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Conservation and Sustainable Use of Tropical Fruit Species Diversity: Bioversity's Efforts in Asia, the Pacific and Oceania

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Asia, the Pacific and Oceania region is very rich in genetic diversity of tropical fruits. Although, fruits have always been important agricultural species, it is only in recent years that there is an increasing awareness of the potential of native tropical fruit species as good sources of dietary vitamins, minerals and energy. They also play a very significant role for the wellbeing of the people through enhancing household income, employment generation particularly for women, and environmental protection. At the same time, their genetic diversity and even the species diversity is threatened due to various human interventions and concerted efforts are required to take corrective measures. Bioversity International, in collaboration with national partners, implemented in recent past several programmes for effective conservation and sustainable use of genetic resources of tropical fruits in the region and is continuing to do so. This paper describes the results of studies on various aspects of tropical fruit genetic diversity and species diversity as well as their sustainable use in major fruit growing countries in Asia, the Pacific and Oceania in the last decade and half. The studies included exploration and collecting, characterization and evaluation, identification of promising/elite lines, documentation, conservation, training and capacity building, socio-economic analysis, information dissemination, collaboration and networking, impacts and sustainability of efforts. The paper also touches on the current efforts and future thrusts for tropical fruit species genetic resources conservation, management and sustainable use.

Key Words: Characterization, Conservation, Documentation, Genetic resources, Species diversity, Sustainable use, Tropical fruits

Introduction

Mostly neglected in the past, tropical fruits have received high priority among the horticultural crops for agricultural development and over the last decade Asia recorded a 66% increase in fruit production, the highest in the world. The region of South, Southeast and East Asia is important in this respect and four countries, namely, India, Indonesia, Thailand and China account for 50% of the total global fruit production. Also in this region, tropical fruits account for 30-59% of total farm income especially for small holders and marginal farmers (TFNet, 2004), thus, contributing to better livelihood of the rural people largely the farming community. It is well established that the tropical fruits contribute significantly towards improved human nutrition and health. These are rich sources of vitamins and minerals and possess high dietary energy (Pareek *et al.*, 1998; Hoe and Siong, 1999; Reddy *et al.*, 2010). Native tropical fruit species are very important for the economic welfare of small farmers in Asia. Most of these species have multi-purpose use for food, shelter, timber, fuel, medicine

and other uses (Bhag Mal and Ramanatha Rao, 2003; Hodel and Gessler, 1999). Thus, in view of their diverse uses, tropical fruits contribute considerably to food and nutritional security, income generation, poverty reduction and ecosystem and environmental sustainability. The rapid agricultural development and industrialization, changing land use patterns, large scale deforestation, accompanied by other social and cultural pressures have resulted in large scale degradation of natural habitats *vis-à-vis* loss of native diversity. Hence, this diversity needs to be conserved by adopting diverse conservation and management techniques and approaches so as to utilize tropical fruit species diversity effectively.

Recognizing the increasing importance and the need of conservation and utilization of tropical fruit tree species (TFT) diversity, Bioversity International (Bioversity in short; formerly IPGRI) initiated research on conservation and use of TFT species in Asia in 1993 in collaboration with national partners which was subsequently followed by large regional projects funded by several donor agencies that strengthened

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Bioversity's work on TFT genetic resources management. Bioversity played a significant role towards TFT genetic resource management and use, in changing the perspective about tropical fruits' contribution to economy in general and specifically, in strengthening the national research programmes on TFT (Arora, 1995; Arora and Ramanatha Rao, 1995; Arora and Ramanatha Rao, 1998; Ramanatha Rao and Arora, 1999; Ramanatha Rao and Bhag Mal, 2002; Bhag Mal and Ramanatha Rao, 2003; IPGRI 2003a, b; Bhag Mal *et al.*, 2004; Ramanatha Rao *et al.*, 2005; Bhag Mal *et al.*, 2007).

Fruit Diversity in Asia

Asia is characterized by rich fruit diversity and about 500 species are distributed in its diverse ecosystems. Thus, a wide range of natural diversity occurs, well adapted to sub-humid, humid tropical and semi-arid conditions. In addition to the native fruit species that have been domesticated and diversified in this region, a large number of species of tropical American origin introduced in the distant past have developed agro-ecological niches and are well acclimatized (Verheij and Coronel, 1991; Arora and Ramanatha Rao, 1995). Over 70 cultivated species of major and minor fruits are presently grown in the region, along with some of the promising exotic tropical fruits (Arora and Ramanatha Rao, 1995). However, only about 20 species are better known under cultivation and these include banana, citrus, mango, pineapple, papaya, durian, rambutan, jackfruit, litchi, longan, tamarind, chempedak, carambola, langsat, guava, sour sop, custard apple, salak, passion fruit and jujube (Verheij and Coronel, 1991; Singh, 1993; Arora and Ramanatha Rao, 1995), the predominant fruits being banana, pineapple, citrus, mango and papaya.

In the humid tropics which hold very rich species diversity, TFT are a major component of multi-crop farming systems including home gardens. Some of these species have been well adapted to marginal lands, and in agroforestry and farm-forestry systems (Verheij and Coronel, 1991).

An example of rich fruit diversity in Asia is the genus *Mangifera* which comprises 58 species (Kostermans and Bompard, 1993) and is naturally distributed in south, southeast and east Asia. The Malay Peninsula, the Indonesian Archipelago, Thailand, Indo-China and the Philippines are the seats of diversity for *Mangifera*

species (Mukherji, 1985; Bompard, 1988; Kostermans and Bompard, 1993). About 26 species have edible fruits, either eaten as fresh fruits or used to prepare jams, jellies or preserves, the most important of which is mango (*Mangifera indica*).

The other important species, which produce edible fruits, are *M. caesia* Jack, *M. foetida* Lour, *M. kemanga* Bl., *M. laurina* Bl., *M. odorata* Griff. Lour. (Bompard 1992; Tanaka, 1976), *M. pajang* Kostermans (Bompard, 1992) and *M. sylvatica* Roxb. (Tanaka, 1976) which, with the exception of the later, are mostly distributed in Malaysia and Indonesia. Besides mango, the other *Mangifera* species reported from India include *M. andmanica*, *M. khasiana* and *M. sylvatica* and *M. camptosperma* (Mukherji, 1985). A large array of cultivated and wild types occur in India. Seedling races derived from monoembryonic mango stones are the most important components of diversity available in India. Almost all commercial cultivars of mango have arisen as a result of seedling selection. Although, most other countries in APO have 2-10 commercial cultivated mango varieties, India has around 1000 distinct varieties and about 30 of them are commercially grown.

Another good example is of *Citrus*. The genus *Citrus* occurs naturally from North-eastern India and Southern China to Northern Australia and New Caledonia. The cultivated species are native to the tropical and subtropical regions of Southeast Asia. The taxonomy of *Citrus* is not precisely established. Most researchers utilize the Swingle system (Swingle, 1943) which recognizes 16 species, or one of its modifications which recognizes 17 species (Bhattacharya and Dutta, 1956; Stone, 1994), 36 species (Hodgson, 1967), or 31 species (Singh and Nath, 1969). The recent taxonomy of Mabberly (1997, 1998) is essentially a modification of the Swingle system, with several genera being reabsorbed into *Citrus*. In contrast, the Tanaka taxonomy recognizes up to 162 species (Tanaka, 1977). This lack of agreement reflects differences of opinion as to what degree of difference justifies species status and whether or not supposed hybrids among naturally occurring forms should be assigned species status. There is no definitive work on *Citrus* taxonomy, and many workers use a sort of ad hoc system somewhat intermediate between the two systems. It is probable that natural hybridization took place between species and varieties resulting in an array

of complex hybrids. The commonly grown citrus fruits belong to three genera, *Citrus*, *Fortunella* and *Poncirus*. All these genera are closely related, have intergeneric fertility and readily hybridize resulting in the development of several unusual plant forms with different names. There is a great amount of variation among *Citrus* species and cultivars as a result of frequent bud mutation, interspecific and intergeneric hybridization, apomixis and long history of cultivation (Shahsavari *et al.*, 2007). The existence of intergeneric hybrids is common among these three genera (Nito, 2003). Some examples are Tangor (mandarin×sweet orange), Tangelo (mandarin×grapefruit), Lemonlime (lemon×lime), Citrange (sweet orange×*Poncirus trifoliata*), Citromelo (grapefruit×*Poncirus trifoliata*), Limquat (lime×*Fortunella* spp.), Citrangequat (*Fortunella margarita*×Rusk citrange), and Calamansi/Calamondin (mandarin×*Fortunella* spp.), etc. There are five citrus groups that are commercially important and these include sweet orange, mandarin (including Satsuma), grapefruit, lemon and lime and numerous varieties and cultivars exist. Kumquat (*Fortunella* spp.) is grown to a limited extent for fresh fruit and processing. Pummelos are of economic importance in many areas within Southeast Asia and China.

Rambutan (*Nephilium lappaceum*) is the most important species in the genus *Nephilium*. Three different forms of rambutan (var. *lappaceum*, var. *pallen* and var. *xanthioides*) are recognized based on leaflet characteristics. Rambutan occurs from southern China through Indo-China region, Malaysia, Indonesia and the Philippines. All cultivars of rambutan have been produced by cloning superior trees found in natural habitats. Jackfruit (*Artocarpus heterophyllus*) is a major fruit in south and Southeast Asia. It is usually classified in two major types based on the quality of its edible pulp. Many cultivars exist within both of these types and all the currently used cultivars are direct selections of desirable trees found in natural habitats. Similarly, durian (*Durio zibethinus*) and litchi (*Litchi chinensis*) are also important priority fruits in South and Southeast Asia and considerable diversity occur in these fruit species.

Need for Intensified Work on Priority Fruit Tree Species

As noted earlier, the number of TFT species in the region is too large and it would not be possible for any organization to focus on so many species. The

information synthesis carried out in 1993 revealed a strong need to identify a few major and minor (but still commercially important) fruit species for conducting detailed research. Based on the collaborative efforts between Bioversity-APO and International Centre for Underutilized Crops (ICUC), a survey was conducted in 15 countries in South Asia (Bangladesh, Bhutan, India, Pakistan, Nepal and Sri Lanka), Southeast Asia (Brunei, Indonesia, Malaysia, Myanmar, Papua New Guinea (PNG), the Philippines, Thailand and Vietnam) and East Asia (China) and a number of priority species were identified. Subsequently in the 'Expert Consultation on Tropical Fruits' held at the Malaysian Agricultural Research and Development Institute (MARDI), Kuala Lumpur, Malaysia in 1994, six priority species (species of major importance-mango, citrus and rambutan; and of minor importance-durian, jackfruit and litchi) and a few others, namely, carambola, mangosteen and longan were identified for intensified work at regional level and individual country level (Arora and Ramanatha Rao, 1995).

The research and development activities with emphasis on genetic resources conservation and use of these priority species were initiated by Bioversity International in Asia, the Pacific and Oceania. The rationale warranting intensified work included nutritional importance, diversified uses, economic/higher monetary return, better employment, suitability to diverse agrohorticultural and fruit based cropping systems, and agroecological considerations. Conservation efforts for fruit crops at the national and international levels had also been very limited (Bhag Mal *et al.*, 2004) and hence deserved utmost consideration.

Major Programmes/Activities

The regional collaborative research and development work focused on priority TFT species identified through regional survey and validated through an expert consultation. The major programmes/activities undertaken by Bioversity through several projects in collaboration with national programmes covered several important aspects of conservation and use of tropical fruit species. In order to implement various activities, the human resource and capacity building and networking approaches were adopted to enhance efficiency of collaboration and sustainability of efforts. The major activities included: i) information synthesis on the extent and distribution of genetic diversity, ii) identification of priority gene pools of major and minor

fruit tree species of national and regional importance, iii) studies on the status of existing collections of TFT species, iv) characterization, evaluation, documentation, maintenance, conservation and utilization of priority fruit species, v) supporting research on developing *ex situ* and *in situ* conservation methods and their adoption in national programmes, vi) genetic diversity studies to assess the status of diversity, genetic threat and promoting *in situ* conservation, vii) studies on socio-economic, indigenous knowledge and sustainable livelihood aspects, viii) human resource and capacity building, consultation meetings and workshops, and ix) promoting national, regional and international collaboration to facilitate networking and dissemination of information.

Salient Achievements

Bioversity has taken several initiatives aimed at conservation and use of native TFT species diversity in Asia, the Pacific and Oceania (APO) region. In 1990s, the activities were mostly supported from Bioversity's core budget. However, the work gained momentum from January 2000 onwards with the initiation of Asian Development Bank (ADB) funded project on 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia' which was implemented in ten Asian countries, namely, Bangladesh, China, India, Indonesia, Malaysia, Nepal, the Philippines, Sri Lanka, Thailand and Vietnam. Subsequently, the work on cryopreservation of citrus was undertaken in collaboration with Universiti Kebangsaan Malaysia (UKM) and Universiti Putra Malaysia (UPM) in Malaysia. To promote the work on *in vitro* conservation and cryopreservation, a three year project on 'Development of Advanced Technologies for Germplasm Conservation of Tropical Fruit Species' funded by the Australian Centre for International Agricultural Research (ACIAR) was implemented in five countries, namely, Australia, Malaysia, the Philippines, Thailand and Vietnam (IPGRI 2003b). During 2004-05, a project proposal on "Conservation and Sustainable Use of Cultivated and Wild Tropical Fruit Diversity: Promoting Sustainable Livelihood, Food Security and Ecosystem Services" was developed under PDF-B Phase and submitted to UNEP/GEF for funding. This five year project was approved and its implementation started in January, 2009.

The successful implementation of Bioversity's programmes on TFT species in the region resulted in

significant achievements. The ADB funded project on six priority TFT species was successfully implemented and its objectives were fully achieved as is evident from country reports for Bangladesh, China, India, Indonesia, Malaysia, Nepal, the Philippines, Sri Lanka, Thailand and Vietnam (Budathoki 2003; Dela Cruz 2003; Hue 2003; Idris 2003; Kalloo 2003; Shantha Peiris 2003; Purnomo, 2003; Somsri 2003a; Uddin 2003; Zushang 2003). Significant outputs were delivered in securing valuable fruit crop germplasm in ten countries through collecting and conserving threatened diversity of priority fruit species, identifying gaps in collections as well as areas for future collecting, documenting information to promote access and sharing of germplasm, characterizing accessions and identifying elite lines for direct use by farmers or use in breeding programmes. In addition, socio-economic surveys for identifying constraints and opportunities in promoting potential development of fruit crops at the local and national levels were undertaken. The ACIAR funded project had also been very successful in developing and standardizing the techniques for *in vitro* conservation and cryopreservation of different fruit species which greatly helped in developing suitable strategies/plans for conservation of TFT genetic resources. These projects/programmes have been able to put fruit crops on a higher development agenda of the national governments and assisted the national agricultural research systems (NARS) in TFT germplasm collecting, characterization and evaluation, conservation, human resource development and capacity building and also in strengthening collaboration among the partners.

The country-wise and crop-wise details of accessions collected, characterized, documented, conserved and the elite lines selected are summarized in Table 1 and Table 2, respectively.

The collaborating countries have been able to collect the threatened and rare diversity of identified priority TFT species including their wild relatives and related species and identify gaps for future collecting missions. The diversity collected has been saved from loss and is safely conserved in genebanks for current and future use. Several elite lines and useful germplasm with specific desirable traits were identified and are now available for use in breeding programmes aimed at developing better varieties or for direct use by farmers.

Table 1. Country-wise details of accessions collected, characterized, documented, conserved and elite lines identified in six priority fruit tree species

Country	Existing accessions documented	Accessions databased in CD-ROM	New accessions collected	Accessions characterized	Accessions added to field genebanks	Elite lines identified
Bangladesh	857	159	206	196	199	26
China	833	833	129	326	129	28
India	404	552*	316	513*	316	30
Indonesia	110	47	127	107	52	17
Malaysia	165	108	100	140	45	6
Nepal	265	134	96	265	72	44
Philippines	419	519*	419	299	232	9
Sri Lanka	271	185	271	185	120	18
Thailand	982	982	279	799	279	3
Vietnam	661	548	241	529	241	9
Total	4967	4067	2184	3359	1685	190

*Includes additional accessions

Table 2. Crop-wise details of accessions collected, characterized, documented, conserved and elite lines identified in 10 countries in South and Southeast Asia

Country	Existing accessions documented	Accessions databased in CD-ROM	New accessions collected	Accessions characterized	Accessions added to field genebanks	Elite lines identified
Mango	2368	1665	1003	1804	734	93
Citrus	1453	1775*	555	983	511	51
Rambutan	316	265	288	285	195	17
Jackfruit	522	131	180	152	126	20
Litchi	185	143	60	40	60	1
Mangosteen	123	88	98	95	59	8
Total	4967	4067	2184	3359	1685	190

*Includes additional accessions

Locating and Collecting Diversity

Ecogeographic Studies and Distribution of Genetic Diversity

The ecogeographic studies were carried out with focus on surveys based on the ecological and climatic parameters of major distribution areas of TFT species in different countries. These studies provided better understanding of the distribution patterns, and agroecosystems of TFT species. Twenty eight ecogeographic surveys were conducted. By mapping the collected accessions, it was possible to map the areas with high diversity of TFT, predict their possible distribution in other similar agroclimatic areas and identify gaps in existing collections. The countries were able to produce the distribution maps for their respective TFT collections with the geographic information system (GIS) tools such as DIVA-GIS and FloraMap. One such good example was for *Citrus* in India (Singh and Singh, 2003). The 42 diversity maps were produced for six crops, namely, citrus, jackfruit, litchi, mango, mangosteen and rambutan showing overlapping distribution of several species. These distribution maps, which represent a first major attempt by national programmes to use GIS technologies for germplasm management, were

very useful in identifying diversity-rich areas for further collecting and *in situ* conservation and also predicting new areas with similar climatic conditions for cultivation of these TFT (IPGRI, 2003a).

Exploration and Germplasm Collecting

Germplasm collecting was done in the areas identified for further exploration through ecogeographic studies. A total of 2,184 accessions of six target TFT species were collected. This included 1,003 accessions of mango, 555 of citrus, 288 of rambutan, 180 of jackfruit, 60 of litchi, and 98 of mangosteen (IPGRI, 2003a). Thus, the collecting strategies based on sound scientific basis were developed and suggested to the national partners for making further collections for different species.

Evaluation and Utilization of Diversity

Germplasm Characterization

In a fairly large scale effort on characterization, a total of 3,359 accessions of target fruit species, namely, mango, citrus, rambutan, jackfruit, litchi and mangosteen held in the field genebanks in different countries were characterized (IPGRI, 2003a). These included 1,804 accessions of mango in 9 countries,

983 of citrus in 6 countries, 285 of rambutan in 3 countries, 152 of jackfruit in 2 countries, 40 of litchi in 2 countries and 95 of mangosteen in 2 countries. These extensive characterization and evaluation studies helped to identify elite germplasm lines that could be used in crop specific breeding programmes or directly for cultivation by farmers.

Identification of Elite Lines with Specific Desirable Traits

Based on specific desirable attributes, 190 elite lines/promising accessions were identified for further evaluation and use by the breeders in the breeding programmes or directly by the farmers for commercial cultivation. These included 93 promising lines in mango, 51 in citrus, 17 in rambutan, 20 in jackfruit, 8 in mangosteen and 1 in litchi.

Elite lines or promising accessions identified (IPGRI, 2003a) based on the evaluation studies in different participating countries included: i) Bangladesh: 4 mango elite lines possessing year-round bearing, 9 with off-season bearing and one possessing sweetness at green stage; ii) China: 8 citrus elite lines including seedless types for fresh fruits market and processing industry; 2 superior rootstocks of pummelo with vigorous growth habit, large fruit size and better fruit quality; 4 mango elite lines with dwarf growth habit, disease resistance, early bearing and large fruit size along with better quality; iii) India: 4 mango elite lines for high yield, 3 for short height, 5 for high total soluble solids (TSS), 8 for red peel with good consumer appeal, 8 for high pulp recovery, 5 for large fruits, 5 for regular bearing, 4 for early maturity, 3 for high tolerance to shoot borer and 2 hybrids for export possessing medium size fruits with high TSS, high acidity and high pulp recovery; In Rangpur lime, 4 elite lines, one each for large fruit size, thinnest peel, less seedy fruits and very high TSS; In rough lemon, 4 for low seed number and one for large fruits; In trifoliate orange, one for thin peel and one for high TSS; In litchi, 3 elite lines, one each for high fruit weight, low peel percentage and high sugar percentage; iv) Indonesia: 2 elite lines of rambutan for large fruit size, flesh quality and ease of rind opening; 2 of mangosteen for dark purple rind; v) Malaysia: 3 elite lines of pulasan (*Nephilium ramboutan-ake*) and 3 of kuini (*Mangifera odorata*) possessing desirable traits; vi) Nepal: 2 seedless varieties of mandarin, one of sweet orange and one of mango for earliness

and very high TSS; vii) Philippines: 2 elite lines of mango for large fruit with small stone, 3 of citrus and 3 of mangosteen for large fruit size, high TSS and regular bearing; viii) Sri Lanka: 2 elite lines of mango, one edible at green stage and the other for pickle, and 2 of jackfruit for good fruit quality and attractiveness; ix) Thailand: 2 elite lines of mango for high fruit weight, firm and thick pulp texture, sweet, yellow peel, small stone and longer shelf life; one of rambutan with firm aril texture, thick aril, normal skin thickness, orange red skin, high TSS, high fruit weight, long shelf life and rind and hair colour not fading even after 30 days after maturity on the tree; x) Vietnam: two best rootstocks of trifoliate orange (*Poncirus trifoliata*) and one of litchi.

Some of the promising elite lines identified were multiplied and given to the farmers for cultivation in China, Nepal, Sri Lanka and Vietnam, thus demonstrating direct application of the findings in the field. In China, one elite line of mango and one of citrus were included in the recommendation package for farmers and mass propagated for distribution to fruit growers. A total of 1,20,000 plants and 8,00,000 buds of 8 elite citrus types, and 4 of mango were multiplied and distributed to farmers. Also, the early and late Ponkan, seedless Ponkan, early and late Navel orange are becoming popular. Mango Carabao, the high quality type currently released was planted on 9000 ha covering nearly one third of mango acreage in Hainan province. In Nepal, 40,000 seedlings of citrus and 3,000 seedlings of mango produced by the government and private nurseries were distributed to men and women farmers. In Vietnam, 4000 grafted seedlings of mango, citrus and litchi were produced through two community nurseries and distributed to 87 farmer households. In Sri Lanka, high quality varieties of mango and jackfruit for a range of uses (fresh, processing, vegetable uses) were identified. These were mass propagated and supplied to farmers for cultivation and enhancement of fruit production. These efforts will not only ensure good quality planting material to farmers but will also contribute to the improvement of quality of fresh and processed products made out of these crops in the future. Similar efforts are underway in other collaborating countries.

In all partner countries, the information on the elite materials was shared with the agricultural departments of the provincial governments for further dissemination to farmers and other growers for their wider use.

Promoting Diversity in Orchards and Home Gardens

In order to promote the use of diversity in the orchards and home gardens, as part of conservation through use, assessment of diversity of different crops was considered important. In Nepal, assessment of diversity of citrus and mango was carried out with the active participation of grower groups and individual orchardists and home gardeners. These groups provided detailed information of the fruit quality, maturity, tree morphology, tree canopy, tolerance to diseases, pests and abiotic stress conditions with respect to the genotypes they had in their villages and neighbouring areas. This fruit growers' evaluation was based on their long experience of cultivation, fruit consumption and fruit selling, which proved to be very useful in identifying the diversity to be collected (Budathoki, 2003). Similar assessment of diversity with communities and home gardens was done in Sri Lanka (Shantha Peiris, 2003), Bangladesh (Uddin, 2003) and Vietnam (Hue, 2003). The women growers predominantly contributed to growers' evaluation. Through their help, it was possible to identify the high diversity areas of citrus and mango, high diversity orchards, home gardens and also the location of orchards and home gardens as well as the owners having very popular elite lines in the villages.

Inclusion of a large number of cultivars and species in the semi-commercial and commercial orchards is a recent practice and was further encouraged and enhanced. This was done in view of consumer preferences and market choices and to reduce the risks from natural biotic and abiotic stress conditions. The cultivars used by the growers on commercial and semi-commercial scales were mostly improved varieties and a very few local landraces were grown. In contrast, indigenous and unique types of fruit germplasm were found in the home gardens which could be further capitalized in the market. The elite lines identified in different fruit species were distributed to semi-commercial orchards and home gardens to promote diversity deployment and enhanced production.

Using Indigenous Knowledge to Improve Productivity

Documenting indigenous knowledge (IK) is extremely important as it gives very useful information on growers' preferences and uses, indigenous production

methods and on the role of growers in conservation and use, which could be used in developing appropriate research and development strategies on target fruit tree species. Some examples of IK gathered are briefly presented below:

In Nepal, IK was documented for citrus, which included varied types of information (Budathoki, 2003) such as: i) *in situ* manuring by keeping animals in the orchards, ii) use of temporary 'mobile' toilets near the trees for manuring, iii) planting of whole fruits in the field after removing the peel, iv) smoking of trees in the evenings and nights to repel the insect pests, and v) spraying small seedlings with slurry of fresh cow dung and urine to repel animals. Such information could be very useful in increasing fruit production and thereby enhancing farmers' income and can be validated by formal and more controlled research.

In Sri Lanka, IK on mango and jackfruit documented with the help of different communities (Maharouf, 2003a, b) indicated the existence of varieties that were used for a long time in specific food items and treatment of various diseases. IK on mango was gathered by interviewing the priests, village leaders, Ayurvedic doctors and the ethnic communities, namely, Singhalese and Tamils. Information pertaining to the use of mango and its plant parts in food, medicine and in festivities, weddings and other rituals was gathered. Jackfruit in Sri Lanka is also known as '*Bath Gasa*' reflecting its prime value as a food which is similar to that of the staple food rice known as *Bath* in Sinhala.

In Malaysia, decoction of roots of pulasan has been reported to be used as vermifuge for fever; and the roots are boiled and used for bathing patients inflicted with fever (Idris, 2003). The dried seed kernels with faintly sweet smell oil are suitable for use in food. In the Philippines, decoction of dried mangosteen rind is used to cure stomach-ache (Dela Cruz, 2003).

In Vietnam, litchi has been reported to have medicinal value. It is traditionally used to treat stomach-ache and the pain in small intestine. The traditional uses included the use of litchi flesh to prevent tiredness and to treat bronchocele or growth on the neck, fruit skin to treat diarrhoea and leaves to treat animal bites. Litchi tree productivity was enhanced with the use of poultry manure. The other

traditional practices included the cutting of trunk vertically in the middle to induce branching and slicing of trunk for inducing fruiting (Hue, 2003).

Conservation of Tropical Fruit Tree Genetic Resources

In situ Conservation

Under the ADB funded project on tropical fruits, Bioversity promoted the concept of on-farm conservation of fruit genetic resources (Nares *et al.*, 2001). *In situ* conservation activities were initiated in a few countries, namely, Bangladesh, India, Nepal, the Philippines, Sri Lanka and Vietnam and suitable *in situ* conservation sites were identified (IPGRI 2003a). These included: i) Ipilan-Alitao for mangosteen in the Philippines, ii) Ramnagar Mirchaiya for mango, and Karki Gaon and Banskharka village for *Citrus* spp. in Nepal, iii) Gazipur for jackfruit, Chapai Nawabganj for mango and Maulibazar for citrus in Bangladesh, iv) Garo Hills for citrus, Paiyur in Tamil Nadu and Lucknow in Uttar Pradesh for mango in India, v) Bac son district, Lang son province for mandarin; Phuc Trach commune, Huong Khe district, Ha Tinh province for pummelo; Thanh son commune, Thanh Ha district, Hai duong province for litchi; and Chiengpan commune, Yenchau district, Son la province for mango in Vietnam, and vi) several home gardens for jackfruit and mango in Sri Lanka and semi-domesticated, natural diversity sites for litchi in Southern China. These constituted the first efforts on *in situ* conservation of TFT genetic resource in APO region. These efforts also highlighted the issues arising out of on-farm/*in situ* conservation of group of species such as perennial tree species as opposed to annual crops on which fairly large amount of data could be found in the literature.

The principles of on-farm/*in situ* conservation recognize that such efforts will be successful and sustainable only through the active participation of communities who depend and enjoy the fruits of the available resources. Hence, efforts were made to encourage the farmers and communities to participate in the conservation of TFT genetic resource. In Nepal, farmer group meetings were organized with the help of Agriculture Development Department and awareness was created about the value of their fruit germplasm materials in terms of income generation, socioeconomic aspects and conservation for future use. Fruit diversity fairs, fruit shows and fruit festivals were organized

in Nepal, Bangladesh, Vietnam, Thailand and the Philippines during socioeconomic surveys and germplasm collecting missions. Close interaction with farmers and communities also motivated them to participate in the germplasm conservation efforts. What was important was that, although several farmers were carrying out *in situ* conservation (as they continue to grow traditional varieties over generations and practice some level of selection while planting new orchards or home gardens) in an unconscious manner, they became more aware of the value of what they have been doing. Farmer organization leaders, village leaders, monks in village temples, women and youth organizations helped in organizing the socioeconomic activities in the villages and provided valuable information during the socio-economic surveys. In Bangladesh, fruit tree plantation fortnight was organized in which mango growers were trained in propagation techniques and production practices. In India, a biodiversity workshop was organized in Karnataka State to create awareness amongst the people to participate in conservation of mango diversity and Snehakunj, an NGO, helped in collecting germplasm through the help of communities. A national exhibition was organized in Indonesia to create awareness among the communities for conservation and use of TFT species. In Vietnam, under the project in collaboration with Centro Internazionale Crocevia (CIC), two community nurseries for propagation of TFT species were established in Phuson, Ninh binh and Chiengpan, Sonla. The grafted seedlings of elite varieties of litchi, mango and pummelo were produced with the participation of local farmers. Two training programmes on grafting and pruning for mango and citrus were organized for these communities. As a result, a community nursery run by farmers produced materials and distributed these to other communities (IPGRI, 2003a). It is evident, from the experiences in the project, that interest of farmers to conserve fruit genetic diversity will effectively take place if they find greater use of these materials.

These efforts also indicated that different approaches (including agroforestry systems approach and community biodiversity management (CBM) approach) are required to make *in situ*/on-farm conservation sustainable and beneficial to TFT growers. The results of ADB project helped in planning and developing larger actions under UNEP/GEF project already commenced from January, 2009.

Ex situ Conservation

The national programmes in the collaborating countries are maintaining germplasm of the target species in the field genebanks at different locations in the respective countries. Fifty two field genebanks were identified/established for different crops, viz., mango (21), citrus (13), rambutan (8), jackfruit (4), litchi (4) and mangosteen (2). These field genebanks were enriched with more accessions collected during the ADB project, thus enriching the accessible genetic diversity. This included mango (734 accessions), citrus (511), rambutan (195), jackfruit (126), litchi (60) and mangosteen (59). Out of a total of 2,184 accessions collected, 1,685 accessions of six target crops were added to field genebanks in different countries (Table 1). The remaining collections were planted in the nursery for subsequent transfer to field genebanks at appropriate growth stage.

Ex situ conservation of TFT genetic resource is an expensive and labour intensive programme requiring considerable land resources. Hence, any effort in developing and managing fruit tree genebank should be based on sound strategy. To promote improved establishment and management of field genebanks, the guidelines for field genebank management developed by Bioversity may be used (Saad and Ramanatha Rao, 2001).

Development of Advanced Technologies for Conservation

Since seed conservation is not an option for most of the TFT species, Bioversity assisted the national programmes in developing advanced techniques for conserving TFT germplasm in different countries. Studies on *in vitro* conservation of citrus conducted at the Citrus Research Institute, Chongqing, China during 1993-96 resulted in *in vitro* storage of 60 accessions of citrus and further development of protocols for citrus under slow growth conditions. Cryopreservation studies in mango conducted in 1995-96 in collaboration with the School of Life Sciences, Zhongshan University, Guangzhou, China confirmed recalcitrant nature of mango seeds although no workable protocols for *in vitro* conservation could be established (Bhag Mal and Ramanatha Rao, 2003; Bhag Mal *et al.*, 2004). Cryopreservation studies in different fruit species (Chaudhury *et al.*, 2000a; Sudarmonowati, 2000) revealed varying degrees of success with different techniques and types of material used (Table 3).

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Table 3. Success of cryopreservation using various techniques in different fruit species

Species	Technique	Type of material	Survival (%)
<i>Litchi chinensis</i>	Vitrification	Embryonic axes	50
	Air desiccation	Embryonic axes	22-35
<i>Euphoria longan</i>	Vitrification	Embryonic callus	30
		Anthers	15
<i>Nephelium lappaceum</i>	Two step freezing	Shoot tips	10
<i>Citrus sinensis</i>	Encapsulation-Vitrification dehydration	Shoot tips	25
		Embryonic axes	62.5

Bioversity, with funding from the Department for International Development (DFID), UK collaborated with NBPGR, New Delhi, India on the development of cryopreservation techniques for long-term conservation of some fruit tree species. For the first time, in litchi (*Litchi chinensis* Sonn.), embryonic axes from seeds harvested 60-80 days after anthesis survived liquid nitrogen exposure (Chaudhury *et al.*, 2000b, 2001; Bhag Mal and Ramanatha Rao, 2003). Successful cryopreservation was noted in jackfruit (*Artocarpus heterophyllus* Lamk.) with 25-30 per cent survival of cryopreserved axes from partially mature and fully mature seeds (Chandel *et al.*, 1995). There was an improvement in recovery percentage of cryopreserved axes in jackfruit and litchi as compared to air desiccation.

The studies carried out in collaboration with Universiti Kebangsaan Malaysia (UKM) and Universiti Putra Malaysia (UPM), Malaysia with support from the Rural Development Administration (RDA), Republic of Korea revealed that seed survival decreased below 16 per cent seed moisture content (MC) in *Citrus aurantifolia* (Cho *et al.*, 2002) and that seeds cryopreserved without testa survived better than those with seeds at about 7 per cent seed MC. Protocol for cryopreservation of zygotic embryonic axes of *C. madurensis* were developed (Cho *et al.*, 2001).

Bioversity's work on *in vitro* conservation and cryopreservation was further strengthened through a project supported by Australian Centre for International Agricultural Research (ACIAR), which resulted in development of conservation techniques for target TFT species (IPGRI, 2003b; Drew *et al.*, 2006). In papaya, protocols for vitrification-based shoot tip cryopreservation were refined and applied successfully to a range of papaya genotypes and *Vasconcellea pubescens* (a wild relative). Papaya seeds could be

stored up to 12 months at a range of moisture content and a range of temperature including cryostorage. Protocols for slow-growth of papaya *in vitro* were developed.

It was observed that seeds of *Citrus australasica* could tolerate desiccation and ultra low temperatures indicating possibilities for seed storage along with seed of *C. inodora* and *C. garrawayi*. A micropropagation protocol was established for three Australian native *Citrus* species (*C. australasica*, *C. inodora* and *C. garrawayi*) suitable for mass multiplication and medium-term storage. Protocols for adventitious root formation and regeneration of shoot for *C. hystrix* were developed. Regeneration *via* somatic (nucellar) embryogenesis was developed for calamansi (*Citrofortunella macrocarpa*) and mandarin (*C. reticulata*). For pummelo (*C. grandis*), callus was induced from juice vesicles and albedo tissues but somatic embryogenesis and shoot regeneration was observed only in callus from albedo. Regeneration system *via* somatic embryogenesis was developed for lime using undeveloped ovules (immature seeds) (IPGRI, 2003b).

Studies also indicated the feasibility of low temperature storage of desiccated seed of calamansi, mandarin, pummelo, native lime, limon and kubot for a short-term (Philippine native *Citrus* sp.). Cryopreservation of embryogenic callus using encapsulation dehydration technique was feasible for *C. reticulata* and *C. sinensis*. For *C. hystrix*, vitrification method was modified to obtain acceptable level of survival (IPGRI, 2003b). In mango, even though 70 per cent recovery of somatic embryos was observed, a major problem was the repeatability of these results and thus more research is required to optimize the protocol.

A micropropagation system was developed in *Davidsonia* spp., an underutilized native fruit of Australia, through the production of microcuttings *in vitro*. Media for litchi and longan micropropagation were also developed. In persimmon, a suitable medium was identified for embryo culture and nodal cutting. The results of cryopreservation studies concluded that vitrification was not suitable for persimmon shoot tips (IPGRI, 2003b). Protocols for adventitious root formation and regeneration of shoot in *Nephelium* spp. were developed. Slow growth technique had shown the potential for short to medium-term storage of germplasm.

Cryopreservation is a well established method for long-term conservation of recalcitrant plant species

that include most of the TFT species. These examples showed that the work done by Bioversity and national partners in the APO region successfully demonstrated a considerable progress towards the cryopreservation of a few fruit species. However, it must be realized that a lot of research still needs to be done to refine and standardize the existing cryopreservation protocols so that these could be effectively used for conservation for TFT genetic resources.

Need for Complementary Conservation Strategy

It is now well recognized that no single approach can take care of conserving the maximum genetic diversity that is normally the goal of conservation efforts. The concept of application of the most appropriate conservation technique to appropriate portion of a gene pool has been referred to as complementary conservation strategy (CCS) or integrated conservation strategy. Such a strategy would employ different conservation options for different types of material in a gene pool under conservation— *in situ* and *ex situ* conservation, *in vitro* conservation, cryopreservation, etc. To assess this need and its implementation in wider context, the status of germplasm conservation of target fruit species in the region was reviewed (Drew and Ashmore, 2003). Various conservation options such as *in situ* conservation in nature reserves and on-farm/home gardens and *ex situ* methods such as field genebanks, seed genebanks, *in vitro* genebanks, cryobanks and pollen genebanks and their advantages and disadvantages were considered in order to crystallize ideas to develop appropriate complementary conservation strategies. A number of important issues that should be considered while developing complementary conservation strategies for topical fruit genetic resources include: i) biological factors, ii) methodologies available, iii) conservation objectives, iv) socioeconomic issues, and v) organizational issues (Brodbeck *et al.*, 1999; Ramanatha Rao and Arora, 1999; Ramanatha Rao and Bhag Mal, 2002; Drew and Ashmore, 2003).

The framework for developing a CCS for TFT requires concrete and appropriate actions to be taken at different stages, namely, i) networking of stakeholders at national, regional or international level, ii) defining the objectives and sub-objectives in accordance with 'Global Strategy for Plant Conservation' and determination of species of major importance for each of the participating countries, iii) analysis of feasibility of each option for each objective or sub-objective in terms of infrastructure needs, costs and

risks involved, iv) decision on conservation options for each objective or sub-objective relevant to each species of major importance, v) setting up enabling environment – policy and legal issues and funding source, vi) elaboration of strategic action plan by stakeholders, and vii) effective implementation of the action plan/process (Drew and Ashmore, 2003; IPGRI, 2003a).

Knowledge Documentation

Country Status Reports

Based on the recommendations of the Expert Consultation on TFT Species in Asia, the information was gathered and six priority species were identified for intensified work in national and regional context (Haq, 1994; Arora and Ramanatha Rao, 1995). During 1995-1998, Bioversity-APO brought out 23 country status reports on genetic resources of the six priority fruit species, namely, mango, citrus, rambutan, litchi, jackfruit and durian in collaboration with the key national programmes (Arora *et al.*, 1996a, b; IPGRI, 2003a; Bhag Mal *et al.*, 2004). Subsequently, status reports on minor fruits of Southeast and South Asian region, namely, litchi, kuini, pulasan, mangosteen and *aonla* (Indian gooseberry) were developed (Ghosh and Mitra, 2000; Dela Cruz, 2001; Idris and Mat Lin, 2002a,b; Pathak, 2003). These reports contain valuable information on distribution; extent of genetic diversity of cultivated and wild genepools; the status of germplasm collection, characterization, evaluation, documentation, conservation, improvement and utilization; diseases and pests; and production, processing and marketing aspects (Table 4).

Based on country status reports, the regional synthesis reports were developed for the two most important crops in the region, namely, mango (Sant Ram and Rajan, 2003) and citrus (Nito, 2003) containing consolidated information on various aspects ranging from origin and distribution through genetic resources to future prospects. In addition, the information on distribution of species of underutilized fruits and nuts was synthesized in order to provide a wider awareness. Inventory of Underutilized Edible Fruits and Nuts (Pareek *et al.*, 1998) and a monograph on durian (Brown, 1997) were also published.

Data Documentation

Documentation of information on existing collections was mostly carried out under the ADB funded TFT

Table 4. Country/regional status reports of priority fruit species

Fruit species	Botanical name	Country/regional report
Mango	<i>Mangifera indica</i>	Bangladesh, China, India, Indonesia, the Philippines, Sri Lanka, Thailand
Citrus	<i>Citrus</i> spp.	India, China, Nepal, Japan, Sri Lanka
Rambutan	<i>Nephelium lappaceum</i>	Indonesia, Malaysia, Thailand
Durian	<i>Durio zibethinus</i>	Indonesia, Malaysia, Thailand
Jackfruit	<i>Artocarpus heterophyllus</i>	Bangladesh, India, Sri Lanka
Litchi	<i>Litchi chinensis</i>	China, India, Thailand and Myanmar
Kuini	<i>Mangifera odorata</i>	Southeast Asia
Pulasan	<i>Nephelium ramboutan-ake</i>	Southeast Asia
Mangosteen	<i>Garcinia mangostana</i>	Southeast Asia
Indian gooseberry (<i>Aonla</i>)	<i>Emblica officinalis</i>	South and Southeast Asia

project. The information on extant collections gathered and synthesized by all participating countries was shared among partners. The amount of information available for different countries varied greatly, which indicated the gaps that existed. The data were standardized according to descriptors published by Bioversity for different fruit crops as well as those developed by relevant national programmes (IPGRI, 2003a). The passport and characterization data were compiled on the existing 4,967 accessions which included 2,368 accessions of mango, 1,453 of citrus, 316 of rambutan, 522 of jackfruit, 185 of litchi, and 123 of mangosteen (Table 5). Bioversity assisted national partners in setting up databases, providing guidelines and descriptors, imparting training to documentation staff, making available the tools and software and worked closely with national staff in developing appropriate documentation systems in different countries. A CD-ROM containing databases from 10 countries was produced and made available to all partners. This database contains the passport and characterization data on 4067 accessions (Table 5) of six TFT crops viz., mango (1,665), citrus (1,775), rambutan (265), jackfruit (131), litchi (143), and mangosteen (88). This laid the foundation for the use of computerized information documentation for fruit tree genetic resources in most of the countries.

New Descriptor Lists Published

To facilitate the systematic characterization and evaluation of TFT genetic resources, new descriptor lists were developed, published and widely distributed

Table 5. Existing accessions documented for passport and characterization data and accessions in databases compiled in CD-ROM for sharing

Countries	Fruit crops						Total
	Mango	Citrus	Rambutan	Jackfruit	Litchi	Mangosteen	
Bangladesh	321	96(89)	-	440(70)	-	-	857(159)
China	80(82)	653(651)	-	-	100(100)	-	833(833)
India	404(151)	-(384)	-	-	-(17)	-	404(552)
Indonesia	-	-	48(21)	-	-	62(26)	110(47)
Malaysia	99(66)	-	66(42)	-	-	-	165(108)
Nepal	130(87)	135(47)	-	-	-	-	265(134)
Philippines	265(356)	93(101)	-	-	-	61(62)	419(519)
Sri Lanka	189(124)	-	-	82(61)	-	-	271(185)
Thailand	780(780)	-	202(202)	-	-	-	982(982)
Vietnam	100(19)	476(503)	-	-	85(26)	-	661(548)
Total	2368(1665)	1453(1775)	316(265)	522(131)	185(143)	123(88)	4967(4067)

Figures in parentheses indicate the accessions in databases in CD-ROM for sharing

to the partners for crops on which no descriptors were available, such as jackfruit, litchi, rambutan, and mangosteen and the descriptors for citrus and mango were revised (IPGRI, 1999, 2000, 2002, 2003c, 2003d, 2006)

Germplasm Catalogues Developed

The participating countries identified and catalogued important varieties of relevant fruit species and these catalogues contained information on passport and characterization. For example, India produced two catalogues on mango with information on 404 accessions and the Philippines prepared a catalogue of 265 accessions of mango, 93 accessions of citrus and 61 accessions of mangosteen. The catalogues were produced in hardcopy and/or electronic versions and were made available to the partners (IPGRI, 2003a; IPB 2003a, b; Rajan, 2003; Rajan *et al.*, 2002; Dinesh and Vasugi, 2002; Somsri, 2003b, c).

Information Dissemination

Information dissemination is extremely important for their use by diverse stakeholders. The outputs and achievements made under different programmes were disseminated through research papers in scientific journals, country status reports, crop descriptors, germplasm catalogues, inventories, monographs, books and proceedings of the meetings relating to TFT species. These have also been placed on website <http://tftgrn.net/> of TFT Genetic Resources Network (TFTGRN). A CD-ROM was developed by Bioversity which contained available databases of fruit tree genetic resources from 10 countries and was made available to all the partners. All these status reports and publications were widely distributed to the national programmes and other partners in the region

which assisted in promoting research and development programmes, facilitating the exchange of materials and also in developing complementary conservation strategies providing an overall regional perspective for South and Southeast Asia and hence proved to be extremely useful.

Training and Capacity Building

Skill Enhancement/Human Resource Development

The highest priority was accorded to human resource development to improve effective conservation and sustainable utilization of TFT genetic resources in Asia and Bioversity was instrumental in imparting training to 382 personnel including researchers, technicians, and farmers on various aspects of TFT genetic resources (Arora and Ramanatha Rao, 1998; Stapleton, 2002; IPGRI, 2003a). Training opportunities were provided in various aspects of plant genetic resources including characterization, evaluation, conservation and utilization, and several related topics such as molecular marker studies, *in vitro* conservation and cryopreservation techniques, ecogeographic surveys and use of GIS tools, socioeconomic studies, data documentation and information management, grafting methods, pruning and nursery management and scientific writing and proposal development. Emphasis was also placed on in-country training courses so that a fairly large number of genebank staff could be trained in one go, which would not have been possible in regional training programmes due to costs involved. Fruit festivals were organized to enhance farmers about the variability present and the characteristics of the varieties grown by them and value of conservation efforts that they might be doing depending on availability of funds. The study visits and technical sessions back to back

with the annual project meetings were organized to promote close interaction of various partners involved. Some of the more advanced courses organized were used to turn the contents into 'reference book', for example, the proceedings of regional training course on 'In vitro Conservation and Cryopreservation of Tropical Fruit Genetic Resources' organized at NBPGR, New Delhi, India, were published which serves as a good manual for the scientists and technicians engaged in this field (Chaudhury *et al.*, 2003).

Bioversity's efforts also gave rise to the concept to 'Centres of Excellence (CoE) for regional/international training on various aspects of plant genetic resources. The National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India is now recognized globally as a CoE for training in *in vitro* conservation and cryopreservation, while Huazhong Agricultural University (HAU), Wuhan, China for training in molecular characterization and Institute of Plant Breeding and the University of Philippines, Los Baños (UPLB), the Philippines for data documentation. These CoEs are continuing to play a significant role in improving the capacity for plant genetic resources education and training in the region.

Strengthening laboratories and infrastructure support under various projects during the past one and a half decade, several laboratories in over 15 collaborating countries were strengthened by providing equipments such as global positioning system (GPS), laboratory equipments, software for geographic information system (GIS), STAT packages, important publications and electronic descriptor software to facilitate their work on ecogeographic studies, mapping, diversity analysis and database development. This kind of support significantly improved the capacity of the national programmes to undertake systematic collecting and evaluation of the collected germplasm and deliver better research outputs. Twenty one field genebanks in ten countries were assisted through scientific/technical advice and funding to ensure continued maintenance of the collected materials. Technical consultancy services were provided from the developed laboratories to developing national programmes in the region, such as using expertise of NBPGR, India for developing tissue culture facilities in Nepal Agricultural Research Council (NARC), Kathmandu, Nepal and the scientific advice in establishing National Biodiversity Centre in Bhutan.

Socio-economic Studies

Socio-economic studies were conducted on several fruit species so as to understand grower and consumer preferences *vis-à-vis* production and marketing constraints. For this, participatory research appraisals (PRA) and rapid market appraisals (RMA) were carried out. Analytical methods used in the study included simple tabular analysis and percentages to more complex one such as calculating internal rate of return (IRR). During the proposal development phase of UNEP/GEF Project, Bioversity carried out market research to better understand the role of markets in the maintenance of TFT diversity on-farm. A few case studies on integrating biodiversity conservation and livelihood improvement were undertaken by Bioversity to study the role of markets of mango and kokum (*Garcinia indica*) in India and to identify good practices for on-farm biodiversity management in Indonesia and Thailand. The focus of these studies was on linking farmers to markets *vis-à-vis* improving their livelihoods through better income generation. The studies revealed the usefulness of maintaining a mix of varieties of mango as a strategy to ensure better distribution of income due to differential ripening period and mitigating the risk of low production of some varieties (Sudha and Kruijssen, 2007). Secondly, rich genetic diversity provides major potential for income enhancement. Maintaining particular underutilized fruits may provide a market niche and ensure income for a group of farmers as observed in a case study in Thailand (Kruijssen and Somsri, 2006). It was also observed in India where many fruit trees species with several different uses are available, that some varieties may be more suitable for a certain use than others and farmers take advantage of this (Sudha and Kruijssen, 2007). Similar observations were made in studies on pummelo in Indonesia where the thickness of spongy white skin under the rind of the fruit was considered advantageous. The differences in soil composition and water availability also resulted in differences in the distribution of pummelo varieties between the sub-districts (Kruijssen and Hardiyanto, 2007). Understanding this G X E interaction is the key to develop intervention on value chain of local produces. The studies indicated that the socio-economic characteristics of the farm households utilizing tropical fruits and the market forces play an important role in their decision making for on-farm conservation and

the sustainable livelihoods. These results were used in designing the full scale proposal that includes studies on marketing and value adding activities that is currently being implemented by Bioversity.

The salient findings of the socioeconomic studies and the policy perspectives (Chengappa, 2003; IPGRI, 2003a; Kruijssen and Somsri, 2006; Kruijssen and Hardiyanto, 2007; Sudha and Kruijssen, 2007) included: i) Low investment and high return makes the target TFT ideal intercrops especially in the home gardens, ii) Commercial orchards growing native TFTs have relatively less maintenance cost, iii) Analysis of marketing constraints such as location, transportation, perishability of produce, distribution and supply revealed the need for establishing farmers' cooperatives and common facilities so as to provide a viable alternative to the farmers to realize greater share of the sale price. Appropriate institutional support will help in this regard, iv) Value addition was considered more important for the minor fruits. The use of diversity for product development and appropriate linkages between processing units and growers will result in improving supply of such products to consumers and generating more income for the rural sector, v) Establishment of processing centres in high production areas is vital in addressing the economic viability of this sector through improved utilization, product diversification of fruit genetic resources, vi) Documentation and dissemination of knowledge on nutritive and medicinal values of native tropical fruits helps to improve the level of consumption creating the demand minor fruits, vii) Training and awareness programmes to disseminate technology and knowledge on consumption patterns, post-harvest management and processing are essential to enhance utilization and conservation of diversity of these fruit crops, vii) There is the vast scope for expansion of area under native tropical fruits with good varieties and exploiting the untapped potential diversity to meet the domestic and international demand both for fresh and processed fruits, vii) Studies clearly indicated the narrow genetic base, limited number of varieties in commercial cultivation, lack of classification and indexing of local varieties, and the need to conserve the rare types possessing desirable characters are the important issues of concern and need immediate attention.

Some of these socio-economic and market related aspects will be studied under the UNEP/GEF project

that is being implemented in four countries in the region.

Collaboration and Linkages

Bioversity believes that successful conservation and use of plant genetic resources is possible only through multidisciplinary and multisectoral collaboration. In addition, as plant genetic resources are not bound by country boundaries, gene pools can only be conserved through collaboration between countries in which such genetic resource are distributed. Hence, the varied activities carried out on TFTs genetic resource as described so far were possible through Bioversity's links with a number of national, regional and international organizations. Some of these collaborative activities are briefly mentioned below:

Exchange of Information and Germplasm

Sharing of germplasm and information on them has become fairly difficult since the Convention on Biological Diversity (CBD) came into existence in 1992. However, under activities supported by Bioversity, national partners agreed to share information on fruit genetic resource and in some cases even germplasm, albeit on a limited scale. Data sharing was achieved through i) developing a central data base, ii) publishing catalogues of fruit crop varieties, and iii) placing information on tropical fruit tree website. Bangladesh shared the passport and characterization data on mango, citrus and jackfruit germplasm and elite materials with the partners in other countries. Database on citrus, mango and litchi developed in China is available for to researchers interested in exchange of materials. Malaysia exchanged information on characterization of the underutilized fruit species, pulasan and kuini, with the partner countries.

The lists of material in mango and citrus that can be exchanged from Nepal for research purpose under the material transfer agreement (MTA) were developed. The Philippines exchanged passport and characterization information of priority fruit species with several countries in the region. Accession information and databases developed in Sri Lanka were shared with the other countries. Germplasm of mango (3 cultivars) and lemon (one cultivar) were received by Sri Lanka from India under the MTA between the two countries. Thailand shared accession information, catalogue and databases with partners. The information on exchangeable varieties of litchi,

mango and citrus was made available by Vietnam to other countries in the region. Also, the seminars and workshops organized in Indonesia in collaboration with the International Tropical Fruits Network (TFNet) programme facilitated exchange of information with partners.

Collaboration with Regional and International Organizations

Bioversity's programme on tropical fruit species over the past two decades had been very successful in establishing close collaboration among the participating countries. It also facilitated its linkages and interaction with national partners and donors and international organizations such as Food and Agriculture Organization of the United Nations (FAO), Centre de Cooperation International en Recherche Agronomique pour le Developpement (CIRAD), Asian Development Bank (ADB), Australian Centre for International Agricultural Research (ACIAR), International Centre for Underutilized Crops (ICUC), Underutilized Tropical Fruits in Asia Network (UTFANET), and the International Tropical Fruits Network (TFNet) for promoting research on plant genetic resources aspects in fruit crops. Collaboration with sub-regional networks, such as the South Asia Network on Plant Genetic Resources (SANPGR), Regional Cooperation in Southeast Asia for Plant Genetic Resources (RECSEA-PGR) and the East Asia Network on Plant Genetic Resources (EA-PGR) was established for exchange of technology and information. Collaborative links were also established between different research institutions in several countries.

Such regional and/or international collaboration proved particularly useful in capacity building of the partners. Bioversity-APO and ACIAR jointly organized Citrus Germplasm Conservation Workshop at Griffith University, Brisbane, Australia on 6-7 October 1997 which was attended by several partners. At this Workshop, further plans to promote conservation and use of citrus genetic resources were made (Broadbent *et al.*, 1999) and (Ramanatha Rao and Arora, 1999; Ramanatha Rao and Bhag Mal, 2002; and Drew and Ashmore, 2003). Collaboration with the International Centre for Underutilized Crops (ICUC) resulted in identifying priority fruit species for the Asia-Pacific region (Arora and Ramanatha Rao, 1995). Collaboration with DFID resulted in the publication of several monographs, namely, tamarind (*Tamarindus indica*) ber (*Ziziphus mauritiana*), baobab (*Adansonia*

digitata), ndjanssang (*Ricinodendron heudelotii*); safou (*Dacrylodes edulis*) and *Annona* species were published (Gunasena and Hughes, 2000; Pareek, 2001; Sidibe and Williams, 2002; Kengue, 2002; Pinto *et al.*, 2005; Tchoundjeu and Atangana, 2006). Bioversity and UTFANET supported each other in the training and meetings relating to conservation and use of tropical fruit species and signed the Memorandum of Understanding (MOU) to collaborate on various activities

Impact and Sustainability

Bioversity's work on tropical fruit tree species to date has been able to successfully promote awareness about the conservation and use of TFT genetic resources at various levels including researchers, farmers, administrators and policy makers. As a result, there is now a greater commitment by the national governments in the collaborating countries to support fruit crops research and development programmes. For example, a number of related and additional research is being promoted (e.g. *in situ* conservation – botanical gardens by Forestry Department; *ex situ* conservation by MARDI, Department of Agriculture (DOA) and NGOs (CPCP); Cryopreservation by several Universities; On-farm conservation by TFNet, MARDI and DOA; Genetic diversity research by MARDI and universities; work on pests and diseases by MARDI and socioeconomic studies by MARDI) have been funded by the Governments in Malaysia. In the Philippines, the projects on 'Conservation and Use of Tropical Fruit Species Diversity in the Philippines' and 'Introduction, Evaluation and Adoption of Improved and Superior Landraces of Banana for Food and Income Alleviation' have been funded by the Department of Agriculture-Bureau of Agricultural Research (DA-BAR). In China, the central and local governments have paid great attention to the tropical and sub-tropical fruits. Some projects, such as field genebank maintenance, wild and semi-wild germplasm exploring and collecting, variety improvement etc. on citrus, have received additional assistance and funding from Agricultural Department in 2001 and 2002. The project 'Mango Genebank and Database Establishment' was mainly funded by the Ministry of Science and Technology in 2002. In Vietnam, research on tropical fruit crops has been identified as one of the ten priority areas to be given due attention by the Government. In India, fruit crop research programme has been

financially supported under the National Agriculture Technology Project (NATP) and has been included in the National Agricultural Innovation Project (NAIP) funded by World Bank to carry forward the ongoing activities. In Thailand, as a result of the awareness generated through Bioversity supported activities, more attention is now being paid by the national government to mango and rambutan research and development, especially for plant improvement and molecular biology programmes. Thus, Bioversity's TFT programme and activities triggered the placement of fruit crops on the higher development agenda of the national governments in the collaborating countries.

The countries have been able to collect the threatened and rare diversity of identified priority TFT crops including their wild relatives and related species. The use of new tools such as DIVA-GIS and Flora Map has been found very successful in identifying the hot spots of diversity, prepare diversity distribution maps and plan the future collecting missions. The diversity collected has been saved from extinction and is safely conserved in genebanks for current and future use, which will have long-term impact on the fruit crop research and development programme in the collaborating countries.

The regeneration and micropropagation techniques for rapid propagation of disease free planting material and *in vitro* conservation/cryopreservation techniques for conservation of germplasm of different fruit species such as citrus, litchi, longan, rambutan and papaya proved very useful and these advance techniques are being used by the national programmes and are also available for use in other fruit crops in different countries.

The useful diversity comprising several elite lines and germplasm accessions with specific desirable attributes is now available for use by the researchers in the breeding programmes. The elite lines identified in different fruit species having added value for specific purposes such as suitability for crop diversification, product development and market demand had great impact and the farmers had access to these lines/cultivars which proved useful in enhancing their conservation and use. For example, Tai Ya variety of mango with red rind colour and good storage quality and Boloxiamyoer with pine apple fragrance and seedless variety Anjianwyhaou of pummelo in China; and Me Amba, Atamba and Valamba varieties of mango with

bark of root and stem used for fixing broken limbs in Sri Lanka exhibited great potential for large scale cultivation in these countries. Good examples that have created impact through the application of results in the field are propagation and direct cultivation of elite varieties of citrus in Nepal and China, litchi in Vietnam and jackfruit in Sri Lanka by farmers and private nurseries.

Dissemination and sharing of the information on community participation in conservation of fruit germplasm has motivated and sensitized the researchers and fruit growers in many countries in aspects related to on-farm conservation and making better use of available diversity. The strong human resource development programme providing training to researchers, technicians and farmers for enhancing their skills on different aspects of fruit genetic resources resulted in the availability of trained human resource in the collaborating countries for enhanced utilization and conservation of fruit genetic resources.

Bioversity projects on TFT facilitated the establishment of the Tropical Fruit Tree Genetic Resources Network (TFTGRN). The Network helped to promote regional cooperation to access and share information through its website <http://tftgrn.net/> which serves as a platform for exchange of information on the progress of work on TFT species in the collaborating countries and thus sustains collaboration between the partners in the Asia region. Information was also shared through GlobalHort Portal (www.globalhort.org) which is a horticultural platform for collaboration and knowledge management.

Expanding from *Ex situ* Conservation to *In situ* Conservation: The Current Approach

Bioversity's earlier work focused mostly on *ex situ* conservation related activities. Considering the need for increased efforts on on-farm (for cultivated) and *in situ* (for wild relatives), Bioversity in collaboration with its partners developed a short proposal under PDF- B Phase with support from the Global Environment Facility (GEF) and its execution resulted in the development of a full scale project proposal which was approved by GEF and the implementation of the project on "Conservation and Sustainable Use of Cultivated and Wild Tropical Fruit Diversity: Promoting Sustainable Livelihood, Food Security and Ecosystem Services" started in January 2009. The project is focusing on

four TFT species, namely, citrus (*Citrus* spp.), mango (*Mangifera indica*), mangosteen (*Garcinia mangostana*), rambutan (*Nephelium lappaceum*) and their wild relatives (some of which are edible). These are commercially important TFT species in the region with high diversity levels, both at intraspecific and interspecific levels. This GEF funded project is being implemented by the United Nations Environment Programme (UNEP) and executed by Bioversity International in four countries, namely, India, Indonesia, Malaysia and Thailand. These four countries were selected as these are located in the centres of diversity of these species.

This new project aims to help farmers to make use of selected TFT species to sustain their communities and by doing so to conserve the genetic diversity of TFT species and their wild relatives. The project will contribute to improvement of livelihoods and food security of target beneficiaries through conservation and use of fruit tree genetic resources. The project aims to promote conservation *in situ* and on-farm of TFT genetic resources through strengthened capacity of farmers, user groups, local communities and institutions to sustainably apply good practices and secure benefits. The major outcomes expected from this project are i) diversity of TFT genetic resources is conserved *in situ* and on-farm through improved knowledge of its value, use and sustainable management, ii) rural communities benefit by using methodologies and good practices for the management and conservation of TFT species and intra-specific diversity, and iii) stakeholders have the capacity and leadership skills to apply good practices for managing TFT diversity for sustainable livelihoods, food security and ecosystem health. The species complexes chosen for this project represent a reasonably comprehensive for providing methods and lessons to other countries and regions. Two of the genera (citrus and mango) are of worldwide importance while the other two (rambutan and mangosteen) are regionally important. These contrasts provide important learning opportunities for the project partners as they seek to improve incomes by developing markets for less commercialized tree fruit species.

Future Thrusts

In order to improve the conservation and utilization of fruit genetic resources in the APO region, an integrated approach needs to be adopted. This would improve productivity and quality as well as enhance

income from cultivation of native TFT species, and contribute towards food and nutritional security, poverty alleviation and the protection of environment in the rural sector in the region. The following important areas need greater thrust for research and development for effective and efficient conservation and use of TFT genetic resources:

- The existing gaps in the collections need to be filled by targeted collecting of rare and threatened materials using the improved techniques of DIVA-GIS and FloraMap and the collected diversity needs to be characterized.
- The utilization of diversity collected and conserved in the genebanks needs a focused attention and the elite lines/germplasm with specific desirable traits need to be used by the breeders to develop improved varieties. The TFT genebank managers should find ways and means for enhancing the use and should increase their involvement in pre-breeding so that they can sell their genetic resource to the plant breeders.
- Diversity of TFT genetic resources needs to be conserved *in situ*/on-farm through improved knowledge of its value, use and sustainable management practices by way of documentation of farmers' and users' knowledge, identification of market and non-market values, identifying populations under threat and developing key methodologies and good practices such as participatory rapid appraisal, genetic diversity mapping, developing descriptors, efficient conservation techniques, etc.
- TFT genetic resource should be used as a major tool to promote diversity for nutrition security. Sincere efforts need to be made for large scale evaluation of germplasm for their nutrient contents and nutraceutical properties and elite lines possessing better quality traits need to be promoted for wider use.
- Appropriate tools for quick estimation of genetic diversity at the field level need to be developed. Greater thrust also needs to be given for developing appropriate methodologies and good practices for the management and conservation of TFT species and intraspecific diversity. A sustainable livelihood approach for promoting TFT conservation needs to be developed.

- Greater focus needs to be placed on the use of TFT genetic resources for upgrading marginal and degraded lands and combating adversities due to climate change by selecting matching species for the changing sites. Integrated farming with perennial fruits in orchards can be potential research scope for mitigating and adapting climate change.
- Product development, processing, post-harvest handling and marketing aspects of TFT species need to be paid adequate attention for income enhancement of the farmers and the benefits to the consumers. Research and development programmes addressing these aspects need to be strengthened.
- The full value of TFT being perennial tree crops must be fully accounted for in terms of its contribution to carbon sequestration and other environmental services. Application of economic valuation methodologies can be applied for this purpose.
- There is a greater need to further promote networking and collaboration at the regional and international level and facilitate sharing of information, technologies and germplasm among the partners in order to exploit the native tropical and subtropical TFT diversity in the region. The existing Tropical Fruit Genetic Resources Network (TFTGRN) could be further strengthened to enhance conservation and use of TFT species. The list of exchangeable varieties of priority fruit tree species in different countries need to be developed and the material exchanged based on mutually agreed terms and under a material transfer agreement (MTA) for the benefit of collaborating countries.
- Bioversity has been supporting the idea of regional or sub-regional genebanks and sharing the responsibilities and benefits from such an effort. For example, Bioversity through its International Coconut Genetic Resources Network (COGENT) has established a multi-site International Coconut Genebank (ICG) consisting of a regional genebank in each of the five COGENT regions (Batugal and Oliver, 2004). Such an approach could be followed for TFT species also for the sustainability of regional efforts towards conservation and use of TFT species.

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References

- Arora RK (1995) Role of IPGRI in the collection, conservation and utilization of tropical and subtropical fruit tree genetic resources. In: *Fruit Production in the Tropics and Subtropics*. JIRCAS International Symposium Series No.3. 1st International Symposium of JIRCAS. Symposium of the XXIVth International Horticultural Congress, Kyoto International Conference Hall, Japan, 22-23 August 1994, pp 7-15.
- Arora RK and V Ramanatha Rao (eds.) (1995) *Proceedings of Expert Consultation on Tropical Fruit Species of Asia*. 17-19 May 1994, Malaysian Agricultural Research and Development Institute, Serdang, Kuala Lumpur, Malaysia. IPGRI Office for South Asia, New Delhi, India, 116 p.
- Arora RK, V Ramanatha Rao and AN Rao (eds.) (1996a) *Status Reports on Genetic Resources of Mango in South, Southeast and East Asia*. IPGRI Regional Office for Asia, the Pacific and Oceania, Singapore.
- Arora RK V Ramanatha Rao and AN Rao (eds.) (1996b) *Status Reports on Genetic Resources of Citrus in East (China, Japan) and South Asia (India)*. IPGRI Regional Office for Asia, the Pacific and Oceania, Singapore.
- Arora RK and V Ramanatha Rao (eds.) (1998) *Tropical Fruits in Asia, Diversity, Maintenance, Conservation and Use*. Proceedings of the IPGRI/ICAR/UTFANET Regional Training Course on the Conservation and Use of Germplasm of Tropical Fruit in Asia, 19-31 May 1997, IIHR, Hesaraghatta, Bangalore, India. IPGRI Office for South Asia, New Delhi, India.
- Batugal PA and J Oliver (2004) The International Coconut Genetic Resources Network. In: Bhag Mal, PN Mathur, V Ramanatha Rao and AHM Jayasuriya (eds.) *South Asia Network on Plant Genetic Resources (SANPGR)*. Proceedings of the Sixth Meeting, Peradeniya, Sri Lanka, 9-11 December 2002. IPGRI Office for South Asia, New Delhi, pp 106-111.
- Bhag Mal and V Ramanatha Rao (2003) Tropical Fruit Genetic Resources Activities in Asia, the Pacific and Oceania Region: Role of IPGRI. In: R Chaudhary, R Pandey, SK Malik and Bhag Mal (eds) *In Vitro Conservation and Cryopreservation*

- of Tropical Fruit Species. IPGRI Office for South Asia, New Delhi/NBPGR, New Delhi, India. 293 p.
- Bhag Mal, V Ramanatha Rao and YS Ramamani (2004) *Status of Tropical Fruit Genetic Resources Activities in Asia, the Pacific and Oceania: IPGRI's efforts*. In: Proceedings of Sixth Meeting of South Asia Plant Genetic Resources (SANPGR) held at PGRC, Peradeniya, Sri Lanka, 9-11 December 2002. IPGRI Office for South Asia, New Delhi, India, 92-100.
- Bhag Mal, V Ramanatha Rao, RK Arora and SE Percy (2007) *Conservation and Use of Tropical Fruit Species Diversity in Asia: IPGRI's Contributions*. In: KV Peter and Z Abraham (eds) *Biodiversity in Horticultural Crops* (Vol. 1). Daya Publishing House, Delhi 110035, 365 p.
- Bhattacharya SC and S Dutta (1956) Classification of the citrus fruits of Assam. ICAR monograph No 25, ICAR, Delhi.
- Bompard JM (1988) *Wild Mangifera species in Kalimantan (Indonesia) and in Malaysia*. Final report on the 1986-88 collecting missions. Report to IUCN-WWF/IBPGR.
- Bompard JM (1992) *Mangifera species*. In: EWM Verheij and RE Coronel (eds) *PROSEA: Plant Resources in South-East Asia No. 2. Edible Fruits and Nuts*. Pudoc. Wageningen, pp 207-220.
- Broadbent P, SR Sykes, KB Bevington and D Hailstones, editors (1999) *Proceedings of Citrus Germplasm Conservation Workshop*, 6-7 October 1997. Brisbane Australia, NSW Agriculture/CSIRO/ACIAR/IPGRI, Canberra, Australia, 158 p.
- Brown, MJ (1997) *Durio—A Bibliographic Review*. RK Arora, V Ramanatha Rao and AN Rao (eds.). IPGRI Office for South Asia, New Delhi, India, 188 p.
- Budathoki K (2003) *Conservation and Use of Mango and Citrus Species Biodiversity in Nepal*. Final Country Report for Nepal submitted to IPGRI under the ADB-funded project on Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia. Nepal Agricultural Research Council, Kathmandu, Nepal, 90 p.
- Chandel KPS, R. Chaudhury, J Radhamani and SK Malik (1995) Desiccation and freezing sensitivity in recalcitrant seeds of tea, cocoa and jackfruit. *Ann. Bot.* **76**: 443-450.
- Chaudhury R, BB Mandal and SK Malik (2000a) Development of cryopreservation techniques for the long-term conservation of recalcitrant seed and vegetatively propagated plant species in India. IPGRI-NBPGR project report (1996-2000), IPGRI, Rome, Italy.
- Chaudhary R, S K Malik and F Engelmann (2000b) Application of Cryopreservation technology for storage of recalcitrant and intermediate seed species. In: *Abstract of International Conference on Science and Technology for Managing Plant Genetic Diversity in the 21st Century*, Kuala Lumpur, Malaysia, 12-16 June, 2000.
- Chaudhury R, R Pandey, BB Mandal, N Sharma, RK Tyagi, A Agarwal, S Gupta, SK Malik and Z Hussain (2001) Germplasm conservation: *In vitro* repository and cryobank. In: BS Dhillon, KS Varaprasad, K Srinivasan, M Singh, S Archak, U Srivastava and GD Sharma (eds) *A Compendium of Achievements*. National Bureau of Plant Genetic Resources, New Delhi, 329 p.
- Chaudhury R, R Pandey, SK Malik and Bhag Mal (eds) (2003) *In Vitro Conservation and Cryopreservation of Tropical Fruit Species*. IPGRI Office for South Asia, New Delhi, India/NBPGR, New Delhi, India, 293 p.
- Chengappa PG (2003) *Socio-economic Studies on Conservation and Use of Native Tropical Fruit Genetic Resources in Asia*. Consultancy Report. IPGRI-ADB-TFT Project 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia'. IPGRI Office for South Asia, New Delhi, India, 53 p.
- Cho EG, YL Hor, HH Kim, V Ramanatha Rao and F Engelmann (2001). Cryopreservation of *Citrus madurensis* zygotic embryonic axes by vitrification: Importance of pregrowth and preculture conditions. *CryoLetters*, **22**: 391-396.
- Cho EG, MN Normah, HH Kim, V Ramanatha Rao and F Engelmann (2002). Cryopreservation of *Citrus aurantifolia* seeds and embryonic axes using a desiccation protocol. *CryoLetters*, **23**: 309-316.
- Dela Cruz, FS (2001) *Status Report on Genetic Resources of Mangosteen (Garcinia mangostana L.) in Southeast Asia*. IPGRI Office for South Asia, New Delhi, India. 24 p.
- Dela Cruz, FS (2003) *Conservation and Utilization of Germplasm of Mango, Citrus spp. and Garcinia spp. in the Philippines*. Final Country Report for Philippines submitted to IPGRI under the ADB-funded project on 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia'. National Plant Genetic Resources Laboratory, Institute of Plant Breeding, College of Agriculture, University of the Philippines, Los Baños (UPLB), Laguna, Philippines.
- Dinesh MR and CS Vasugi (2002) *Catalogue of Mango Germplasm*. Indian Institute of Horticulture Research, Bangalore, India, 160 p.
- Drew R and S Ashmore (2003) Complementary Conservation Strategy for Tropical Fruit Species. Consultancy Report under ADB funded project on 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia. IPGRI South Asia Office, New Delhi, India, 68 p.
- Drew R, A Ashmore, S Somsri, N Noor, TT Hoa, O Damasco, and VRamanatha Rao (2006). *Development of Advanced Technologies for Germplasm Conservation of Tropical Fruit Species*. Paper presented at the International Horticultural Congress. October 2006, Suwon, R. Korea.
- Ghosh SP and SK Mitra (2000) *Status Report on Genetic Resources of Litchi in India, Thailand and Myanmar*. IPGRI Office for South Asia, New Delhi, India, 56 p.
- Gunasena HPM and A Hughes (2000) *Tamarind*. International Centre for Underutilized Crops, Southampton, UK, 171 p.
- Haq N (1994) *Identification of Priority Species of Tropical Fruits for Research and Development*. Final Report, IPGRI Project No.93/11 (AOG-APO) ICUC in collaboration with IPGRI-APO. International Centre for Underutilized Crops, Department of Biology, Southampton University, UK.
- Hodel Urs and M Gessler (1999) *In situ Conservation of Plant Genetic Resources in Home Gardens of Southern Vietnam*. A report of home gardens surveys in Southern Vietnam. December 1996-May 1997, 106 p.

- Hodgson RW (1967) Horticultural varieties of citrus. In: W Reuther, HJ Webber, and LD Batchelor (eds) *The Citrus Industry*. Vol I. History, World Distribution, Botany, and Varieties. Univ. of California, Div. of Agricultural Sci, Berkeley, 431-591.
- Hoe VB and KH Siong (1999) The nutritional value of indigenous fruits and vegetables in Sarawak. *Asia Pacific Journal of Clinical Nutrition* **8(1)**: 24-31.
- Hue NTN (2003) *Conservation and Use of Diversity in Citrus, Mango and Litchi in Vietnam*. Final Country Report for Vietnam submitted to IPGRI under the ADB-funded project on "Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia". Vietnam Agricultural Science Institute, Thanh Tri, Hanoi, Vietnam.
- Idris S and R Mat Lin (2002a) *Status Report on Genetic Resources of Kuini (Mangifera odorata Griff.) in Southeast Asia*. IPGRI Office for South Asia, New Delhi, India, 23p.
- Idris S and R Mat Lin (2002b) *Status Report on Genetic Resources of Pulasan (Nephelium ramboutan-ake (Labill.) Leech in Southeast Asia*. IPGRI Office for South Asia, New Delhi, India, 28 p
- Idris S (2003) *Genetic Conservation and Utilization of Nephelium ramboutan-ake and Mangifera odorata in Malaysia*. Final Country Report for Malaysia submitted to IPGRI under ADB-funded Project on 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia'. Malaysian Agricultural Research and Development Institute, Kuala Lumpur, Malaysia.
- IPB (2003a) *Germplasm Catalogue on mango*. Institute of Plant Breeding, College of Agriculture, University of the Philippines, Los Baños (UPLB), Laguna, Philippines.
- IPB 2003(b) *Germplasm Catalogue on Garcina spp*. Institute of Plant Breeding, College of Agriculture, University of the Philippines, Los Baños (UPLB), Laguna, Philippines.
- IPGRI (1999) *Descriptors for Citrus*. International Plant Genetic Resources Institute, Rome, Italy, 66 p.
- IPGRI (2000) *Descriptors for Jackfruit (Artocarpus heterophyllus)*. International Plant Genetic Resources Institute, Rome, Italy, 58 p.
- IPGRI (2002) *Descriptors for Litchi (Litchi chinensis)*. International Plant Genetic Resources Institute, Rome, Italy, 64 p.
- IPGRI 2003(a) *Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia*. Final Project Report, Asian Development Bank, RETA 5866, September 2003. IPGRI-APO, Serdang, Malaysia, 89 p.
- IPGRI 2003(b). *Development of Advanced Technologies for Germplasm Conservation of Tropical Fruit Species*. Final Project Report. Australian Centre for International Agricultural Research. CP/2000/002. IPGRI-APO, Serdang, Malaysia, 12 p.
- IPGRI (2003c) *Descriptors for Rambutan (Nephelium lappaceum)*. International Plant Genetic Resources Institute, Rome, Italy, 54 p.
- IPGRI (2003 d) *Descriptors for Mangosteen (Garcinia mangostana)*. International Plant Genetic Resources Institute, Rome, Italy, 56 p.
- IPGRI (2006) *Descriptors for Mango (Mangifera indica)*. *Indian J. Plant Genet. Resour.* **24(1)**: 1-22 (2011)
- International Plant Genetic Resources Institute, Rome, Italy, 57 p.
- Kaloo G (2003) *Conservation and Use of Diversity in Mango, Citrus and Litchi in India*. Final Country Report for India submitted to IPGRI under ADB-funded Project on "Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia". Indian Council of Agricultural Research, Krishi Anusandhan Bhavan, Pusa Campus, New Delhi.
- Kengue J (2002) *Safou (Dacryodes edulis)*. International Centre for Underutilized Crops, Southampton, UK, 147 p.
- Kostermans AJGH and JM Bompard (1993) *The Mangoes: Their Botany, Nomenclature, Horticulture and Utilisation*. IPGRI and Linnean Society of London, Academic Press, London.
- Kruijssen F and S Somsri (2006) *Marketing local biodiversity in Thailand: Identification of a possible good practice for on-farm biodiversity management of tropical fruit trees*. Contributed paper for the Deutscher Tropentag, "Prosperity and Perty in a Globalised World- Challenges for Agricultural Research". Bonn, Germany, 11-12 October 2006.
- Kruijssen F and A Hardiyanto (2007) *Marketing Local Biodiversity in Indonesia: Analysis of a Possible Good Practice for On-farm Biodiversity Management of Tropical Fruit Trees (Unpublished manuscript)*.
- Mabberley DJ (1997) A classification for edible *Citrus* (Rutaceae). *Telopea* **7**: 167-172.
- Mabberley DJ (1998) Australian Citrae with notes on other Aurantioideae (Rutaceae). *Telopea* **7**: 333-344.
- Mahrouf ARM (2003a) *Socio-economic Dimensions in Conservation and Use of Mango Species Biodiversity in Sri Lanka*. Final Report on Socioeconomic Aspects studied under IPGRI-ADB-TFT Project "Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia". Socio-economics & Planning Centre, Department of Agriculture, Peradeniya, Sri Lanka, 75 p.
- Mahrouf ARM (2003b) *Socio-economic Dimensions in Conservation and Use of Jackfruit Species Biodiversity in Sri Lanka*. Final Report on Socioeconomic Aspects studied under IPGRI-ADB-TFT Project "Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia". Socioeconomics & Planning Centre, Department of Agriculture, Peradeniya, Sri Lanka, 81 p.
- Mukherjee SK (1985) *Systematic and Biogeographic Studies of Crop Genepools*. Vol.1, *Mangifera* L. IBPGR, 86p.
- Nares D, V Ramanatha Rao, and D Jarvis (2001) In situ conservation of tropical fruit trees in Southeastern Asia. In: Bhag Mal, YS Ramamani and V. Ramanatha Rao (eds) *Proceedings of the First Annual Meeting of the Project, 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia*, 6-9 February 2001. IPGRI South Asia Office, New Delhi, pp 51-60.
- Nito N (2003) *Status Report on Genetic Resources of Citrus in Asia-Pacific Region*. Bhag Mal, V. Ramanatha Rao and R.K. Arora (eds). IPGRI South Asia Office, New Delhi, India, 104 p.
- Pathak RK (2003) *Status Report on Genetic Resources of Indian Gooseberry – Aonla (Emblica officinalis Gaertn.) in South*

- and Southeast Asia. Bhag Mal, V Ramanatha Rao and RK Arora (eds). IPGRI Office for South Asia, New Delhi, India, 99 p.
- Pareek OP, Suneel Sharma and RK Arora (1998) *Underutilized Edible Fruits and Nuts: An Inventory of Genetic Resources in Their Regions of Diversity*. IPGRI Office for South Asia, New Delhi, India, 235 p.
- Pareek OP (2001) *Ber*. International Centre for Underutilized Crops. Southampton, UK. 292 p.
- Pinto AC de Q, MCR Cordeiro, SRM de Andrade, FR Ferreira, HA de CFilgueiras, RE Alves and DI Kimpura (2005) *Annona* species. International Centre for Underutilized Crops, University of Southampton, Southampton, UK, 263 p
- Purnomo S (2003) *Conservation and Use of Diversity on Rambutan and Mangosteen in Indonesia*. Final Country Report for Indonesia submitted to IPGRI under ADB-funded Project on 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia'. Indonesian Fruit Research Institute, Solok, West Sumatra, Indonesia.
- Rajan S, SS Negi and Ram Kumar (2002) *Catalogue on Mango (Mangifera indica L.) Germplasm*. Central Institute for Subtropical Horticulture, Lucknow, India, 66 p.
- Rajan S (2003) *Electronic Catalogue of Mango (Mangifera indica)*. Central Institute for Subtropical Horticulture, Lucknow, India.
- Ramanatha Rao V and RK Arora (1999) Conservation Strategy In: P Broadbent, SR Sykes, KB Kenington and D Hailstones (eds) *Proceedings Citrus Germplasm Conservation Workshop*, Brisbane, Australia. 6-7 October 1997, 158 p.
- Ramanatha Rao V and Bhag Mal (2002) Tropical fruit species in Asia: diversity and conservation strategies. In: Rod Drew (ed) *Proceedings of the International Symposium on Tropical and Subtropical Fruits; Acta Horticulturae 575*. International Society for Horticulture Science, 405 p.
- Ramanatha Rao V, Bhag Mal and Z Zongwen (2005) Exploration of Native Tropical and Subtropical Fruit Species Diversity: Asian Perspective. In: KL Chadha, BS Ahloowalia, KV Prasad and SK Singh (eds) *Crop Improvement and Production Technology of Horticultural Crops*. Horticulture Society of India, New Delhi, 764 p.
- Reddy CVK, D Sreeramulu and M Raghunatha (2010) Antioxidant activity of fresh and dry fruits commonly consumed in India. *Food Res. International* **43(1)**: 285-288.
- Saad MS and V Ramanatha Rao (eds) (2001) *Establishment and Management of Field Genebank: A Training Manual*. IPGRI-APO, Serdang.
- Shahsavari AR, K Izadpanah, E Tafazoli, BE Sayed Tabatabaei (2007) Characterization of citrus germplasm including unknown variants by inter-simple sequence repeat (ISSR) markers. *Scientia Hort.* **112**: 310-314.
- Sant Ram and Shailendra Rajan (2003) Status Report on Genetic Resources of Mango in Asia-Pacific Region. In: Bhag Mal, V Ramanatha Rao and RK Arora (eds) IPGRI Office for South Asia, New Delhi, India, 196 p.
- Shantha Peiris KH (2003) *Exploration, Collection, and Conservation of Genetic Diversity of Mango and Jackfruit in Sri Lanka*. Final Country Report for Sri Lanka submitted to IPGRI under Indian J. Plant Genet. Resour. **24(1)**: 1-22 (2011)
- the ADB-funded project on 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia'. Horticultural Crop Research and Development Institute, Gannoruwa, Peradeniya, Sri Lanka.
- Sidibe M and JT Williams (2002) *Baobab (Adansonia digitata)*. International Centre for Underutilized Crops, Southampton, UK. 96 p.
- Singh R and N Nath (1969) Practical approach to the classification of citrus. *Proc, 1st Intl Citrus Symposium*, pp 435-440.
- Singh RB (1993) Fruit production in Asia-Pacific region. In: RB Singh (ed) *Research and Development of fruits in Asia-Pacific Region*. RAPA/FAO, Bangkok, 207 p.
- Singh IP and Shyam Singh (2003) *Exploration, Collection and Mapping of Citrus Genetic Diversity in India*. Technical Bulletin No.7, National Research Centre for Citrus, Nagpur, Maharashtra.
- Somsri S (2003a) *Conservation and Use of Mango and Rambutan Diversity in Thailand*. Final Country Report for Thailand submitted to IPGRI under ADB-funded Project on "Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia". Horticulture Research Institute, Department of Agriculture, Chatuchak, Bangkok, Thailand.
- Somsri S (2003b) *Electronic Catalogue of Mango Germplasm*. Horticulture Research Institute, Bangkok, Thailand.
- Somsri S (2003c) *Electronic Catalogue of Rambutan Germplasm*. Horticulture Research Institute, Bangkok, Thailand.
- Sudarmonowati E (2000) Cryopreservation of tropic plants: current reserach status in Indonesia. In: F Engelmann and H Takagi (eds) *Cryopreservation of Tropical Plant Germplasm: Current research progress and application* (JIRCAS, Tsukuba, Japan/IPGRI, Rome Italy, pp. 291-296.
- Sudha M and F Kruijssen (2007) Economic analysis of value addition along the supply chain for fresh and semi-processed products- the case of totapuri mango in South India. In: P Batt and J Cadhilon (eds) *Proceedings of International Symposium on Fresh Produce Supply Chain Management*, FAO, AFMA, Curtin University of Technology, Department of Agriculture of Thai Ministry of Agriculture and Cooperatives. RAP Publication 2007/21.
- Stapleton P (2002) Project Proposal Development and Scientific/ Technical Report Writing. Consultancy Report prepared under IPGRI-ADB-TFT Project 'Final Report on Socioeconomic Aspects studied under IPGRI-ADB-TFT Project 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia'. Bogor, Indonesia, 65 p.
- Stone BC (1994) Citrus Fruits of Assam: A New Key to Species, and Remarks on *C. assamensis* Bhattacharya and Dutta, 1956. *Gardens' Bulletin* (Singapore) **46**, 105-112.
- Swingle WT (1943) The botany of citrus and its wild relatives of the orange subfamily. In: HJ Webber and LD Batchelor (eds) *The Citrus Industry. Vol I. History, Botany and Breeding*. Univ. of California Press, Berkeley, pp 129-474.
- Tanaka T (1976) Tanaka's Encyclopaedia of edible plants of the world. Keigaku Publishing Co., Tokyo.
- Tanaka T (1977) Fundamental discussion of citrus classification. *Stud Citrol.* **14**: 1-6.

- Tchoundjeu Z and AR Atangana (2006) *Ndjanssang (Ricinodendron heudelotii)*. Southampton Centre for Underutilized Crops, University of Southampton, Southampton, UK, 74 p.
- TFNet (2004) Global Production of Tropical and Sub-tropical Fruits. Tropical Fruit Nut, Issue No. 3, Kuala Lumpur, Malaysia.
- Uddin Md Nazim (2003) *Survey, Collection, Evaluation, Conservation and Utilization of Jackfruit, Mango and Citrus of Bangladesh*. Final Country Report for Bangladesh submitted to IPGRI under the ADB-funded project on 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia'. Bangladesh Agricultural Research Institute, Dhaka, Bangladesh
- Verheij EWM and RE Coronel (1991) *Plant Resources of South-East Asia*, No. 2. Edible Fruits and Nuts. Pudoc. Wageningen, the Netherlands.
- Zushang C (2003) *Conservation and Utilization of Citrus, Mango and Litchi in China*. Final Country Report for China submitted to IPGRI under the ADB-funded project on 'Conservation and Use of Native Tropical Fruit Species Biodiversity in Asia'. Citrus Research Institute, Chinese Academy of Agricultural Sciences, Beibei, Chongqing, China.

Genetic Evaluation and Characterization of Sunflower (*Helianthus annuus* L.) Genotypes as per DUS Guidelines

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Sixty-seven genotypes of sunflower were evaluated for yield and yield components to study the extent of variation for different quantitative traits. Analysis of variance revealed significant differences among the genotypes for all the quantitative traits. High heritability coupled with low genetic advance was recorded in respect of days to initiation of disk floret opening (96.3%), complete anthesis (92.2%) and days to maturity (84.6%). High heritability coupled with high genetic advance was observed for 1000 seed weight (88.2 and 55.06) and seed yield g/plant (73.7 and 59.1). Large head size was observed for P62R, P64R, P74R, P81R and NDR-2. Nineteen lines had high self-fertility exceeding 94.0%. Bold seeds (1000 seed weight >80 g) was the characteristic feature of P72R. The lines viz. P63R, P64R and P86R were found to be promising for developing short duration hybrids.

Key Words: Characterization, Genetic evaluation, Heritability, Phenotypic and genotypic Coefficients of variation

Introduction

Sunflower is one of the important edible oilseed crops of the world. The crop is spreading to diverse agroclimatic conditions and shows adaptability to all types of soils, which necessitates the development of more productive hybrids of diverse duration. Success of plant breeding, depends upon the nature and magnitude of variability present in the germplasm. Further more, the assessment of heritable and nonheritable components of total variability will have immense value in the choice of suitable breeding procedure. Characterization of germplasm is useful to identify suitable lines and also to avoid duplication. Qualitative characters being more stable over generations and environments are reliable for characterization of germplasm. Hence, the present study was planned to genetically evaluate the available germplasm for yield and related attributes. Attempt has also been made to identify some promising genotypes for use in sunflower breeding programme.

Material and Methods

The material for the present study comprised of 67 (55 restorers and 12 maintainers) genotypes of sunflower. The experiment was conducted at Punjab Agricultural University, Ludhiana, over two years during spring 2006 and 2007. The material was grown in a randomized block design with three replications. Each plot consisted of a single row of 4.5 m length with row to row spacing of 60 cm and plant to plant spacing of 30 cm. Recommended

cultural practices were followed to raise the crop. The data were recorded in each genotype for days to initiation of disk floret opening (number of days from sowing to the date when one plant in a line showed disk floret opening), complete anthesis (when all the plants in the lines flowered), days to physiological maturity (when the back side of the heads turned yellowish brown) and on five plants for head diameter, plant height, autogamy (%), 1000 seed weight, seed yield/plant and oil content (%), in both the years. The overall means were calculated and used for statistical analysis. The phenotypic and genotypic coefficients of variation (PCV and GCV) were computed and classified as suggested by Burton and Dewana (1953), heritability (h^2) as per Hanson *et al.* (1956) and expected genetic advance (GA) as suggested by Johnson *et al.* (1995). The genotypes were characterized for 27 distinguishing morphological characters as per guidelines (Anonymous, 2009)

Results and Discussion

Analysis of variance revealed highly significant differences amongst genotypes for all the traits (Table 1). The study has also revealed that the genotypes performed differently in two environments for 1000-seed weight, autogamy (%), plant height and head diameter. For these characters, genotype environment interaction was also observed to be significant. Different parameters *i.e.*, range, mean, phenotypic and genotypic coefficients of variance, heritability estimates and predicted genetic advance for the quantitative traits are presented in Table 2. The PCV and GCV was found to be the highest

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Table 1. Analysis of variance for nine quantitative characters in 67 genotypes of sunflower (Pooled over environments)

Source of Variation	d.f.	Mean Squares								
		Initiation of disk floret opening (days)	Complete anthesis (days)	Physiological maturity (days)	Head diameter (cm)	Plant height (cm)	Autogamy (%)	1000 seed weight (g)	Seed yield (g/pl)	Oil content (%)
Rep. (within Env.)	4	4.9	2.6	3.7	21.4**	180.8**	7.2	3.0	112.5	0.8
Genotypes	66	29.5**	30.1**	33.9**	45.5**	1635.8**	84.2**	1218.1**	414.9**	97.9
Environment	1	37.0**	5.9	2.9	59.3**	10100.0**	573.5**	3746.2	58.0	547.7**
Genotype × Environment	66	1.1	2.3	5.2	7.2**	130.8**	48.6**	139.8**	109.0	32.3
Error	264	1.8	2.4	4.1	2.9	40.7	3.3	4.4	109.9	2.8

* Significant at 5% level.

** Significant at 1% level.

Table 2. Mean, Range and components of variability for nine quantitative traits in 67 genotypes of sunflower

Character	Mean ± SE	Range	PCV%	GCV%	h ²	GA
Initiation of disk floret opening (days)	61.1 ± 0.5	52.0–70.2	3.6	3.6	96.3	7.2
Complete anthesis (days)	66.9 ± 0.6	58.2–73.4	3.3	3.2	92.2	6.3
Physiological maturity (days)	90.6 ± 0.8	83.8–95.2	2.6	2.4	84.6	4.5
Head diameter (cm)	13.7 ± 0.8	7.9–19.2	20.1	18.4	84.3	34.3
Plant height (cm)	117.8 ± 3.1	77.8–151.7	14.0	13.4	92.0	26.5
Autogamy (%)	91.7 ± 1.4	80.3–95.9	4.8	0.0	42.3	3.5
1000 seed weight (g)	46.7 ± 2.3	21.8–89.3	30.5	28.7	88.3	55.6
Seed yield (g/plant)	21.4 ± 4.3	10.3–50.6	38.9	33.4	73.7	59.1
Oil content (%)	33.0 ± 1.2	22.3–42.8	12.2	10.0	67.0	16.9

PCV = Phenotypic coefficient of variance; GCV = Genotypic coefficient of variance; h² = heritability; GA = Genetic advance.

for seed yield/plant (38.9% and 33.4%) followed by 1000-seed weight (30.5% and 28.7%) and head diameter (20.1 and 18.5). This indicated presence of more variability which gives scope for improvement of these traits by selection. The high PCV and GCV observed for these traits is in conformation with earlier reports of Reddy and Reddy (2006). Moderate PCV and GCV were observed for plant height (14.0% and 13.4%) and oil content (12.2% and 10.0%). Very low variability was recorded for days to flowering, days to maturity and autogamy (%) thereby emphasizing the need for generating more variability with respect to these characters so that the germplasm lines having diverse maturity period could be effectively utilized in synthesizing hybrids having different maturity duration.

High heritability was recorded for days of initiation of disk floret opening (96.3%), complete anthesis (92.2%) and days to maturity (84.6%), but these traits exhibited low genetic advance. High heritability coupled with high genetic advance was observed for 1000-seed weight (88.2 and 55.6) and seed yield (g/plant) (73.7 and 59.1), suggesting better scope for improvement of these characters through direct selection. Similar results have been reported by Reddy and Reddy (2006), Gangappa

(1991) and Jayaramaiah *et al.* (1994). Moderate heritability with low genetic advance (67.01 and 16.89) was recorded for oil content. Low heritability (42.2) was observed for autogamy (%) along with very low genetic advance (3.5) which shows the greater influence of environment in the expression of these characters. On the contrary, Reddy and Reddy (2006) observed high heritability along with high genetic advance for these traits.

The characterization of genotypes revealed wide variation for all the qualitative characters among the genotypes. Earlier reports by Virupakshappa and Sindagi (1987) and Reddy and Reddy (2006) have also shown the presence of variation for these qualitative traits in sunflower accessions. Distinguishing characters of different genotypes are given in Table 3. Promising lines with desirable traits were identified as presented in Table 4. The genotype viz. P63R, P64R, P86R being early maturing were found to be promising for developing short duration hybrids. The genotypes P86R, P68R, P74R, P69R were dwarf with plant height of less than 100 cm. Large head size (>15 cm) was observed for P62R, P64R, P81R, P74R, P69R, NDR-2. A total of 19 genotypes were found to be having more than 94% self fertility. Bold seed (1000-seed weight >80.0 g) was the characteristic

Table 3. Distinguishing morphological characters of the genotypes

Character	Category	Genotype
Hypocotyle: Anthocyanin Coloration	Absent	P68R, SF-7R, NDR-2, CMS-44B, CMS-32B
Leaf size	Very Large	PISF-9R, RHA-856, PISF-3R, 179-2RP2, 12B
Leaf: colour	Light green	P84R, P81R, P69R
	Dark green	P62R, P64R, P83R, RCR8297
Leaf: blistering	Absent	P86R, P65R, P68R, P67R, P63R, P73R, PISF-12R, RHA83R6, PISF-18, LTRR-341, CMS-7-1B, CMS-10B, P69R
	Strong	P81R, P78R, P88R, P70R, P66R, P72R, RHA-297, RHA-265, R-801, RHA-17, LTRR-1822, RHA-859, 179-2RP2, CMS-18B, CMS-44B, CMS-12B, CMS-395, CMS-234B.
Leaf: fineness of Serration	Fine	P88R, P72R, RHA-856, LTRR-1822, 32B, 207B.
	Acute	P69R
Leaf: angle of lateral veins	Right angle	PISF-9R, R273, 32B, RCR-8297
	Obtuse	P65R, P83R, P74R, P75R, 44B, 234B.
Leaf: hairiness	Dense	P64R, P84R, P83R, P73R, RHA-271, PISF-3R, PISF-1R, R-801, 1147-4, PISF-13R, 32B
Stem: pigmentation	Absent	P62R, P87R, P84R, P68R, P78R, P74R, P67R, P72R, RHA-297, P69R, SF-7R, RHA-265, PISF-9R, PISF-12R, PISF-18R, P35R, PISF-3R, R-272-IP9, NDR-2, RHA-17, LTRR-1822, 1147-4, SF-4R, PISF-13R, SF-1R, 179-2RP2, CMS-18B, CMS31B, CMS-44B, CMS-7-1B, CMS-32B, CMS853B, CMS-10B, CMS-395B, CMS-234B, CMS207B.
	Strong	P86R, P83R, P70R, R-17, RHA-296, LTRR-341, RR-1, MR-6, RHA-85, RCR8297
Stem: flower: shape	Ovoid	P78R, P71R
Ray flower: colour	Orange	CMS-32B
Disk flower: Anthocyanin Coloration of stigma	Absent	P62R, P87R, P68R, P74R, P66R, P67R, P71R, P63R, P82R, P72R, RHA-297, P69R, SF-7R, RHA-265, RHA-856, RHA-271, PISF-1R, NDR-2, RHA-214, CMS-31B, CMS-7-1B, CMS-304B, CMS-32B, CMS-12B, CMS-853B, CMS-10B, CMS-395B, CMS-207B
Disk flower pollen Colour	White	MR-6
Bract: shape	Rounded	P68R, P78R, P70R, PISF-9R, PISF-12R, PISF-3R, P61R, P-801-RHA-17, 1147-4, 179-2RP2, 188, 31B, 853b, RCR-8297
Head: shape of grain side	Flat	395B, 234B, RCR8297
Plant: branching	Present	P86R, P68R, P70R, P72R, RHA-297, R-17, P69R, SF-7R, RHA-271 RHA-296, P61R, PISF-1R, RCR-8297, R273, R-802, LTRR-1822, RR-1, MR-6, PISF-13, 395B

Table 4. Promising genotypes for different characters

Days to flowering	< 60	P86R
Days of maturity	< 90	P64R, P86R, P63R, R-17, RHA-856, RHA-296, PISF-1R, R-801
Plant height (cm)	< 100	P86R, P68R, P74R, P69R, RHA-83R6
Head diameter (cm)	> 15	P62R, P64R, P81R, P74R, P69R, RHA-83R6, R-801, NDR-2
Autogamy (%)	> 94	P87R, P65R, P83R, P81R, P88R, P66R, P75R, P71R, RHA-297, RHA-256, NDR-2, RHA-214, 234B, 853B, 12B, 7-1B, 44B, 18B, RHA-859
1000-Seed weight (g)	> 60.0	P64R, P83R, P66R, P82R, PISF-3R, 179-2RP2, 12B, 853B, P69R
	> 80.0	P72R
Seed yield (g/plant)	> 30	P62R, P78R, PISF-18R, NDR-2
	> 40	PISF-9R, PISF-3R, 1147-4, 234B
Oil content (%)	> 37	P65R, RHA-271, PISF-1R, 234B

feature of P72R. For seed yield P62R, P78R, PISF-18R and NDR-2 had more than 31g seed yield/plant while PISF-9R, PISF3R, 1147-4 and 234 recorded more than >40 g seed yield/plant. Oil content was recorded to be high (>37%) for P65R, RHA271, PISF-1R, while 234B recorded the highest oil content of 42.8%.

The study revealed sufficient genetic variability both for quantitative and morphological characters among the genotypes, which can be exploited for developing superior hybrids. Different accessions have different promising

traits. Therefore, a gene pool can be generated by crossing the germplasm lines of interest which can be further used as a source material to develop promising inbreds.

References

- Anonymous (2009) Guidelines for the conduct of test for distinctiveness, uniformity and stability (DUS) on Sunflower. *Plant Variety J. India* **3(10)**.
- Burton GW and EM Dewane (1953) Estimating heritability in tall fescue (*Festuca circulinaccae*) from replicated clonal material. *Agrono. J.* **45**: 478–481.

- Gangappa E (1991) Evaluation of sunflower germplasm lines. *Crop Sci.* **15**: 77–78.
- Jayaramaiah H, Virupakshappa K, Jayaram Gowda and Nagaraju (1994) Germplasm utilization and enhancement in sunflower. In: MVR Prasad *et al.* (eds) *Sustainability in Oilseeds*. Indian Society of Oilseeds Research, Hyderabad, pp 113–115.
- Hanson GH, HF Robinson and RE Comstock (1956) Biometrical studies of yield in segregating population of Korean lespedeza, *Agron. J.* **48**: 267–282.
- Johnson HW, HF Robinson and RE Comstock (1955) Estimates of genetic and environmental variability in soybean. *Agron. J.* **47**: 314–318.
- Reddy A Vishnuvardhan and R Nagaraja Reddy (2006) Evaluation and characterization of sunflower, *Helianthus annuus L.* germplasm accessions. *J. Oilseeds Res.* **23**: 161–164.
- Virupakshappa K and SS Sindagi (1987) Characterization, evaluation and utilization of sunflower germplasm accessions. Catalogue, Unit of the Project Coordinator, (Sunflower) GKVK, Bangalore.

Important Crop Germplasm Introduced in Field Crops in India during 2009

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Germplasm Exchange Unit of NBPGR is constantly working towards introduction of promising trait specific germplasm having tolerance/resistance to various biotic and abiotic stresses. India has been benefited tremendously by importing germplasm and varieties and new crops in various field crops from other countries, which have improved productivity and lead to diversification of crop species. Exchange of plant genetic resources (PGR) offers enormous opportunity for addressing these issues and there is continuous need of genetic resources for developing varieties resistant to various pests and diseases and to improve quality, quantity and other value addition traits. During 2009, the Bureau introduced 28,225 accessions in field crops from 43 countries which included trait-specific germplasm in crops namely wheat, barley, rice, maize, soybean, lentil and cotton.

Key Words: Exotic, Field crops, Germplasm, Introduction, Trait

Introduction

National Bureau of Plant Genetic Resources (NBPGR), New Delhi under Indian Council of Agricultural Research and Department of Agricultural Research and Education (DARE) of the Government of India, is playing a very dynamic and key role in overall regulation and management of Plant Genetic Resources (PGR) in India. NBPGR is augmenting the large amount of variability for broadening the genetic base by importing genetic wealth of different crop plants from different ecological areas of the world. These materials have been used all over the country by various institutes in various crop improvement programmes. Field crops are crops (other than fruits or vegetables) grown for agricultural purposes over a wide area and constitute mainly cereals, grain legumes, oilseeds, fibres and forages. In the current scenario, particularly with technological advances in the field of molecular biology and genetic engineering appreciation of the monetary and non-monetary value of genetic resources have led to inequity of historical free flow of germplasm. Access to genetic resources are now based on the principle of 'Sovereign rights of Nations' as promulgated under the legally binding Convention on Biological Diversity (CBD), 1992. The Convention provides for appropriate access to genetic resources and transfer of relevant technologies on mutually agreed terms, subject to prior informed consent. At national level various regulatory mechanisms have been put in place, which govern access to PGR occurring in India (Brahmi, 2009).

Materials and Methods

As per the existing procedure for import of germplasm for research or experimental purposes, the Government of India by enacting the New Seed Development Policy (1989) and Plant Quarantine (Regulation of Import into India) Order 2003 (PQ Order 2003), has made it obligatory for all plant breeders and researchers intending to import seed/planting materials, to fulfill the two mandatory requirements, first the import permit before import of any material and second the phytosanitary certificate from the country of origin. These two documents must accompany every consignment of seed/planting material imported from abroad for research purposes. The provisions of PQ Order are applicable to import of transgenic seeds as well.

The requests received for importing seed material in different field crops for research/experimental purposes in the name of the Director, NBPGR, New Delhi, on a prescribed application form (PQ 08), were facilitated for the issuance of Import permit and import of seed material into the country. Based on survey of literature and other references, applications for procurement of trait-specific germplasm were forwarded to various source institutes. Germplasm Exchange Unit, NBPGR, is continuously making all efforts for introducing diverse PGR by way of bibliography screening of various journals/ periodicals, reports, catalogues, index seminums and online databases. The widely searched websites are detailed at the end for reference.

Results and Discussion

In the year 2009, a total of 429 import permits were issued to public and private organisations for import of germplasm

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of field crops for research purposes. Of the total import permits issued, 47% belonged to private seed companies/sector and 53% to public organizations/institutes. Of the public sector, 39% were issued to applicants from NBPGR, 17% to ICAR institutes, 30% to SAUs, 2% to ICRISAT and 12% to other government organizations. During the period, 28,225 accessions in field crops were introduced from 43 countries which included trait-specific germplasm in crops namely wheat, barley, rice, maize, soybean, lentil and cotton. The trait-specific germplasm and wild

species introduced during 2009 are given in Table 1 and 3 respectively. A total of 170 accessions of transgenic seed material were also introduced as described in Table 2.

The seed material was procured for various biotic and abiotic stresses and value added traits. Important traits which were procured include tolerance to drought, lodging, submergence and heat in paddy, wheat, and barley; biotic stresses primarily resistant to rust, smut, sheath blight, blast, fusarium. *Tungro virus*, mosaic, and nematode in paddy, wheat, barley and soybean. Agronomic traits

Table 1. Trait-specific germplasm introduced in field crops during 2009

Crop/EC No.	Country	Specific traits	Distribution
<i>Hordeum vulgare</i> (Barley) EC657889 EC657888	Canada Canada	High yielding for both grain and biomass, good grain quality for malting, resistant to the spot form of net blotch, surface borne smuts and spot blotch Six rowed, hulled, smooth-awned, spring feed barley, lodging resistance, higher plump seed percentage, good resistance to covered smut and false loose smut	DWR, Karnal
<i>Oryza sativa</i> (Paddy) EC637732–35 EC659913–14	USA	High yielding lines	BASF India Limited
EC637984	Philippines	Improved resistance to sheath blight, bacterial panicle blight, and narrow brown leaf spot Submergence tolerant	NBPGR Regional Station, Cuttack Annamalai University, Annamalainagar
EC638154–161, 166–178	Philippines	Blast resistant	Rice Research Station, Chinsurah, WB
EC639758–797, 820–822	Kenya	Blast resistant	Devgen Seeds and Crop Technology Pvt. Ltd
EC657109–118 EC638162–165	France Philippines	Blast resistant Tungro virus tolerant	TNAU, Coimbatore Rice Research Station, Chinsurah, WB
EC659921	Vietnam	Drought tolerant	NBPGR Regional Station, Cuttack
EC639584–757, 798–819, 823–826	Kenya	Drought tolerant	Devgen Seeds and Crop Technology Pvt. Ltd
<i>Triticum aestivum</i> (Wheat) EC638278 EC638314	USA USA	Alien disomic addition line with resistance to fusarium head blight Winter wheat, white grained, excellent bread baking quality, good pre-harvest sprouting tolerance	DWR, Karnal DWR, Karnal
EC638315 EC641860	USA USA	Good disease resistance and excellent yield potential Var. NEO16432, superior grain yield performance, winter hardy, resistant to fusarium head blight, stem rust, moderately resistant to leaf rust, stripe result and Hessian fly	DWR, Karnal DWR, Karnal
EC665054 EC664600	UK Argentina	Winter type Hard red winter wheat, excellent grain yield potential, resistance to leaf rust, conferred mainly by the Lr 47 gene, and good bread making quality	BCKV, Kalyani DWR, Karnal
<i>Zea mays</i> (Maize) EC659915–17	Nigeria	Lower levels of aflatoxin, good agronomic traits and resistance to important diseases in the lowlands, including southern corn leaf blight, southern corn rust and ear rot	DMR, New Delhi
<i>Glycine max</i> (Soybean) EC638228 EC638229	USA USA	Excellent yield potential. Resistant to soybean mosaic virus, stem canker, bacterial pustule and frog-eye leaf spot Resistant to <i>Soybean mosaic virus</i> and peanut root knot nematode, frog-eye leaf spot and bacterial pustule	NRC Soybean, Indore NRC Soybean, Indore

contd.

Table 1 contd.

Crop/EC No.	Country	Specific traits	Distribution
EC644409	USA	Small seeded, 100 seed weight is 7.3g, resistant to shattering, <i>Soybean mosaic virus</i> , frog eye leaf spot and bacterial pustule	NRC Soybean, Indore
EC644410	USA	Variety N 8001 has purple flowers, gray pubescence, tan pod wall color at maturity, and shiny yellow seeds with imperfect black hila, resistant to <i>Soybean mosaic virus</i> and stem canker	NRC Soybean, Indore
EC656640	USA	High yield potential and broad resistance to soybean cyst nematode, southern root knot nematode and reniform nematode	NRC Soybean, Indore
EC656641	USA	High yield potential, broad resistance to soybean cyst nematode, southern root knot nematode and sudden death syndrome	NRC Soybean, Indore
EC656642	USA	High yield potential, higher seed protein and resistance to root knot nematode	NRC Soybean, Indore
EC656643 <i>Lens culinaris</i> (Lentil)	USA Syria	High yield potential and disease resistant Early maturing	NRC Soybean, Indore ICRISAT Patancheru, AP
EC666214–952, 5016–5052 <i>Gossypium hirsutum</i> (Cotton)	Israel	Restorers and maintainer	Bayer Bioscience Pvt. Ltd, Hyderabad
EC657081–104 <i>Gossypium barbadense</i> (Cotton) EC657105–108	Israel	Restorer lines	Bayer Bioscience Pvt. Ltd, Hyderabad

Table 2. Details of transgenic seed material introduced in field crops

Crop/EC No./ Source Country	Specific Traits	Distribution
<i>Gossypium hirsutum</i> EC654298–303 Texas Tech University USA	Coker 312 with 35S promoter and npt II as selectable marker	Ankur Seeds Pvt. Ltd. Aurangabad
<i>Gossypium hirsutum</i> EC640276–285 Hazera Seeds Limited, Israel	Containing stacked traits bollgard II and Roundup Ready flex (Event MON 88913 X Event MON 15985) gene	Monsanto India Limited, New Delhi
<i>Oryza sativa</i> EC660466–660500 EC636963–637009 Bayer Bio Science, Belgium	Containing <i>Cry 1Ab</i> , <i>Cry1Ca</i> and <i>bar</i> genes	Bayer Bioscience Pvt. Ltd., Gurgaon
<i>Oryza sativa</i> EC659713–721 Huazhong Agricultural University, China	Bt rice lines containing <i>Cry1c</i> , <i>Cry 1Ac</i> and <i>Cry 2A</i> genes to conduct efficacy evaluation against rice stem borers and rice leaf folder	Pioneer Overseas Corporation, Bangalore
<i>Oryza sativa</i> ssp. <i>japonica</i> EC657644–656 Australia	Variety Nipponbare silenced for the rice <i>Myc</i> gene and rice Phytochrome and Flowering Time 1 (<i>PFT1</i>) gene by RNA interference (RNAi) conferring resistance to sheath blight, rice fungal diseases and other pathogens	TNAU, Coimbatore
<i>Oryza sativa</i> EC660501–505 Bayer Crop Science USA	Transgenic rice of event LLRICE62 containing <i>bar</i> gene	Bayer Bioscience Pvt. Ltd, Gurgaon
<i>Zea mays</i> EC643857–62 Pioneer Hi Bred, USA	Transgenic seed material expressing stacked event IARI 1507 (<i>cry IF & PAT</i> gene) and NK 603 (<i>CP4EPSPS</i> gene)	Pioneer Overseas Corporation, Bangalore
<i>Zea mays</i> EC648319, EC661295–96 Syngenta, Philippines	Seeds containing <i>Cry 1Ab</i> gene (Bt 11event)	Syngenta India Limited,
<i>Zea mays</i> EC664605 Syngenta Agro SA, Argentina	Containing <i>Cry1Ab</i> gene (Bt 11 event) and <i>MEPSPS</i> gene GA21 event	Syngenta India Ltd, Pune

Table 3. Wild species imported in different field crops

Genus (Country)	Species	Distribution
<i>Aegilops</i> (USA)	<i>A. comos</i> , <i>A. geniculata</i> , <i>A. markgrafii</i> , <i>A. neglectal</i> , <i>A. peregrina</i> , <i>A. searsii</i> , <i>A. speltoide</i> , <i>A. tauschii</i> , <i>A. triuncialis</i> , <i>A. umbellulata</i>	Bioinformatics Centre School of agricultural Biotechnology, PAU, Ludhiana
<i>Brassica</i> (Japan)	<i>B. barrellieri</i> , <i>B. cretica</i> , <i>B. elongata</i> , <i>B. gravinae</i> , <i>B. maurorum</i> , <i>B. souliei</i>	Zakir Husain College, New Delhi
<i>Bunium</i> (USA)	<i>B. persicum</i>	SKUAST (S), J&K
<i>Cicer</i> (Syria)	<i>C. echinospermum</i> , <i>C. reticulatum</i>	Department of Botany, University of Delhi
<i>Diploaxis</i> (Japan)	<i>D. assurgens</i> , <i>D. catholica</i> , <i>D. eruroides</i> , <i>D. virgata</i>	Zakir Husain College, New Delhi
<i>Eucalyptus</i> (Australia)	<i>E. camaldulensis</i> ig. <i>camaltereti</i> , <i>E. cameldulensis</i> var. <i>cameldulensis</i> , <i>E. gomphocephala</i> , <i>E. pellita</i> , <i>E. pellita x brassiana</i> , <i>E. smithii</i>	Tamil Nadu Newsprint and Papers Limited, Karur, Kagithapuram, Tamil Nadu
<i>Helianthus</i> (USA)	<i>H. anomalus</i> , <i>H. atrorubens</i> , <i>H. bolanderi</i> , <i>H. debilis</i> subsp. <i>cucumerifolius</i> , <i>H. debilis</i> subsp. <i>debilis</i> , <i>H. debilis</i> subsp. <i>silvestris</i> , <i>H. debilis</i> subsp. <i>tardiflorus</i> , <i>H. debilis</i> subsp. <i>vestitus</i> , <i>H. decapetalus</i> , <i>H. deserticola</i> , <i>H. exilis</i> , <i>H. giganteus</i> , <i>H. hybrid</i> , <i>H. maximilianii</i> , <i>H. mollis</i> , <i>H. niveus</i> subsp. <i>canescens</i> , <i>H. niveus</i> subsp. <i>tephrodes</i> , <i>H. occidentalis</i> subsp. <i>plantagineus</i> , <i>H. pauciflorus</i> , <i>H. pauciflorus</i> subsp. <i>subrhomboides</i> , <i>H. petiolaris</i> subsp. <i>petiolaris</i> , <i>H. praecox</i> , <i>praecox</i> subsp. <i>hirtus</i> , <i>H. praecox</i> subsp. <i>praecox</i> , <i>H. praecox</i> subsp. <i>runyonii</i> , <i>H. strumosus</i>	Directorate of Oilseeds Research, Rajendra Nagar, Hyderabad
<i>Oryza</i> (Philippines)	<i>O. alta</i> , <i>O. australiensis</i> , <i>O. barthii</i> , <i>O. glumaepatula</i> , <i>O. grandiglumis</i> , <i>O. granulata</i> , <i>O. latifolia</i> , <i>O. atifolia</i> , <i>O. longiglumis</i> , <i>O. longistaminata</i> , <i>O. meridionalis</i> , <i>O. officinalis</i> , <i>O. minuta</i> , <i>O. nivara</i> , <i>O. punctata</i> , <i>O. rhizomatis</i> , <i>O. rufipogon</i>	NDUAT, Faizabad; Ankur Seeds, (MS); ANGRAU, Hyderabad
<i>Triticum</i> (Mexico)	<i>T. monococcum</i> , <i>T. turgidum</i> subsp. <i>dicoccum</i>	PAU, Ludhiana
<i>Vicia</i> (Syria)	<i>V. hyaeniscyamus</i> , <i>V. hybrida</i> , <i>V. johannis</i> , <i>V. johannis</i> var. <i>johannis</i> , <i>V. kalakhensis</i> , <i>V. melanops</i> , <i>V. narbonensis</i> , <i>V. serratifolia</i>	Botany Department, University of Delhi

include high yielding lines, good grain quality, higher plump seed percentage, early maturing types in paddy, wheat, barley, maize, soybean and lentil.

References

- Brahmi P, V Tyagi and A Lal (2009) Regulatory mechanisms for access to plant genetic resources In: RK Tyagi et al. (eds), Souvenir and Abstracts. *National Symposium on Recent Global Developments in the Management of Plant Genetic Resources*. Indian Society of Plant Genetic Resources Publication, New Delhi, 97 p.
- Plant Quarantine (Regulation of Import into India) Order (2003) The Gazette of India, Extraordinary, Part-II-Section 3-Subsection (ii) www.plantquarantineindia.org
- Singh RV, D Chand and V Tyagi (2001) Exchange procedure of transgenic plants. In: GJ Randhawa, RK Khetarpal, RK Tyagi and BS Dhillon (eds) *Transgenic Crops and Biosafety Concerns*. NBPGR New Delhi, pp 96–100.
- <http://www.ars-grin.gov/npgs/searchgrin.html>
- http://www.bioversityinternational.org/nc/scientific_information/information_sources/germplasm_databases/list_of_germplasm_databases.html
- <http://eurisco.ecpgr.org>
- <http://www.ngb.se/Material/>
- <http://www.ngb.se/sadc/Material/accsadc.html>
- <http://www.singer.cgiar.org/>

Developing Descriptors for Dioecious *Momordica* Species for Germplasm Characterization and Evaluation

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Momordica L. is a genus of tropical wild and underutilized vegetables of medicinal importance. The descriptions of morphological and agronomic traits would unravel their potential for successful utilization. A set of highly discriminating descriptors and descriptor states for the dioecious *Momordica* species of India comprising *M. dioica*, *M. sahyadrica*, *M. subangulata* ssp. *renigera* and *M. cochinchinensis* is proposed. The descriptors are proposed based on a study of morphological variability in over 667 herbarium specimens and 164 live collections of India.

Key Words: Characterization, Descriptors, Evaluation, Genetic diversity, *Momordica* L., Spine gourd, Sweet gourd, Teasle gourd

Introduction

The importance of germplasm as a basic tool for crop improvement is well recognized. Wild relatives and progenitors of cultivated plants together with semi-domesticates represent a strategic group of germplasm collections. As the genetic base of modern varieties is narrow and variability fast eroding, introgression of genes from wild species can substantially influence the breeding progress. Thus, the knowledge of their taxonomic range, morphological similarities, crossing ability and reaction to various biotic and abiotic stress are not only important from a botanical view point, but also to accelerate and increase their potential for utilization (Dolezalova *et al.*, 2003). Identifying a limited set of accessions likely to be of most interest to specific users from a large collection necessitates the use of a full-fledged descriptor as a tool to provide a generalized search strategy. It helps to differentiate between accessions and to describe the variability in characters of interest. Preliminary characterization and evaluation are pre-requisites for successful utilization of plant genetic resources.

The future strategies for horticulture and genetic resources management should focus on not only the already commercialized crop species but also on many relatively neglected minor vegetables that have received very little attention hitherto. In fact, these high quality minor crops are a better route to food security than many of today's tailor made varieties, which are low in vitamins and minerals (Padulosi *et al.*, 2001). It is rather ironic that

malnutrition and under nutrition are more prevalent in the diversity-rich zones where plenty of wild edible fruits and leafy green vegetables with rich nutritive potential are available (Pradheep *et al.*, 2003). These vegetables and fruits still have large genetic diversity, which should be collected, characterized, conserved and utilized. These crops can play an important role in the diversification of agriculture and production of eco friendly-organically grown vegetables. By working on the genetic resources of these potential taxa, wild foods can be made more popular and can also develop new crop domesticates (Rathore *et al.*, 2005).

Momordica L.: Taxonomy and Diversity

Momordica L. is a genus of tropical wild and under-utilized vegetables native to Asia and Africa. Fruits are rich in vitamins and minerals and are ascribed with many medicinal properties by indigenous communities. The genus *Momordica*, even though has high potential as nutraceutical vegetable, it remains under-utilized (with the exception of bitter gourd) as no concerted research and development efforts have been made to promote them as cultivated crops. Of about 40 *Momordica* species, there are approximately less than five species represented in world germplasm collections (Bettencourt and Konopka, 1990). The purpose of this article is to present a proposal of detailed descriptors for the dioecious, perennial *Momordica* species comprising sweet, spine and teasle gourd of South-East Asia.

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Descriptors for Wild Dioecious

Momordica Species

As a first step to study of genetic resources of these under-utilized vegetables, a database of herbarium and germplasm holdings was prepared. The observed variability in national collections (herbarium specimens and germplasm collections comprising of *M. dioica* Roxb., *M. sahyadrica* Joseph & Antony and *M. subangulata* Blume ssp. *renigera* WJJ de Wilde and *M. cochinchinensis* [Lour.] Spreng) together with published descriptions of these taxa in various flora were used as a source for preparation of descriptor and descriptor states for wild *Momordica*. The taxonomic validity of the entities is as per the recent

taxonomic revisions (Joseph, 2005; Joseph and Antony, 2006; 2007). The proposed descriptors and descriptor states are presented according to guidelines and definitions provided by IPGRI (2003, 2005 and 2007) and National Institute of Agrobiological Resources, Ibaraki, Japan (Nagamine and Takeda, 1999). The botanical terminology regarding plant morphology and elaboration of figures is based on Jackson (1965), Robinson and Walters (1997) and Nayar and More (1998).

The proposed list of descriptors and descriptor states for the wild dioecious *Momordica* species is given in Tables 1 and 2. The set provides tool for species determination within the genus *Momordica* and

Table 1. Descriptors for characterization

Descriptor number	Descriptor name	Descriptor state (with code)
1. Vegetative characters		
1.1. Tuber		
(Specify age of tuber - only seedling tuber to be observed)		
1.1.1	Tuber (tap root) shape	1 conical 2 napiform 3 round bulged 4 fusiform 5 other (specify)
1.1.2	Protrusion of lenticels on tuber surface	1 weak 2 medium 3 strong
1.1.3	Tuber branching	1 absent 2 present
1.1.4	Occurrence of adventitious tuber	1 absent 2 present
1.1.5	Life span of tuber	1 ~5 years 2 < 5 years 3 > 5 years
1.1.6	Surface colour of tuber	1 light brown 2 dark brown 3 other (specify)
1.1.7	Inside colour of tuber	1 pale yellow 2 white 3 other (specify)
1.2. Seedling		
(Except 1.2.1, all other traits may be recorded in tuber sprouts/ratoon crop also)		
1.2.1	Germination	1 epigeal 2 hypogeal
1.2.2	Seedling vigour (visual score at 3-5 leaf stage)	1 low 2 medium 3 high
1.2.3	Primary leaf size	1 minute 2 small 3 medium 4 large
1.2.4	Primary leaf shape	specify
1.2.5	Primary leaf margin	1 smooth 2 wavy 3 dentate 4 lobed
1.3. Plant		
1.3.1	Growth habit	1 less viny 2 moderately viny 3 highly viny

contd.

Table 1 contd.

Descriptor number	Descriptor name	Descriptor state (with code)
1.3.2	Vine tip pubescence	1 glabrous 2 scarcely pubescent 3 pubescent
1.3.3	Stem nodal region - shape	1 quadrangular 2 round
1.3.4	Leaf shape (to be recorded at flowering stage)	
1.3.5	Leaf margin	1 entire 2 serrate 3 dentate 4 wavy 5 other (specify)
1.3.6	Leaf pubescence	1 glabrous 2 sparse 3 medium 4 dense 5 wooly 6 other (specify)
1.3.7	Lamina - gland dottedness (at 10X magnification) on lower surface	1 sparse 2 dense 3 medium
1.3.8	Leaf colour (fresh leaf)	1 light green 2 green 3 dark green
1.3.9	Leaf venation	1 fine network (aeroles) 2 spaced network 3 intermediate
1.3.10	Leaf lobing (1 st flowering node)	1 entire 2 lobed 3 mixed occurrence in same plant 4 other (specify)
1.3.11	Extent of lobing	1 shallowly lobed 2 broadly angled margins 3 deeply lobed and sub lobed
1.3.12	Lobe tip	1 acute 2 acuminate 3 ovate 4 obovate 5 other (specify)
1.3.13	Leaf odour	1 mild 2 not foetid 3 foetid (intense)
1.3.14	Leaf thickness	1 thin 2 medium 3 thick
1.3.15	Extent of leaf margin dentation	1 close 2 spaced 3 remote
1.3.16	Petiole-Lamina juncture shape	1 subangulate 2 round 3 cordate 4 other (specify)
1.3.17	Petiole-umbilical glands (viewed with naked eye)	1 absent 2 present
1.3.18	Tendrill robustness	1 robust 2 fragile 3 medium
1.3.19	Tendrill length (when uncoiled)	1 short (5-10 cm) 2 medium (11-20 cm) 3 very long (21-30 cm)

contd.

Table 1 contd.

Descriptor number	Descriptor name	Descriptor state (with code)
2. Inflorescence seed and fruit, 2.1. Male inflorescence and flower 2.1.1 Male inflorescence - nature of branching		1 solitary 2 psuedoraceme 3 loose fascicle 4 truly branched (above the bract)
2.1.2	Bract - position on peduncle	1 at base 2 midway 3 at tip
2.1.3	Male bract shape	1 scar like 2 small foliar 3 reniform 4 fan shaped (cleft) 5 hooded 6 frilled 7 any other (specify)
2.1.4	Male bract size	1 minute 2 small 3 medium 4 large
2.1.5	Male bract pubescence	1 absent 2 sparse 3 stiff short hairy-conspicuous
2.1.6	Male bract colour	1 light green 2 dark green 3 whitish green
2.1.7	Male bract tip	1 colored black-purple 2 no colour distinction
2.1.8	Flower colour (petal colour at full bloom). Use RHS colour charts (1995)	1 lemon yellow 2 dull yellow 3 bright yellow 4 creamish yellow 5 whitish yellow 6 any other (specify)
2.1.9	Flower size	1 small 2 medium 3 large
2.1.10	Male flower receptacle size	1 small 2 medium 3 large
2.1.11	Floral scent	1 odourless 2 faint 3 detectable from 1m distance
2.1.12	Floral odour	1 musky 2 other (specify)
2.1.13	Nectar guides (on petals)	1 absent 2 present
2.1.14	Nature of nectar guides	1 purple blotch on 3 inner petals 2 on all 5 petals 3 light greenish yellow region on base of petals 4 other (specify)
2.1.15	Male flower calyx shape	1 linear acute 2 round oval 3 broad elliptic 4 ovate oblong 5 other (specify)

contd.

Table 1 contd.

Descriptor number	Descriptor name	Descriptor state (with code)
2.1.16	Calyx cup colouration	1 non pigmented 2 pigmented purple-blackish 3 light creamish yellow 4 greenish yellow 5 blackish
2.1.17	Corolla tip	1 acute 2 broad ovate 3 round 4 other (specify)
2.1.18	Aestivation	1 just touching each other 2 overlapping 3 spaced 4 other (specify)
2.1.19	Petal pubescence	1 glabrous 2 glandular hairy
2.1.20	Petal shape	1 ovate 2 linear acute 3 rhomboid 4 other (specify)
2.1.21	Petal spur (at base)= scale	1 absent 2 present, but inconspicuous 3 prominent
2.1.22	Petal venation	1 less prominent 2 medium 3 high (embossed)
2.1.23	Pollen dust colour	1 yellow 2 orange 3 brown
2.1.24	Pollen abundance	1 scanty 2 medium 3 abundant
2.1.25	Male flower anthesis	1 early morning 2 evening
2.1.25	Insect visitors observed (list out)	
2.2. Female inflorescence and flower		
2.2.1	Female flower bract size	1 minute (scar like) 2 medium large 3 large
2.2.2	Female flower bract position	1 just below gynoeceium 2 midway on pedicel 3 near axis
2.2.3	Gynoeceium	1 small 2 medium 3 large
2.2.4	Ovary surface	1 smooth 2 warty 3 tubercled 4 echinate (softly) 5 ridged 6 other (specify)
2.3. Fruit		
2.3.1	Fruit size	1 small 2 medium 3 large
2.3.2	Immature fruit colour	1 whitish green 2 light green 3 dark green
2.3.3	Fruit surface echination	1 absent=smooth 2 mild-sparcely echinate 3 densely echinate

contd.

Table 1 contd.

Descriptor number	Descriptor name	Descriptor state (with code)
2.3.4	Fruit surface bumps & ridges	1 no ridges 2 obscurely ridged (feeble) 3 clearly ridged 4 ridged at base only 5 ridged at base and top 6 other (specify)
2.3.5	Fruit C.S (mature fruit at equatorial point)	1 uniformly soft echinate 2 clear cut ridges and echination 3 ridges faint but echinate 4 other (specify)
2.3.6	Fruit shape	1 round oval 2 winged 3 doom shaped 4 ellipsoid oblong 5 top shaped 6 others (specify with drawing)
2.3.7	Fruit pericarp ripening	1 slow 2 sudden
2.3.8	Fruit (blossom end) rostration	1 faint 2 medium 3 appreciable length
2.3.9	Fruit blossom end surface murication	1 ridged and flat 2 ridged and echinate 3 uniformly echinate 4 uniformly smooth 5 other (specify)
2.3.10	Calyx persistence	1 caducous 2 semi persistent 3 persistent
2.3.11	Fruit bitterness	1 not bitter 2 slightly bitter 3 very bitter
2.4. Seed		
2.4.1	Seed aril colour (at ripening)	1 yellow 2 orange 3 scarlet 4 blood red
2.4.2	Seed shape	1 oval 2 round 3 globular 4 stellate 5 squarish 6 cog-wheel 7 rectangular 8 other (specify)
2.4.3	Seed sculpturing	1 absent 2 present
2.4.4	Extent of sculpturing	1 faint 2 medium 3 filigree type 4 pitted and ridged 5 other (specify)
2.4.5	Seed ornamentation	1 absent 2 present
2.4.6	Type of ornamentation	1 golden lines on black seed coat 2 other (specify)
2.4.7	Seed sides (margins)	1 smooth 2 wavy = bitten

Table 2. Descriptors for evaluation

Descriptor no.	Descriptor name	Descriptor state with code
3. Seedling		
3.1	Days to emergence (specify after ripening period)	
3.2	Germination percentage	
4. Plant		
4.1. Stem		
4.1.1	Vine length (measured at senescence) [m]	
4.2. Leaf		
4.2.1	First flowering node leaf size (L x B)	
4.2.2	Petiole length (avg. of 5 leaves at flowering node) [cm]	
4. 3. Inflorescence		
4.3.1. Male flower		
4.3.1.1	Days to first male flower opening (specify seed or tuber origin)	
4.3.1.2	Days to 50% male flowering	
4.3.1.3	Male flower prolificacy - No. of flowers/plant/day (avg. count of 5 days)	
4.3.1.4	Male bract size (L x B - avg. of 5 flowers)	
4.3.1.5	Male Peduncle length (axis to base of bract) [cm]	
4.3.1.6	Male pedicel length (bract to calyx base) [cm]	
4.3.1.7	Male flower diameter (average of 5 flowers) [cm]	
4.3.2. Female flower		
4.3.2.1	Days to first female flower opening	
4.3.2.2	Days to 50% female flowering	
4.3.2.3	Female flower prolificacy (avg. count of 5 days)	
4.3.2.4	Female bract size (L x B - avg. of 5 flowers)	
4.3.2.5	Female peduncle length (axis to bract base) [cm]	
4.3.2.6	Female pedicel length (bract to gynoecium) [cm]	
4.3.2.7	Female flower diameter (avg. of 5 flowers) [cm]	
4.4. Fruit		
4.4.1	Days to first fruit maturity (flowering to fruit-split)	
4.4.2	Fruit length (including rostration) [cm]	
4.4.3	Fruit circumference (around fruit) [cm]	
4.4.4	Fruit diameter [cm] (measured in C.S of fruit)	
4.4.5	Cavity size (measured at widest point in fruit CS) [cm]	
4.4.6	Flesh thickness (measured from C.S of ripe fruit) [cm]	
4.4.7	Single fruit weight (average of 5 fruits) [g]	
4.4.8	No. of fruits/plant/season	
4.4.9	Seediness (No. of seeds/fruit, avg. of 5 fruits)	
4.4.10	Fruit stalk length (avg. of 5 fruits) [cm]	
4.4.11	Fruiting period (No. of days from first to last female flower opening)	
4.5. Seed		
4.5.1	100-seed weight [g]	
4.5.2	Seed storability (viability under normal storage)	1 6 months 2 1 year 3 above one year
4.6. Biotic and abiotic stress susceptibility		
4.6.1	Biotic stress susceptibility (on a 0-9 scale)	0 no incidence 1 very low 3 low 5 intermediate 7 high 9 very high
4.6.1.1	Witches broom /little leaf disease	
4.6.1.2	Seedling damping off (<i>Pythium affanidermaticum</i>)	
4.6.1.3	Fruit black rot (<i>Dydimella</i> sp.)	
4.6.1.4	Powdery mildew (<i>Oidium</i> spp.)	
4.6.1.5	Anthracnose (<i>Colletotricum lagenerium</i>)	
4.6.1.6	Root knot nematode (<i>Meladogyne incognita</i>)	
4.6.1.7	Fruit fly (<i>Bactocera cucurbitae</i>)	
4.6.1.8	Lady bird beetle (<i>Epilacna septima</i>)	
4.6.1.9	Vine gall fly (<i>Lasioplera falcata</i>)	

contd.

Table 2 contd.

Descriptor no.	Descriptor name	Descriptor state with code
4.6.1.10	Pumpkin caterpillar (<i>Margaronia indica</i>)	
4.6.1.11	Leaf minor (<i>Liriomyza trifoli</i>)	
4.6.1.12	Leaf hopper (<i>Hishimonus phycitis</i>)	
4.6.1.13	Red Pumpkin beetle (<i>Aulocophora fevicolii</i>)	
4.6.2	Abiotic stress susceptibility (indicator- yield performance)	
4.6.2.1	Susceptibility to shade	1 low 2 medium 3 high
4.7	Biochemical evaluation of (a) Tender fruits (b) Green leaves/tips	
4.7.1	Moisture	
4.7.2	Carbohydrates	
4.7.3	Proteins	
4.7.4	Fat	
4.7.5	Calcium	
4.7.6	Phosphorus	
4.7.7	Iron	
4.7.8	Magnesium	
4.7.9	Vitamin A	
4.7.10	Antioxidants	
4.7.11	Flavonoids	
4.7.12	Dietary fibre	
5. Evaluation for value addition/quality traits		
5.1	Fruit tenderness index (from pollination to seediness calculated as days up to which a sharp knife easily passes through)	
5.2	Suitability for vegetable preparation (based on consumer preference after organoleptic tests)	1 excellent 2 good 3 average 4 poor
5.3	Suitability of ripe fruits as vegetable salads (based on organoleptic tests and visual appeal)	1 excellent 2 high 3 medium 4 low
5.4	Usefulness as pot herb and leafy vegetable	1 excellent 2 good 3 average 4 poor
5.5	Fruit shelf life under room temperature	1 high (1 week) 2 medium (3 days) 3 low (1day)
5.6	Fruit shelf life under refrigeration (vegetable stage)	1 high (2 weeks) 2 medium (1 week) 3 low (< 1 week)

for characterization of infra-specific morphological variability. Morphological variability encountered at seedling, vegetative, flowering and fruiting stages of the plant has been included for preliminary characterization. Descriptor for evaluation consists of traits of crop husbandry value and response to biotic and abiotic stresses. Exploitation of some characters for inter- and infra-specific categorization is based on the personal experience of the authors at both levels of variation. Passport data descriptors, handling site descriptor and environmental descriptors are not provided for sake of brevity, which may be followed, as it is common for all cucurbits. Present treatment of extent of

variability for some traits such as leaf shape, fruit shape etc. are not exhaustive as numerous types difficult to describe in technical terms, but easy to depict through illustrations have been found in the existing collection. Further collection and study of variability across the country may lead to spotting of more diverse types and accordingly the descriptor states may need elaboration and modification in future.

There is no published descriptor for bitter gourd, teasle gourd, sweet gourd or spine gourd or any *Momordica* species by IPGRI. The lone reference to a descriptor to *Momordica* was seen in NATP Minimal Descriptor for

Vegetable Crops (Anon., 2001) where bitter gourd, sweet gourd and spine gourd are treated together. They, being evolutionarily divergent groups (bitter gourd on the one hand, sweet gourd and spine gourd on the other hand), should be treated separately as they vary for more than 75% characters by virtue of their breeding behaviour and growth forms (Joseph, 2005).

A descriptor based on experience of dealing with four species of less cultivated or wild gathered dioecious, perennial species of *Momordica* from India and South-East Asia is presented here. A critical review of the user community is invited to improve and revise this descriptor for the benefit of vegetable researchers, dealing with crop improvement of sweet, spine and teasle gourd.

References

- Anonymous (2001) *NATP Minimal Descriptors for Vegetable Crops*. National Bureau of Plant Genetic Resources, New Delhi, pp 61–66.
- Bettencourt E and J Konopka (1990) *Directory of Crop Germplasm Collections*. 4. Vegetables, International Bureau of Plant Genetic Resources, Rome, 147 p.
- Dolezalova I, E Kristkova, A Lebeda, V Vinter, D Astley and IW Boukema (2003) Basic morphological descriptors for genetic resources of wild *Lactuca* spp. *Plant Genet. Resour. Newsl.* **134**: 1–9.
- IPGRI (2003) *Descriptors for Melon (Cucumis melo L.)*. International Plant Genetic Resources Institute, Rome, Italy (<http://www.ipgri.cgiar.org/publications/pubselect.asp>).
- IPGRI (2005) *Minimum Descriptor Lists for Cucurbita, Cucumber, Melon and Watermelon*. International Plant Genetic Resources Institute, Rome, Italy.
- IPGRI (Bioversity International) (2007) *Guidelines for the Development of Crop Descriptor Lists*. Bioversity Technical Bulletin Series. Bioversity International, Rome, Italy (<http://www.bioversityinternational.org>).
- Jackson BD (1965) *A Glossary of Botanical Terms with their Definition and Accent* (4th edition), Hafner Publishing Co., London.
- Joseph John K (2005) *Studies on Ecogeography and Genetic Diversity of the Genus Momordica L. in India*. Ph.D. Thesis, Mahatma Gandhi University, Kottayam, Kerala, India, 315 p.
- Joseph John K, VT Antony and YC Roy (2006) On the occurrence, distribution and taxonomy of *Momordica subangulata* Blume ssp. *renigera* (G. Don) de Wilde in India. *Genet. Resour. Crop Evol.* **54**(6): 1327–1332.
- Joseph John K and VT Antony (2007) *Momordica sahyadrica* sp.nov. (Cucurbitaceae), an endemic species of Western Ghats of India. *Nord. J. Bot.* **24**(5): 539–542.
- Nagamine T and H Takeda (1999) *The Descriptors for Characterization and Evaluation in Plant Genetic Resources* (Vol. 2), National Institute of Agrobiological Resources, Ibaraki, Japan.
- Nayar N.M and TA More (1998) *Cucurbits*, Science Publishers, Enfield, NH, USA.
- Padulosi S, T Hodgkin, JT Williams and N Haq (2001) *Underutilized Crops: Trends, Challenges and Opportunities in the 21st century*, International Plant Genetic Resources Institute, 222 p.
- Pradheep K, SM Gomez and A Kalamani (2003) Possibilities of broadening plant wealth of horticulture from existing flora of Tamil Nadu, India: an overview. *Asian J. Plant Sci.* **2**(9): 719–730.
- Rathore DS, U Srivastava and BS Dhillon (2005) *Management of Plant Genetic Resources of Horticultural Crops: Issues and Strategies* In: BS Dhillon, RK Tyagi, S Saxena, GJ Ramdhawa (eds) *Plant Genetic Resources: Horticultural Crops*, Narosa Publishing House Pvt. Limited, New Delhi, India, pp 1–18.
- Robinson RW and DS Decker-Walters (1997) *Cucurbits*. CAB International, London.

Characterization of an Indian Mustard (*Brassica juncea*) Indigenous Germplasm Line Bio-YSR for White Rust Resistance

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White rust, caused by *Albugo candida* is one of the major diseases of Indian mustard in India, causing heavy yield losses ranging from 17 to 34%. The breakdown of resistance is the prime concern to search for new genes to develop a durable resistance against white rust in mustard. A stable donor Bio-YSR (INGR No. 04099) has been developed indigenously, which need genetical characterization. Bio-YSR, the resistant donor germplasm line was crossed with popular, widely grown and high yielding susceptible cultivars Varuna and Bio-902 (Pusa Jai Kisan), to study the mode of inheritance of white rust resistance gene. The F₁ plants of these crosses were resistant indicating the dominant nature of the resistance. The segregation pattern in F₂ of the crosses fits well in 3 resistant (R): 1 susceptible (S) ratio indicating Bio-YSR carries a single dominant gene. This monogenic dominant nature was confirmed from the results of backcross populations as well. Hence, the major gene governing white rust resistance in the indigenous germplasm line Bio-YSR, will be of immense use in breeding for durable resistance by the way of diversification of resistant sources and gene pyramiding.

Key Words: Indian mustard, Indigenous germplasm, Inheritance, Resistance, White rust

Introduction

White rust, caused by *Albugo candida*, is a common disease of many economically important cruciferous vegetables and oilseed crops. It is most wide-spread and highly destructive to *Brassica juncea*, reported to cause 17–34 % yield losses (Kolte, 1985). The Indian genotypes are highly susceptible to white rust (Li *et al.*, 2008) and an appreciable loss in seed yield has been reported to the extent of 50% under late sown conditions (Saharan *et al.*, 1984). Amongst the four oleiferous *Brassica spp.* grown in India, *B. juncea* is the predominant one and occupies more than 80% of the total area under rapeseed-mustard. Though, *B. juncea* is hardy in comparison to other oilseed Brassicas, yet it is highly susceptible to white rust. This disease is recurring every season with different degrees of intensity at different stages of crop growth, causing significant reduction in yield. The disease is characterized by the formation of white pustules on the cotyledons, leaves, stems and inflorescence. Systemically infected inflorescence becomes hypertrophied, causing the characteristic staghead galls (Verma and Petrie, 1980). It has been estimated that combined infection of leaf and inflorescence causes yield losses to the extent of 62.7%, the loss being more severe (89.8%) as a result of staghead formation in the susceptible cultivars (Lakra and Saharan, 1989). The most cost-effective way of protecting

mustard plants from white rust is through introgression of genetic resistance. Identification of different sources of resistance to white rust is an important prerequisite in managing this disease by means of effective and durable genetic resistance.

Genetic analysis of available white rust resistance has elucidated a digenic mode of inheritance with duplicate gene action in *B. napus* (Fan *et al.*, 1983; Verma and Bhowmik, 1989) and monogenic dominant resistance in *B. juncea* (Tiwari *et al.*, 1988; Bansal *et al.*, 1999; Sachan *et al.*, 2000; Chauhan and Sharma, 2001) as well as in *B. rapa*, *B. carinata* and *B. nigra* (Delwiche and Williams, 1974; 1981). The earlier studies were based on the exotic sources of white rust resistance. A stable donor Bio-YSR has been developed indigenously, and the genetics of this resistance source has not been studied. In comparison to the different exotic sources taken for genetic studies and used in white rust resistance breeding programme, Bio-YSR is agronomically superior and also stable under Indian conditions (Katiyar and Chopra, 1990).

Dynamic changes in race composition of the pathogen have often resulted in short-lived efficiency of host resistance in the improved varieties which necessitates identification and characterization of new sources of white rust resistance. Hence, the present study was undertaken to investigate the nature and inheritance of white rust

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resistance in an indigenous germplasm for their use in future crop improvement programme for breeding for durable resistance for this disease.

Materials and Methods

Development of experimental material

The experimental material used in the study includes two popular, widely grown, high yielding cultivars viz., Varuna and Bio-902 (Pusa Jai Kisan) of *B. juncea*, which are highly susceptible to white rust. The resistant source used was Bio-YSR, a somaclone of *B. juncea* developed by NRCPB, IARI, New Delhi, and registered with NBPGR (INGR No. 04099). Bio-YSR, the resistant donor of *B. juncea*, was crossed with susceptible cultivars Varuna and Bio-902, during rabi 2006–07 at IARI Experimental Farm, New Delhi to study the mode of inheritance of white rust resistance gene. The F_1 s, thus, obtained were advanced during rabi 2007–08 to derive F_2 population by selfing, and backcrossed to both the parents to obtain Backcross1(B_1) (with susceptible parent, $F_1 \times P_1$) and Backcross2(B_2) (with resistant parent, $F_1 \times P_2$) generations for studying the genetics of white rust resistance.

Inoculum preparation and incubation conditions

The inoculum was prepared by collecting the white rust zoosporangia from heavily infected fresh leaves of the susceptible *B. juncea* cultivar Varuna and Pusa Bold maintained in the National Phytotron Facility, IARI, New Delhi. The zoosporangia were collected in sterile distilled water and allowed to germinate for 4 hours at 8°C. The zoospore suspension was sprayed on the foliage with a hand atomizer until runoff. Dark conditions were maintained for 24 hrs after the spray for development of the disease by covering the entire plot with light blocking PVC sheet. To maintain high humidity, which is congenial for the disease development, experimental plot was irrigated frequently and water was kept standing in the channels surrounding the plots during the period of inoculation.

Phenotyping for white rust resistance

The parents, F_1 , B_1 , B_2 and F_2 generations of these crosses were grown and their white rust reaction was observed during Rabi, 2008–09. Two rows of parents and F_1 , five rows of B_1 and B_2 and ten rows of F_2 were planted with a spacing of 30 cm between rows, and 10 cm between plants within row. Recommended package of practices were followed to raise a good crop. The plants were rated for white rust reaction two weeks after inoculation. For recording the observations for white rust a minimum

of 20 plants each from P_1 , P_2 , F_1 , 100 plants in B_1 and B_2 and 250 plants in F_2 were taken. The plants on which observations for white rust were recorded, were tagged from seedling stage and scoring was done upto the stage of staghead formation. The disease scoring was done as per the method described by Fox and Williams (1984). Chi-square (χ^2) test was employed to test goodness of fit of observed and expected frequency in segregating generations.

Results and Discussion

The results of the present study are based on the observations recorded and analysis carried out for inheritance of white rust resistance in Parents, F_1 , B_1 , B_2 and F_2 generations of the two crosses involving Bio-YSR as a white rust resistance donor.

Mode of inheritance

Disease scores of parental lines indicated that the indigenous germplasm line Bio-YSR was resistant to local *A. candida* population. The observations on P_1 , P_2 , F_1 , B_1 , B_2 , and F_2 generations of these crosses are given in the Table 1. The F_1 plants of these crosses Varuna $\times$ Bio-YSR and Bio-902 $\times$ Bio-YSR were resistant to white rust indicating the dominant nature of the resistance.

The segregation pattern in F_2 of the two crosses fits well in 3 resistant (R):1 susceptible (S) ratio ($\chi^2 = 1.58$, and 0.79, respectively) (Table 1) indicating that the donor carries a single dominant gene. This monogenic dominant nature of the resistance gene to white rust was confirmed from the results of backcross populations as well. In the backcrosses 2 (B_2) with the resistant parent, all the plants were resistant, whereas, in the backcrosses1 (B_1) with susceptible parents, test cross progenies segregated in 1R:1S ratio. These results of monogenic dominant nature of resistance to white rust are in agreement with the earlier findings (Tiwari *et al.*, 1988; Bansal *et al.*, 1999; Sachan *et al.*, 2000; Chauhan and Sharma, 2001).

The study revealed that the resistance is monogenic in the indigenous resistant source Bio-YSR. Hence, the major gene governing white rust resistance could be easily transferred to the well adapted, high yielding but susceptible genotypes by backcross breeding. The presence of monogenic resistance gene in the indigenous source Bio-YSR will be very useful in breeding for durable resistance by the diversification of resistant sources and gene pyramiding. However, more detailed studies would have to be conducted to analyse the virulence spectra and diversity in the pathogen population through controlled experiments.

Table 1. Segregation pattern for white rust resistance in the crosses between Bio-YSR and susceptible genotypes

Cross	Generations	Total plants	Observed		Expected ratio	Expected		χ^2	P value
			Resi.	Susc.		Resi.	Susc.		
Varuna x Bio-YSR	P ₁	27	0	27	—	0	27	—	—
	P ₂	21	21	0	—	21	0	—	—
	F ₁	23	23	0	—	23	0	—	—
	F ₂	257	184	73	3:1	192.75	64.25	1.58	0.20 – 0.30
	B ₁	112	64	48	1:1	56	56	2.28	0.10 – 0.20
	B ₂	109	109	0	1:0	109	0	—	—
Bio-902 x Bio-YSR	P ₁	25	0	25	—	0	25	—	—
	P ₂	22	22	0	—	22	0	—	—
	F ₁	20	20	0	—	20	0	—	—
	F ₂	263	191	72	3:1	197.25	65.75	0.79	0.30 – 0.50
	B ₁	119	52	67	1:1	59.5	59.5	1.89	0.10 – 0.20
	B ₂	113	113	0	1:0	113	0	—	—

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References

- Bansal VK, MR Thiagarajah, GR Stringam and JP Tewari (1999) Inheritance of partial resistance to race 2 of *Albugo candida* in canola-quality mustard (*Brassica juncea*) and its role in resistance breeding. *Plant Pathol.* **48**: 817–822.
- Chauhan SK and JB Sharma (2001) Inheritance of white rust resistance in Indian mustard incorporated from *Brassica napus*. *Indian J. Genet.* **61**: 250–252.
- Delwiche PA and PH Williams (1974) Resistance to *Albugo candida* race 2 in *Brassica* spp. *Proc. Am. Phytopathol. Soc.* **1**: 66.
- Delwiche PA and PH Williams (1981) Thirteen marker genes in *Brassica nigra*. *J. Hered.* **72**: 289–290.
- Fan Z, SR Rimmer and BR Stefanson (1983) Inheritance of resistance to *Albugo candida* in rape (*Brassica napus* L.). *Can. J. Genet. Cytol.* **25**: 420–42.
- Fox DT and PH Williams (1984) Correlation of spore production by *Albugo candida* in *Brassica campestris* and a visual rating scale. *Can. J. Plant Pathol.* **6**: 175–176.
- Katiyar RK and VL Chopra (1990) Somaclonally induced earliness in *Brassica juncea* germplasm accessions with field resistance to important disease. *Plant Breed.* **104**: 262–264.
- Kolte SJ (1985) Diseases of Annual Edible Oilseed Crops. Volume II Rapeseed-Mustard and Sesame diseases. CRC press, Boca Raton, Florida, 135 p.
- Lakra BS and GS Saharan (1989) Correlation of leaf and staghead infection intensities of white rust with yield and yield components of mustard. *Indian J. Mycol. Plant Pathol.* **19**: 279–281.
- Li CX, K Sivasithamparam, G Walton, P Fels and MJ Barbetti (2008) Both incidence and severity of white rust disease reflect host resistance in *B. juncea* germplasm from Australia, China and India. *Field Crops Res.* **106**: 1–8.
- Sachan JN, SJ Kolte and B Singh (2000) Inheritance of white rust (*Albugo candida* race 2) in *Brassica juncea*. *Indian Phytopathol.* **53**: 206–209.
- Saharan GS, CD Kaushik, PP Gupta and NN Tripathi (1984) Assessment of losses and control of white rust of mustard. *Indian Phytopathol.* **37**: 397.
- Tiwari AS, GA Petrie and RK Downey (1988) Inheritance of resistance to *A. candida* race 2 in mustard (*B. juncea* (L.) Czern). *Can. J. Plant Sci.* **68**: 297–300.
- Verma PR and GA Petrie (1980) Effect of seed infestation and flower inoculation on systemic infection of turnip rape by *Albugo candida*. *Can. J. Plant Sci.* **60**: 267–271.
- Verma V and OP Bhowmik (1989) Inheritance of resistance to a *Brassica juncea* pathotype of *Albugo candida* in *Brassica napus*. *Can. J. Plant Pathol.* **11**: 443–444.

Genetic Variability Studies in Minicore Collections of Chickpea (*Cicer arietinum* L.) under Different Environments

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The present investigation was carried out on chickpea germplasm lines representing minicore collection obtained from ICRISAT, Patancheru (AP) for assessing genetic variability under three environments. Considerably high variability was observed for most of the productivity related traits in E3 (irrigated 2005–06). This was evidenced by high range of mean performance for different traits in E3 compared to E1 (rainfed 2004–05) and E2 (rainfed 2005–06). Moderately high heritability and genetic advance (GA) was observed for many productivity related traits under E3. The higher PCV, although, heritability was reduced or remained same as that under E2. These findings revealed the importance of productivity related traits giving more response under E3 than E1 and E2 for better expression for crop improvement in chickpea. Over three environments, genotype ICC 6279 was found to be early flowering irrespective of the environmental effect while ICC 1882 was found to be early flowering in E1 and E2 whereas ICC 13124 and ICC 6279 were early in flowering in both E2 and E3 compared to early flowering check JGK-1. For seed yield/plant, 24, 22 and 17 genotypes showed significantly higher yield over check A-1 in E1, E2 and E3, respectively. Out of these, ICC 13124 (31.25 g, 32.85 g and 32.95 g) is the only top yielder in all the three environments. While genotypes ICC 6279 (28.9 and 27.85 g), ICC 13892 (30.05 g and 27.65 g) and ICC 13187 (27.45 g and 36.55 g) were top yielders in both E1 and E2 and ICC 12866 (27.65 and 40.15 g) and ICC 4533 (29.38 and 38.8) were identified as top yielders in E2 and E3, while ICC 12947 (27.9 g and 40.9 g) and ICC 6877 (18 g and 35.33 g) were top yielders in E1 and E3, respectively. On overall basis, the genotype ICC 13124 was found promising for earliness, large seed size and high yield/plant in all the environments suggesting that this accession is best suited for both rainfed and irrigated condition during the *rabi* season.

Key Words: Chickpea, Environments, Genetic advance, Genetic variability, Heritability, Minicore

Introduction

Chickpea (*Cicer arietinum* L.) is an important pulse crop of the semi-arid tropics, particularly in the rainfed ecology and resource poor farmers of the Indian subcontinent, the Mediterranean region, the west Asian and North American region, Eastern Africa and Latin America. In the recent past, this crop has experienced an export-driven expansion in new niches such as Australia and Canada. Globally, chickpea is cultivated on about 10.4 million hectare area adding 8.8 million tonnes of grains to the global food basket, with an average productivity of 826 kg/ha (FAO, 2007). It is cultivated in about 50 countries in the arid and semi arid regions. India grows chickpea on about 7.29 million hectare producing 5.77 million tonnes seed, which represents 30% and 38% of the national pulses acreage and production respectively with an average productivity of 792 kg/ha. In Karnataka, it is grown on an area of 0.33 million ha with a production of 0.18 million tonnes with an average productivity of only 578 kg/ha (Anonymous, 2007).

The variability for the characters of economic importance is the basic pre-requisite for improvement of any crop species. Lack of adequate variability has been implicated as one of the major limitation in improving the productivity of chickpea. There have been reports on genetic variability in chickpea but mostly based on limited number of germplasm lines (Arunkumar *et al.*, 1998; Sivakumar and Muthiah, 2001). Upadhyaya and Ortiz (2001) developed chickpea minicore of 211 accessions that represent the core collection of 1956 accessions (Upadhyaya *et al.*, 2002) and entire collection of about 17,000 accessions at ICRISAT. A set of minicore of chickpea (Upadhyaya and Ortiz, 2001) received from ICRISAT, Patancheru, which represents the whole range of variation of cultivated chickpea is an ideal material for assessing the exact nature of diversity, which helps in inferring about the extent of diversity in the entire collection and to determine how far it acts as limiting factors in improving productivity. Hence, the present investigation was carried out to gather information on

variability under three different environments in minicore collections of chickpea for eight quantitative characters of economic importance.

Materials and Methods

The experimental material for the present study comprised of 203 chickpea germplasm lines from the minicore collection (Upadhyaya and Ortiz, 2001) obtained from ICRISAT. These lines were evaluated for assessing genetic variability under three environments (E_1 , E_2 and E_3) for agronomic traits. Three experiments were conducted during *rabi* 2004–05 and 2005–06 under rainfed and irrigated situation at Genetics and Plant Breeding Garden, College of Agriculture, Dharwad, in medium black soils in randomized complete block design with two replications. Each genotype was grown in a single row of 4 m length with 30 cm spacing between rows and 10 cm within the row. Recommended agronomic practices were followed during the period of crop growth in both the situation. The crop was maintained free from weeds, diseases and pests by adopting appropriate plant protection measures. In irrigated situation, two irrigations were provided one at flowering and other at pod formation stage. The observations were recorded on eight quantitative characters viz., Days to 50% flowering (DFF), Plant height (PLHT), Number of primary branches/plant (PB), Number of secondary branches/plant (SB), Number of tertiary branches/plant (TB), Number of pods/plant (PPP), 100-seed weight (SDWT) (g) and seed yield/plant (YPP) (g). The data collected were subjected for statistical analysis. The analysis of variance for different characters was carried out using the mean data in order to partition variability due to different sources by following Panse and Sukhatme (1961). In order to assess and quantify the genetic variability among the genotypes for the characters under study, estimated the genetic parameters such as genotypic coefficient of variability (GCV%), phenotypic

coefficient of variability (PCV%), heritability (h^2), genetic advance (GA) and genetic advance as % mean (GAM). Heritability in the broad sense was derived based on the formula given by Hansan *et al.* (1956). GA was obtained by the formula prescribed by Johnson *et al.* (1955). The method adopted by Burton and Devane (1953) was used to calculate phenotypic and genotypic coefficient of variation.

Results and Discussion

Mean, range and environmental index for different quantitative traits in minicore collection of chickpea were depicted in Table 1. The results of the present investigation indicated the prevalence of significant differences among 203 genotypes studied during the three environments for all the eight characters (Table 2). A narrow difference was observed between PCV and GCV for days to 50% flowering. These results are in conformity with the reports of many researchers (Chavan *et al.*, 1994; Vijay Laxmi *et al.*, 2000; Jeena and Arora, 2001). The present findings suggest negligible influence of extraneous factors on this trait.

For the character plant height, narrow difference between PCV and GCV were recorded in all the three environments. Similar observations were made by Lawrence and Kabbar (2004) and Jeena and Arora (2000). Narrow difference observed in the present investigation between PCV and GCV indicate negligible influence of environmental factors on plant height. For the characters number of primary branches, secondary branches and tertiary branches/plant, large difference between PCV and GCV were observed in E_1 whereas difference in E_2 and E_3 were low to moderate. These observations are in accordance with the results of Chavan *et al.* 1994 and Patil (1996). This finding suggest that environmental factors have a role to play in influencing this trait.

Table 1. Mean, range and environmental index for different quantitative traits in minicore collection of chickpea

Characters	Mean			Range			Environmental index		
	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
DFF	60.26	56.9	56.13	38 to 78	38 to 77	36 to 76	1.27	0.80	0.80
PLHT (cm)	37.19	39.96	48.34	28 to 64	26 to 66	30 to 69	2.23	1.51	1.65
PB	2.55	3.71	3.91	2 to 4	2 to 6	2 to 8	0.22	0.32	0.38
SB	14.17	8.81	10.07	8 to 18	5 to 17	5 to 19	0.75	0.80	0.60
TB	18.87	17.08	20.23	11 to 28	6 to 40	9 to 34	0.95	1.30	1.38
PPP	91.05	114.35	126.78	21 to 162	25 to 182	27 to 200	4.06	9.54	7.65
SDWT (g)	16.28	17.40	18.58	9 to 38	11 to 36	13 to 39.9	0.53	0.45	0.69
YPP (g)	17.71	18.16	20.85	7 to 31	8 to 33	10 to 49	1.07	0.67	1.53
E_1-04-05 rainfed	E_2-05-06 rainfed			E_3-05-06 irrigated					

Table 2. Genetic variability, heritability and genetic advance for seed yield and its component traits evaluated under rainfed conditions of 2004–05(E1) and 2005–06(E2) and irrigated condition of 2005–06(E3)

Characters	E1				E2				E3			
	GCV %	PCV %	h ² (%)	GAM (%)	GCV %	PCV %	h ² (%)	GAM (%)	GCV %	PCV %	h ² (%)	GAM (%)
DFF	16.29	16.30	99.87	33.54	18.02	19.42	86.10	34.44	17.39	17.48	98.68	35.65
PLHT (cm)	23.07	27.56	70.07	39.80	15.06	18.29	67.83	25.55	14.99	15.95	88.24	29.00
PB	12.69	24.04	27.87	13.73	21.29	25.37	70.46	36.82	24.70	34.17	52.26	36.79
SB	19.05	49.91	14.57	14.98	25.75	26.78	99.80	55.06	30.17	58.34	26.74	32.13
TB	15.92	25.62	38.61	20.37	33.34	54.37	37.62	42.13	23.10	24.08	92.4	45.66
PPP	18.90	29.47	41.13	24.97	33.17	41.43	64.08	54.70	38.68	51.33	56.78	60.03
SDWT (g)	34.65	35.35	96.07	69.97	26.94	27.70	94.59	53.99	29.58	38.87	57.90	46.35
YPP (g)	27.85	29.79	87.36	53.63	32.30	32.34	89.75	66.46	31.51	35.17	80.29	58.18

The phenotypic and genotypic coefficient of variations were high for number of pods/plant in all the three environments. Similar results were reported by Yaman *et al.* 1997) and Jeena and Arora, 2001). The present finding suggests the role of environmental factors in influencing this trait. For the character 100 seed weight, the genotypes recorded a wide range of variation in E3 whereas low variations were observed in E1 and E2. These results are in accordance with the results of several workers (Salimath and Bahl, 1985; Salimath and Patil, 1990; Upadhyaya *et al.*, 2002). For seed yield/plant, high values of PCV and GCV were recorded in all the three environments. Similar results were reported in chickpea by Wanjari *et al.*, 1996; Yaman *et al.*, 1997).

The coefficient of variation indicates only the extent of variability present for different characters and do not indicates the heritable portion. To obtain the heritable portion of variability, it is essential to compute the heritability estimates for different characters. The heritability estimate separate the environmental influence from the total variability and indicate the accuracy with which a genotype can be identified by its phenotypic performance, thus, making the selection more effective. As such the heritability in a broader perspective is the proportion of genotypic variability to the total variability. Its importance has been emphasized by Lush (1949) in animals and Johnson *et al.* (1955) in plants. Heritability estimates in the broad sense alone is not a true indicator of effectiveness of selection for the trait since their scope is restricted by their interactions with the environment (Johnson *et al.*, 1955). Hence, heritability values considered along with predicted genetic gain increases the reliability of the parameter as a tool in selection programme.

High amount of heritability estimates were recorded for days to 50% flowering coupled with moderate genetic advance in all the three environments, respectively. Similar results were also reported by Agarwal (1985) and

Chavan *et al.* (1994). The results obtained in the present investigation suggest that high heritability with moderate GAM is the indication of presence of both additive and non-additive gene action operating for this character. Plant height showed high heritability coupled with low GAM in all the three environments. But Singh and Rao (1991) and Patil (1996) have reported high heritability coupled with high GAM for the trait. High heritability with low GAM recorded for the traits in the present investigation indicated that they are controlled to greater extent by non-additive gene action.

Low heritability coupled with low GAM was observed for primary branches/plant in E1 whereas in E2 and E3 high heritability with moderate GAM was noticed for this trait. Low GA reflects higher influence of environment on this trait. This is in contrast to the results of Patil (1996). Low heritability estimates coupled with low GAM were observed for secondary branches/plant in E1 and E3 whereas, high heritability estimate with moderate GAM was observed for this trait in E2, while many researchers (Jahagirdar *et al.*, 1994; Patil, 1996; Chauhan and Singh, 2000) reported higher estimate of heritability and GA. Moderate heritability estimates coupled with low GAM were recorded for tertiary branches in E1 and E2, while high heritability estimate along with high GAM were observed in E3 suggesting this trait could be improved through simple selection. These results are in accordance with the findings of Patil (1996). For the character number of pods/plant, it was observed that the heritability was moderate to high coupled with moderate to high GAM in all the three environments. But several workers (Singh and Rao, 1991; Chavan *et al.*, 1994, Mishra, 1991; Patil, 1996) reported high heritability coupled with high GAM for number of pods/plant. Moderate heritability with high GAM is the indication of presence of both additive and non-additive gene action in the control of this character.

High estimates of heritability along with high GAM were noticed for 100-seed weight and seed yield/plant in all the environments and this is in line with the findings of earlier workers including Singh and Rao (1991) and Jahagirdar *et al.* (1994) for test weight and seed yield/plant. High heritability coupled with high GAM values for characters studied suggest the importance of additive gene action for these traits (Sidramappa, 2003). These traits could be improved through simple selection

Mean performance of minicore germplasm

In order to identify the elite lines the mean performance of the test entries for different traits with checks has been compared. Annigeri-1 and KAK-2 were used as check varieties. The genotype performing significantly higher than their checks in all the environments for various characters are presented in Table 3. Since chickpea is mainly grown as a *rabi* crop, the terminal water stress is going to affect the yield potentiality of the crop. So one has to identify the genotypes which are early in flowering and maturity and hence, they can escape the terminal drought condition. The lines which are early in flowering and maturity have been identified in three different environments (E1, E2 and E3). In E1, out of 203 genotypes, 10 genotypes showed significantly lower value for days to 50% flowering. ICC 6279, ICC 1882, ICC 14699 were significantly early in flowering (38 days) as compared to other genotypes. In E2, among 203 genotypes only six genotypes showed significantly lower value for

days to 50% flowering. ICC 6279, ICC 13124, ICC 1882 and ICC 14669 were significantly early in flowering (less than 38 days). In E3, out of 203 genotypes, nine showed significantly lower value for days to 50% flowering. ICC 6279 and ICC 13124 were significantly early in flowering (39 days). These results are in conformity with the report of Upadhyaya *et al.* (2007).

Out of 203 genotypes 21, 19 and 17 genotypes expressed significantly higher pods/plant over check Annigeri-1 in E1, E2 and E3, respectively. ICC 14831 was found to be promising for pods/plant in both rainfed and irrigated condition suggesting that the genotype is fairly tolerant to drought. With regard 100 seed weight, out of 203 genotypes 22, 21 and 18 genotypes had significantly higher seed weight over check A-1 in E1, E2 and E3, respectively. ICC 8261, ICC 13357, ICC 16903, ICC 10341, ICC 13124, ICC 15406, ICC 2969, ICC 7315 and ICC 1915 are the top bold seeded genotypes ranging from 23 g to 40 g in all the 3 different environment suggesting that their characteristic feature of bold seededness. In general, *kabuli* types had higher seed weight in the study.

In respect of seed yield/plant 24, 22 and 17 genotypes showed significantly higher yield over check A-1 in E1, E2 and E3, respectively. Out of these, ICC 13124 (31.25 g, 32.85 g and 32.95 g) is the only top yielder in all the 3 environments. While genotypes ICC 6279 (28.9 and 27.85 g), ICC 13892 (30.05 g and 27.65 g) and ICC 13187 (27.45 g and 36.55 g) were top yielders in both E1 and E2 and ICC 12866 (27.65 and 40.15 g) and ICC

Table 3. Promising accessions in respect of seed yield and its component traits identified based on the evaluation of chickpea minicore in three different environments (E1, E2 and E3)

Trait	E1	E2	E3
DFP	(< 40 days): ICC 16903, 13357, 6279 , 13124, 1882 , 14669 , 15888, 1164, 8318, JGK 1	(< 38 days): ICC 8058, 6279 , 13124 , 12824, 1882 , 14669	(<39 days): ICC 6279 , 13124 , 506, 11879, 15888, 6874, 1164, 1356, JGK 1
PPP	(>153 pods): ICC 13523, 637, 10341, 1230, 6279, 12824, 3325, 4872, 13863, 15888, 14051, 1397, 3512, 7819, 12155, 3421, 6877, 6537, 3776, 2507, L 550	(> 161 pods): ICC 14831 , 6816, 2969, 5434, 4918, 14402, 10945, 2277, 13764, 12726, 1205, 9402, A-1, ICC 708, 1164, KAK-2, ICC 12328, 6293, 10399	(> 169 pods): ICC 14831 , 2969, 13124, 2065, 4182, 2720, 12866, 15264, 2580, 2263, 4463, 6571, 13816, 1710, 1052, 8318, 4567
Bold seed	(Seed weight >24.0 g): ICC 8261 , 13357, 10341 , 15406 , 2969 , 2242, 13124 , 1923, 15518, 7315 , 1915 , 16261, 2919, 12947, 3512, 13219, 1164, KAK 2, 5879, 1356, 12492, JGK 1	(seed weight >25.0 g): ICC 16903 , 8261 , 13357 , 10341 , 15406 , 13124 , 1923, 7315 , 1915 , 16261, 13892, 2072, 456, 12947, 11284, 3512, 11627, 2720, 7272, 6263, 7554	(seed weight >26.4 g): ICC 16903 , 8261 , 13357 , 10341 , 15406 , 2969 , 13124 , 7315 , 1915 , 16261, 2072, 12947, 1397, 3512, 11627, 1164, 7272, JGK 1
High yield	(>24.85 g/plant): ICC 1230, 6279 , 5504, 13124 , 506, 7315, 13892 , 15333, 12947, 11284, 3512, 13187 , 6877 , KAK 2, 12328, 6537, 15606, 2580, 5879, 5383, 1431, 1715, L 550, ICC 7554	(>26.5 g/plant): ICC 16903, 15406, 6279 , 2242, 13124 , 4841, 14402, 15610, 13892, 2072, 2919, 12947, 13077, 13187 , 12866 , 2990, 9848, 67, 7867, 5135, 10399, 4533	(>30.4 g/plant): ICC 637, 13124, 8195, 7308, 6816, 11879, 15888, 16796, 12947 , 1510, 13524, 13219, 12866 , 6877 , 13816, 12928, 4533

Table 4. Mean, range and co efficient of variation for eight quantitative traits in minicore of chickpea

Trait	Mean		Range		Coefficient of variation (%)	
	Present study	Upadhyaya & Ortiz, 2001	Present study	Upadhyaya & Ortiz, 2001	Present study	Upadhyaya & Ortiz, 2001
DFF	60.3	62.2	38–78	33–82	16.30	14.21
PLHT (cm)	37.2	46.7	28–69	12.8–78.6	27.56	18.01
PB (no.)	2.55	2.89	2–4	0–6	24.04	82.96
SB (no.)	14.17	4.07	8–18	1.3–5.3	49.90	39.82
TB (no.)	18.87	2.28	11–28	0–7	25.62	80.69
PPP (no.)	91.1	83.3	21–162	13.3–247.3	29.47	45.34
SDWT (g)	16.28	17.21	9–38	8.3–57.2	35.35	44.54
YPP (g)	17.70	15.0	7–31	5.3–46.0	29.79	36.45

4533 (29.38 and 38.8) were identified as top yielders in E2 and E3, while ICC 12947 (27.9 g and 40.9 g) and ICC 6877 (18 g and 35.33 g) were top yielders in E1 and E3, respectively. The promising accessions identified for different traits from different environments are represented in Table 3. On overall basis, it was noticed from the present study that the genotype ICC 13124 is found promising for earliness, bold seed and yield/plant in all the environments suggesting that this entry is best suited for both rainfed and irrigated condition during rabi season.

Upadhyaya and Ortiz (2001) evaluated minicore consisting of 216 genotypes at ICRISAT. The same set of genotypes except 13 have been evaluated in this study during 2004–05 to 2005–06 at Dharwad. It thus, provides an opportunity to compare the performance of minicore at Dharwad and Hyderabad with the average of different years and the place in which they are evaluated (Table 4). Of the eight quantitative traits, a good correspondence between the studies at Dharwad and Hyderabad for days to 50% flowering in respect of mean, range and coefficient of variation. Despite the influence of environment, days to 50% flowering is fairly stable trait. It is reported to be controlled by few oligogenes (Kumar and van Rheena, 2000) and hence, the effect of environment is less. Even for complex trait like yield/plant a reasonably high degree of correspondence was observed particularly in respect of mean and coefficient of variation and to some extent in respect of range also. Similarly, seed weight which is again reported to be additive gene controlled (Salimath and Bahl, 1985; Sarode *et al.*, 2000) there was good correspondence in respect of mean performance. A good correspondence with respect to mean was observed in respect of number of pods/plant also. However, the estimates of coefficient of variation are slightly higher in Hyderabad report. The range of expression was also at variance between the two reports

for both these traits. For the three traits concerning the number of branches some correspondence is observed in respect of mean performance for primary branches. However, the number of secondary and tertiary branches, the mean values in the present study are much higher than at Hyderabad. We believe that this might be due to the error in the way of recording observation on these traits. However, for an important trait like yield/plant, pods/plant, seed weight and days to 50% flowering, it may be inferred that the expression of these traits was not very different than at Hyderabad. Thus, it may be concluded that the minicore obtained from ICRISAT can be very well used as a source population for genetic and breeding investigation.

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References

- Agarwal (1985) Genetic variability in segregating populations of desi x kabuli crosses. *Indian J. Agric. Sci.* **55**(7): 456–459.
- Anonymous (2007) Hindu Survey of India. *Agriculture* pp 63–70.
- Arora PP (1991) Genetic variability and its relevance in chickpea. *Int. Chickpea Newsl.* **25**: 9–10.
- Arunkumar, A Kumar and R Krishna (1998) Heritability and genetic advance in gram (*Cicer arietinum* L.) genotypes of diverse origin. *Indian J. Agric. Sci.* **68**: 747–749.
- Burton GW and EH Devane (1953) Estimating heritability in tall Fescue (*Festuca circulinaceae*) from replicated clonal material. *Agron. J.* **45**: 478–481.
- Chavan VW, HS Patil and PN Rasal (1994). Genetic variability correlation studies and their implications in selection of high yielding genotypes of chickpea, *Madras Agric. J.* **81**: 463–465.

- Chauhan MP and IS Singh (2000) Variability estimates and identifying chickpea genotypes for yield and yield attributes in salt affected soil. *Legume Res.* **23(3)**: 199–200.
- Jahagirdar JE, RA Patil and PR Khare (1994) Genetic variability and its relevance in chickpea improvement. *Indian J. Pulses Res.* **7(2)**: 179–180.
- FAO (2007) Food and Agricultural Organization. *Bulletin of Statistics*, **14**: 35.
- Hanson GH, HF Robinson and RE Comstock (1956) Biochemical studies of yield in segregating populations of Korean lespezea. *Agron. J.* **48**: 267–282.
- Jeena AS and PP Arora (2000) Genetic variation in chickpea evaluated at Pantnagar. *Indian Agric. Sci. Digest* **20**: 50–51.
- Jeena AS and PP Arora (2001) Role of variability for improvement of chickpea. *Legume Res.* **24(2)**: 135–136.
- Johnson HW, HF Robinson and RF Comstock (1955) Estimation of genetic and environmental variability of soybean. *Agronomy J.* **47**: 314–318.
- Kumar J and HA van Rheena (2000) A major gene for time of flowering in chickpea. *J. Heredity*, **91**: 67–68.
- Lawrence D and V Kabbar (2004) Studies on genetic divergence in advanced generation breeding lines of chickpea (*Cicer arietinum* L.). M.Sc. (Ag.) Thesis, University of Agricultural Science, Dharwad, India.
- Lush JL (1949) Heritability of quantitative characters in farm animals. Proc. 8th Congress of Genetics Hereditas (suppl) **35**: 356–375.
- Mishra RC (1991) Stability of heritability, genetic advance and character association estimates in chickpea. *Int. Chickpea Newsl.* **25**: 10–11.
- Panse VG and PV Sukhatme (1961) Statistical methods for Agricultural workers. ICAR, New Delhi, 359 P.
- Patil SB (1996) Variability studies in segregating populations of chickpea. *Legume Res.* **13(1)**: 36–46.
- Salimath PM and PN Bahl (1985) Early generation selection in chickpea (*Cicer arietinum* L.). Variability, correlations and predication of direct and correlated responses in F₂ populations. *Indian J. Genet.* **45**: 101–104.
- Salimath PM and PN Bahl (1989) Combining ability studies in crosses involving tall and dwarf types of chickpea. *Indian J. Genet.* **49(1)**: 29–35.
- Salimath PM and SS Patil (1990) Genetic study in F₃ and F₄ generations of chickpea. *Indian J. Genet.* **50(4)**: 378–381.
- Sarode ND, RB Deshmukh, JV Patil, MR Manjare and LB Mhase (2000) Heterosis and combining ability in chickpea (*Cicer arietinum* L.). *Legume Res.* **23(3)**: 206–209.
- Siddramappa B (2003) Relationship of phonological traits with productivity in chickpea (*Cicer arietinum* L.). M.Sc. (Ag.) Thesis, University of Agricultural Science, Dharwad, India.
- Singh RK and SK Rao (1991) Heritability and genetic advance in segregating populations of chickpea. *Res. Dev. Report* **8**: 21–26.
- Sivakumar S and Muthiah (2001) Genetic divergence in chickpea germplasm. *Madras Agric. J.*; **87**: 48–50.
- Upadhyaya HD and R Ortiz (2001) A minicore subset for capturing diversity and promoting utilization of chickpea genetic resources in crop improvement. *Theor. Appl. Genet.* **102**: 1292–1298.
- Upadhyaya HD, R Ortiz, PJ Bramel and S Singh (2002) Phenotypic diversity for morphological characteristics in chickpea core collection. *Euphytica* **12**: 333–342.
- Upadhyaya HD, PM Salimath, CLL Gowda and Subesingh (2007) New early maturing germplasm lines for utilization in chickpea improvement. *Euphytica* **157(1/2)**: 195–208.
- Vijayalaxmi NVS, Kumar and T Nageshwar Rao (2000) Variability and correlation studies in desi, kabuli and intermediate chickpea. *Legume Res.* **23(4)**: 232–236.
- Wanjari KB, AJ Patil and PB Ghawghawe (1996) Genetic variability in F₅ progenies derived from bulk populations in chickpea. *Ann. Plant Physiol.* **10**: 83–86.
- Yaman M, A Kitiki, AS Kinsoy and N Acikgoz (1997) Characterization of chickpea (*Cicer arietinum* L.) genetic resources material collected from the Asian region. *Anadolu* **7**: 43–59.

Genetic Divergence in Snowball Cauliflower (*Brassica oleracea* var. *botrytis* L.)

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The genetic divergence analysis using Mahalanobis D^2 statistics was carried out in 52 snowball cauliflower germplasm including 3 superior CMS (Ogura) lines based on 12 quantitative characters. These 52 germplasm lines were grouped in 10 clusters, of which cluster IX accommodates 13 genotypes, while cluster VII was solitary. Morphological characterization for curd colour and compactness, leaf colour and plant types was also performed for all the lines. The snowball cauliflower lines under present investigation showed little deviation from original snowball group for plant type and their adaptability. High inter-cluster distance indicated considerable amount of diversity in the present population. Cluster I, II and VIII were important because they had high yield potential. First two clusters also accommodate 3 CMS lines (Ogu1A, Ogu 2A and Ogu 3A). These CMS lines would be immensely useful in heterosis breeding after crossing with divergent genotypes based on cluster distance.

Key Words: CMS lines, D^2 analysis, Genetic diversity, Heterosis, Snowball cauliflower

Introduction

Snowball cauliflower represents the late group of Indian cauliflower cultivated during *rabi* season throughout the Indian sub-continent. In the hilly temperate regions of India, they are cultivated almost year round. Cauliflower contributes around 5% of total vegetable production (NHB Database, 2008) in India and major chunk of it is represented by the snowball types. Snowball cauliflowers are also known as 'Erfurt' or 'Alpha' in Europe. Snowball cauliflower is characterized by dwarf plant with short stem, erect glaucous green leaves, solid and well protected curd. The genetic base of the snowball cauliflower is very narrow. Low genetic diversity is because of high degree of self-compatibility and consequent selfing to a considerable percentage (Watts, 1963; Nieuwhof, 1963). Moreover, most of the snowball cauliflower lines in India were derived from European materials. Genetic base of Indian snowball cauliflower is low as the base population have low genetic diversity. Astrini *et al.* (2006) also reported narrow genetic base in cauliflower. However, there is wide variability among different groups of cauliflower (Quamruzzaman *et al.*, 2007). Early types are very distinct from late snowball types. However, group III of Indian cauliflower (~ December maturity group) shares few similarities with snowball group because of possible gene flow between these two groups because of simultaneous flowering at high altitudes. However, the present snowball lines in India are not exactly similar to European summer cauliflower. Snowball cauliflowers in India are adapted to comparatively higher temperature and rainfall in contrast to European summer cauliflowers.

Semi-erect and spreading plant types have also evolved in the Indian snowball cauliflowers.

Information on nature and magnitude of variability present in a population is an important pre-requisite for starting any systematic breeding programme. Identification of superior genotypes among the existing germplasm becomes imperative for promoting production/unit area of this crop. Three superior CMS (Ogura) lines were also included to identify divergent genotypes from these lines for their use in heterosis breeding. Considering these points, studies on genetic variability in snowball group of cauliflowers were undertaken.

Materials and Methods

The present investigation was carried out at the Research Farm of Indian Agricultural Research Institute, Regional Station, Katrain, Kullu Valley, Himachal Pradesh, during *rabi* season of 2009-10. The experimental materials comprised of 52 genotypes of snowball cauliflower including 4 commercially released varieties from our station and 3 promising CMS (Ogura) lines. All the lines were characterized for morphological traits, like curd colour and compactness, and leaf colour and plant type. Lines were divided into four groups (loose, medium compact, compact and very compact) based on curd compactness. Curd compactness was determined physically by the pressure applied to the curd with the help of fingers and thumb. Similarly, all the lines were classified into two groups for curd colour (cream and white), four groups for leaf colour (light green, green, dark green and blue green) and three groups for plant type (erect, semi erect and semi

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spreading). The experiment was laid out in random block design (RBD) with 3 replications in 3 rows with 6 plants/row with spacing of 45 cm × 45 cm. Standard cultural practices as suggested by Singh *et al.* (1959) were followed to raise a successful crop. Observations were recorded for 12 quantitative characters viz., (i) Days to 50% curd initiation, (ii) Days to 50% curd maturity, (iii) Plant height (cm), (iv) Number of leaves, (v) Leaf length (cm), (vi) Leaf width (cm), (vii) Gross plant weight (kg), (viii) Curd length (cm), (ix) Curd width (cm), (x) curd depth (cm), (xi) Net curd yield (t/ha), and (xii) Harvest index (%). Five plants were selected randomly for recording observation. The D^2 statistics was used for assessing the genetic divergence among the populations as suggested by Mahalanobis (1936). Based on the D^2 values thus obtained, the entire germplasm was classified into distinct clusters, grouping together the less divergent genotypes (Rao, 1952).

Results and Discussion

Evaluation of Curd Quality, Leaf Colour and Plant Type

All the genotypes were characterized for curd quality (colour and compactness), leaf colour and plant type (Table 1). Leaf colour and curd compactness varied widely. Most of the lines possessed white but few had cream curd. Very compact curd was produced by Kt-33, Kt-16 and Kt-20 and loose curd was found in the lines, Kt-18 and RSK-119. Majority of the lines had compact curd and few lines showed medium compactness of curd. Most of the lines had semi-erect plant stature except Kt-16, Jonavon, EC-162587, Composite and King Kong with erect plant type where as CIF No. 1 had semi-spreading plant type. Morphological characterization depicts that changes might have occurred in the snowball lines in India from the original population. Majority of the lines had semi-erect plant type in contrast to the erect in original snowball population. The Indian lines are more tolerant to high temperature and rainfall and less prone to the riceyness. Astrini *et al.* (2006) also reported significant deviation in the Indonesian cauliflower lines from European snowball types. The available lines in India would be highly useful in the development of cultivars with wider adaptability.

Grouping of Genotypes into Various Clusters

Based on D^2 analysis the 52 lines were classified into 10 clusters (Table 2). The cluster IX had maximum lines (13) and cluster VII had only one line. The cluster III and cluster II had 9 and 8 lines, respectively. Three identified cultivars for commercial cultivation (Pusa Snowball-1,

Pusa Snowball K-1 and Pusa Snowball K-25) were grouped together in cluster II along with Kt-22, Kt-9, Kt-16 and two CMS lines, Ogu1A and Ogu 2A. However, the remaining CMS line, Ogu 3A was placed with Helna, Kt-2, White Gold and Kt-8 in cluster I. The clustering pattern depicts the close ancestry of almost all the identified lines for commercial cultivation. In snowball cauliflower there are no identified F_1 hybrids in India. This was mainly attributed to the non-availability of suitable pollination control mechanism. Self-incompatibility is very weak and promising CMS lines with good setting are not available in this group (Sharma *et al.*, 2004). However, three CMS (Ogura) lines developed in this station were free from any floral deformities and had good seed setting (data not shown). These lines will be useful in the development of F_1 hybrids in snowball cauliflower after identification of suitable parent combinations.

Intra- and Inter-cluster Distances

There was considerable amount of genetic divergence in the present collection as evident from inter- and intra-cluster distances among ten clusters (Table 3). Intra-cluster distance was highest in cluster V with four lines and lowest in cluster VII as represented by only one line (Pyramis). Highest inter-cluster distance, however, was between cluster VI vs VII (12654.1) followed by VI vs IX (9767.2), VI vs II (9418.5) and VII vs IV (8185.5). The lowest inter cluster distance was between cluster I vs VIII (554.3) followed by II vs VIII (600.1), II vs IX (616.1) and III vs IX (742.4). Cluster II which contain two CMS lines, Ogu1A and Ogu 2A was highly divergent from the cluster VI, IV and X. According to Arunachalam *et al.* (1984), the optimum level of genetic divergence between the parents gives the best heterosis and better segregants. However, Shwe *et al.* (1972) and Sichkar *et al.* (1988) suggested that hybridization between highly divergent parents generate promising breeding material. Thus, there is possibility in developing heterotic CMS based F_1 hybrids through selection of parents from highly divergent clusters with similar flowering time. Divergent genotypes can also be used in different breeding schemes for developing snowball cauliflower lines with better adaptability and high yield potential.

Cluster Mean Analysis

The study of cluster mean value of 10 clusters indicated considerable differences for the character studied (Table 4). After leaving out the solitary cluster, range of variation for curd length, curd width, curd depth and number of

Table 1. Characterization of 52 snowball cauliflower genotypes for important morphological traits

Genotype	Curd colour and compactness	Leaf colour and plant type	Genotype	Curd colour and compactness	Leaf colour and plant type
Helna	White, compact	Blue green, semi-erect	Kibogiant	Cream, medium compact	Green, semi-erect
Kt-2	White, compact	Green, semi-erect	Jonavon	White, compact	Green, erect
DB-187-1	Cream, compact	Green, semi-erect	Doc Elgon	Cream, medium compact	Dark green, semi-erect
Pushpa	Cream, medium compact	Light green, semi-erect	Helna-1	White, compact	Blue green, semi-erect
HL	Cream, medium compact	Green, semi-erect	Grodan	Cream, compact	Dark green, semi-erect
Kt-33	White, very compact	Blue green, semi-erect	Autumn Giant	Cream, compact	Green, semi-erect
White Gold	Cream, compact	Green, semi-erect	White Satin	White, compact	Blue green, semi-erect
Kt-9	White, very compact	Green, semi-erect	Early Snowball	Cream, compact	Green, semi-erect
Kt-15	White, medium compact	Light green, semi-erect	RSK-1385	White, compact	Blue green, semi-erect
RSK-1301	Cream, compact	Light green, semi-erect	Kn-81	White, compact	Dark green, semi-erect
Kt-22	White, compact	Light green, semi-erect	EC-162587	White, compact	Green, erect
Kt-18	White, loose	Light green, semi-erect	ACC-329	White, medium compact	Green, semi-erect
RSK-119	White, loose	Blue green, semi-erect	ACC-330	White, compact	Blue green, semi-erect
Agrotech	Cream, compact	Dark green, semi-erect	NCFH-23	White, medium compact	Dark green, semi-erect
White Fox	Cream, compact	Dark green, semi-erect	Igloo	Cream, compact	Green, semi-erect
SR-05	Cream, medium compact	Green, semi-erect	Composite	Cream, medium compact	Green, erect
Hermia	White, medium compact	Light green, semi-erect	Dominate	White, medium compact	Light green, semi-erect
PSBK-25	White, compact	Dark green, semi-erect	King Kong	White, medium compact	Blue green, erect
PSB-1	White, compact	Blue green, semi-erect	Himlata-2	White, compact	Blue green, semi-erect
PSBK-1	White, compact	Blue green, semi-erect	CIF No. 1	White, compact	Light green, semi-spreading
Kt-8	White, compact	Blue green, semi-erect	Pyramis	Cream, compact	Blue green, semi-erect
Kt-16	White, very compact	Green, erect	Kt-17	White, compact	Blue green, semi-erect
Kt-20	White, very compact	Dark green, semi-erect	Kt-44	White, compact	Dark green, semi-erect
Kt-6	White, compact	Light green, semi-erect	Ogu1A	White, compact	Blue green, semi-erect
Kt-19	White, compact	Blue green, semi-erect	Ogu2A	White, compact	Dark green, semi-erect
Alpha	Cream, compact	Blue green, semi-erect	Ogu3A	White, compact	Blue green, semi-erect
Alpha	Cream, compact	Blue green, semi-erect	Ogu3A	White, compact	Blue green, semi-erect

Table 2. Cluster classification of 52 genotypes of snowball cauliflower based on D² analysis

Cluster No	Genotypes
I	Helna, Kt-2, White Gold, Kt-8, Ogu3A
II	Kt-9, Kt-22, Pusa Snowball K-25, Pusa Snowball-1, Pusa Snowball K-1, Kt-16, Ogu1A, Ogu2A
III	DB-187-1, White Fox, Kt-6, Kibogiant, RSK-1385, EC-162587, ACC-330, Dominate, Kt-17
IV	Pushpa, Agrotech
V	Kt-33, Kt-18, RSK-119, Kt-19
VI	Igloo, Himlata-2, CIF No.1
VII	Pyramis
VIII	Kt-15, SR-05, Jonavon, Kn-81
IX	HL, Hermia, Kt-20, Alpha, Doc Elgon, Helna-1, Grodan, Autumn Giant, White Satin, Early Snowball, NCFH-23, Composite, Kt-44
X	RSK-1301, ACC-330, King Kong

Table 3. Inter- and Intra-cluster distances among 10 clusters based on D² analysis

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	337.8	586.6	1069.2	3321.2	1371.2	6889.1	2233.1	554.3	1131.8	1767.8
II		323.8	1091.9	5061.2	2373.3	9418.5	1992.7	600.1	616.1	2467.8
III			342.4	2971.6	1156.6	6703.9	3560.7	898.9	742.4	1159.1
IV				589.3	899.0	1327.5	8185.5	3857.6	5198.9	2244.7
V					899.0	3087.6	4924.4	1688.8	2451.4	1166.3
VI						843.9	12654.1	7944.6	9767.2	5783.9
VII							0.0	3063.8	2465.2	5419.3
VIII								388.1	918.4	1474.8
IX									417.1	2241.4
X										581.1

leaves were low among the multi-member cluster. The characters viz., leaf length, leaf width, gross plant weight, plant height, net curd yield and harvest index exhibited

moderate variation. The high range of variation was observed for days to 50% curd initiation and days to 50% curd maturity among the different clusters.

Table 4. Cluster means of 52 genotypes for 12 characters based on D² analysis

Cluster	Days to 50% curd initiation	Days to 50% curd maturity	Plant height (cm)	Number of leaves	Leaf length (cm)	Leaf width (cm)	Gross plant weight (kg)	Curd length (cm)	Curd width (cm)	Curd depth (cm)	Net curd yield (t/ha)	Harvest index (%)
I	114.02	123.94	46.66	18.61	47.41	25.42	1.80	10.92	12.99	5.86	41.85	43.53
II	124.58	135.36	44.20	19.32	46.65	23.45	1.90	11.14	13.24	6.45	38.97	36.59
III	116.51	123.64	39.12	18.89	34.34	16.75	0.90	9.80	11.20	5.18	20.39	40.98
IV	79.48	89.00	39.14	21.78	34.73	17.73	0.94	9.77	10.93	4.53	24.69	49.48
V	94.80	106.50	42.57	18.01	36.69	19.96	1.06	10.95	12.52	5.75	26.25	45.54
VI	56.68	72.28	42.79	19.40	36.79	21.86	0.99	10.78	11.55	6.08	22.58	42.31
VII	131.00	139.60	73.63	20.33	70.27	36.11	1.26	9.96	11.14	6.76	28.16	45.71
VIII	119.96	127.55	44.69	18.53	35.00	18.11	1.68	10.39	11.99	6.22	43.48	43.14
IX	127.56	137.26	42.27	18.03	39.86	20.27	1.24	10.33	12.38	5.82	24.64	36.96
X	107.86	116.37	37.67	17.97	26.47	11.91	0.78	9.49	11.14	5.41	27.62	64.33
Overall mean	107.245	117.15	45.274	19.08	40.82	21.15	1.25	10.35	11.91	5.81	29.86	44.86

The variation observed in cluster means also point out the degree of variability. In the present investigation, cluster IV, V and VI contain genotypes with early maturity, whereas, cluster II, VII and IX were represented by genotypes with late maturity. Thus, considerably good amount of diversity was recorded for days to maturity. For vegetative traits, like plant height, numbers of leaves, leaf length and width significant amount of variability was also observed. Dwarf plants (< 40 cm) was observed in the clusters III, IV and X. All the clusters had plant height in the range of 40–50 cm except the solitary cluster VII which had plant height of 73.63 cm. The numbers of leaves/plant was 17–22 among the clusters. Smallest leaf size (26.47 × 11.91 cm²) was recorded in the cluster X. The solitary cluster VII had very large leaf size with length and width of 70.27 cm and 36.11 cm, respectively. All the remaining clusters had medium leaf size. Gross plant weight was highest (1.90 kg) in cluster II while it was lowest (0.78 kg) in cluster X. The genotypes included in cluster I, II, V, VI and VIII had more curd length than population mean and similarly genotypes in the cluster I, II, V, VIII and IX had greater curd width whereas clusters I, II, VI, VII, VIII and IX had greater curd depth. Cluster III with 9 genotypes had lowest curd yield (20.39 t/ha) while it was highest (43.48) in cluster VIII with four genotypes. The population mean for yield was 29.86 t/ha and the clusters with better yield than population were I (5 genotypes), II (8 genotypes) and VIII (4 genotypes). Cluster I, II and VIII had all the desirable yield related traits. Moreover, three CMS lines were also included in the cluster I and II. Desirable horticultural traits of parents are important for their utilization in heterosis breeding (Sharma *et al.*, 2004). Therefore, these CMS lines could be utilized in the heterosis breeding programme after testing their combining ability.

References

- Arunachalam V, A Bandopadhyay, SN Nigam and RW Gibbons (1984) Heterosis in relation to genetic divergence and specic combining ability in groundnut (*Arachis hypogaea* L.) *Euphytica* **33**: 33–39.
- Astarini IA, JA Plummer, RA Lancaster and G Yan (2006) Genetic diversity of Indonesian cauliflower cultivars and their relationships with hybrid cultivars grown in Australia. *Sci. Hort.* **108**:143–150.
- Mahalanobis PC (1936) On the generalized distance in statistics. *Proceedings of National Institute of Science, India* **2**: 49–55.
- Nieuwhof M (1963) Pollination and contamination of *Brassica oleracea* L. *Euphytica* **12**: 17–26.
- Quamruzzaman AKM, MM Rahman, MN Uddin, MA Siddiky and MDH Prodhan (2007) Genetic diversity in cauliflower (*Brassica oleracea* var. *botrytis* L.) *Indian J. Hortic.* **64**: 50–52.
- Rao CR (1952) *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons, Inc Macmillan Pub Co New York, 460 p.
- Sharma SR, PK Singh, V Chable and SK Tripathy (2004) A Review in Hybrid Cauliflower Development. In: Singh PK, Dasgupta SK, Tripathi SK (eds) *Hybrid Vegetable Development*, The Haworth Press, New York, pp 217–221.
- Shwe UH, BR Murthy, HB Singh, UMB Rao (1972) Genetic divergence in recent elite strains of soybean and groundnut in India, *Indian J. Genet.* **32**: 285–295.
- Sichkar VI, EM Grigoryan and AP Loguval (1988) Multivariate analysis of Mahalanobis distance parameters for economically useful characters in different group of soybean. *Tsitol. Genet.* **22**: 37–43.
- Singh HB, MR Thakur, PM Bhagchandani (1959) Vegetable seed production in Kullu Valley – I. *Indian J. Hort.* **16**:92–101
- Watts LE (1963) Investigations into the breeding system of cauliflower I: Studies on self-incompatibility. *Euphytica* **12**: 323–340.

Inter-trait Relationship and Variability in Segregating Population of Muskmelon Derived from Intra-specific Cross for Total Soluble Solids and Yield

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Variability, character association, and path analysis were carried out in 599 individual plants of F_2 population derived from an intra-specific cross of *Cucumis melo* x *Cucumis melo* var. *Momordica*. The observations were recorded on nine horticultural traits viz. number of branches/plant, vine length (cm), number of fruits/plant, polar circumference and equatorial circumference of fruit (cm), flesh thickness (cm), fruit weight (kg), total soluble solid (%) and yield/plant (kg). The analysis of variance revealed remarkable variation within population for concerned characters. The maximum range of mean value was recorded in vine length and minimum in flesh thickness. Regression analysis revealed that number of fruits contribute maximum towards increase of fruit yield, followed by fruit weight and polar circumference of fruit. Yield has positive and significant association with all other characters except total soluble solids (TSS). Number of fruits had the highest direct effect on yield followed by fruit weight. Therefore, number of fruits and fruit weight should be considered during selection for yield. These populations will be converted into Recombinant Inbred Lines (RILs) by selfing following the Single Seed Decent (SSD) methods will be very useful to map the Quantitative Trait Loci (QTLs) for horticultural traits and TSS.

Key Words: Muskmelon, Phenotypic correlation, Regression analysis, TSS, Variability

Introduction

Muskmelon (*Cucumis melo* L.) is an important member of family Cucurbitaceae marketed and consumed as dessert all over the world. An intra-specific taxa *Cucumis melo* var. *momordica* Duthie & Fuller, commonly known as snapmelon or phoot consumed as vegetable and found only in Indian subcontinent. The morphological intra-specific variations were observed in genus *Cucumis* (Krikbride, 1993; Stepansky *et al.*, 1999). The variation in morphological characters *i.e.*, growth habit, maturity, fruit shape flesh color and external skin texture of different botanical variety of *C. melo* in India as well as other part of world provide relatively broad phenotypic variation (Dhillon *et al.*, 2007). In India, this group of melon has not been exploited in crop improvement programme as they have several desirable traits. Creation of variability in the cultivated melon by using the unexploited melon would be of great importance. Evaluation of variability is pre-requisite for planning the quality improvement programmes. Knowledge of the nature and magnitude of variation promotes a rational choice of the character in which selection can be exercised.

The regression analysis is useful for prediction of extent of contribution of other traits towards yield. The correlation and path analysis will establish the extent of

association between yield and its contributing components and also bring out relative importance of their direct and indirect effects. The correlation of economic yield component with yield and the partitioning of the correlation coefficient into its component of direct and indirect effect have been extensively studied in individual crops. Highly significant associations of yield with contributing traits were studied by Chaudhary *et al.* (2003) in muskmelon and Pandey *et al.* (2003, 2005) in snapmelon and muskmelon. Therefore, an attempt was made to reveal direct and indirect influences of some important yield components on fruit yield in the segregating population through regression, correlation, path coefficient analysis and to know the extent of variability in F_2 population.

Materials and Methods

The study comprised of 599 F_2 population of melon generated from an intra-specific cross between cv. Kashi Madhu (*Cucumis melo*) and genotype B-159 (*Cucumis melo* var. *momordica*). Seeds of F_1 were selfed and advanced as F_2 . Individual F_2 plants have been treated as an identical genotype (family). All F_2 lines have been planted at experimental block at Indian Institute of Vegetable Research (IIVR), maintaining a row to row and plant to plant spacing of 1.8 m × 0.8 m. Standard

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cultural practices were adopted to raise a healthy crop as recommendation of De *et al.* (2003).

The observation were recorded on individual plant for nine characters viz., number of branches/plant, vine length (cm), number of fruits/plant, polar circumference and equatorial circumference of fruit (cm), flesh thickness (cm), fruit weight (kg), total soluble solid (%) and yield/plant (kg). The data were analyzed for standard statistical procedure followed for estimating correlation and regression analysis and selection of best regression equation was done through backward elimination as per the procedure described by Mead *et al.* (1993). The analysis of descriptive statistics was done through statistical software SPSS 11 and regression, correlation and path through SPAR1.

Results and Discussion

Descriptive statistics of different characters under study were presented in Table 1. All characters were fitted on normal frequency distribution curve indicating that population was polymorphic for respective traits. An

increase in yield and nutritional content of snakemelon has been obtained by utilizing intraspecific genetic variation of diverse melons (Pandey *et al.*, 2010). The maximum range of variation was recorded in vine length followed by polar circumference and equatorial circumference of fruit and minimum range of variation was recorded in flesh thickness followed by fruit weight and TSS. On the basis of skewness and kurtosis was recorded maximum in yield plant followed by equatorial and polar circumference of fruit. It indicated that yield is complex traits and influenced by its contributed components. These results were in agreement to the findings of Pandey *et al.* (2005) and Singh (2008).

Regression analysis (Table 2) indicated increase in fruit yield due to increase in all the remaining eight characters. Average fruits weight was found to increase the yield to maximum level, followed by fruits number. The backward regression analysis was carried out to point out the contribution of independent variables to yield in linear fashion according to (Kempton and Fox, 1997).

Table 1. Descriptive statistics for yield and yield related traits of population

Variable	No. of branches /plant	Vine length (cm)	No. of fruits /plant	Polar circumference of fruit (cm)	Equatorial circumference of fruit (cm)	Flesh thickness (cm)	Fruit weight (kg)	TSS (%)	Yield/plant (kg)
Mean	4.100	270.785	2.425	56.399	33.059	2.414	1.420	2.870	3.366
Sum of square	10778	45754400.690	4795.000	2023171.640	678513.222	3651.380	1541.560	5072.420	11481.400
SD	1.088	55.360	1.457	14.036	6.314	0.514	0.746	0.480	2.801
Variance	1.183	3064.804	2.124	197.018	39.867	0.264	0.556	0.231	7.846
Minimum	2.000	123.000	1.00	24.000	15.000	1.000	0.200	2.000	0.200
Maximum	9.000	429.000	10.00	124.500	80.500	4.200	4.550	8.200	26.250
Skewnes	0.323	0.159	1.470	0.812	1.197	0.273	1.049	0.230	2.628
Kurtosis	3.450	3.029	5.785	4.445	8.336	3.066	4.403	2.746	14.530

Table 2. Regression analysis for yield related traits of muskmelon population

Variable	No. of branches /plant	Vine length (cm)	No. of fruits/ plant	Polar circumference of fruit (cm)	Equatorial circumference of fruit (cm)	Flesh thickness (cm)	Fruit weight (kg)	TSS (%)
	V ₁	V ₂	V ₃	V ₄	V ₅	V ₆	V ₇	V ₈
R ²	0.845	0.843	0.842	0.841	0.841	0.841	0.696	0.484
St. Error	18.191	18.95	22.235	23.747	25.650	36.278	40.438	47.792
F – value	266.989	287.353	395.909	447.716	523.162	1049.995	685.347	562.108
Probability	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Intercept	-1.681	-1.967	-2.066	-2.532	-2.572	-2.507	-5.340	0.1200
V ₁	0.032	0.031	0.026	0.024	0.024	—	—	—
V ₂	0.0003	0.0004	0.0004	0.0003	0.0003	—	—	—
V ₃	1.387	1.392	1.395	1.402	1.402	1.409	1.442	1.338
V ₄	-0.021	-0.019	-0.019	-0.020	-0.020	-0.021	0.092	—
V ₅	-0.0109	-0.023	-0.023	—	—	—	—	—
V ₆	0.0106	0.042	0.031	-0.024	—	—	—	—
V ₇	2.709	2.654	2.649	2.574	2.566	2.561	—	—
V ₈	-0.116	-0.113	—	—	—	—	—	—

Seven morphological and one quality traits viz., number of branches/plant, vine length, number of fruits/plant, polar circumference and equatorial circumference of fruit, flesh thickness, fruit weight, total soluble solid were able to explain variation up to nearly 85% in fruit yield ($R^2 = 0.845$). However, average fruit weight alone was able to explain 69% of total yield variation ($R^2 = 0.696$). The results indicated that above traits are important during selection.

The traits were significantly correlated with yield at the 1% level of significance (Table 3). Number of branches, vine length, polar and equatorial circumference of fruit, and number of fruits, flesh thickness and fruit weight showed higher correlation coefficient except TSS. Therefore, these characters should be considered while making selection for yield improvement. Most of the variables had positive significant association among themselves except number of fruits/plants had negative significant association with fruit weight and equatorial circumference of fruit. Kalloo *et al.* (1983), Pandey *et al.* (2005, 2009) observed similar results where yield was significantly and positively associated with the number

of fruit, fruit weight, and number of branches and length of vine, which supports present findings.

The contribution of these characters was further analyzed by computing their direct and indirect effect on yield (Table 4). The findings revealed that fruits number had highest direct effect on yield followed by fruit weight. However, other yield contributing traits i.e., number of branches/plant, vine length, and flesh thickness provided a positive direct contribution to yield at low level. While highest negative direct effect on yield was exerted by polar and equatorial circumference of fruit and TSS. TSS showed negative direct effect on yield in spite of positive correlation with yield. Number of fruits/plant, fruit weight, and number of branches/plant, vine length, and flesh thickness contributed maximum positive indirect effect for all the characters, whereas, TSS, equatorial and polar circumference of fruit contributed negative indirect effects *via* all the characters to yield. These results were found in accordance to several other reports on melon and cucurbit crops Chaudhary *et al.* (2003), Kalloo *et al.* (1983) and Pandey *et al.* (2003, 2005, 2009).

Table 3. Inter-traits correlation coefficient for fruit yield and yield attributes in muskmelon

Characters	No. of branches / plants	Vine length (cm)	No. of fruits/ plant	Polar circumference of fruit (cm)	Equatorial circumference of fruit (cm)	Flesh thickness (cm)	Fruit weight (kg)	TSS (%)	Yield/plant (kg)
	V ₁	V ₂	V ₃	V ₄	V ₅	V ₆	V ₇	V ₈	V ₉
V ₁	—	0.1204**	0.230**	0.117**	0.074	0.072	0.110**	0.095*	0.240**
V ₂	—	—	0.235**	0.170**	0.154**	0.143**	0.216**	0.059	0.308**
V ₃	—	—	—	0.116**	-0.096*	-0.028	-0.072	-0.078	0.696**
V ₄	—	—	—	—	0.547**	0.581**	0.830**	0.143**	0.376**
V ₅	—	—	—	—	—	0.463**	0.594**	0.127**	0.246**
V ₆	—	—	—	—	—	—	0.536**	0.189**	0.291**
V ₇	—	—	—	—	—	—	—	0.162**	0.541**
V ₈	—	—	—	—	—	—	—	—	0.021

*, ** Significant at 5% and 1% level of probability, respectively

Table 4. Direct (Diagonal) and indirect effects of independent traits on yield in muskmelon (phenotypic level)

Characters	No. of branches /plants	Vine length (cm)	No. of fruits/ plant	Polar-circumference of fruit (cm)	Equatorial circumference of fruit (cm)	Flesh thickness (cm)	Fruit weight (kg)	TSS (%)	Correlation with yield
	V ₁	V ₂	V ₃	V ₄	V ₅	V ₆	V ₇	V ₈	V ₉
V ₁	0.0123	0.0008	0.16663	-0.0124	-0.0018	0.0001	0.0795	-0.0019	0.240**
V ₂	0.0015	0.0069	0.1701	-0.0180	-0.0038	0.0003	0.1560	-0.0012	0.308**
V ₃	0.0028	0.0016	0.7219	0.0123	0.0024	-0.0001	-0.0523	0.0016	0.696**
V ₄	0.0014	0.0012	-0.0842	-0.1055	-0.0135	0.0009	0.5595	-0.0029	0.376**
V ₅	0.0009	0.0011	-0.0698	-0.0578	-0.0247	0.0009	0.4289	-0.0026	0.246**
V ₆	0.0009	0.0010	-0.0208	-0.0509	-0.0114	0.0019	0.3875	-0.0038	0.291**
V ₇	0.0014	0.0015	-0.0523	-0.0877	-0.0147	0.0010	0.7218	-0.0033	-0.541**
V ₈	0.0012	0.0004	-0.0563	-0.0151	-0.0032	0.0004	0.1176	-0.0200	0.021

**, Significant at 5% level of probability; Residual effect: 0.1546

In the light of above finding it may be concluded that beside direct selection for fruit yield, other traits like the fruits number, polar circumference of fruit, fruit weight should also taken in consideration for improvement of yield in muskmelon. On the basis of regression analysis, number of fruits and fruit weight contribute maximum to increase the yield. The variation in TSS was very low in the population and had not contributed in yield. The results might be used to know the variation in the population, adopt the selection criteria in advance stage and increase the selection efficiency. These genomic resources may be further utilized for molecular mapping to detect the QTL for horticultural traits and TSS after regress phenotyping at different environment.

References

- Chaudhary BR, RS Dhaka and MS Fageria (2003) Association studies in muskmelon correlation and path coefficient analysis in muskmelon *Cucumis melo* L. *Haryana J. Hort. Sci.* **32(1&2)**: 98–101.
- De N, S Pandey, KP Singh and M Rai (2003) Integrated development of gourds and melon. IIVR, *Tech. Bull.* **No. 13**.
- Dhillon NPS, R Ranjana., K Singh, I Eduardo., AJ Monfort, M Pitrat, NK Dhillon and PP Singh (2007) Diversity among landraces of Indian snapmelon (*Cucumis melo* var. *momordica*). *Genet. Resour. Crop. Evol.* **54**: 1267–1283.
- Kaloo G, J Dixit and AS Sidhu (1983) Studies on genetic variability and characters association in muskmelon (*Cucumis melo* L.). *Indian J. Hort.* **40(181)**: 79–85.
- Kempton RA and PN Fox (1997) *Statistical Methods for Plant Variety Evaluation*. Chapman and Hall, London.
- Kirkbride HJ Jr (1993). *Biosystematics monograph of the genus Cucumis (Cucurbitaceae)*. Parkway Publishers, Boone, North Carolina.
- Mead R, RN Curnow and AM Hasted (1993) *Statistical Method in Agriculture and Experimental Biology*. Chapman and Hall, London.
- Pandey S, M Rai, D Ram, B Singh and PK Chaubey (2003) Component analysis in snapmelon (*Cucumis melo* var. *momordica*). *Veg. Sci.* **30(1)**: 64–67.
- Pandey S, M Rai and B Singh (2005) Genetic Variability and Character association in muskmelon (*Cucumis melo* L.). *Indian J. Plant Genet. Resour.* **18(2)**: 212–216.
- Pandey S, SK Kashya, A Jha, BR Chaudhary, S Kumar, DK Singh and M Rai (2009) Inter-trait association and genetic variability assessment in snapmelon (*Cucumis melo* var. *momordica*). *Indian J. Plant Genet. Resour.* **22(2)**: 113–116.
- Pandey S, NPS Dhillon, AK Sureja, D Singh and AA Malik (2010) Hybridization for increased yield and nutritional content of snakemelon (*Cucumis melo* L. var. *flexuosus*). *Plant Genet. Resour.: Character. Utiliz.* **1**: 1–5.
- Singh PK (2008) Intertrait relationship and variability in intervarietal cross of melon. *M. Sc. (Ag) Thesis*, UP College (Autonomous Institution), Varanasi, pp 1–72.
- Stepansky A, I Kovalski and R Perl-Treves (1999) Intraspecific classification of melons (*Cucumis melo* L.) in view of their phenotypic and molecular variation. *Plant System. Evol.* **217**: 313–332.

Genetic Variability and Divergence Analysis in Oat (*Avena sativa*) under Rainfed Environment of Intermediate Himalayan Hills

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On the basis of D^2 analysis 70 oat genotypes were grouped into seven clusters and two ungrouped clusters. Cluster I was the largest and contained 16 genotypes. The genotype belonging to ungrouped cluster IX, namely, SJO-47 showed promise for green fodder yield, dry matter yield, green fodder productivity/day, tillers/plant and dry matter (%). The highest intra-cluster distance was observed in cluster VIII containing five genotypes. The most distant clusters were cluster II and cluster VIII followed by cluster II and VII and Cluster II and IX. The genotypes SJO-14, SJO-16, SJO-17, SJO-13, SJO-15, SJO-12, SJO-11 were distantly related with JO-55, SJO-56, SJO-54, SJO-52, SJO-53. The maximum (%) contribution towards genetic divergence was contributed by crop duration, followed by green fodder yield and plant height. High phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance as (%) of mean were reported for green fodder productivity, plant height, tillers/plant, dry matter yield and green fodder yield.

Key Words: *Avena sativa*, Clusters, Divergence, Green fodder, Oat, Variability

Introduction

Oat is one of the most nutritious non-leguminous fodder crops and is mainly grown during *rabi* season under irrigated as well as rainfed conditions in India. It provides green fodder during scarcity period in winter season of Himalayan regions. Oat green fodder contains 20% dry matter, 10% crude protein, 91% organic matter (DM basis) (Gupta *et al.*, 2004). In addition to green fodder, oat grains are also used for cattle feeding and preparation of nutritious instant foods for humans. Assessment of variability for the yield and its components becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement. The role of plant genetic resources in the improvement of cultivated plants has been well recognized. Characterization and evaluation of both exotic and indigenous collections to get information on useful traits forms the basic step for crop improvement programmes. Like any other crop species the first step in oat improvement is full assessment of the local materials, including collection, evaluation and molecular characterization of germplasm lines. Often, local varieties of crops are of excellent quality and flavour, have a good level of resistance to pests and diseases and may be superior to exotic materials (Abbas *et al.*, 2008). Study of genetic divergence among a set of genotypes will, therefore, enable a plant breeder to choose suitable parents and plan appropriate hybridization

programme. Diederichsen (2008) characterized 10,105 accessions of hexaploid cultivated oat (*Avena sativa* L. *sensu lato*) from 85 countries. Eight environmentally stable morphological characters differentiated into 18 character states, were used to define genetically distinct morphological groups. The greatest richness of diversity was found in oat from countries with temperate climates and intensive oat breeding programmes. Achleitner *et al.* (2008) studied genetic diversity among 114 oat (*Avena sativa* L.) varieties of worldwide origin based on 77 molecular polymorphisms produced by eight selective AFLP primer combinations used for cluster analysis and principal component analysis. Their study demonstrated that diversity could be significantly enhanced using a global collection, and provides evidence for marker-trait associations that can be validated in segregating populations and exploited through marker-assisted selection. D^2 statistics has proved to be a powerful tool in discerning genetic divergence among groups based upon multiple growth characters, assessing relative characters and relative contribution of different components of total divergence. In fodder crops such informations are limited.

The present study was conducted to determine the magnitude of variability for green fodder yield and genetic divergence among the oat genotypes. Parameters such as genotypic and phenotypic coefficient of variability

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are useful in detecting the amount of variability present in the germplasm. Heritability and genetic advance help in determining the influence of environment on the expression of the genotype and the reliability of characters. Like grain yield in cereals, green fodder yield in oat is also not a unitary character but depends on a number of plant characters. Being highly influenced by environmental changes direct selection for green fodder yield is often not effective. The estimation of correlation coefficient among yield and its components has been useful to the breeders in selecting suitable plant type. Thus, in the present study efforts were made to explore the extent of genetic variability for the nine characters, to obtain information on genetic diversity present among the genotypes and to classify them into clusters.

Materials and Methods

The present investigation was carried out at the Regional Agricultural Research Station, (SKUAST-J), Rajouri. The experimental material for the present study consisted of 70 diverse genotypes of oat (*Avena sativa* L). All the genotypes were evaluated in randomized block design with three replications during *rabi*-2007-08 and 2008-09 under rainfed environment. Each plot consisted of five rows of 4 m length, spaced 25 cm apart and maintaining an inter-plant distance of 10 cm within rows. All the recommended agronomic practices were followed to raise the good crop. The crop experienced moisture stress during early development in November-December in both the years. However, the crop recovered well following sufficient rains from the month of January onwards. Observations were recorded on nine characters. Observations on plant height, tillers/plant and leaf stem ratio were recorded on randomly selected five plants in each plot and in each replication, whereas observations on days to flowering, crop duration (days), dry matter (%), green fodder productivity, green fodder yield and dry matter yield were recorded on plot basis. Standard statistical procedures were followed for estimating genetic constants *i.e.* phenotypic and genotypic coefficients of variation (Burton, 1952), heritability in broad sense (Hanson *et al.*, 1956) and expected genetic advance (Johnson *et al.*, 1955). Pooled analysis of variance (ANOVA) was used to quantify the genetic differences among the genotypes. The multivariate analysis was performed through Window State Software (Indostat Service, India) using Mahalanobis's D^2 statistics (Mahalanobis,

1936). Treating D^2 as a generalized statistical distance, the criteria used by Toucher (Rao, 1952) was applied for determining the group constellation and clustering was done accordingly (Fig. 1). The character-wise rank totals were used to calculate the % contribution of each character to the total divergence. Average inter- and intra-cluster distances were estimated as per the method recommended by Singh and Chaudhary (1985).

Results and Discussion

A wide range of phenotypic variability was observed for all the characters studied. The mean squares (ANOVA) for nine characters indicated highly significant differences between genotypes for all the characters (Table 1). The estimates of both phenotypic (PCV) and genotypic coefficients of variation (GCV) for the nine characters were studied and are presented in Table 2. The variability estimates, in general, revealed that the estimates of PCV were greater than the estimates of GCV for all the traits. This suggested the role of environment in the expression of the characters (Singh and Singh, 2009). PCV/GCV ratio was highest for leaf stem ratio and was lowest for plant height. Highest GCV was obtained for dry matter yield (35.82%) followed by green fodder yield productivity (30.14%), green fodder yield (29.86%) plant height (24.34%) and tillers/plant (21.98). Moderate estimates of GCV were obtained for dry matter percent, for all other characters GCV was low. The green fodder yield showed the estimate of PCV (38.28%) in comparison to GCV of 35.82% suggesting environmental influence on this character, which was confirmed by its heritability. The least difference between PCV and GCV for plant height suggested that this character is least affected by environment. In such a situation, selection can be effective on the basis of phenotype alone with equal probability of success.

On the basis of GCV, it is possible to determine the amount of heritable variation. It can be found out with greater degree of accuracy when heritability in conjunction with genetic advance is studied. Hence, both heritability and genetic advance were determined to study the scope of improvement in various characters through selection. The heritability estimates ranged from 53.50% for leaf stem ratio to 97.50% for plant height. High estimates of heritability were also observed for green fodder productivity, days to flowering, crop duration and dry matter yield and moderate estimates for tillers/plant, dry matter (%), green fodder yield and

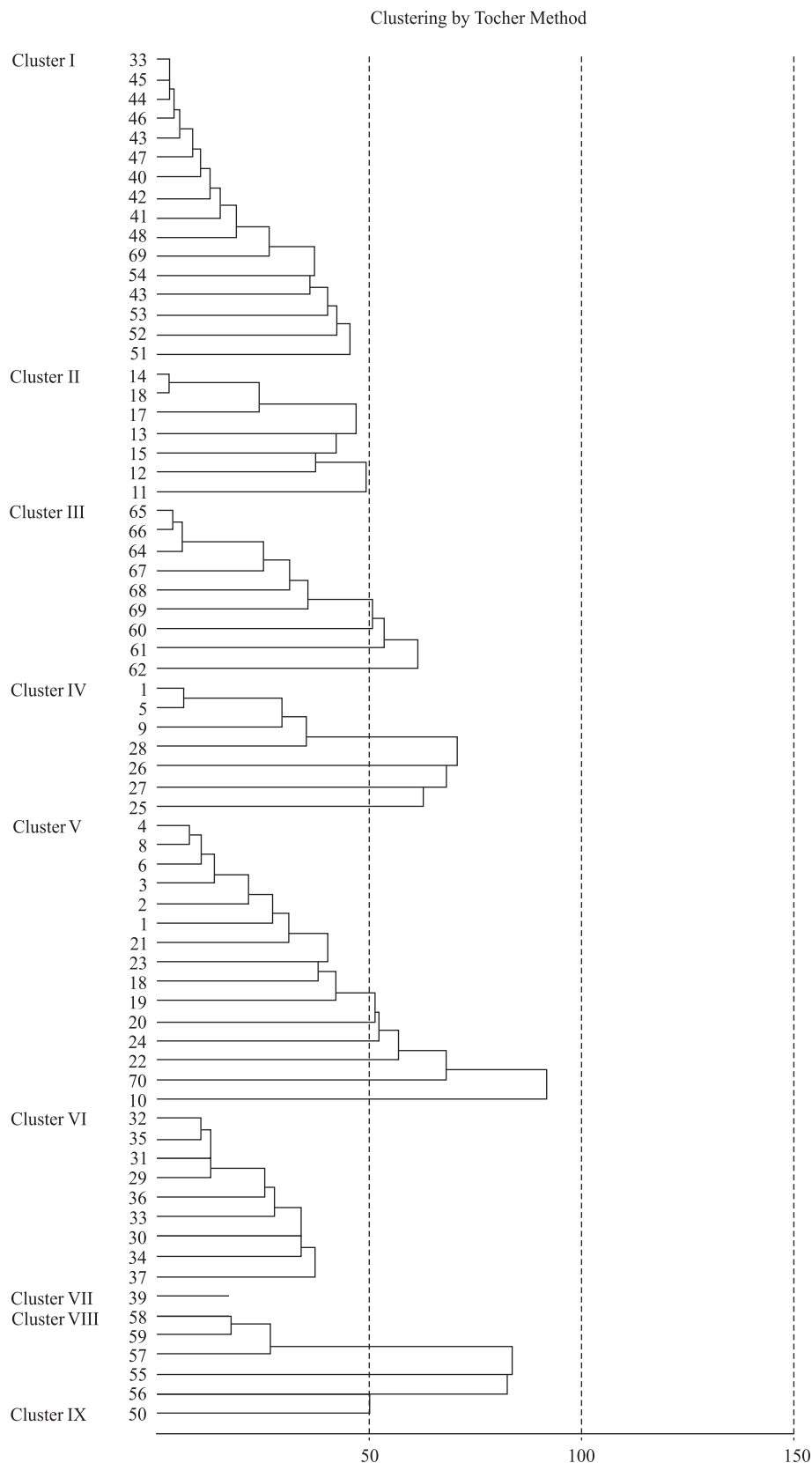


Fig. 1. Different clusters showing the position of genotypes (mentioned by serial numbers)

Table 1. Estimates of mean, range, mean square, genotypic coefficient of variation, (GCV), phenotypic coefficient of variation (PCV), genetic advance (GA) as percent of mean, heritability for eight characters in oat.

Character	Mean	Range		Mean square	GCV	PCV	GA as % of Mean	h ² (broad sense)	r _g with green fodder yield
		Min.	Max.						
Days to flowering	139.05	121.33	165.33	296.02**	7.05	7.32	13.99	92.70	0.232**
Crop duration(days)	151.43	135.33	171.33	226.24**	5.64	5.91	11.10	91.20	0.290**
Plant height (cm)	119.15	57.33	172.73	2544.94**	24.34	24.65	49.50	97.50	0.101
Tillers / plant	22.42	14.55	31.52	79.81**	21.98	24.93	39.93	77.70	0.970**
Leaf/stem ratio	0.46	0.39	0.57	0.006**	8.40	11.47	12.65	53.50	0.134*
Dry matter (%)	21.12	17.20	30.63	24.21**	12.67	14.88	22.24	72.60	0.404**
Green Fodder Productivity (q/ h/ d)	2.07	1.16	3.70	1.17**	29.86	30.93	59.38	93.20	0.985**
Green Fodder Yield (q/ h)	313.86	169.48	553.48	30496.85**	30.14	35.77	52.31	71.00	—
Dry Matter Yield (q/ h)	69.45	33.45	170.54	1944.35**	35.82	38.28	69.05	87.60	0.933**

*, ** = Significant at 5% and 1% level, respectively.

leaf/stem ratio. Moderate estimates of heritability for these characters indicated that environmental effects constitute a sufficient portion of the total phenotypic variation and hence, selection for these characters will be less effective. Expected genetic advance as % of mean for various characters (Table 1) revealed that dry matter yield, green fodder productivity, green fodder yield, tillers/plant and plant height exhibited the high genetic advance. These characters exhibited high GCV, heritability together with high genetic advance indicated the predominance of additive gene effects in controlling these characters. Therefore the characters like dry matter yield, green fodder productivity, green fodder yield and plant height possessing high GCV, heritability and genetic advance as % of mean could be effectively used in selection, as it has been suggested that characters with high heritability coupled with high GA as % of mean would respond to selection better than those with high heritability and low genetic advance.

The 70 genotypes were grouped into seven grouped clusters and two ungrouped clusters (Fig. 1) using Tocher's method with variable number of entries (Table 2), suggesting adequate scope for selecting superior and diverse parents to be exploited for any breeding programme. Cluster I had the maximum number of genotypes (16) with intra-cluster distance 5.50, indicating diversity within the cluster but not to the extent so that they can form separate clusters as there existed genetic similarities among themselves on the basis of multiple characters causing them to belong into a single character. Cluster V consisted of 15 genotypes while cluster III and VI contained 9 genotypes each representing different eco-geographical regions. Cluster II and IV also had equal number of genotypes (7 each). Further, cluster VIII had 5 genotypes while rests of two clusters were solitary entry clusters. The intra- and inter-

cluster distances (D² values) are presented in Table 3. Cluster VIII recorded maximum intra-cluster distance (9.21) followed by cluster IV (8.30) and cluster V (7.54), indicating existence of considerable genetic divergence among constituent genotypes. Hence, parents within the cluster can also be chosen for hybridization programme. The relative distance of each cluster from other clusters (inter-cluster distances) indicated greatest divergence between cluster II and cluster VIII (D=24.28) followed by cluster II and VII (D=23.7), II and IX (D=21.66), V and VIII (D=20.02), indicating greater diversity between genotypes belonging to respective pairs of clusters. The genotypes of the most distant cluster i.e. cluster II and VIII were quite contrasting in performance with respect to plant height, tiller/plant, days to flowering and crop duration. The genotypes of cluster II showed promise with regard to plant height. Ungrouped genotype in cluster IX (SJO-47) seem to be quite promise for many of the green fodder yield attributing traits as it had the highest mean performance for green fodder yield, dry matter yield, green fodder productivity/day, tillers/plant and dry matter (%). This genotype also had contrasting traits with cluster II with respect to plant height, tillers/plant, dry matter (%), and green fodder yield. The contrasting genotypes of these clusters are expected to yield desirable segregants upon hybridization following single plant selection in later generations, suitable for rain-fed conditions with early maturing and high green fodder yield. The clusters I and VII had the lowest inter cluster genetic distance (D = 8.35), suggesting that the cluster VII which have solitary genotype represents more similarity with cluster I, which differed mainly for characters plant height and dry matter (%). The small inter-cluster distance indicates less diversity between the genotypes contained in the clusters. However, these genotypes can be undertaken for hybridization in order to exploit variability for the

specific characters for which the genotype of the two clusters showed marked difference.

In the present study, hybridization between genotypes having higher D-distance are expected to generate exploitable variability for the improvement in the fodder yield and yield related traits as well as are likely to throw desirable transgressive segregants in later generations of hybridization. In the present study, D² analysis revealed the presence of considerable diversity among the genotypes and was observed to be distributed into nine different clusters. Since, the genotype present in the same cluster indicate their close relationship as compared to others (Table 3), it could be expected that all the 16 genotypes present in cluster I were some how genetically related among themselves and were diverse from the genotypes belonging to other classes.

The cluster means of genotypes (Table 4) revealed considerable genetic differences between the groups. The cluster IX registered the highest mean value for green fodder yield (553.48q/h) dry matter yield (170.54q/h), green fodder productivity/day (3.70q/h), tillers/plant (31.52) and dry matter (30.63%). The highest average cluster mean for plant height was reported in cluster II (162.94) followed by cluster V (148.47), whereas, highest cluster mean value for crop duration was observed in cluster IV. The lowest mean value of character days to flowering, which is desirable, was reported in cluster VIII (125.13). The clusters contributing maximum to D² values are to be given greater emphasis for deciding the clusters for the purpose of further selection and hybridization. The maximum percent contributing towards genetic divergence was showed by the characters crop duration

Table 2. Grouping of 70 genotypes into nine clusters

Cluster	No. of genotypes	Genotypes
I	16	SJO-35, SJO-42, SJO-41, SJO-43, SJO40, SJO-44, SJO-37, SJO-39, SJO-38, SJO-45, SJO-66, SJO51, SJO-46, SJO-50, SJO-49, SJO-484
II	7	SJO-14, SJO-16, SJO-17, SJO-13, SJO-15, SJO-12, SJO-11
III	9	SJO-62, SJO-63, SJO-61, SJO-64, SJO-65, SJO-60, SJO-57, SJO-58, SJO-59
IV	7	SJO-1, SJO-5, SJO-9, SJO-25, SJO-23, SJO-24, Palampur-1
V	15	SJO-4, SJO-8, SJO-6, SJO-3, SJO-2, SJO-7, OS-6, SJO-21, Kent, SJO-18, SJO-19, SJO-22, SJO-20, Sabzar, SJO-10
VI	9	SJO-29, SJO-32, SJO-28, SJO-26, SJO-33, SJO-30, SJO-27, SJO-31, SJO-34
VII	1	SJO-36
VIII	5	SJO-55, SJO-56, SJO-54, SJO-52, SJO-53
IX	1	SJO-47

Table 3. Average intra-cluster (diagonal bold) and inter-cluster distances (D values) among the nine clusters in oat

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	5.60	18.47	12.14	11.79	13.83	15.40	8.35	13.12	11.27
II		7.07	18.58	15.03	11.60	17.98	23.79	24.28	21.66
III			7.16	15.51	14.30	12.78	13.30	10.86	17.86
IV				8.30	12.71	16.76	15.86	19.68	17.45
V					7.54	18.76	19.55	20.02	19.83
VI						5.89	15.05	14.63	17.09
VII							0.00	10.47	12.16
VIII								9.21	16.47
IX									0.00

Table 4. Cluster means and (%) contribution of characters towards divergence in oat

Clusters	Days to flowering	Crop duration (days)	Plant height (cm)	Tillers/plant	Leaf/stem ratio	Dry matter (%)	Green fodder productivity (q/ h/d)	Green fodder yield (q/h)	Dry matter yield (q/h)
I	138.13	152.13	110.81	27.96	0.46	22.09	2.85	434.01	95.72
II	145.00	153.57	162.94	21.22	0.46	19.05	1.86	286.25	65.51
III	130.89	144.89	98.93	15.89	0.43	21.58	1.35	195.69	42.36
IV	157.48	167.81	132.18	26.35	0.46	22.83	2.14	358.60	82.15
V	135.60	146.89	148.47	21.94	0.48	21.36	1.99	292.83	62.69
VI	143.74	156.74	92.30	17.29	0.47	17.96	1.41	222.15	47.86
VII	139.67	153.67	78.67	28.15	0.49	19.81	2.87	442.00	87.66
VIII	125.13	139.13	72.60	20.28	0.42	21.06	1.95	272.77	57.24
IX	135.33	149.33	111.67	31.52	0.48	30.63	3.70	553.48	170.54
Contribution (%)	2.17	35.88	14.87	10.83	0.15	14.12	1.04	19.46	1.49

(35.88) followed by green fodder yield (19.46), plant height (14.87) and dry matter (14.12%) tiller/plant (10.83). More than 80% contribution towards total genetic divergence was mainly because of these five characters. Hence, these traits may be considered to be the more important traits for higher green fodder yield. It is observed that the genotypes desirable for different traits belonged to different clusters. On the basis of inter-cluster distances genotypes in cluster II (SJO-14, SJO-16, SJO-17, SJO-13, SJO-15, SJO-12, SJO-11) and in cluster VIII (SJO-55, SJO-56, SJO-54, SJO-52, SJO-53) were found suitable for hybridization programme. The selection of diverse genotypes with desirable traits and in turn utilizing them for multiple crossing programmes amongst themselves is expected to be effective in accumulation of favourable genes for bringing together different desirable traits in to the common genetic background. On the other hand genotype included in the same cluster with a high order of divergence will be expected to provide the best breeding material for achieving the maximum genetic gain for yield *per se*, provided other factors do not operate to limit the realization of the potential. It is encouraging that the divergence revealed in the present genotypes studied due to these characters will offer a good scope of improving green fodder yield in oat. Thus, a crossing programme involving parents selected on the basis of divergences for yield traits may likely to produce an improved genotype of oat suitable for rainfed ecosystem of intermediate Himalayan hills.

References

- Abbas SJ, SRU Shah, G Rasool and I Munir (2008) Analysis of genetic diversity in *genusaavena* Pak. *J. Weed Sci. Res.* **14(1-2)**: 33–41.
- Achleitner A, NA Tinker, E Zechner and H Buerstmayr (2008). Genetic diversity among oat varieties of worldwide origin and associations of AFLP markers with quantitative traits. *Theor. Appl. Genet.* **117(7)**: 1041–53.
- Burton GW (1952) Quantitative inheritance in grasses. Proc. IV Institute Grassland Congress **1**: 155–157.
- Diederichsen A (2008). Assessments of genetic diversity within a world collection of cultivated hexaploid oat (*Avena sativa* L.) based on qualitative morphological characters *Genet. Resour. Crop. Evol.* **55**: 419–440.
- Gupta BK, Bhardwaj BL and Ahuja A (2004) Nutritive value of Fodder crops of Punjab. Punjab Agricultural University, Ludhiana.
- Hanson CH, HF Robinson and RE Comstock (1956) Biometrical studies of yield in segregating population of Korean lespedza. *Agron. J.* **48**: 268–272.
- Johnson HW, HF Robinson and RE Comstock (1955) Estimates of genetic and environmental variability in soybeans. *Agron. J.* **47**: 314–318.
- Mahalanobis PC (1936) On the generalized distance in statistics. *Proc. Nat. Acad. Sci. India* **12**: 49–55
- Rao CR (1952). Advanced biometrical methods in biometric research. John Wiley and Sons Inc., New York, pp 357–363.
- Singh RK and BD Chaudhary (1985) Biometrical methods in quantitative genetic analysis, Kalyani Publishers, New Delhi, pp 229–252.
- Singh SB, BB Gupta and AK Singh (2009) Genetic divergence for morpho-physiological traits and yield components associated to drought tolerance in maize (*Zea mays* L) inbreds. *Indian J. Plant Genet. Resour.* **22**: 102–107.
- Singh SB and AK Singh (2009) Genetic variability, character association and path analysis for green fodder yield and its component characters in oat (*Avena sativa*). *Progressive Res.* **4**: 159–162.

Evaluation of Lettuce Genotypes for Growth and Yield Attributes in Kashmir Valley

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The experiment was conducted during 2006 and 2007 at Sher-e-Kashmir University of Agricultural Sciences & Technology (K), Shalimar, with 25 genotypes of lettuce. Among all the genotypes, LS-2 proved significantly superior to rest of the genotypes in terms of yield (362.60 g/plant) and most of the yield attributing characters. It was statistically comparable with LS-17 (342.31 g/plant). The genotypes LS-11 exhibited highest plant height of 29.09 cm where as maximum plant spread was recorded in LC-4 (37.37cm) followed by LS-15 (37.01cm) and LS-2 (35.98 cm). The genotypes LS-2 (49.26), LS-15 (47.16) and LC-5 (45.46) gave maximum number of leaves/plant, whereas average leaf weight was highest in LS-18 (11.54 g). The leaf area was maximum in SS-12 (246.84 cm²) followed by LS-18 (242.90 cm²). Genotype LS-11 and LS-17 were early in picking recording the value of 45 days under the investigation during individual as well as on pooled data basis. LC-18 and LS-19 were late in picking which took 53 days and 60 days, respectively, with less picking duration of 16 days on pooled data and individual basis. The LS-2 genotype can be recommended for cultivation in this area as they are high yielding and early in picking and given good performance during winter as well as in summer.

Key Words: Evaluation, Improvement, *Lactuca sativa* L., Lettuce, Selection, Variability

Introduction

Lettuce (*Lactuca sativa* L.) is an important salad vegetable and popular in USA, Australia and Europe. Now a days, it has started gaining importance in India especially in big markets of metropolitan cities. It is rich source of Vitamin C, pro-vitamin A and minerals such as calcium, phosphorous, potassium and iron. Vitamins, fibre, folic acid, high potassium and high volume of water make it a heart healthy green vegetable as it helps in lowering cholesterol, blood pressure and other risk factors for heart diseases and also have medicinal properties (Sharma, 2002). Lettuce is used fresh in salads, sandwiches and for garnishing. Besides domestic markets, it has great potential for exporting to neighbouring Middle East countries. The present study was, therefore, undertaken to identify suitable genotypes with desirable yield potential and horticultural characteristics for Kashmir region.

Materials and Methods

The present investigation was carried out at Sher-e-Kashmir University of Agricultural Science and Technology, Kashmir, Srinagar, during winter 2006 and summer 2007. Twentyfive genotypes of lettuce were utilized for the study in randomized block design with three replications. Sowing was done in mid August 2006 for winter crop in raised bed and first week of

February 2007 in hot beds for summer crop. Hot beds prepared with the help of bamboosticks and paddy straw, and beds covered by polythene-sheet during night for protection of nursery from cold air in winter. Five-week-old seedlings were transplanted in the field at 45×45 cm spacing in three rows of 2.25 m accommodating 15 plants of each genotypes in each replication on 15th September and 8th March for winter and summer season, respectively. The FYM and fertilizers were applied as per recommended package of practices i.e. 20 tonnes FYM and 120:90:60 kg NPK/ha. Irrigation was applied at the time of transplantation and subsequent as and when required. Intercultural operations like hoeing, weeding and insecticide application were carried out according to the normal practice to raise a successful crop.

For each growing season, lettuce genotypes were picked when they reached commercial size and subsequent picking was done at 10 days interval. The observation was recorded on five randomly selected plant for each genotype replication-wise on 8 quantitative characters viz. plant height (cm), plant spread (cm), number of leaves/plant, average leaf weight (g), leaf area (cm²), days to first picking, duration of picking and leaf yield/plant (g). Statistical analysis was done according to the methods suggested by Panse and Sukhatme (1967).

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Results and Discussion

Analysis of variance showed highly significant differences among genotypes for all the character under study. The genotypes tested, expressed significant variability for all the traits both in winter as well as in summer indicating a good amount of variability in the present material. The data pertaining to leaf yield and its contributing characters and best five genotypes on mean performance were given in Table 1 and 2, respectively. In regards to plant height, highest plant height was noted in SS-11 during winter, summer as well as on pooled basis, but it was at par with Simpson and LS-2 during winter as well as on pooled basis. The plant spread was recorded as the average spread from North to South and East to West direction which varied from 16.76 cm (LS-19) to 36.33 cm (LC-4) with over all mean value of 29.99 cm during winter and 24.93 cm (LS-20) to 39.13 cm (LC-4) with over all mean of 34.91 cm during summer season. The maximum plant spread was recorded in LC-4 (37.73 cm) which was statistically at par with LS-15 (37.01 cm), LS-2 (35.98 cm) and SS-12 (35.46 cm) on pooled basis.

As regard to number of leaves/plant, genotypes LS-2 (49.26) proved best among all the genotypes studied under this experiment for obtaining maximum number of leaves/plant in both season as well as on pooled basis while, LS-15 (47.16), LC-5 (45.46) and Simpson (44.62) being similar in the respect to descending order. Further, it ranged from 23.30 (LS-20) to 49.26 (LS-2) with over all mean of 37.92 on pooled data basis. In respect of average leaf weight, LS-18 (12.93 g) had highest leaf weight among all the genotypes during winter and on pooled basis, but second position in summer and statistically par with LS-11 (12.53 g) during winter. The leaf area ranged from 151.90 (LS-20) to 277.76 cm² (SS-12) with mean value of 221.59 cm². Maximum leaf area was found in SS-12, during both the seasons, while it was statistically at par with LC-9 (272.50 cm²) and RM (266.18 cm²) during winter and LC-29 (244.00 cm²) and Simpson (222.56 cm²) during summer season.

Genotypes LS-11, LC-24, LS-17, SS-12 and LS-2 were early in picking recording 45 days from date of transplanting with picking duration of 30 days while genotypes LS-19, LS-20 and LS-8 were late in picking recording 65.0, 61.66, and 58.33 days from date of transplanting with picking duration of 13.33, 23.33, 20.0 days, respectively, during winter indicating that these genotypes required considerably more period of time

for their initial establishment in the field than the other genotypes. Whereas in summer, genotypes DPHL-1, LS-11, LC-24, LS-17 and LS-2 were early in picking and recording 45 days from date of transplanting with picking duration of 30 days. LS-19, LS-20 and LS-8 were late in picking, recording 55 days from date of transplanting with picking duration of 20.0, 26.66 and 26.66 days, respectively.

In critical analysis of the data on leaf yield/plant, it was observed that the genotypes LS-2 (362.66g) proved its superiority over rest of the genotypes, except that it was statistically comparable with LS-17 on pooled and winter season, however, during winter. DPHL-1 record highest leaves yield (385.0g) and were statistically at par with LS-2 (347.60 g), Simpson (322.66 g) and LS-17 (321.33 g). Similar observation on mean performance were observed by Singh *et al.* (2000), Sharma (2003) and Araujo *et al.* (2007) for leaf yield/plant in lettuce; Leeper and Scully (1991), Komissarov *et al.* (1980) and Ledo *et al.* (2001) for different traits in lettuce.

Mean performance of the genotypes (Table 1) in both the seasons revealed that no single genotypes were superior for all the traits. Different genotypes were identified to be superior for different traits. The genotypes SS-11, Simpson, LS-2, SS-7 and LC-15 were superior in respect of plant height, and LC-4, LS-15, LS-2, SS-12, LC-15 were desirable in respect of plant spread in both the seasons. The genotypes which were desirable for number of leaves in both the seasons were LS-2, LS-15, LC-5 and LS-17. The desirable genotypes in respect of leaf area were SS-12, Simpson, LS-2 and LS-21, while LS-18 and LS-11 for average leaf weight in both seasons. The desirable genotypes in respect of early picking were LS-11, LS-17, SS-12, LC-9, LS-2, LC-24 and DPHL-1, while the genotypes LC-29, LC-5, LS-18, LS-19, LS-20 and LS-8 were in general late in picking as these genotypes required considerably more period of time for their initial establishment in the field than the other genotypes in winter as well as in summer. Genotypes, LS-2, LS-17, LC-24 and LC-4 exhibited better performance for leaf yield/plant in both the seasons. However, DPHL-1 performed better only in summer.

An overall perusal of Table 2, indicated that the genotypes LS-2, LS-17, in both seasons; LC-24, LC-4 and LC-9 in winter; Simpson, LC-5 and LS-15 in summer besides being high yield also exhibit superior performance for other important yield attributing traits

Table 1. Mean performance of various lettuce genotypes for different characters under winter and summer season

Genotypes	Plant height (cm)		Pooled	Plant spread (cm)		Pooled	Number of leaves/plant		Pooled	Average leaf weight (g)		Pooled
	Winter	Summer		Winter	Summer		Winter	Summer		Winter	Summer	
LC-2	14.80	18.00	16.40	31.80	35.40	33.65	32.60	39.40	36.00	10.73	8.00	9.36
LC-4	16.76	18.80	17.78	36.33	39.13	37.73	43.33	40.93	42.93	9.66	8.56	9.11
LC-5	17.26	19.36	18.31	32.03	35.70	33.86	38.06	52.86	45.46	9.06	7.00	8.03
LC-9	16.46	20.00	18.29	30.63	36.93	33.78	35.33	41.00	38.16	10.20	8.63	9.41
LC-14	16.33	17.16	16.74	30.13	35.00	32.61	32.80	53.46	43.13	7.40	6.20	6.80
LC-15	17.46	19.13	18.29	32.03	37.10	34.56	34.73	49.73	42.23	7.86	7.06	7.46
LC-16	17.13	17.60	17.36	28.76	38.60	33.68	33.00	38.80	35.90	10.13	7.96	9.04
LC-24	16.50	18.33	17.41	33.26	33.83	33.54	35.06	41.46	38.26	12.40	9.70	11.05
LC-29	13.40	18.63	16.01	24.36	28.73	26.54	22.66	27.0	24.83	10.46	9.66	10.06
LS-2	17.46	19.66	18.53	34.73	37.23	35.98	43.53	55.00	49.26	10.06	7.56	8.81
LS-8	14.20	19.40	16.80	30.16	34.83	32.54	34.36	43.66	39.01	7.06	7.00	7.03
LS-11	17.10	17.80	17.45	33.23	35.90	34.36	31.33	42.26	36.79	12.53	10.30	11.42
LS-15	16.33	18.90	17.61	36.00	38.03	37.01	39.86	54.46	47.16	8.70	6.96	7.83
LS-16	15.80	18.20	17.00	31.53	37.06	34.29	35.00	41.86	38.40	7.76	7.26	7.51
LS-17	17.46	19.33	18.39	34.80	33.90	34.35	35.73	48.93	42.33	10.73	7.10	8.91
LS-18	13.60	19.66	16.60	25.60	33.03	29.31	22.06	32.93	27.49	12.93	10.16	11.54
LS-19	10.86	17.46	14.16	16.76	32.00	24.38	22.46	33.33	27.89	10.40	9.40	9.90
LS-20	10.06	17.13	13.59	16.83	24.93	20.80	18.20	28.40	23.30	8.96	7.10	8.03
LS-21	13.40	18.03	15.71	27.83	31.10	29.46	29.20	27.33	28.26	11.60	8.33	9.96
SS-7	18.46	19.53	18.99	31.73	33.43	32.58	34.73	48.86	41.79	10.13	7.26	8.69
SS-11	18.66	21.53	20.09	32.16	35.70	33.93	33.73	45.26	39.49	10.46	7.46	8.96
SS-12	16.80	19.93	18.36	32.46	38.46	35.46	31.86	43.60	37.73	8.93	8.23	8.58
DPHL-I	16.33	18.66	17.46	28.10	35.50	31.80	33.40	53.73	43.56	9.96	7.76	8.86
Simpson	17.60	20.00	18.60	28.76	36.16	32.47	35.06	54.33	44.62	10.06	7.50	8.78
RM (C)	16.46	18.76	17.61	29.86	35.03	32.44	30.86	38.40	34.63	10.40	8.83	9.61
G. Mean	15.75	18.59	17.17	29.99	34.91	32.45	32.76	43.08	37.92	9.94	8.04	8.99
LSD at 5%	1.63	0.96	1.29	2.73	2.61	2.67	2.42	4.66	3.59	1.12	0.84	0.98
SED	0.81	0.48	0.64	1.36	1.30	1.33	1.20	2.32	1.76	0.55	0.41	0.48
CV%	6.30	3.16	4.73	5.56	4.56	5.06	4.50	6.59	5.54	6.88	6.36	6.62
Genotypes	Leaf area (cm ²)		Pooled	Days to first picking		Pooled	Duration of picking (days)		Pooled	Leaf yield/plant (g)		Pooled
	Winter	Summer		Winter	Summer		Winter	Summer		Winter	Summer	
LC-2	204.51	148.43	176.47	48.33	48.33	48.33	26.66	26.66	26.66	297.00	251.60	274.30
LC-4	240.46	183.63	212.04	51.66	48.33	49.96	26.66	30.00	28.33	335.60	288.60	312.30
LC-5	182.28	148.00	165.04	51.66	48.33	49.96	23.33	26.66	24.99	258.66	291.60	275.13
LC-9	272.50	177.34	224.92	45.00	45.00	45.00	26.66	30.00	28.33	333.60	285.60	194.60
LC-14	180.71	151.92	166.32	55.00	51.66	53.30	20.00	23.33	21.65	250.30	262.30	256.30
LC-15	195.96	207.70	201.83	51.66	51.66	51.66	20.00	20.00	20.00	241.00	285.30	263.15
LC-16	215.83	170.53	193.18	51.66	48.33	49.96	23.33	26.66	24.99	258.00	244.00	251.00
LC-24	259.74	199.30	229.52	45.00	45.00	45.00	30.00	30.00	30.00	363.33	306.00	334.66
LC-29	206.95	224.00	215.47	51.66	48.33	49.96	33.33	36.66	34.99	189.66	179.06	184.36
LS-2	252.16	227.60	239.88	45.00	45.00	45.00	30.00	30.00	30.00	377.60	347.60	362.60
LS-8	193.63	199.34	196.49	58.33	55.00	56.65	20.00	26.66	23.30	214.60	250.30	232.45
LS-11	241.53	193.29	217.41	45.00	45.00	45.00	30.00	30.00	30.00	322.66	356.00	314.33
LS-15	179.77	188.38	184.07	51.66	45.00	48.33	30.00	30.00	30.00	317.00	293.60	305.00
LS-16	193.56	144.73	169.15	48.33	48.33	48.33	20.00	23.33	21.65	256.30	222.60	239.45
LS-17	247.29	161.00	204.15	45.00	45.00	45.00	30.00	30.00	30.00	373.33	321.33	342.31
LS-18	262.15	223.76	242.90	55.00	51.66	53.30	23.33	23.33	23.33	225.66	266.60	246.13
LS-19	191.66	192.41	192.04	65.00	55.00	60.00	13.33	20.00	16.66	202.60	259.33	230.97
LS-20	151.90	142.86	147.38	61.66	55.00	58.30	23.33	26.66	24.99	138.00	125.33	131.67
LS-21	246.01	216.83	231.16	51.66	51.66	51.66	30.00	30.00	30.00	285.30	276.30	280.80
SS-7	242.10	188.40	215.30	48.33	48.33	48.33	26.66	26.66	26.66	296.33	274.60	285.47
SS-11	187.88	207.11	197.49	48.33	45.00	46.65	20.00	20.00	20.00	317.66	266.00	291.83
SS-12	277.76	217.93	246.84	45.00	45.00	45.00	30.00	30.00	30.00	266.60	283.60	275.10
DPHL-I	192.50	198.23	195.36	48.33	45.00	46.66	23.33	30.00	26.66	272.00	385.00	328.50
Simpson	254.80	222.56	238.68	48.33	45.00	46.65	26.66	30.00	28.33	278.60	322.66	302.30
RM (C)	266.18	148.60	207.09	48.33	48.33	48.33	23.33	26.66	24.99	262.33	260.00	261.17
G. Mean	221.59	187.34	204.44	50.60	48.33	49.46	25.20	27.20	26.20	277.37	276.25	276.81
LSD at 5%	16.14	11.91	14.02	7.70	6.69	7.19	6.84	6.46	6.65	20.19	23.60	21.89
SED	8.02	5.92	6.97	3.83	3.32	3.57	3.40	3.21	3.30	10.02	11.76	10.89
CV%	4.43	3.87	4.15	9.28	8.43	8.85	16.54	14.47	15.50	4.40	5.21	4.80

Table 2. Best five genotypes on the basis of mean performance for different characters in lettuce genotypes

Traits	Winter	Summer	Pooled
Plant height (cm)	SS-11 (18.66)	SS-11 (21.53)	SS-11 (20.09)
	SS-7 (18.46)	LC-9 (20.00)	SS-7 (18.99)
	Simpson (17.60)	Simpson (20.0)	Simpson (18.60)
	LS-2 (17.46)	SS-12 (19.93)	LS-2 (18.53)
	LS-17 (17.46)	LS-2 (19.60)	SS-12 (18.36)
Plant spread (cm)	LC-4 (36.33)	LC-4 (39.13)	LC-4 (37.73)
	LS-15 (36.00)	LC-16 (38.6)	LS-15 (37.01)
	LS-17 (34.80)	SS-12 (38.46)	LS-2 (35.98)
	LS-2 (34.73)	LS-15 (38.03)	SS-12 (35.46)
	LC-24 (33.26)	LS-2 (37.23)	LC-15 (34.86)
No. of leaves/plant	LS-2 (43.53)	LS-2 (55.0)	LS-2 (49.26)
	LC-4 (43.33)	LS-15 (54.46)	LS-15 (47.16)
	LS-15 (39.86)	DPHL-1 (53.73)	LC-5 (45.46)
	LC-5 (38.06)	LC-14 (53.46)	Simpson (44.62)
	LS-17 (35.73)	LC-5 (52.86)	DPHL-1 (43.56)
Average leaf weight (g)	LS-18 (12.93)	LS-11 (10.3)	LS-18 (11.54)
	LS-11 (12.53)	LS-18 (10.16)	LS-11 (11.42)
	LC-24 (12.4)	LC-24 (9.7)	LC-24 (11.05)
	LS-21 (11.6)	LC-29 (9.66)	LC-29 (10.06)
	LC-2 (10.73)	LS-19 (9.4)	LS-21 (9.96)
Leaf area (cm ²)	SS-12 (277.76)	LS-2 (227.60)	SS-12 (246.84)
	LC-9 (272.50)	LC-29 (224.0)	LS-18 (242.90)
	RM (266.15)	LS-18 (223.76)	LS-2 (239.88)
	LS-18 (262.15)	Simpson (222.56)	Simpson (238.68)
	LC-24 (259.74)	SS-12 (217.93)	LS-21 (231.16)
Days to first picking	LS-11 (45.00)	DPHL-1 (45.00)	LS-11 (45.00)
	LS-17 (45.00)	LS-11 (45.00)	LC-24 (45.00)
	SS-12 (45.00)	LC-24 (45.00)	LS-17 (45.00)
	LC-9 (45.00)	LS-17 (45.00)	LS-2 (45.00)
	LS-2 (45.00)	SS-12 (45.00)	LC-9 (45.00)
Duration of picking (days)	LC-29 (33.3)	LC-29 (36.66)	LC-29 (34.98)
	LS-11 (30.0)	LS-11 (30.0)	LC-24 (30.0)
	LS-12 (30.0)	LC-24 (30.0)	LS-17 (30.0)
	LS-2 (30.0)	LS-17 (30.0)	LS-2 (30.0)
	SS-12 (30.0)	LS-2 (30.0)	SS-12 (30.0)
Leaf yield/plant (g)	LS-2 (377.60)	DPHL-1 (385.00)	LS-2 (362.6)
	LS-17 (373.33)	LS-2 (347.6)	LS-17 (342.31)
	LC-24 (363.33)	Simpson (322.6)	LC-24 (334.6)
	LC-4 (335.60)	LS-17 (321.33)	DPHL-1 (328.5)
	LC-9 (333.30)	LC-24 (306.0)	LS-11 (314.33)

namely, plant spread, number of leaves, leaf area, days to first picking and duration of picking. Since different genotypes were identified to be performing differently for yield attributing and quality traits, hence, these diverse genotypes with superior characters could be involved in the hybridization programme for assembling of desirable traits in single genotypes or could be very well utilized for commercial growing in the valley. Similar observations on mean performance of lettuce have been reported by Singh *et al.* (2000), Sharma (2003) and Araujo *et al.* (2007) for yield.

On the basis of above results the genotypes LS-2, LS-17, LC-4 and LC-24 was found to be performing better in terms of yield and yield attributing characters

like number of leaves/plant, plant spread, early in picking which in turn gives longer duration of picking.

References

- Araujo WF, EP Trajano, JLR Neto, MR Mourao and PRVS Pereira (2007) Evaluation of lettuce cultivars under protected cultivation in Boa Vista, Roraima, Brazil. *Acta Amazonica* **37(2)**: 299–302.
- Komissarov A, NI Timin and VA Popova (1980) Study of variation in yield and head quality character in lettuce varieties, *Doklady. TSKHA* **226**: 107–111
- Ledo FJS, VWD Casali and CD Cruz (2001) Genetic analysis in a lettuce diallel. *Pesquisa Agropecuaria Brasileira* **36(3)**: 493–499.
- Leeper PV and B Scully (1991) Valcus a cos lettuce cultivars for Southern Texas. *Hort. Sci.* **26(7)**: 928–929.

- Panse VG and PV Sukhatme (1967) Statistical Methods of Agriculture Workers, Indian Council of Agricultural Research, New Delhi, pp 58–67.
- Sharma DK (2003) Studies on evaluation and commercialization of exotic vegetables for sustainable agriculture production in Himachal Pradesh. *Haryana J. Hort. Sci.* **32**: 130–133.
- Sharma JP (2002) Crop production technology for cold arid region. Kalyani Publishers, Ludhiana, New Delhi, pp 220–226.
- Singh D, AK Atwal and KL Bajaj (2000) Evaluation of some promising type lettuce cultivars for leaf and quality characters. *Veg. Sci.* **27**: 92–93.

Studies on Genetic Variability and Divergence in Sweet Gourd (*Momordica subangulata* ssp. *renigera* [(G. Don) W.J. de Wilde]) Accessions Collected from West Bengal

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Eleven genotypes were evaluated for 14 quantitative and two qualitative components during the rainy season of 2007–08 and 2008–09. The genotype $\times$ environment interactions were non-significant for all the characters, hence, the data were pooled over the years and discussed on the basis of mean of two years. Analysis of variance indicated significant differences for all the characters investigated. High GCV and PCV values were observed for characters like primary branches/vine followed by total fruit yield/vine, fruit weight and protein content. High heritability coupled with low genetic advance was observed for almost all the quantitative and qualitative characters. High heritability coupled with exceptional high genetic advance was found for total fruit yield/vine. Correlation studies in relation to various characters revealed that total fruit yield/vine was positively and significantly correlated to fruit weight, fruit length, fruit diameter, fruit girth and protein content. Days to first female flower appearance which reflects the earliness to fruiting was positively and significantly associated with days to first male flower appearance and pedicel length. Among the biochemical traits, protein content showed significant and positive correlation with fruit weight, fruit length, fruit diameter, fruit girth and total fruit yield/vine. Path analysis at phenotypic level revealed that total fruit yield/vine was positively dependent on characters like number of fruits/vine and fruit weight.

Key Words: Correlation, Genetic divergence, *Momordica subangulata*, Path Analysis, Variability

Introduction

Momordica subangulata ssp. *renigera* [(G. Don) W.J. de Wilde] belongs to the melon family (Cucurbitaceae) and is indigenous to South-East Asia. It is also known as baby jackfruit, spiny bitter gourd and sweet gourd. Its Latin name is *Momordica subangulata* ssp. *renigera* (G. Don) W.J. de Wilde, “Bhat karela” (Indian name), “spiny bitter gourd, sweet gourd (English), “*Kakrol* or *Kakur*” (Hindi). Different research workers in India and South-East Asia treat dioecious species in the genus *Momordica* differently. The cultivated ‘*bhat karela*’ of East and North-East India is referred to as *Momordica dioica* Roxb. by botanists and herbarium curators whereas agricultural scientists in general designate it as *Momordica cochinchinensis*. A critical study of 266 herbarium sheets housed at CAL and BSISH and *in situ* field studies at specific pockets in the North East India followed by preliminary characterization revealed its correct identity as *Momordica subangulata* ssp. *renigera* [(G. Don) de Wilde]. The species was found in wild as well as in homestead cultivation in North-East India and exemplify direct utilization of biodiversity

by indigenous people. The vegetable is rich in calcium, phosphorous, iron, carotene, lycopene and protein. It is mostly dioecious and propagated vegetatively through tuberous roots/vine cuttings. They grow in warm and humid weather and tuberous roots are planted in pits. The vines are trained on bowers and 5 to 10 % of male parents are provided for good fruit setting. Plantation is done at the onset of summer with the first shower, flowering starts in April and fruiting ends in October-November. The plants remain dormant in winter. The tubers are left *in situ* and they over winter. It is an important summer vegetable crop in West Bengal. It has many advantages like high market price, good nutritional value and keeping quality is longer. Being a minor crop not much attention was focused on improvement of this crop in the past but with its popularity gaining high among the masses, development programmes had been initiated on this crop. Collection and evaluation of the existing germplasm and selection of better parents are pre-requisite for commencing a breeding programme in any crop. Besides, knowledge of genetic diversity and relationship among the sets of

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germplasm is critical to plant improvement. Keeping the importance of this cucurbit and the lack of information on genetic architecture of the breeding population the present investigation was under taken to know the genetic divergence, correlation and path coefficient among yield and it's contributing characters.

Materials and Methods

The experimental material consisted of 11 genotypes of sweet gourd collected from different parts of West Bengal viz., Malda Selection-1, Malda Selection-2, Malda Selection-3, Malda Selection-4, Joynagar Selection-1, Joynagar Selection-2, Baruipur Selection-1, Barasat Selection-1, Bonga Selection-1, Bonga Selection-2 and Bonga Selection-3. The experiment was laid out in randomized block design (RBD) during the onset of rainy season during 2007–08 and 2008–09 having three replications of each genotype. The tuberous roots were sown on two ridges in each plot, having a spacing of 0.75 m between plant-plant and 1.0 m in between the ridges, ensuring 8 plants/plot. Manures like - FYM @ 20–25 t/ha as basal dose along with half dose of nitrogen @ 35kg/ha, full dose of P_2O_5 @ 25kg/ha and full dose of K_2O @ 25kg/ha were applied during field preparation. The remaining amount of nitrogen i.e. 35 kg was applied in two split doses, the first being applied one month after sowing and the second one at the initiation of flowering and fruit setting. Nitrogen in the form of urea and phosphorus in the form of single super phosphate and potash in the form of murate of potash were applied to the experimental plots. Essential intercultural operations such as weeding, staking, trailing and timely irrigation were carried out as and when required. Plant protection measures were carried out at regular intervals by application of pesticides to protect and prevent the incidence of pests like fruit fly, red pumpkin beetle, aphid and red spider mite.

Observations on various morphological, biochemical and other yield-contributing traits viz., vine length (m), primary branches/vine, node to which first female flower appears, days to first male flower appearance, days to first female flower appearance, fruit length (cm), fruit girth (cm), fruit diameter (cm), pedicel length (cm), number of fruits/vine, average fruit weight (g), days taken from fruit set to edible maturity, total fruit yield/vine (g), number of seeds/fruit, protein (g/100 g) and calcium content (mg/100 g) were scored on five plants randomly selected from each plot of the designated replications, representing

the genotypes of sweet gourd. The estimation of calcium and protein was done as per the method described by Rangana (1986) and Lowry (1951), respectively. Plot Means were used for standard analysis using the statistical package SPAR-2 developed by Indian Agricultural Statistical Research Institute (IASRI) and Genres (version 2.01) developed by Pascal International Software Solutions. The genotypic (GCV) and phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance were worked out as per the formula given by Johnson *et al.* (1955). The genotypic and phenotypic correlations were calculated as per the method of Al-Jibouri *et al.* (1958). Path coefficient analysis was done according to the method given by Dewey and Lu (1959). Mahalanobis (1936) D^2 statistics was used to assess genetic diversity. Genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952).

Results and Discussion

Analysis of variance for all the quantitative and qualitative characters revealed that mean squares were highly significant for all the characters. The interactions between genotype $\times$ environment were non-significant for all the traits, hence, the generated data were pooled and discussed on the basis of mean of two years. Substantial variability as evidenced from range, PCV and GCV was noted for all the quantitative and qualitative traits (Table 1). The PCV was slightly higher to more or less similar to the corresponding GCV for all the traits, justifying that variability is due to genetic constitution. Among the quantitative traits, the PCV and GCV values were higher for characters like primary branches/vine i.e. 33.56 and 34.11, respectively, followed by total fruit yield/vine (32.17 and 32.91) and fruit weight (30.90 and 31.17). Among qualitative traits PCV and GCV was high for protein content (22.53 and 22.91). Selection of these traits offers good opportunity for improvement of this crop and probability of getting high performance recombinant segregants will be more. Moderate GCV and PCV values were obtained for number of seeds/fruit, number of fruits/vine, pedicel length, node to which first female flower appears, vine length, fruit length and calcium content. The coefficient of variation under both GCV and PCV was low for days to first female flower appearance, days to first male flower appearance, fruit girth, fruit length and days taken from fruit set to edible maturity. Our findings are in accordance to those of Maharana *et al.* (1995), Rasul *et al.* (2002), Ram *et al.* (2004) and Bharathi *et al.* (2006).

Table 1. Grand mean, range, phenotypic and genotypic coefficient of variation, heritability (h^2), genetic advance and genetic advance as percent of mean for different quantitative and qualitative characters among 11 accessions of sweet gourd

Characters	Grand mean	Range	GCV	PCV	h^2 (%)	GA	GA as % of Mean
Vine length (m)	2.64	1.86–3.50	15.12	17.84	71.84	0.70	26.40
Primary branches/vine	4.32	1.35–7.80	33.56	34.11	96.78	2.94	68.01
Node to which first female flower appears	23.35	15.00–36.00	18.08	18.62	94.23	8.44	36.15
Days to first male flower appearance	53.18	46.00–62.00	11.05	11.52	91.96	11.61	21.83
Days to first female flower appearance	61.31	50.00–72.00	11.45	11.95	92.03	13.91	22.69
Fruit weight (g)	45.47	18.90–68.50	30.90	31.17	98.28	28.70	63.11
Fruit length (cm)	6.09	3.85–7.80	16.21	16.53	96.15	1.99	32.75
Fruit diameter (cm)	4.53	3.20–5.90	10.58	10.88	94.61	0.26	21.21
Fruit girth (cm)	13.59	9.90–15.80	10.91	11.18	95.32	2.98	21.95
Pedicle length (cm)	12.89	7.50–17.90	20.97	21.06	99.15	5.55	43.02
Days taken from fruit set to edible maturity	16.36	12.00–19.00	7.96	9.16	75.47	2.00	14.24
Number of fruits per vine	23.16	13.00–36.00	20.19	21.41	88.88	9.08	39.21
Protein content (g/100g)	0.48	0.30–0.72	22.53	22.91	96.61	0.22	45.61
Number of seeds per fruit	45.65	24.00–68.00	24.09	24.13	99.66	22.61	49.55
Calcium content (mg/100g)	60.35	32.60–72.56	15.56	15.90	95.61	18.91	31.34
Total fruit yield per vine (g)	1022.06	580.0–1490.0	32.17	32.91	95.53	661.89	64.76

The magnitude of heritability in broad sense was high for most of the traits under study except for vine length and days taken from fruit set to edible maturity (Table 1) thus, suggesting that the highly heritable traits were least affected by environmental variation and selection based on phenotypic performance would be reliable. Similar findings were also reported by Ram *et al.* (2004) and Bharathi *et al.* (2006). High heritability coupled with low genetic advance were observed for almost all the quantitative and qualitative characters like protein content, fruit diameter, fruit length, primary branches/vine, fruit girth, pedicle length, node to which first female flower appears and number of fruits/vine except for total fruit yield/vine indicating that these characters are mostly controlled by non-additive genes either dominant or epistasis and improvement can be made by intermating the superior genotypes of the segregating population to develop multiple crosses and the desirable genes can be accumulated in the lines. High heritability coupled with exceptional high genetic advance was found for total fruit yield/vine thus indicating that this trait was controlled by additive gene action and offers the more selective criteria for selection. High heritability coupled with moderate genetic advance were observed in traits like fruit weight, number of seeds/fruit and calcium content. High heritability coupled with extremely low genetic advance was observed for protein content. Moderate heritability coupled with low genetic advance was observed in vine length and days taken to first female flower appearance which might be attributed to non-additive gene action and thereby, simple selection would not be rewarding.

The genotypic correlation in general was higher in magnitude than corresponding phenotypic correlation (Table 2) thereby indicating that there was inherent association among various characters. Genotypic correlation studies in relation to various characters revealed that total fruit yield/vine was positively and significantly correlated to fruit weight, fruit length, fruit diameter, fruit girth and protein content. Phenotypic correlation to different characters revealed that total fruit yield/vine was significantly and positively associated with traits like fruit weight, fruit length, fruit diameter, fruit girth and protein content. Days taken from fruit set to edible maturity was significantly and positively associated with vine length and negatively associated with fruit diameter in a significant manner. Node to which first female flower appears was significantly and negatively correlated to primary branches/vine. Similar findings were observed by Bharathi *et al.* (2005). Days to first female flower appearance which reflects the earliness to fruiting was positively and significantly associated with days to first male flower appearance and pedicle length. Fruit weight showed positive and significant association with fruit length, fruit diameter, fruit girth, protein content and total fruit yield per vine. Among the biochemical traits protein content showed significant and positive correlation with fruit weight, fruit length, fruit diameter, fruit girth and total fruit yield/vine while calcium content showed significant and positive correlation only with number of fruits/vine at genotypic level. Bharathi *et al.* (2005) in their study observed that total yield/vine was negatively

Table 2. Correlation coefficients at phenotypic (P) and genotypic (G) levels among different traits

Characters	Vine length (m)	Primary branches per vine	Node to which first female flower appears	Days to first male flower appearance	Days to first female flower appearance	Fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit girth (cm)	Pedicel length (cm)	Days taken from fruit set to edible maturity	Number of fruits per vine	Protein content (g/100g)	Number of seeds per fruit	Calcium content (mg/100g)	Total fruit yield per vine (g)
Vine length (m)	P 1.000	0.258	-0.470	0.297	0.403	-0.439	-0.602*	-0.414	-0.610	0.561	0.545	0.122	-0.281	0.307	-0.253	-0.221
Primary branches/vine	G 1.000	0.323	-0.556	0.344	0.432	-0.531	-0.684*	-0.471	-0.705*	0.680*	0.785**	0.224	-0.351	0.357	-0.295	-0.230
	P 1.000	0.323	-0.635*	0.045	0.112	0.320	-0.005	0.288	0.013	0.429	0.152	0.148	0.583	0.276	0.098	0.240
Node to which first female flower appears	G 1.000	0.323	-0.663*	0.047	0.098	0.323	-0.017	0.284	-0.001	0.445	0.168	-0.122	0.601	0.287	0.088	0.271
	P 1.000	0.323	-0.663*	-0.337	-0.408	0.084	0.426	0.282	0.373	-0.565	-0.349	0.344	-0.018	-0.291	0.148	0.282
Days to first male flower appearance	G 1.000	0.323	0.901**	-0.384	-0.389	0.093	0.432	0.320	0.418	-0.578	-0.413	0.377	-0.033	-0.302	0.144	0.295
	P 1.000	0.323	0.901**	1.000	0.967**	-0.465	-0.354	-0.289	-0.342	0.801**	0.086	0.246	-0.364	0.154	0.352	-0.294
Flower appearance	G 1.000	0.323	0.967**	1.000	0.967**	-0.485	-0.365	-0.320	-0.369	0.838**	0.165	0.313	-0.381	0.166	0.360	-0.292
	P 1.000	0.323	0.967**	1.000	0.967**	-0.369	-0.342	-0.286	-0.286	0.845**	0.229	0.258	-0.245	0.091	0.414	-0.190
Days to first female flower appearance	G 1.000	0.323	0.967**	1.000	0.967**	-0.391	-0.336	-0.333	-0.312	0.890**	0.298	0.326	-0.253	0.101	0.434	-0.181
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.741**	0.762**	-0.312	-0.184	-0.272	-0.870**	0.103	0.102	0.711*
Fruit weight (g)	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Fruit length (cm)	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Fruit diameter (cm)	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Fruit girth (cm)	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Pedicel length (cm)	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Days taken from fruit set to edible maturity	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Number of fruits/vine	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Protein content (g/100 g)	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Number of seeds/fruit	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Calcium content (mg/100 g)	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
Total fruit yield/vine (g)	G 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**
	P 1.000	0.323	0.967**	1.000	0.967**	1.000	0.865**	0.766**	0.784**	-0.320	-0.237	-0.295	0.894**	0.102	0.166	0.735**

Note: *and **significant at 5% and 1% levels of significance, respectively

correlated with the number of days to flowering which is in agreement to our findings.

Path analysis at phenotypic level (Table 3) revealed that the largest direct effect on total fruit yield/vine was through traits like number of fruits/vine (0.631) and fruit weight (0.461). The phenotypic direct effect was positive but moderate for protein content, fruit length and vine length. Days to first female flower appearance, number of seeds/fruit and pedicel length contributed the least towards total fruit yield/vine. Rest of the characters exhibited negative direct effect towards total fruit yield/vine, the highest being contributed by days to first male flower appearance (−0.229) followed by fruit girth, calcium content, days taken from fruit set to edible maturity and fruit diameter. Thus, it can be ascertained that for selecting high yielding types emphasis should be laid on traits like number of fruits/vine and fruit weight. The residual effect was low suggesting the inclusion of maximum fruit yield influencing characters in analysis. Our findings could be related to those of Dey *et al.* (2007), Bhawe *et al.* (2003) and Sharma and Bhutani (2001).

Multivariate analysis based on D^2 statistics indicated the presence of considerable amount of genetic diversity among the genotypes studied. The genotypes were grouped

into three clusters with cluster I being the largest having five genotypes, followed by cluster III and II having four and two genotypes, respectively. Genotypes from different geographical regions were grouped in the same cluster indicating no relationship exists between geographical distribution and genetic divergence. The intra- and inter-cluster distance represented the index of genetic diversity among the clusters (Table 5). The data suggest that intra-cluster distance was high in Cluster I followed by Cluster III and Cluster II. Inter-cluster distances between II and III was maximum followed by I and III. Genotypes belonging to the cluster having maximum inter-cluster distance are genetically more divergent and hybridization between genotypes of divergent cluster is likely to produce wide variability. The cluster-wise mean values (Table 6) showed that the differences in cluster means were substantially high for characters like days to first male flower appearance, days to first female flower appearance, fruit weight, protein content, number of seeds/fruit and calcium content. Cluster I was having maximum number of genotypes and was not having any highest mean values for any of the traits under study. Cluster II had highest mean values for characters like node to which first female flower appears, fruit weight, fruit length, fruit diameter,

Table 3. Phenotypic path values among fifteen characters in sweet gourd (*Momordica subangulata* ssp. *renigera* (G.Don) W.J. de Wilde). (Dependent Variable – Total fruit yield/vine)

Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	0.155	−0.046	0.068	−0.079	0.030	−0.245	−0.193	0.001	0.032	0.013	−0.012	0.141	−0.118	0.017	0.005
2	0.050	−0.142	0.081	−0.011	0.006	0.149	−0.005	−0.001	−0.001	0.008	−0.003	−0.077	0.202	0.014	−0.001
3	−0.086	0.094	−0.123	0.088	−0.027	0.043	0.119	−0.001	−0.019	−0.011	0.006	0.238	−0.011	−0.015	−0.002
4	0.053	−0.007	0.047	−0.229	0.067	−0.223	−0.103	0.001	0.017	0.015	−0.002	0.198	−0.128	0.008	−0.006
5	0.067	−0.013	0.048	−0.221	0.069	−0.181	−0.095	0.001	0.014	0.016	−0.004	0.203	−0.086	0.005	−0.007
6	−0.082	−0.046	−0.011	0.111	−0.027	0.461	0.252	−0.002	−0.035	−0.006	0.004	−0.186	0.300	0.005	−0.002
7	−0.106	0.002	−0.052	0.084	−0.023	0.413	0.282	−0.002	−0.040	−0.007	0.005	0.012	0.248	−0.001	−0.004
8	−0.073	−0.040	−0.039	0.073	−0.023	0.353	0.215	−0.002	−0.036	−0.004	0.010	0.031	0.220	0.016	−0.003
9	−0.109	−0.001	−0.051	0.084	−0.022	0.361	0.248	−0.002	−0.046	−0.007	0.008	0.040	0.207	0.003	−0.004
10	0.105	−0.063	0.071	−0.192	0.061	−0.147	−0.112	0.001	0.016	0.018	−0.004	0.176	−0.034	0.021	−0.005
11	0.122	−0.024	0.051	−0.038	0.021	−0.109	−0.097	0.001	0.026	0.006	−0.015	−0.044	−0.019	−0.014	0.005
12	0.035	0.017	−0.046	−0.072	0.022	−0.136	0.005	−0.001	−0.003	0.005	0.001	0.631	−0.025	−0.001	−0.011
13	−0.054	−0.085	0.004	0.087	−0.018	0.412	0.208	−0.001	−0.028	−0.002	0.001	−0.046	0.336	−0.001	−0.005
14	0.055	−0.041	0.037	−0.038	0.007	0.047	−0.004	−0.001	−0.003	0.008	0.004	−0.012	−0.002	0.048	0.003
15	−0.046	−0.012	−0.018	−0.082	0.030	0.054	0.070	−0.001	−0.012	0.005	0.004	0.443	0.111	−0.010	−0.016

Residual effect = 0.109

1. Vine length (m), 2. Primary branches/vine, 3. Node to which first female flower appears, 4. Days to first male flower appearance, 5. Days to first female flower appearance, 6. Fruit weight (g), 7. Fruit length (cm), 8. Fruit diameter (cm), 9. Fruit girth (cm), 10. Pedicel length (cm), 11. Days taken from fruit set to edible maturity, 12. Number of fruits/plant, 13. Protein content (g/100 g), 14. Number of seeds/fruit, 15. Calcium content (mg/100 g).

Table 4. Grouping of 11 genotypes of sweet gourd in clusters

Clusters	Number of genotypes	Name of genotypes
I	5	Malda Selection-1, Malda Selection-2, Malda Selection-3, Bonga Selection-2 and Bonga Selection-3.
II	2	Baruipur Selection-1 and Joynagar Selection-1.
III	4	Malda Selection-4, Joynagar Selection-2, Barasat Selection-1 and Bonga Selection-1.

Table 5. Average inter and intra-clusters D² values among three clusters in 11 sweet gourd genotypes

Clusters	I	II	III
I	16088.36	11892.57	30235.22
II		4845.04	30779.83
III			13532.11

Table 6. Clusters-wise mean values of 16 characters in sweet gourd

Characters	Cluster I	Cluster II	Cluster III
Vine length (m)	2.353	2.717	2.942
Primary branches/vine	3.153	4.600	5.600
Node to which first female flower appears	25.162	25.750	19.758
Days to first male flower appearance	52.653	46.833	56.850
Days to first female flower appearance	59.627	57.250	65.342
Fruit weight (g)	42.573	62.217	40.608
Fruit length (cm)	6.167	7.083	5.533
Fruit diameter (cm)	4.353	4.867	4.492
Fruit girth (cm)	13.847	14.450	12.775
Pedicle length (cm)	11.600	11.400	15.283
Days taken from fruit set to edible maturity	15.893	17.400	16.467
Number of fruits/vine	22.180	22.583	24.617
Protein content (g/100 g)	888.307	1410.933	1999.742
Number of seeds/fruit	46.680	41.683	50.942
Calcium content (mg/100 g)	58.560	58.983	63.050
Total Fruit yield/vine (g)	0.429	0.598	0.478

fruit girth, days taken from fruit set to edible maturity and total fruit yield per vine. Cluster III had highest mean values for characters like vine length, primary branches/vine, days to first male flower appearance, days to first female flower appearance, pedicle length, number of fruits/vine, calcium content, number of seeds/fruit and protein content. Hence, selection for divergent parents based on these characters will be useful for heterosis breeding in sweetgourd. In general, the pattern of distribution of genotypes from different region to different cluster was random. Similar observations were reported by Wahab and Gopalakrishnan (1993) in bittergourd. One of the possible reasons may be the difficulty in establishment of actual location of the origin of the genotype. Further, the free exchange of genetic material among the farmers in the country makes it very difficult for the breeders to recognize or maintain the real identity of the genotypes on the basis of morphological characters. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographic origin such as exchange of genetic stock, genetic drift, spontaneous variation, natural and artificial selection may be responsible for genetic diversity.

References

- Al-Jibouri HA, PA Miller and HF Robinson (1958) Genotypic and environmental variances and covariances in upland cotton cross of inter-specific origin. *Agron. J.* **51**: 633–636.
- Bharathi LK, G Naik, HS Singh and DK Dora (2005) Correlation and path analysis in spine gourd (*Momordica dioica* Roxb.). *Orissa J. Hort.* **33(2)**: 105–108.
- Bharathi LK, G Naik and DK Dora (2006) Studies on genetic variability in spine gourd. *Indian J. Hort.* **63(1)**: 96–97.
- Bhave SG, VW Bendale, UB Pethe, SA Berde and JL Mehta (2003) Correlation and path analysis in segregating generations of bitter gourd. *J. Soil Crops* **13(1)**: 33–40.
- Dewey DR and KH Lu (1959) A correlation and significant at 5 per cent path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* **51**: 515–518.
- Dey SS, TK Behera, AD Munshi and PS Sirohi (2007) Studies of genetic divergence in bitter gourd (*Momordica charantia* L.). *Indian J. Hort.* **64(1)**: 53–57.
- Johnson HW, HF Robinson and RE Comstock (1955) Genotypic and phenotypic correlations in soybean. *Agron. J.* **47(10)**: 477–482.
- Lowry et al. (1951) Protein estimation by Lowry's method. *J. Biol. Chem.* **193**: 265.
- Mahalanobis PC (1936) On the generalized distance in statistics. *Proc. Nat. Inst. Sci., India*, pp.12–49.

- Maharana UK, P Tripathy and T Maharana (1995) Genetic variability and heritability studies in spine gourd. *Current Research Univ. Agri. Sci. Bangalore* **24(7)**: 122–124.
- Ram D, S Kumar, A Verma and M Rai (2004) Variability analysis of underutilized nutritive vegetable kartoli: Indian collection. *Cucurbit Gene Cooperative* **27**: 66–68.
- Rangana S (1986) Handbook of Analysis and Quality Control for Fruit and Vegetable Products. Tata McGraw–Hill Pub. Co., pp 126–127.
- Rao CR (1952) Advanced statistical methods in biometrical Research. John Wiley and Sons. Inc. New York, USA.
- Rasul MG et al., (2002) Genetic diversity in teasle gourd (*Momordica dioica* Roxb.). *Bangladesh J. Plant Breed. Genet.* **15**: 7–15.
- Sharma NK and RD Bhutani (2001) Correlation and path analysis studies in bitter gourd (*Momordica charantia* L.). *Haryana J. Hort. Sci.* **30**: 84–86.
- Wahab MA and PK Gopalakrishnan (1993) Genetic divergence in bitter gourd. *South Indian Hort.* **41**: 232–234.

Notes on Naturalized Taxa of Plant Genetic Resource Value in Himachal Pradesh

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Several exotic species were observed to be part of the natural flora in parts of Himachal Pradesh in the Western Himalayan region of India. This paper highlights 56 species occurring in this region at different altitudes and diverse habitat range, identified for potential use as weedy race/close relatives of crops, having economic potential in terms of edible, forage, aesthetic, soil conservation value, etc. The available information on nativity, habitat, distributional range, genetic resource value, other uses and authors' own observations during explorations has been included to observe the potential of these taxa.

Key Words: Exotic, Himachal Pradesh, Naturalized, Plant Genetic Resources

Introduction

Introduction of species for agriculture, horticulture, forestry, etc. or accidentally through human delivery systems as well as natural migration of species from adjacent areas due to landmass connections with isoclimatic conditions had resulted in tremendous influx of many exotic species in Western Himalaya. All introduced taxa may not enter into series of steps viz. establishment-naturalization-invasiveness, as the thumb rule goes that one out of ten introduced taxa become naturalized while one among the ten naturalized taxa may become invasive (Williamson and Fitter, 1996). Chatterjee (1947) reported about 38% of Indian flora comprised foreign elements. More than 500 new records were reported in India in 20th century (Sharma, 2000). Eradication attempts on various naturalized and invasive species have miserably failed. Hence, it would be appropriate to suggest making use of those naturalized taxa, usually left uncared though rendering the services which can be immediately exploited in contrast with the wild flora. Dekkar (2005) emphasized the need for preserving and exploiting germplasm of best adapted invasive and weedy species, which may provide novel solutions to the problems associated with human altered earth's habitats in future. Leaving this aside, it is quite common that being unaware of occurrence of these taxa in the region, researchers make request for their germplasm from foreign countries. Therefore, the purpose of this paper is to record notes on such taxa of exotic origin occurring in Himachal Pradesh and finding out the means of harnessing the desirable traits.

Materials and Methods

Based on exploratory studies undertaken during 2003-09 supplemented with literature (Collet, 1902; Parker, 1956; Bor, 1960; Raizada, 1976; Nair, 1977; Chowdhery and Wadhwa, 1984; Polunin and Stainton, 1984; Dhaliwal and Sharma, 1999; Kaur and Sharma, 2004; Singh and Sharma, 2006), information on more than 150 exotic taxa naturalized during the last two centuries in HP was gathered. As there is a difference of opinion about defining the terms, the authors followed the definition given by ICUN (McNeely, 2001) which stated that "naturalized species are alien species that reproduce consistently and sustain populations over more than one lifecycle without direct intervention by humans (or in spite of human intervention); they often reproduce freely, and do not necessarily invade natural, semi-natural or human-made ecosystems". Therefore, causal escapes, those undergoing naturalization and invasive plants (based on Reddy, 2008) were not taken into account. Further screening of taxa was made based on their genetic resource value, potential value, new alternate uses, etc. Hence, those taxa already cultivated as ornamental but naturalized for which no potential alternate use noticed (in fact majority are under this group) were not taken into account. The species identity was verified with the help of regional and national floras, published literature and herbarium records. Vouchers of herbarium specimens pertaining to the shortlisted taxa were deposited in the National Herbarium of Cultivated Plants, National Bureau of Plant Genetic Resources (NBPGR), New Delhi and NBPGR, Regional Station, Shimla.

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Results and Discussion

A total of 56 taxa were short-listed as having potential use as genetic resource. Unlike invasive species most of the species included were confined to disturbed sites or not expanding their range, although for some, resident time may determine whether they became invasive or not. In this regard, the species *Nicotiana plumbaginifolia*, *Solanum viarum*, *Melilotus albus*, *Asclepias curassavica* and *Acacia farnesiana* reported by Reddy (2008) being invasive in India, had no longer attained that status in HP. Occurrence of *Cyclanthera brachystachya* as naturalized exotic species in Shimla hills is the first report of its kind in India. Taxa having value as genetic resources (Table 1) are being discussed below:

A. Genetic resource for crop improvement

It is well known that most of the domesticated species have wild/weedy forms. Populations of five such crops of exotic origin were found in naturalized state. Apart from morphological variability, they are known for wider adaptation, stability and tolerance to abiotic stresses particularly frost. Another 14 taxa naturalised are relatives of crop species, of these, contributing traits were known only for a few. Apart from above, there are some species within the genera wherein the cultivated plants fall, whose relationship with the latter is not yet established. For example, *Stevia ovata* Willd., a native of America, is found naturalized in HP but its relation with cultivated *S. rebaudiana* Bertoni is unknown. Similarly, *Solanum asperolanatum* Ruiz & Pav. [syn. *S. hispidum* Pers.], a native of Tropical America is a recent entry to HP up to 1800 m, but its relation with other species is relatively unknown.

B. Edible

Ten taxa of edible value were observed under the present study. Their edibility has been proved in other areas of their occurrence. Apart from their use as famine food, ample scope exists in developing at least a few as commercial crops. In this context, research is underway for popularization of *Diospyros lotus*, *Physalis peruviana*, *Rubus fruticosus*, *Lepidium sativum* and *Nigella sativa* in western Himalaya. Also, there are added advantages in utilizing them to generate sustained income by farmers, provide variety to diets, etc.

C. Forage

Ten species having forage value particularly some temperate grasses and forage legumes were found naturalized in HP. Even though researchers have paid attention to these forages, popularization among end users is still awaited. Few grasses demonstrate a vast array of adaptations to climatic, edaphic or biotic factors, or various combinations of these like *Lolium*, *Festuca*, etc. and hence, in some cases, it is difficult to find out the nativity. Inter-specific hybridization is frequently reported in grasses, in some cases even potential for gene movement across the genera is established (Levy and Feldman, 2002).

D. Aesthetic and others

The plants of aesthetic value included those taxa having ornamental value but nowhere cultivated in HP for that purpose. Observations of nature of plants supplemented with information on past history and their utility in other countries will give clue for new uses thereby it will change the mindset of people from uncared ones to asset. There were many plants introduced for specific purpose, in the due course, remained neglected but new uses pave their way for use as crop, for instance, *Jatropha curcas* for bio-fuel, *Tagetes minuta* for bio-insecticidal, *Silybum marianum* and *Cichorium intybus* for medicinal purposes.

Majority of the short-listed species have more than one use. This is a welcome situation in the sense that they serve manifold purposes spatially as well as temporally. Apart from above there are plants which can suit as biostimulants, greenmanure, mulch, etc. It would be too early to ascribe them as genetic resource. *Lepidium sativum* is an example of a naturalized weed (of wheat fields) entering into domestication process in sub-Himalayan region of HP. Areas of multiple introductions often lead to secondary centre of diversity (Pickersgill, 1998). This is visualized in peach, apricot, and many cultivated grasses in western Himalaya. An area which needs study is impact of the spontaneous introgression of naturalized flora with the wild relatives occurring in the region especially in genera such as *Medicago*, *Chenopodium* and *Lolium*.

Conclusions

Seeking the best in naturalized exotic plants has not gained sufficient impetus in contrast to their customary

Table 1. Some naturalized exotic taxa as potential genetic resource in HP

Sl. No.	Botanical name (Family)†	Native region	Area/habitat	Genetic resource value	Additional uses (if any)
A. Weedy or apparently wild form					
1	<i>Eruca vesicaria</i> (L.) Cav. subsp. <i>sativa</i> (Mill.) Thell. (Brassicaceae)	South America	Up to 1800 m; roadsides	Tolerant to abiotic stresses	High enucic acid for plastic industries
2	<i>Medicago sativa</i> L. (Fabaceae)	Mediterranean	Kangra	Tolerant to abiotic stresses	–
3	<i>Prunus armeniaca</i> L. (Rosaceae)	China, Siberia	1500–3000 m; probably extended distribution	Variability in colour and size of fruit, flesh colour, chilling hour requirement, time of ripening, kernel taste, etc.	As rootstock for cultivated apricot
4	<i>P. persica</i> (L.) Batsch (Rosaceae)	China	700–3000 m; near human habitations	Variability in colour and size of fruit, time of ripening and degree of stone attachment with pulp, resistance to leaf curl and gummosis	As rootstock for cultivated peach
5	<i>Ricinus communis</i> L. (Euphorbiaceae)	South America	Up to 2000 m; grasslands, riparian and disturbed sites	Variability in pigmentation, plant habit and size of capsule	Red-leaved types useful as ornament
B. Crop Relatives					
1	<i>Abelmoschus manihot</i> (L.) Medik. subsp. <i>manihot</i> (Malvaceae)	China	Shimla and Kinnaur (up to 1000 m)	Crossable with okra; resistant to yellow vein mosaic virus (Dhankhar <i>et al.</i> , 2005)	–
2	<i>Avena fatua</i> L. (Poaceae)	Europe; western & central Asia	Lahaul & Spiti; weed of wheat fields; extended distribution	Progenitor of cultivated oat (Holden, 1976)	–
3	<i>Carthamus oxyacanthus</i> Bieb. (Asteraceae)	Lahore westwards to Caucasus	Areas bordering Punjab (400–700 m); field weed	Progenitor of safflower (Ashri and Knowles, 1960)	–
4	<i>Cyclanthera brachystachya</i> (Ser.) Cogn. [syn. <i>C. explodens</i> Naud.] (Cucurbitaceae)	Central America	Shimla (1700–2300 m); becoming weedy	Can contribute earliness in <i>meetha karela</i> (<i>C. pedata</i>)	Fruit-vegetable; suit for bush farming
5	<i>Fragaria vesca</i> L. subsp. <i>vesca</i> (Rosaceae)	Europe & West Asia	1500–2500 m; extended distribution	Crossed with cultivated strawberry (Marta <i>et al.</i> , 2004); resistant to <i>Xanthomonas fragariae</i> (Maas <i>et al.</i> , 2000)	Fruit value
6	<i>Jatropha gossypifolia</i> L. (Euphorbiaceae)	Brazil	Up to 700 m; early colonizer of disturbed lands	Crossed with <i>J. curcas</i> L. (Sujatha and Prabhakaran, 1997)	Ornamental
7	<i>Nicotiana plumbaginifolia</i> Viv.* (Solanaceae)	Mexico & West Indies	Up to 2300 m	Crossable with tobacco (Nikova <i>et al.</i> , 2004); resistant to black shank disease (Nagarajan and Reddy, 1982)	–
8	<i>Paspalum dilatatum</i> Poir. (Poaceae)	South America	Hill stations; grasslands, fresh water wetlands	A gene pool for kodo millet	Forage; soil binder
9	<i>Raphanus raphanistrum</i> L. (Brassicaceae)	Southwest Asia, North Africa, Europe	Up to 1500 m; weed of wheat fields	Contributed to the evolution of cultivated radish (Gill, 1995)	–
10	<i>Rosa foetida</i> Herr. (Rosaceae)	South West Asia	Lahaul	Yellow flower colour is incorporated into garden roses (de Vries and Dubois, 1978)	Ornamental
11	<i>Solanum lycopersicum</i> L. var. <i>cerasiforme</i> (Alef.) Fosberg [syn. <i>Lycopersicon esculentum</i> var. <i>cerasiforme</i> (Dunal) Alef.] (Solanaceae)	South America	Up to 2500 m; near human habitations	Progenitor of cultivated tomato (Rick, 1976); contributes to disease resistance	Fruit as vegetable; salad; processing value
12	<i>S. viarium</i> Dunal* (Solanaceae)	Brazil	1000–2000 m; grasslands, forests, riparian habitats	Crossable with brinjal (Prabhu <i>et al.</i> , 2009); resistant to <i>Fusarium</i> wilt, bacterial wilt and tolerant to frost (Rana <i>et al.</i> , 2006).	Solosodine rich hence commercial value

Contd.

Table 1 Contd.

Sl. No.	Botanical name (Family)†	Native region	Area/habitat	Genetic resource value	Additional uses (if any)
C. Edible Value					
1	<i>Allium tuberosum</i> Rottler ex Spreng. (Amaryllidaceae)	China	Kinnaur (1400–1800 m); probably extended distribution	Leaves as vegetable and condiment	Dried leaves as spice
2	<i>Canna indica</i> L. [syn. <i>C. edulis</i> Ker Gawl.] (Cannaceae)	Andes Region	700–2100 m; only near human habitations	Tuber value	Ornamental
3	<i>Diospyros lotus</i> L. (Ebenaceae)	South West Asia	1000–2200 m; probably extended distribution	Dried fruit taste like date fruit	Rootstock for persimmon
4	<i>Helianthus tuberosus</i> L. (Asteraceae)	North America	1500–2300 m; in forest edges, orchards, riparian habitats	Tuber value; crossable with sunflower and imparts disease resistance (Kalloo, 1993)	Ornamental
5	<i>Lepidium sativum</i> L. (Brassicaceae)	Egypt & West Asia	Up to 2500 m; weed of wheat fields	Leafy vegetable	Medicinal value for joint pain
6	<i>Nigella sativa</i> L. (Ranunculaceae)	West Asia	Weed in Sirmour	Seed as spice	Medicinal; insecticidal
7	<i>Opuntia ficus-indica</i> (L.) Mill. (Cactaceae)	Mexico	Up to 2300 m; rocky places, grasslands	Fruit value; cladode as vegetable	Hedge, ornamental
8	<i>Physalis peruviana</i> L. (Solanaceae)	Tropical America	Up to 2000 m; forest edges, disturbed sites	Fruit value	Ornamental
9	<i>Plantago lanceolata</i> L. (Plantaginaceae)	Europe & West Asia	Shimla (1500–2300 m); probably extended distribution	Leafy vegetable	–
10	<i>Rubus fruticosus</i> L. agg. (Rosaceae)	Europe	Kinnaur & Shimla (1800–2500 m); scrublands and other disturbed sites	Fruit value	Ornamental
D. Forage value					
1	<i>Broussonetia papyrifera</i> Vent. (Moraceae)	China	Up to 1800 m	Leaves as forage	Soil conservation in moist areas
2	<i>Desmanthus virgatus</i> (L.) Willd. (Fabaceae)	America	Up to 1000 m	Leaves as forage	Hedge
3	<i>Lolium temulentum</i> (L.) var. <i>arvense</i> Lilj. (Poaceae)	Mediterranean	Kullu and Kangra (1000–2000 m); due to multiple introduction	Plants as forage	–
4	<i>Medicago polymorpha</i> L. (Fabaceae)	Europe	Up to 2000 m; extended distribution	Plants as forage	Green manure
5	<i>Melilotus albus</i> Desr.* (Fabaceae)	Europe	Up to 4000 m	Plants as forage	Green manure
6	<i>M. indicus</i> (L.) Ali (Fabaceae)	Europe	Up to 2000 m; extended distribution	Plants as forage	Green manure
7	<i>Phleum pratense</i> L. (Poaceae)	Temperate Europe	Kullu; probably as a result of multiple introduction	Plants as forage	–
8	<i>Trifolium dubium</i> Sibth. (Fabaceae)	Europe	Up to 2000 m	Plants as forage	–
9	<i>T. incarnatum</i> L. (Fabaceae)	Europe	Up to 1500 m	Plants as forage	–
10	<i>T. tomentosum</i> L. (Fabaceae)	Europe	Sirmour	Plants as forage	–

Contd.

Table 1 Contd.

Sl. No.	Botanical name (Family)†	Native region	Area/habitat	Genetic resource value	Additional uses (if any)
E. Aesthetic value					
1	<i>Acacia decurrens</i> (Wendl.) Willd. (Fabaceae)	Australia	1500–2200 m	Lean season ornamental	Crossable with <i>A. meensis</i> ; tannin value
2	<i>Asclepias curassavica</i> L.* (Asclepiadaceae)	West Indies	Up to 1500 m; in wet areas	Lean season ornamental; cut flower value	–
3	<i>Briza minor</i> L. (Poaceae)	Mediterranean	Kullu (1000–1800 m); weed of wheat fields	Ornamental grass	–
4	<i>Cymbalaria muralis</i> Gaertn. (Scrophulariaceae/Plantaginaceae)	Europe	Shimla (1800–2300 m); in walls	Hanging baskets	–
5	<i>Dahlia imperialis</i> Roehl. (Asteraceae)	Central America	1500–2500 m; in disturbed sites	One of the parents for present day dahlias	Ornamental
6	<i>Sema × floribunda</i> (Cav.) H.S. Irwin & Barneby [syn. <i>Cassia floribunda</i> Cav.] (Fabaceae)	Mexico	Up to 1500 m	Ornamental hedge value	–
F. Others					
1	<i>Acacia dealbata</i> Link. (Fabaceae)	Australia	1300–2100 m	Windbreak, shelterbelt; afforestation in wasteland	Tannin value; ornamental
2	<i>A. farnesiana</i> (L.) Willd.* (Fabaceae)	Tropical America	Along riversides to 1200 m	Gum; perfume value	–
3	<i>Agave cantala</i> (Haw.) Roxb. (Asparagaceae)	Tropical America	Up to 2400 m	Soil conservation; fibre value	Hedge
4	<i>A. vivipara</i> L. [syn. <i>A. angustifolia</i> Haw., <i>A. wightii</i> J.R. Drumm. & Prain] (Asparagaceae)	Tropical America	Up to 1500 m	Soil conservation	Hedge, flower stalks as famine food
5	<i>Ailanthus altissima</i> (Mill.) Swingle [syn. <i>A. glandulosa</i> Desf.] (Simaroubaceae)	China	Up to 1800 m; along roadsides	Soil erosion control	Silkworm rearing
6	<i>Chenopodium ambrosioides</i> L. (Chenopodiaceae)	Mexico	Up to 3000 m; disturbed sites, weed	Aromatic oil	–
7	<i>Chrysanthemum coronarium</i> L. (Asteraceae)	Mediterranean	Kinnaur Dt. (2500–3100 m)	Ornamental	Vegetable
8	<i>Cichorium intybus</i> L. (Asteraceae)	Europe	Shivalik hills; in fallow fields	<i>Kasni</i> leaves as having medicinal properties i.e. in the treatment of kidney and liver problems (exploited in South India)	Fodder; leafy vegetable
9	<i>Matricaria chamomilla</i> L. (Asteraceae)	Europe & West Asia	Mandi (2000–2300 m); extended distribution	Medicinal value as stimulant, carminative	Ornamental
10	<i>Parkinsonia aculeata</i> L. (Fabaceae)	Northern Mexico to southern USA	Shivalik hills; in fallow lands	Afforestation in sandy, denuded soils and drought-prone areas	Ornamental hedge
11	<i>Silybum marianum</i> Gaertn. (Asteraceae)	Mediterranean	Kangra (500–1200 m); roadsides	Seed act as blood purifier	Ornamental
12	<i>Tagetes minuta</i> L. (Asteraceae)	South America	Up to 2200 m; in disturbed places	Bio-insecticidal	–
13	<i>Triadica sebifera</i> (L.) Small [syn. <i>Sapium sebiferum</i> (L.) Roxb.] (Euphorbiaceae)	China & Japan	Kangra ; wetlands, grasslands	Seeds yield tallow	Ornamental tree

† Taxa with asterisk mark (*) mentioned as invasive in India (Reddy, 2008) were observed not that status in HP.

treatment as ‘annoyance’ in India. This paper attempts to address such naturalized taxa which can be explored as genetic resource of direct value in comparison with wild flora because many of them are cultivated elsewhere and introduced intentionally. Ample scope exists in promotion of few such species as new crops. Alternate uses are highlighted since original intended use was not well appreciated in the region. Overall, this assessment will help in generating primary database on naturalized taxa for the benefit of scientists and policy makers in developing management strategies. Validation of potential value of aforementioned taxa may reveal whether more germplasm needs to be introduced in the region further. This would also give clue on the phenotypic plasticity of these exotic plants.

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References

- Ashri A and PF Knowles (1960) Cytogenetics of safflower (*Carthamus* L.) species and their hybrids. *Agron. J.* **52**: 11–17.
- Bor NL (1960) *The Grasses of Burma, Ceylon, India and Pakistan (excluding Bambuseae)*. Pergamon Press, Oxford, England, 767 p.
- Chatterjee D (1947) Influence of East Mediterranean regions flora on that of India. *Sci. Cult.* **13**: 9–11.
- Chowdhery HJ and BM Wadhwa (1984) *Flora of Himachal Pradesh*. 3 vol., Botanical Survey of India, Calcutta, 860 p.
- Collet H (1902) *Flora Simlensis: a Handbook of the Flowering Plants of Simla and the Neighbourhood* (Reprint 1971). Bishen Singh Mahendra Pal Singh, Dehra Dun, Uttarakhand.
- Dekkar J (2005) Biology and anthropology of plant invasion, In Inderjit (ed) *Invasive Plants: Ecological and Agricultural Aspects*, Birkhauser Verlag, Switzerland, pp 235–250.
- de Vries DP and LAM Dubois (1978) On the transmission of the yellow flower colour from *Rosa foetida* to recurrent flowering hybrid tea roses. *Euphytica* **27**(1): 205–210.
- Dhankhar SK, BS Dhankhar and RK Yadava (2005) Inheritance of resistance to yellow vein mosaic virus in an interspecific cross of okra (*Abelmoschus esculentus*). *Indian J. Agric. Sci.* **75**(2): 87–89.
- Dhaliwal DS and M Sharma (1999) *Flora of Kullu District*. Bishen Singh Mahendra Pal Singh, Dehra Dun, Uttarakhand, 744 p.
- Gill HS (1995) Improvement of root crops. In: KL Chadha and G Kalloo (eds) *Advances in Horticulture Vol. 5. Vegetable Crops*. Malhotra Publishers, New Delhi, pp 201–215.
- Holden JHW (1976) Oats. In: NW Simmonds (ed.) *Evolution of Crop Plants*, Longmans, United Kingdom, pp 86–90.
- Kalloor G (1993) Jerusalem artichoke. In: G Kalloor and BO Bergh (eds) *Genetic Improvement of Vegetable Crops*. Pergamon Press, Oxford, pp 647–651.
- Kaur H and M Sharma (2004) *Flora of Sirmaur (Himachal Pradesh)*. Bishen Singh Mahendra Pal Singh, Dehra Dun, Uttarakhand, 770 p.
- Levy AA and M Fledman (2002) The impact of polyploidy on grass genome evolution. *Plant Physiol.* **130**: 1587–1593.
- Marta AE, EL Camadro, JC Az-Ricci and AP Castagnaro (2004) Breeding barriers between the cultivated strawberry *Fragaria x ananassa* and related wild germplasm. *Euphytica* **136**: 139–150.
- Mass JL, BC Gouin, JS Hartung and SC Hokanson (2000) Sources of resistance for two differentially pathogenic strains of *Xanthomonas fragariae* in *Fragaria* genotypes. *Hort. Sci.* **35**(1): 128–131.
- McNeely JA (ed) (2001) *The Great Reshuffling: Human Dimensions of Invasive Alien Species*. ICUN, Gland, Switzerland and Cambridge, United Kingdom, 242 p.
- Nagarajan K and TSN Reddy (1982) Reactions of *Nicotiana* species and varieties to important diseases in India. *Indian J. Agric. Sci.* **52**(11): 791–795.
- Nair NC (1977) *Flora of Bashahr Himalayas*. International Bioscience Publishers, Hissar, Haryana, 360 p.
- Nikova V, R Pundeva, R Vladora and A Petkova (2004) Application of tissue cultures to overcome the complete sterility of *Nicotiana plumbaginifolia* Viviani x *N. tabacum* F₁ hybrid. *Israel J. Plant Sci.* **52**(1): 45–49.
- Parker RN (1956) *Forest Flora for the Punjab with Hazara and Delhi*. Third Edition. Bishen Singh Mahendra Pal Singh, Dehra Dun, Uttarakhand, 584 p.
- Pickersgill B (1998) Crop introductions and the development of secondary areas of diversity. In: HDV Prendergast, NL Etkin, DR Harris and PJ Houghton (eds) *Plants for Food and Medicine*. Richmond, UK; Royal Botanical Garden, Kew, pp 93–105.
- Polunin O and A Stainton (1984) *Flowers of Himalaya*. Oxford University Press, New Delhi, 580 p.
- Prabhu M, S Natarajan, D Veeraragavathatham and L Pugalandhi (2009) The biochemical basis of shoot and fruit borer resistance in interspecific progenies of brinjal (*Solanum melongena*). *EurAsia J. BioSci.* **3**: 50–57.
- Raizada MB (1976) *Supplement to Duthie's Flora of Upper Gangetic Plain and of adjacent Siwalik and Sub-Himalayan tracts*. Bishen Singh Mahendra Pal Singh, Dehra Dun, Uttarakhand, 353 p.
- Rana, JC, VD Verma and K Pradheep (2006) Management of genetic resources of temperate horticultural crops. In: DK Kishore, SK Sharma and KK Pramanick (eds) *Temperate Horticulture: Current Scenario*. New India Publishing Agency, New Delhi, pp 85–100.
- Reddy CS (2008) Catalogue of invasive alien flora of India. *Life Sci. J.* **5**(2): 84–89.
- Rick CM (1976) Tomato. In: NW Simmonds (ed) *Evolution of Crop Plants*, Longmans, United Kingdom, pp 268–273.

- Sharma BD (2000) Affinities–Paleobotanical and geographical evidences, relationships with adjacent regions, past and recent plant migration. In: NP Singh, DK Singh, PK Hajra and BD Sharma (eds) *Flora of India: Introductory Volume, Part II*, Botanical Survey of India, Calcutta, pp 1–200.
- Singh H and M Sharma (2006) *Flora of Chamba District, Himachal Pradesh*, Bishen Singh Mahendra Pal Singh, Dehra Dun, Uttarakhand.
- Sujatha M and AJ Prabhakaran (1997) Characterization and utilization of Indian *Jatropha*. *Indian J. Plant Genet. Resour.* **10(1)**: 123–128.
- Williamson M and A Fitter (1996) The varying success of invaders. *Ecology* **77**: 1661–1665.

Genetic Variability and Character Association in Common Millet Germplasm of Odisha

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Eleven germplasm collections of common millet (*Panicum miliaceum* L.) along with one check variety were evaluated under 10 environments during *kharif* 2003 to *kharif* 2004 at the Central Research Station, OUAT, Bhubaneswar. Observations recorded on 14 metric traits including grain yield were analyzed to assess the extent of genetic variability and the magnitude of character association in the genotypes tested. Analysis of variance revealed highly significant differences due to genotypes, environments and genotype x environment interactions for all the characters. Germplasm accessions exhibited significant variability for different traits. KCM 120 was the earliest to flower and high yielding with the highest panicle number and harvest index. KCM 424, KCM 14 and KCM 325 were late maturing but high yielders having higher mean performance for most of the characters. Moderate to high estimates of heritability along with moderate to high genetic advance (GA) and genotypic coefficient of variation (GCV) were observed for grain yield and all the component traits except plant height and panicle number. Significant positive association of grain yield with plant height, flag leaf length, flag leaf area, panicle length, panicle weight, panicle yield, biological yield, harvest index and 1000-grain weight was observed. Path analysis pooled over environments revealed that flag leaf length, panicle weight, 1000-grain weight and plant height had maximum contribution towards grain yield.

Key Words: Character association, Common millet, Genetic variability, *Panicum miliaceum*, Proso millet

Introduction

Common millet otherwise known as proso millet (*Panicum miliaceum* L.) is mostly cultivated in India as grain crop under adverse soil and climatic conditions. Nutritionally, the grains are rich in protein, minerals, vitamins and even superior to major cereals in certain nutritional parameters. It occupies substantial area in Bihar, Andhra Pradesh and Odisha as an important constituent of dry land agriculture. The first attempt to collect the available germplasm (250 numbers) was made in 1961 under PL-480 project on 'Storage, maintenance and distribution of millet germplasm'. Realising the importance of conservation of millet genetic resources, a germplasm unit was established at Bangalore in 1980 (Seetharam, 1997; Seetharam and Rao, 1998). The broadening of varietal base by evolving varieties of different maturity periods will definitely impart further stability to production. The knowledge of genetic variability in the available germplasm and association of yield with component traits will be quite helpful in evolving genotypes with higher yield potential.

Materials and Methods

The investigation was carried out at the Central Research Station Orissa University of Agriculture and Technology (OUAT), Bhubaneswar, during the period from *kharif* 2003 to *kharif* 2004 under 10 different environmental conditions generated through different dates of sowing. The test genotypes consisting of 11 local germplasm collected from five tribal districts of Odisha were evaluated along with variety Tarini of OUAT, as check. The local germplasm included KCM 14 and KCM 424 (IC 273532 and 321839, collected from district Gajapati), KCM 120, KCM 122, KCM 285 and KCM 291 (IC 298429, 298431, 321700 and 321706, collected from district Kandhamal), KCM 137 (collected from district Rayagada), KCM 171 (IC No. 298480, collected from district Koraput) and KCM 296, KCM 298 and KCM 325 (IC No. 321711, 321713 and 321741, collected from district Kalahandi). The genotypes were sown in randomized complete block design with three replications and observations were recorded for grain yield and 13 component characters *i.e.* days to

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heading, plant height, flag leaf length, flag leaf area, panicle length, panicle exertion, panicle number, panicle weight, panicle yield, straw yield, biological yield, harvest index and 1000-grain weight. The coefficient of variability, heritability in broad sense and genetic advance (GA) were computed following Hanson *et al.* (1956) and Johnson *et al.* (1955). The genotypic and phenotypic correlations and path coefficients were computed following Al-Jibouri *et al.* (1958) and Dewey and Lu (1959).

Results and Discussion

The pooled analysis over environments showed that differences due to genotypes, environments and genotype x environment interactions were highly significant for all the characters (Table 1). Performance of the genotypes

showed wide range of variation for all the characters (Table 2). The overall varietal means for grain yield ranged from 14.4 g in KCM 171 to 23.4 g in KCM 424. The earliest to flower was KCM 120 (62.7 days), while the late maturing genotype was KCM 424 (100.3 days). Plant height varied from 99.6 cm in KCM 122 to 111.7 cm in Tarini. Mean for flag leaf length ranged from 18.3 cm in KCM 122 to 23.2 cm in KCM 424 and the same varieties had extreme values for flag leaf area ranging from 9.6 sq cm to 13.8 sq cm. KCM 122 registered the lowest panicle length (21.9 cm) while KCM 424, the maximum (28 cm). Panicle exertion among the test entries varied from 2.3 cm in KCM 137 to 7.2 cm in KCM 424. The varietal means over environments for panicle number ranged from 26.3 in KCM 296 to 33.3 in KCM 120. The

Table 1. Analysis of variance for 14 characters of 12 genotypes pooled over 10 environments

Character	Mean square				
	Reps/Env. (20)	Genotype (11)	Environment (9)	G x E (99)	Pooled error (220)
Grain yield (GY)	1.4	281.16**	668.57**	68.08**	1.13
Days to heading (DH)	2.4	2676.75**	15250.14**	147.84**	1.08
Plant height (PH)	0.4	318.53**	5530.39**	107.52**	1.32
Flag leaf length (FLL)	0.2	72.8**	59.25**	6.49**	0.22
Flag leaf area (FLA)	0.1	47.14**	58.81**	6.13**	0.10
Panicle length (PL)	0.3	114.67**	122.66**	8.45**	0.31
Panicle exertion (PE)	0.03	50.62**	16.89**	6.48**	0.10
Panicle number (PN)	0.4	75.27**	3608.03**	55.16**	1.14
Panicle weight (PW)	0.003	0.45**	3.69**	0.11**	0.003
Panicle yield (PY)	0.9	391.97**	1083.41**	78.44**	2.39
Straw Yield (SY)	1.0	863.61**	5112.05**	298.46**	2.05
Biological yield (BY)	2.1	1656.06**	6192.58**	490.49**	3.29
Harvest index (HI)	1.8	214.8**	896.41**	61.39**	2.13
1000-grain weight (GW)	0.01	0.91**	0.14**	0.03**	0.0003

Figures in parentheses indicate the degrees of freedom

Table 2. Mean performance of 12 genotypes for 14 characters pooled over 10 environments

Genotype	GY** (g)	DH	PH (cm)	FLL (cm)	FLA (cm ²)	PL (cm)	PE (cm)	PN	PW (g)	PY (g)	SY (g)	BY (g)	H I (%)	GW (g)
KCM 14	20.9	96.8	108.0	22.4	12.2	27.0	4.5	30.4	0.94	26.4	61.3	87.7	24.8	2.14
KCM 120	20.7	62.7	106.8	21.8	12.4	26.6	3.9	33.3	0.86	27.8	41.2	69.0	29.2	1.69
KCM 122	14.6	92.0	99.6	18.3	9.6	21.9	4.3	29.4	0.79	20.3	49.3	69.6	21.7	1.82
KCM 137	16.1	93.1	106.6	19.8	10.5	25.0	2.3	30.7	0.83	22.3	52.6	74.9	21.8	1.83
KCM 171	14.4*	92.4	104.5	21.4	11.9	24.7	5.1	28.8	0.77	20.4	53.1	73.5	19.6	1.73
KCM 285	16.6	90.0	107.4	19.6	10.6	23.8	3.4	29.1	0.85	22.3	52.4	74.7	22.4	1.80
KCM 291	17.3	94.8	103.2	19.1	9.8	22.8	4.6	28.9	0.90	23.1	49.2	72.3	24.6	1.64
KCM 296	16.1	93.2	105.6	20.3	10.7	25.3	3.5	26.3	0.91	22.2	51.1	73.4	22.2	1.75
KCM 298	17.4	93.8	107.6	22.3	12.1	27.1	3.5	29.5	0.87	23.7	52.4	76.1	22.7	1.78
KCM 325	19.1	96.1	107.2	21.2	11.0	27.9	3.3	29.8	0.98	25.9	53.2	79.1	24.2	1.71
KCM 424	23.4	100.3	111.1	23.2	13.8	28.0	7.2	30.1	1.15	30.9	61.7	92.5	26.1	2.18
Tarini	22.9	92.8	111.7	22.5	12.6	25.7	2.6	29.7	1.13	30.5	54.9	85.4	27.1	1.97
Mean	18.3	91.5	106.6	21.0	11.4	25.5	4.0	29.7	0.91	24.7	52.7	77.4	23.9	1.84
C.D.5%	0.5	0.4	0.5	0.2	0.1	0.2	0.1	0.5	0.02	0.7	0.6	0.8	0.6	0.01
C.D.1%	0.6	0.6	0.7	0.3	0.2	0.3	0.2	0.6	0.03	0.9	0.9	1.1	0.9	0.01

** Abbreviation for characters as in Table 1

* The underlined figures indicate the highest (double) and the lowest (single) values

panicle weight ranged from 0.77 g in KCM 171 to 1.15 g in KCM 424, while the extreme values for panicle yield ranged from 20.3 g in KCM 122 to 30.9 g in KCM 424. Among the test entries KCM 120 recorded the lowest straw yield of 41.2 g whereas KCM 424, the highest (61.7 g) and the same varieties had extreme values for biological yield ranging from 69 g to 92.5 g. The harvest index varied from 19.6% in KCM 171 to 29.2% in KCM 120. Mean for 1000-grain weight varied from 1.64 g in KCM 291 to 2.18 g in KCM 424.

The highest yielder KCM 424 was the late maturing genotype having maximum values for flag leaf length and area, panicle length, panicle exertion, panicle weight, panicle yield, straw yield, biological yield, and 1000-grain weight with higher plant height and harvest index. The earliest flowering genotype KCM 120 was high yielder with the highest panicle number and harvest index possessing the minimum values for straw yield and biological yield. Besides KCM 424 and KCM 120, high grain yield was recorded by KCM 14, KCM 325 and Tarini with relatively higher mean performance for at least 6 to 7 component characters. Thus, it is evident that the germplasm accessions exhibited significant variability for different traits.

The parameters of genetic variability estimated for 14 characters of common millet pooled over 10 environments indicated high genotypic and phenotypic coefficient of variation for panicle exertion, grain yield, panicle yield, panicle weight, flag leaf area and days to heading and it was moderate for harvest index, 1000-grain weight, straw yield, biological yield, flag leaf length and panicle length while low for the remaining two characters i.e. plant height and panicle number (Table 3). The estimates of heritability in broad sense was high ranging from

65.4% to 96.6% for all the characters except panicle number, thus indicating the predominance of heritable component of variation for the traits.

The predicted genetic advance was of moderate to high magnitude for all the characters studied except plant height and panicle number. Moderate to high estimates of heritability along with moderate to high genetic advance and genotypic coefficient of variation (GCV) were observed for grain yield and all the component traits except plant height and panicle number indicating preponderance of additive gene action thus rendering ample scope for selection in varietal improvement.

These parameters of variability unbiased by GE interaction were of great value in selection. The results thus indicate that the evaluation of varietal characters across environments rather than at individual environment leads to precision in predicting probable future performance of the varieties in respect of the characters studied (Bradley *et al.*, 1988).

Positive association of grain yield was significant with all the component characters except days to heading, panicle exertion, panicle number and straw yield in pooled analysis over 10 environments while the correlation coefficients of grain yield with these characters varied greatly from environment to environment indicating differential response of the genotypes for their character expression in different environments (Table 4). It was further revealed that grain yield had significant positive association with days to heading and panicle number in only one environment and significant negative association with days to heading in one environment. Significant positive correlation of grain yield with panicle length, panicle exertion and 1000-grain weight was observed

Table 3. Estimates of coefficient of variability (GCV and PCV), heritability (h^2) in broad sense and genetic advance (GA) for 14 characters of 12 genotypes pooled over 10 environments

Character	GCV	PCV	h^2 (%)	GA	GA (% of mean)
Grain yield (GY)	14.6	16.8	75.8	4.8	26.2
Days to heading (DH)	10.0	10.3	94.5	18.4	20.1
Plant height (PH)	2.5	3.1	66.2	4.4	4.2
Flag leaf length (FLL)	7.1	7.4	91.1	2.9	13.9
Flag leaf area (FLA)	10.2	11.0	87.0	2.2	19.6
Panicle length (PL)	7.4	7.7	92.6	3.7	14.6
Panicle exertion (PE)	30.2	32.3	87.2	2.3	58.0
Panicle number (PN)	2.8	5.3	26.7	0.9	2.9
Panicle weight (PW)	11.5	13.3	74.8	0.2	20.5
Panicle yield (PY)	13.1	14.7	80.0	6.0	24.2
Straw Yield (SY)	8.2	10.2	65.4	7.2	13.7
Biological yield (BY)	8.1	9.6	70.4	10.8	13.9
Harvest index (HI)	9.5	11.2	71.4	3.9	16.5
1000-grain weight (GW)	9.3	9.5	96.6	0.3	18.9

Table 4. Phenotypic (r_p) and genotypic (r_g) correlation coefficients of grain yield with 13 other characters of 12 genotypes in 10 environments and pooled over environments

Env. (D/S)	Corr.	DH	PH	FLL	FLA	PL	PE	PN	PW	PY	SY	BY	HI	GW
1 (5.7.03)	r_p	0.250	0.316	0.188	-0.053	0.481	-0.042	0.373	0.755**	0.928*	0.584*	0.740**	0.727**	0.358
	r_g	0.253	0.316	0.188	-0.056	0.483	-0.037	0.374	0.765	1.167	0.590	0.745	0.723	0.362
2 (20.7.03)	r_p	0.353	0.612*	0.616*	0.763**	0.693*	-0.009	0.187	0.817**	0.972**	0.627*	0.796**	0.614*	0.469
	r_g	0.356	0.618	0.623	0.772	0.701	-0.009	0.187	0.830	0.983	0.632	0.801	0.611	0.473
3 (5.8.03)	r_p	0.547	0.781**	0.684*	0.602*	0.765**	0.211	0.032	0.753**	0.995**	0.720**	0.831**	0.374	0.528
	r_g	0.558	0.789	0.698	0.613	0.777	0.210	0.033	0.767	1.018	0.726	0.839	0.358	0.535
4 (5.9.03)	r_p	0.183	0.299	0.171	0.244	0.069	0.542	0.352	0.649*	0.945**	0.682*	0.859**	0.580*	0.820**
	r_g	0.187	0.301	0.174	0.248	0.072	0.548	0.357	0.670	0.955	0.701	0.872	0.579	0.827
5 (5.10.03)	r_p	-0.306	0.640*	0.666*	0.797**	0.579*	0.229	0.695*	0.973**	0.989**	-0.462	0.488	0.964**	0.337
	r_g	-0.310	0.642	0.675	0.801	0.583	0.231	0.707	0.981	0.992	-0.466	0.490	0.965	0.337
6 (5.11.03)	r_p	-0.675*	0.892**	0.627*	0.720**	0.550	-0.410	-0.311	0.966**	0.992**	0.630*	0.882**	0.744**	0.396
	r_g	-0.686	0.898	0.632	0.725	0.556	-0.413	-0.318	0.970	0.996	0.635	0.887	0.744	0.399
7 (5.12.03)	r_p	-0.250	0.579*	0.330	0.378	0.337	0.327	0.115	0.846**	0.941**	0.135	0.599*	0.844**	0.591*
	r_g	-0.251	0.588	0.340	0.389	0.341	0.331	0.107	0.873	0.962	0.135	0.606	0.843	0.597
8 (20.5.04)	r_p	0.505	0.319	0.669*	0.633*	0.452	0.721**	-0.115	0.608*	0.857**	0.059	0.492	0.849**	0.390
	r_g	0.509	0.325	0.685	0.645	0.458	0.728	-0.121	0.623	0.873	0.062	0.502	0.850	0.394
9 (5.6.04)	r_p	0.679**	0.040	0.034	0.088	0.077	0.661*	-0.231	0.922**	0.985**	0.193	0.640*	0.776**	0.511
	r_g	0.685	0.047	0.027	0.086	0.081	0.672	-0.243	0.938	0.996	0.194	0.645	0.773	0.518
10 (25.6.04)	r_p	0.343	0.392	0.289	0.373	0.229	0.611*	0.038	0.845**	0.940**	0.357	0.590*	0.367	0.651*
	r_g	0.354	0.423	0.296	0.381	0.235	0.634	0.033	0.889	0.974	0.375	0.612	0.321	0.683
Pooled	r_p	-0.049	0.803**	0.762**	0.758**	0.670*	0.240	0.453	0.878**	0.990**	0.390	0.766**	0.858**	0.637*
	r_g	-0.067	0.842	0.793	0.786	0.692	0.242	0.538	0.893	0.997	0.399	0.779	0.873	0.658

*, **Significant at the 5% and 1% level, respectively. (D/S) : Date of sowing

Table 5. Phenotypic path indicating direct and indirect effects of component traits on grain yield of 12 genotypes of common millet pooled over 10 environments

Character	DH	PH	FLL	FLA	PL	PE	PN	PW	PY	SY	BY	HI	GW	Corr. with GY
DH	-1.273	0.158	0.017	0.365	-0.016	0.235	-0.874	1.411	0.457	-1.478	0.012	0.146	0.792	-0.049
PH	-0.130	1.544	4.639	-4.063	-0.772	0.010	0.315	3.449	-4.192	-0.952	0.017	-0.161	1.098	0.803**
FLL	-0.004	1.263	5.672	-4.947	-0.888	0.331	0.447	2.799	-3.977	-0.874	0.015	-0.154	1.077	0.762**
FLA	0.090	1.221	5.462	-5.137	-0.789	0.479	0.515	2.742	-4.043	-0.810	0.015	-0.158	1.172	0.758**
PL	-0.020	1.163	4.912	-3.956	-1.025	0.163	0.448	2.492	-3.427	-0.742	0.013	-0.138	0.786	0.670*
PE	-0.259	0.014	1.622	-2.127	-0.145	1.157	-0.008	1.095	-1.171	-0.703	0.008	-0.025	0.781	0.240
PN	0.795	0.347	1.809	-1.890	-0.328	-0.007	1.400	0.174	-2.338	0.454	0.001	-0.192	0.229	0.453
PW	-0.404	1.197	3.567	-3.164	-0.574	0.285	0.055	4.451	-4.531	-1.033	0.018	-0.191	1.204	0.878**
PY	0.113	1.260	4.390	-4.043	-0.684	0.264	0.637	3.925	-5.138	-0.632	0.016	-0.264	1.145	0.990**
SY	-1.012	0.791	2.666	-2.240	-0.409	0.438	-0.342	2.475	-1.747	-1.858	0.019	0.036	1.575	0.390
BY	-0.681	1.186	4.067	-3.570	-0.639	0.439	0.064	3.716	-3.766	-1.650	0.022	-0.103	1.682	0.766**
HI	0.604	0.806	2.836	-2.641	-0.460	0.094	0.872	2.764	-4.413	0.217	0.007	-0.308	0.480	0.858**
GW	-0.534	0.897	3.233	-3.185	-0.426	0.478	0.169	2.835	-3.113	-1.548	0.019	-0.078	1.890	0.637*

P(R) = .091 R SQR (PC) = 100.820

Bold and diagonal values indicate the direct effect of component traits on grain yield

in three environments whereas in five environments with plant height, flag leaf length, flag leaf area, and straw yield. There was significant positive correlation

of grain yield with biological yield and harvest index in eight environments while with panicle weight and panicle yield in all the ten environments. At the genotypic

level, the correlation of grain yield with the component characters reflected similar pattern of association as at the phenotypic level. But the genotypic correlation coefficients were higher in magnitude (direction remaining same) as compared to phenotypic values in most of the characters. Thus, higher genotypic correlation coefficients in case of positive association and lower in case of negative association would reinforce selection based on these characters would be effective in desired direction as observed in earlier studies (Hawalder, 1991; Prasad *et al.*, 1995; Manoharan and Sibasubramanian, 1984; Sen and Hamid, 1986).

The correlation of grain yield with its component traits at phenotypic level was analyzed over environments to assess the cause and effect relationship of yield *per se* versus other characters by partitioning into direct and indirect effects at phenotypic level. Among the characters with positive direct effect on grain yield it was found that, the direct effect in positive direction was the highest (5.672) for flag leaf length followed by panicle weight (4.451), 1000-grain weight (1.890), plant height (1.544), panicle number (1.400) and panicle exertion (1.157). On the other hand, the highest direct negative effect was exhibited by panicle yield (−5.138) followed by flag leaf area (−5.137), straw yield (−1.858), days to heading (−1.273) and panicle length (−1.025). The positive indirect effect *via* flag leaf length was maximum for flag leaf area (5.462) followed by panicle length (4.912), plant height (4.639), panicle yield (4.390), biological yield (4.067), panicle weight (3.567), 1000-grain weight (3.233), harvest index (2.836), straw yield (2.666), panicle number (1.809) and panicle exertion (1.622). Through panicle weight all the characters had high positive indirect effect, highest being 3.925 for panicle yield followed by biological yield (3.716), plant height (3.449), 1000-grain weight (2.835), flag leaf length (2.799), harvest index (2.764), flag leaf area (2.742), panicle length (2.492) and straw yield (2.475). All characters except days to heading had substantial indirect negative effect *via* flag leaf area and panicle yield. It is evident from both direct and indirect effects of the characters at phenotypic level that flag leaf length, panicle weight and 1000-grain weight contributed substantially towards

grain yield thus suggesting that selection based on these characters would be more effective for yield improvement of common millet.

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References

- Al-Jibouri HA, Miller PA and Robinson HF (1958) Genotypic and environmental variances and covariances in upland cotton cross of interspecific origin. *Agron. J.* **50**: 633–636.
- Bradley JP, Krittie KH and Troyer AF (1988) Statistical methods in seed corn product selection. *J. Prod. Agric.* **1**: 34–38.
- Dewey DR and Lu KH (1959) A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* **51**: 515–518.
- Hanson CH, Robinson HK and Comstock RE (1956) Biometrical studies of yield in segregating population of Korean lespedeze. *Agron. J.* **48**: 268–272.
- Hawalder MSH (1991) Genetic variability and correlation study in proso millet (*Panicum miliaceum* L.). *Ann. Bangladesh Agri.* **1(2)**: 61–64.
- Johnson HW, Robinson HF and Comstock HE (1955) Estimates of genetic and environmental variability in soybean. *Agron. J.* **47**: 314–318.
- Manoharan V and Sibasubramanian V (1984) Association analysis in proso millet (*Panicum miliaceum* L.). *Madras Agric. J.* **71**: 5–10.
- Prasad SG, Nagaraja TE, Seetharam A and Gowda BTS (1995) Genetic variability and character association studies in proso millet. *Crop Improv.* **22**: 225–227.
- Seetharam A (1997) Genetic resources in small millets and their utilization. In: A. Seetharam, M. Rangaswamy and N Jayaraman (eds) *Extended Summaries of National Seminar on Small Millets-Current Research Trends and Future Priorities as Food, Feed and Processing for Value Addition*. Tamil Nadu Agricultural University, Coimbatore, pp 42–44.
- Seetharam A and Prasada Rao KE (1988) Use of minor (small) millets germplasm and its impact on crop improvement in India. In: Proceedings of a Workshop on Germplasm Exploration and Evaluation in India, ICRISAT, Hyderabad, India, 97 p.
- Sen DK and Hamid MA (1986) Character association and path analysis in proso millet (*Panicum miliaceum* L.). *Thai J. Agric. Sci.* **19**: 307–312.

Components of Genetic Variation for Yield Traits in Crosses of Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.]

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A field experiment comprising of 4 F_1 s, derived from crossing of contrasting parents for the characters viz., plant height, primary branches/plant, siliqua/plant seeds siliquae, test weight and seed yield/plant and their $4F_2$ s, $4B_1$ s and $4B_2$ s was carried to study the genetic variability and inheritance of the yield attributing traits during *rabi* season in a non-replicated, compact family block design. A high coefficient of variation was observed in the F_2 of all the crosses, especially for yield/plant and number of siliqua/plant. Higher narrow sense heritability estimates were recorded for seed yield/plant followed by plant height and siliqua/plant in all the four crosses while number of primary branches/plant and seeds/siliquae showed low heritability. Genetic advance as percentage of mean was high for seed yield/plant and siliqua/plant in most of the crosses. Selection for high number of siliqua/plant is expected to be the crucial selection criteria for yield improvement. Component of additive genetic variation for traits viz., plant height, primary branches/plant, siliqua/plant and seed yield/plant in cross QM-2 x Pusa Barani was highest in magnitude compared to other three crosses for these traits. Importance of additive gene action was revealed in the inheritance of most of the characters under study.

Key Words: Coefficient of variation, Genetic advance, Heritability, Mustard, Variability

Introduction

Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] is one of the most important oilseed crops of the country and it covers about more than six million ha during *rabi* season accounting about 13% of world's oilseed area and 7% of production (Singh and Dixit, 2008). Presently, average yield of oilseed is just around one ton/ha which need be increased to at least 1.3 and 1.6 ton by 2010 and 2015, respectively, if the country has to achieve self-sufficiency in edible oil (Hedge, 2006). With limited scope to bring additional area under oilseeds cultivation bulk of future increases in oilseed production have to come primarily from a combination of high yielding plant types and standard crop management practices. Therefore, there is a need of concentrated effort to develop high yielding varieties of this crop for increasing its productivity and production. It is well known that useful biometrical information and the extent of the existing variability of the various economic or agronomic traits in the existing working germplasm are usually required in evolving superior, stable and widely adaptable varieties in field crops. Thus, information on the nature and magnitude of genetic variability operative in the inheritance of various yield component traits and yield itself would always be

helpful to the plant breeders in selecting the parental genotypes to be utilized in breeding programme.

Materials and Methods

A field experiment was carried out during *rabi* season, 2005-06 at the Agriculture Research Farm of the Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. This research farm is situated at 25°2' N latitude and 83°03' E longitude at an altitude of 128.93 meters above the sea level. The material used in the present investigation comprised of four crosses (F_1 s) involving six parental lines, their four F_2 s and eight back crosses of Indian mustard. All the crosses and parental genotypes were evaluated in non-replicated, compact family blocks during *rabi* season 2006-2007. Three rows of parental and F_1 lines, 10 rows of F_2 and 6 rows of each back cross generation were raised for recording data. The spacing between row to row and plant to plant were 30 cm and 45 cm, respectively. Boarder plants were excluded for recording data. All the recommended package of practices for growing good crop were followed. The parental lines utilized were Agrani, NUDH-YJ-1, QM-2, Pusa Barani, Pusa Bahar, and LES-39. Four crosses were made from these parents viz., cross 1 = Agrani × NUDH-YJ-1, cross 2 = QM-2 × Pusa Barani, cross 3 = NUDH-YJ-1 × Pusa Barani

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and cross 4 = LES-39 × Pusa Bahar. Eight back crosses were made by crossing each F_1 with their respective parents. F_2 seeds were obtained by selfing the F_1 plants. Fifteen plants from each parent and F_1 , 100 plants from F_2 of each cross and 50 plants from back cross generations of each cross were selected randomly for recording observations on the traits namely, plant height, number of primary branches/plant, number of siliqua/plant, number of seeds/silique, test weight and seed yield/plant.

Results and Discussion

The extent of variability in the present set of genotypes with respect to yield and yield components was estimated in terms of range, mean and coefficient of variation (CV). The range of variation for the all the traits viz., plant height, primary branches/plant, siliqua/plant, seeds/silique, 1000-seed weight and seed yield/plant was higher in F_2 than both the back crosses (B_1 and B_2) in all the four crosses. Similarly CV for all the traits was higher in the F_2 of all the four crosses as compared to their respective parents, F_1 s and back crosses, except seeds per silique (B_2). High estimates of coefficient of variation ($> 30\%$) were recorded in the F_2 of all the crosses, for traits namely number of primary branches/plant, number of siliqua/plant and seed yield/plant (Table 1). Ali *et al.* (2002) and Singh (2004) working with mustard have also reported high CV for yield and yield components. Presence of considerable amount of variability suggest a good scope of practicing selection for these traits. In oilseed *Brassica*, there is a compensatory relationship between number of seeds/silique and test weight. Hence, an optimum number of seeds/silique coupled with high test weight would be a desirable criterion for improving yield in mustard. Yield as such is a complex trait being an integrated function of action and interaction of a number of yield components which themselves are often very complex quantitative attributes. In order to resolve the nature of inheritance of yield and yield component traits the components of genetic variation viz., additive genetic variation, dominance genetic variation, degree of dominance, heritability estimates in narrow sense, and genetic advance as percentage of mean were estimated for all the characters under study in F_2 of four crosses (Table 2). In cross I and cross II, all the traits under study exhibited preponderance of additive genetic variance as compared to dominance genetic variance. The estimates of average degree of dominance revealed partial dominance in the inheritance of all the traits. In cross III (NUDH-YJ-1 × Pusa Barani), except for seeds/silique, all the

traits exhibited higher magnitude of additive genetic variance than dominance genetic variance. The degree of dominance revealed complete dominance for seeds/silique and partial dominance for rest of the traits. Earlier workers have reported additive gene action (Sheikh and Singh, 2004), dominant gene action (Rai *et al.*, 2005) as well as both (Rishipal and Kumar, 1993) for seeds/silique. In cross IV (LES-39 × Pusa Bahar), primary branches/plant and siliqua per plant exhibited importance of dominance genetic variance over additive genetic variance while rest of the traits exhibited preponderance of additive genetic variance. The degree of dominance revealed over dominance for primary branches/plant and siliqua/plant. Rest of the characters exhibited partial dominance. Earlier workers in mustard have reported preponderance of dominance gene effect (Prakash *et al.*, 1998) for primary branches/plant.

Overall, in all the four crosses, degree of dominance revealed partial dominance for plant height, test weight and seed yield/plant (Table 2). Earlier workers in mustard have reported both partial dominance (Prakash *et al.*, 1998; Rai *et al.*, 2005) as well as additive gene action (Verma and Kushwaha, 1999; Sheikh and Singh, 2004) in the inheritance of plant height. Rishipal and Kumar (1993) have reported importance of both additive and dominance effect for test weight whereas, Singh *et al.* (2002) have reported importance of over dominance for it. Contrary to present finding, seed yield/plant has been reported to be governed mainly by dominance gene effect (Singh, 2004). Where as Rai *et al.* (2005) have reported partial dominance for seed yield/plant as is revealed in the present set of material. Comparison of the estimates of additive and dominant genetic variance in different crosses, it is revealed that the highest magnitude of additive genetic variance was observed in cross II for plant height followed by primary branches per plant, siliqua/plant and seed yield/plant. Seeds/silique and test weight showed nearly equal amount of additive genetic variance in all the crosses. Thus, we may follow single plant selection in F_2 progeny of cross II for improving component traits like plant height, primary branches/plant and siliqua/plant. This may be fruitful in isolating a superior line having increased yield. In cross IV which included parents namely LES-39 and Pusa Bahar, the siliqua/plant showed higher magnitude of dominant genetic variance as well as over dominance for the trait as compared to other crosses. So, we may go for hybrid breeding for this trait. Narrow sense heritability which is heritable portion of variance for

Table 1. Range and coefficient of variation (CV) of four crosses for yield contributing traits in Indian mustard.

Traits/ Crosses			Generations					
			P ₁	P ₂	F ₁	B ₁	B ₂	F ₂
Trait 1	C ₁	Range	136-151	167-188	168-186	125-208	132-198	102-213
		CV	6.40	5.20	5.09	10.30	10.50	13.70
	C ₂	Range	151-172	142-162	147-170	125-220	134-194	97-205
		CV	4.35	4.22	4.58	12.83	8.52	15.32
	C ₃	Range	157-188	142-167	168-183	131-223	145-205	116-200
		CV	5.20	4.56	2.75	8.32	9.57	12.98
	C ₄	Range	159-186	138-156	164-174	147-215	113-207	106-196
		CV	4.93	3.96	1.87	8.11	10.28	12.68
Trait 2	C ₁	Range	4-6	4-6	5-7	3-9	3-8	1-8
		CV	17.87	16.76	10.93	21.87	22.31	30.32
	C ₂	Range	5-6	5-7	4-6	4-9	3-10	3-10
		CV	9.50	12.49	13.04	26.07	27.72	32.27
	C ₃	Range	4-7	5-7	6-8	2-10	4-10	2-10
		CV	16.76	12.49	9.58	25.10	21.08	34.44
	C ₄	Range	4-7	4-6	5-7	4-9	3-9	2-9
		CV	13.58	12.96	12.63	23.34	24.44	30.62
Trait 3	C ₁	Range	167-215	238-304	270-304	168-377	184-399	102-357
		CV	13.38	13.03	4.11	20.03	23.66	34.63
	C ₂	Range	189-256	193-250	202-256	174-436	181-376	89-524
		CV	9.55	9.22	7.40	26.60	23.18	36.42
	C ₃	Range	208-324	193-250	313-380	148-347	144-369	93-369
		CV	13.03	9.22	5.80	21.25	24.92	38.42
	C ₄	Range	181-275	168-211	205-265	111-369	117-433	82-465
		CV	9.35	7.37	6.21	28.11	27.96	33.79
Trait 4	C ₁	Range	11.67-14.67	12.67-15.67	10-12.67	9.33-14.33	9.67-15.33	9.33-16.33
		CV	6.34	5.53	6.84	9.84	11.14	12.08
	C ₂	Range	9.33-14.33	9-12.33	10.33-14.67	9.33-14.33	9-13.67	6.33-17.0
		CV	13.75	8.52	9.94	13.18	14.38	13.36
	C ₃	Range	12.67-15.67	9.33-12.33	11-13.67	8-15	5.33-16.33	8.33-15.67
		CV	5.53	10.31	6.80	14.57	16.43	15.73
	C ₄	Range	15.33-17.67	10.67-12.67	13-14.67	10-17.67	9.33-16.67	7.58-17.0
		CV	4.33	5.26	4.64	10.28	12.83	12.25
Trait 5	C ₁	Range	2.44-3.22	2.73-3.84	2.52-3.83	2.9-4.37	2.40-4.17	2.56-5.0
		CV	6.94	10.83	7.60	15.04	16.44	23.95
	C ₂	Range	7.98-10.95	9.59-13.78	9.76-13.92	9.44-21.57	9.33-16.99	5.15-26.15
		CV	11.57	11.12	11.38	28.23	27.43	40.00
	C ₃	Range	2.73-2.84	2.97-3.86	3.24-3.81	3.27-4.69	2.82-4.62	3.04-5.57
		CV	10.83	11.11	5.83	17.82	20.21	20.21
	C ₄	Range	2.37-2.96	5.02-5.78	3.31-4.23	3.08-5.2	3.2-5.69	2.6-4.48
		CV	4.88	11.05	7.76	25.42	23.68	35.62
Trait 6	C ₁	Range	2.73-2.84	2.97-3.86	3.24-3.81	3.27-4.69	2.82-4.62	3.04-5.57
		CV	10.03	8.42	7.40	11.69	14.24	15.00
	C ₂	Range	2.44-3.16	2.95-3.86	2.76-3.91	2.96-3.87	2.91-3.94	2.32-5.4
		CV	8.22	8.47	9.94	15.65	17.25	18.38
	C ₃	Range	9.3-13.61	9.63-13.78	13.17-16.58	8.63-21.5	8.62-26.32	5.44-17.63
		CV	8.42	7.87	11.15	15.53	14.44	15.76
	C ₄	Range	9.73-11.21	9.12-12.95	9.59-12.63	8-24.66	7.63-26.89	5.53-25.5
		CV	4.88	11.05	7.76	25.42	23.68	35.63

Trait 1 = plant height, trait 2 = number of primary branches/plant, trait 3 = number of siliqua/plant, trait 4 = number of seeds/siliquae, trait 5 = test weight and trait 6 = seed yield/plant.

which selection can successfully be practiced was studied in four crosses. Estimate of narrow sense heritability was highest for seed yield/plant followed by plant height and test weight among all the four crosses under study. Singh *et al.* (2002); Mahala *et al.* (2003) and Rai *et al.*

(2005) reported moderate to high estimates of heritability for yield/plant. High narrow sense heritability for seed yield/plant offers good opportunity for exploiting fixable variability for the improvement in seed yield in mustard. Primary branches/plant and seeds/siliquae, recorded lowest

Table 2. Estimates of degree of dominance, heritability and genetic advance in F₂s of Indian mustard

Estimates	Crosses	Plant Height	Primary branches/Plant	Siliquea/Plant	Seeds/Siliqueae	Test weight	Seed yield/Plant
	Range	11.67-14.67	12.67-15.67	10-12.67	9.33-14.33	9.67-15.33	9.33-16.33
σ^2A	C ₁	305.15	0.79	2570.21	1.36	0.22	5.71
	C ₂	347.73	1.46	4830.03	1.13	0.27	19.67
	C ₃	298.40	1.16	3887.79	1.28	0.27	8.21
	C ₄	286.18	0.65	1940.69	1.32	0.22	14.33
σ^2D	C ₁	64.65	0.49	1279.61	0.33	0.03	0.02
	C ₂	105.03	1.32	1408.47	0.36	0.10	0.84
	C ₃	46.60	0.95	1519.37	1.40	0.09	1.05
	C ₄	68.86	0.92	2279.43	1.09	0.06	1.47
$(\sigma^2D/\sigma^2A)^{1/2}$	C ₁	0.46	0.79	0.71	0.49	0.37	0.06
	C ₂	0.55	0.95	0.54	0.56	0.37	0.21
	C ₃	0.40	0.91	0.62	1.05	0.58	0.36
	C ₄	0.49	1.19	1.08	0.91	0.52	0.32
H ² (ns)	C ₁	67.27	39.90	56.64	58.64	58.57	66.67
	C ₂	69.39	45.38	73.01	36.45	60.00	89.21
	C ₃	75.47	44.27	65.00	36.36	62.79	78.19
	C ₄	73.00	31.25	44.34	46.48	66.67	86.43
GS	C ₁	29.32	1.16	78.60	1.83	0.79	4.58
	C ₂	32.00	1.68	122.33	1.32	0.83	8.63
	C ₃	30.91	1.48	103.82	1.41	0.85	5.22
	C ₄	29.75	0.93	60.43	1.61	0.79	7.25
GSm	C ₁	18.98	24.89	40.41	14.55	20.63	42.76
	C ₂	21.90	30.43	54.77	10.02	22.74	73.51
	C ₃	20.17	31.49	51.44	11.82	20.43	47.20
	C ₄	19.07	19.75	30.86	11.70	22.83	63.43

Abbreviations: σ^2A = Additive variance, σ^2D = Dominance variance, $(\sigma^2D/\sigma^2A)^{1/2}$ = Degree of dominance, Hns = Heritability in narrow sense GS = Genetic Advance, GSm = GS as percentage of Mean, CV = Coefficient of variation, C₁ = Cross 1 (Pusa Agrani × NUDH-YJ-1), C₂ = Cross 2 (QM-2 × Pusa Barani) C₃ = Cross 3 (NUDH-YJ-1 × Pusa Barani) C₄ = Cross 4 (LES-39 × Pusa Bahar).

estimates of narrow sense heritability in all the four crosses. This suggested poor scope of improving yield in mustard through selection for component traits namely primary branches/plant and seed/siliqueae. Beside the heritability, genetic advance accomplishes meaningful genetic progress in crop improvement programme, therefore, selection of a character should be based on high heritability coupled with high genetic advance. High genetic advance as per cent of mean coupled with high heritability was observed for seed yield/plant and siliquea/plant in most of the crosses. Test weight which recorded high narrow sense heritability had poor genetic advance as percent of mean. This suggested that effective improvement in yield can be achieved by practicing selection for siliquea/plant rather than test weight. In cross III (NUDH-YJ-1 x Pusa Barani), highest genetic advance was observed for siliquea/plant followed by plant height (Table 2). Low Genetic advance was recorded for test weight, seeds/siliqueae and primary branches/plant. The present findings regarding heritability and genetic advance are in accordance with those of Mahala *et al.* (2003) and Singh *et al.* (2003).

References

- Ali N, J Farzad and AA Attary (2002) Genetic variability, correlation and path analysis of yield and its components in winter rapeseed (*Brassica napus* L.). *Pak. J. Botany*. **34**: 145-150.
- Hegde DM (2006) The Hindu Survey of Indian Agriculture. Chennai: 66-69.
- Mahala HR, J Jambhulkar, DK Yadava and R Sharma (2003) Genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* (L.) Czern and Coss). *Indian J. Genet.* **53**: 171-172.
- Prakash K, NK Thakral, TP Yadava, Lekhraj and N Chandran (1998) Inheritance of yield attributing traits in Indian mustard (*Brassica juncea* L.). *Cruciferae Newsl.* **20**: 73-74.
- Rai SK, A Verma and DD Pandey (2005) Analysis of combining ability in Indian mustard (*Brassica juncea* (L.) Czern. and Coss.) *Plant Archives* **5(1)**: 69-75.
- Rishipal and P Kumar (1993) Generation mean analysis of yield and yield attributes in Indian mustard (*Brassica juncea*). *Indian J. Agri. Scic.* **63**: 807-813.
- Sheikh IA and JN Singh (2004) Inheritance of seed yield, oil content and some component traits in Indian mustard. *Adv. Plant Sci.* **17(1)**: 307-311.
- Singh B (2004) Character association and path analysis under dry land condition in Indian mustard (*Brassica juncea* L.). *Cruciferae Newsl.* **25**: 99-100.
- Singh RK and P Dixit (2008) Genetics of Quantitative Traits in Indian mustard (*Brassica juncea* L. Czern. and Coss.). *J. Plant Genet. Resour.* **21**: 75-78.
- Singh D, VK Mishra and RP Singh (2003) Studies on heritability and genetic advance of seed yield and its components in

- yellow sarson (*Brassica campestris* L. var. yellow sarson Prain). *Agric. Sci. Digest* **23(1)**: 69-70.
- Singh M, GB Swarnkar, P Lalta, and R Geeta (2002) Genetic variability, heritability and genetic advance for quality traits in Indian mustard [*Brassica juncea* (L.) Czern. and Coss.]. *Plant Archives* **2(1)**: 27-31.
- Verma OP and GD Kushwaha (1999) Heterosis and combining ability of seed quality traits in Indian mustard (*Brassica juncea* (L.) Czern. and Coss.). *Cruciferae Newsl.* **21**: 107-108.

Assessment of Variability Parameters for Agro-morphological and Phyto-chemical Traits in Basil (*Ocimum basilicum* L.) Germplasm

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The variability parameters viz., genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), heritability and genetic advance were studied for agro-morphological and phyto-chemical traits in 30 genotypes of basil during *kharif* 2004 and 2005. Tremendous variability was observed for agro-morphological as well as phyto-chemical characters. The high and medium values of GCV and PCV for seed yield/plant and spike length respectively, showed presence of maximum amount of variability in the germplasm. High heritability estimates were observed for seed yield/plant, leaf stem ratio, 1000 seed weight and plant height. These attributes may be improved further by selection. The estimates of high genetic advance were observed for fresh herbage yield per plant, seed yield per plant, plant height and dry yield/plant. The genetic advance as percentage of mean was recorded high for characters like leaf-stem ratio and spike length. The high estimates of genetic advance coupled with high heritability estimates for seed yield/plant, leaf stem ratio and plant height may be helpful in formulating the selection criteria for improvement of this important medicinal plant.

Key Words: Basil, Coefficient of Variation, Genetic Advance, Genotypic Coefficient of Variation, Medicinal plant, Phenotypic Heritability

Introduction

Basil (*Ocimum basilicum* L.) is a globally important plant and grown since times immemorial due to its medicinal, culinary and other properties. The genus *Ocimum* belongs to family Lamiaceae having around 160 species widely distributed throughout the country from tropical areas to 1800 m in the Himalayas region (Balyan and Pushpangadan, 1988). At global level, it is distributed and grown in Arabia, Australia, Brazil, Egypt Malaya, Nepal, Iran, Philippines and Western Asia (MGrieve, 1992; Pushpangadan and Bradu, 1995; Bhattacharjee, 1998; Verma *et al.*, 1998; Pandey and Chowdhary, 2002). The role of genetic variability is well documented in crop improvement. The selection of the best genotypes for the desirable traits from the variable populations is important for making rapid improvement of the plant. The selection of the potential parents from the variable populations is also important for their use in crossing for further improvement. Genotypic and phenotypic coefficient of variability helps to access the magnitude of variability in population. Selection would be more effective for the traits which exhibit high variability and heritability along with moderate to high genetic gain. Keeping in view of the above, an attempt was made to analyze the variability parameters for agro-morphological and phyto-chemical

parameters of basil germplasm. Realizing the importance of crop, the desired variability for different agronomic traits coupled with quality parameters have been identified for further improvement. The studies will be helpful and of practical significance to the plant breeders to achieve the desired level of improvement in this important medicinal plant.

Materials and Methods

Thirty accessions of basil were augmented from different sources. These comprised of 20 accessions of exotic origin (EC) from five countries (USA-10, USSR-07, Poland-01, Hungary-01 and Germany-01) and rest were indigenous collections (IC) representing the maximum variability by taking into consideration their place of origin (Madhya Pradesh-06, Gujarat-02, Andhra Pradesh-01 and Uttar Pradesh-01). The experimental material was grown in nursery and transplanted in a randomized block design (RBD) with three replications during *kharif* 2004 and 2005 at National Bureau of Plant Genetic Resources (NBPGR) Experimental Farm, Issapur, New Delhi, (latitude 28°36'N, longitude 76°50'E) and at Research Farm, Janta Vedic College Baraut, Baghpat, UP (latitude 29°06'N, longitude 77°15'E). Three rows of each accession/row were transplanted with row to row and plant to plant spacing of 45 and 30 cm, respectively. Observations were recorded

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on five randomly selected plants in each genotype for 16 characters viz., number of primary branches/plant, lamina length (cm), lamina width (cm), leaf-stem ratio, days to flower initiation, number of spikes/plant, spike length (cm), number of flower-whorls/spike, plant height (cm), fresh herbage yield/plant (g), dry herbage yield/plant (g), days to seed maturity, seed yield/plant (g), 1000-seed weight (g), essential oil content (%), and essential oil yield/plant (ml). The Genotypic and phenotypic coefficients of variances were estimated according to Burton and DeVane (1953). Heritability in broad sense was calculated as ratio between genotypic variance to the total phenotypic variance and expected genetic advance was defined as the difference between mean of the progeny of selected individuals and base population as suggested by Johnson *et al.* (1955).

Results and Discussion

Greater variability in the base material ensures higher chances of getting the genotypes of desired traits. The estimates of genetic parameters of variability, viz., genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), heritability in broad sense (h^2) and genetic advance (GA) along with genetic advance as % of mean for different characters is presented in Table 1. The data revealed that there were significant

differences among accessions for various agromorphological and phyto-chemical traits. In overall pooled analysis of the data of both the locations, the high values of GCV for seed yield/plant (50.37) and leaf-stem ratio (29.75); medium values of GCV for spike length (19.73), essential oil yield/plant (12.98), plant height (12.82), fresh herbage yield/plant (11.48), essential oil content (11.46), 1000-seed weight (11.36) and dry herbage yield/plant (11.26) were recorded. The details of the same are presented in Fig. 1.

Similarly, the high values of PCV were observed in seed yield/plant (50.62) and leaf-stem ratio (30.18). Medium values of PCV were observed in spike length (21.80), essential oil yield/plant (19.26), essential oil content (17.98), plant height (14.22), dry herbage yield/plant (13.29), fresh herbage yield/plant (12.93), number of spikes/plant (12.20) and 1000-seed weight (11.60). The details of the same are presented in Fig. 2.

Heritability (bs) is an important selection parameter because it helps in selection of elite genotypes from genetically diverse population. Over all pooled analysis of the data recorded at both the locations revealed that highest heritability estimate was found in seed yield/plant (99.0%) followed by leaf-stem ratio (97.2%), 1000-seed weight (95.8%), spike length (81.9%), plant height

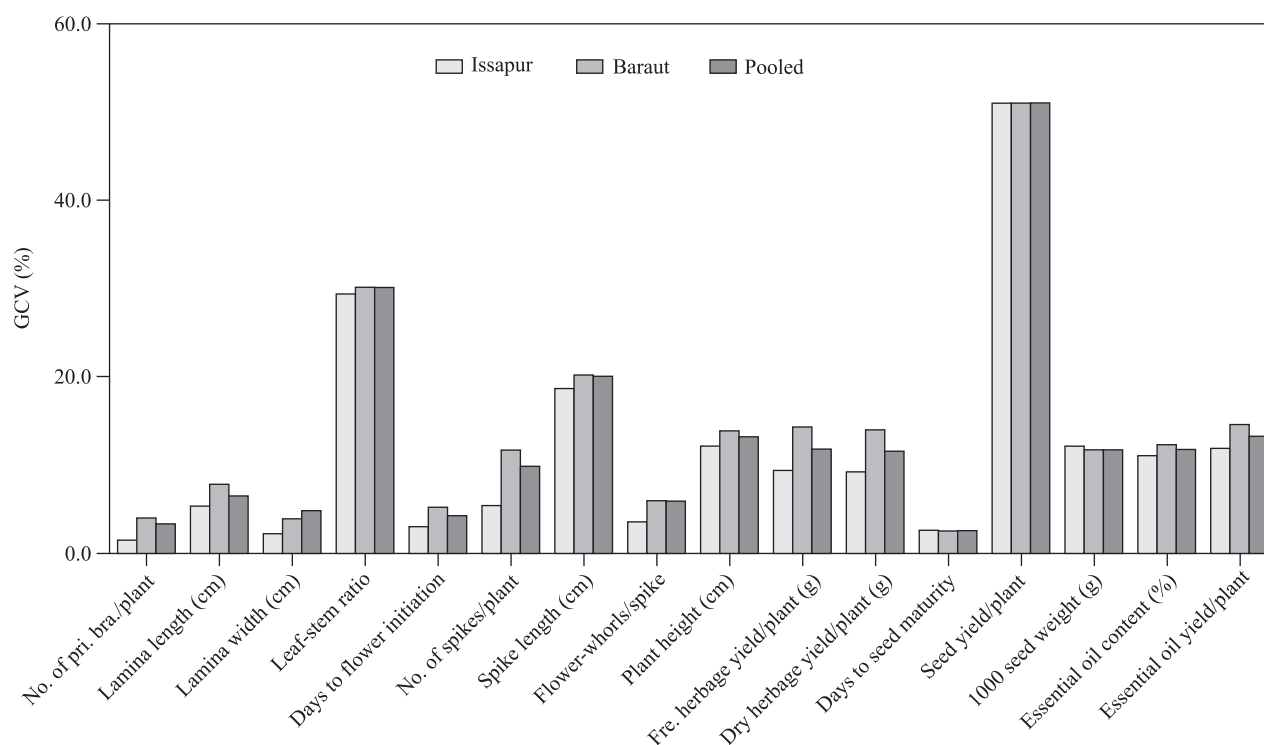


Fig. 1. Genotypic coefficients of variation in 30 accessions of basil

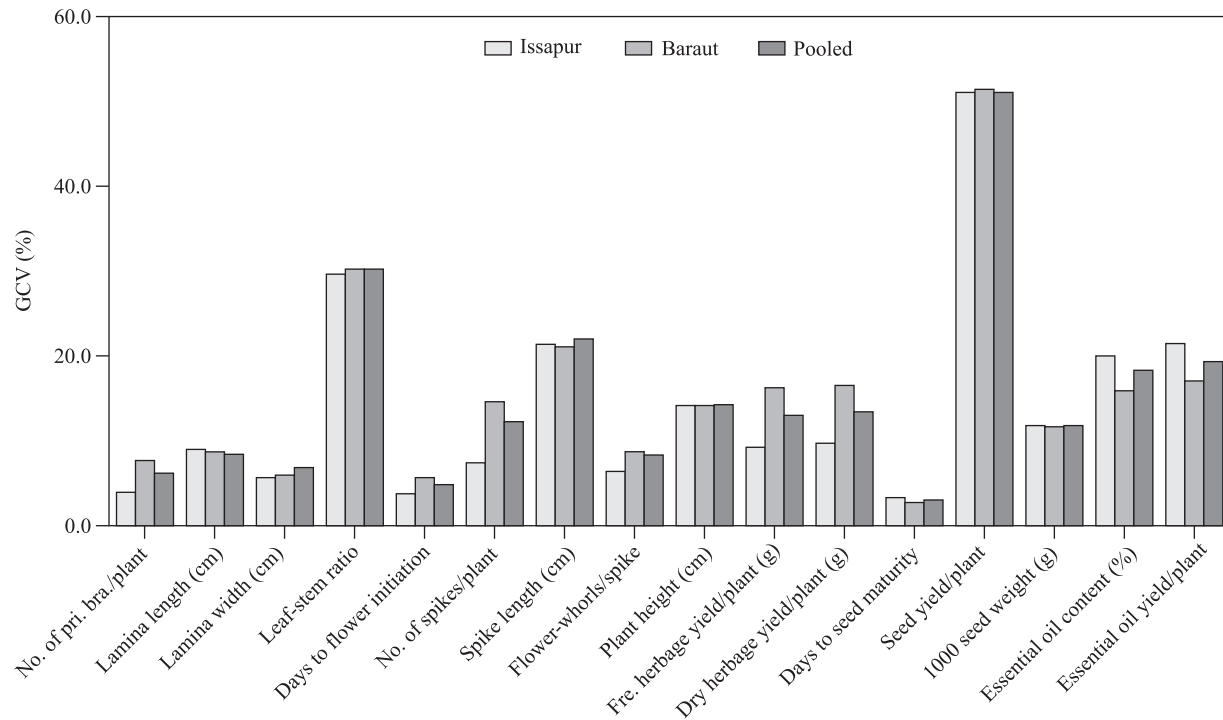


Fig. 2. Phenotypic coefficients of variation in 30 accessions of basil

(81.3%), fresh herbage yield/plant (78.9%), dry herbage yield/plant (71.8%) and days to flower initiation (71.4%). Moderate heritability estimates were observed for number of spikes/plant (62.6%), days to seed maturity (59.8%) and lamina length (53.0%). Low heritability estimates

were observed in number of flower-whorls/spike (48.7%), lamina width (46.7%), essential oil yield/plant (45.4%), essential oil content (40.6%) and number of primary branches/plant (27.1%). The details of the same are presented in Fig. 3.

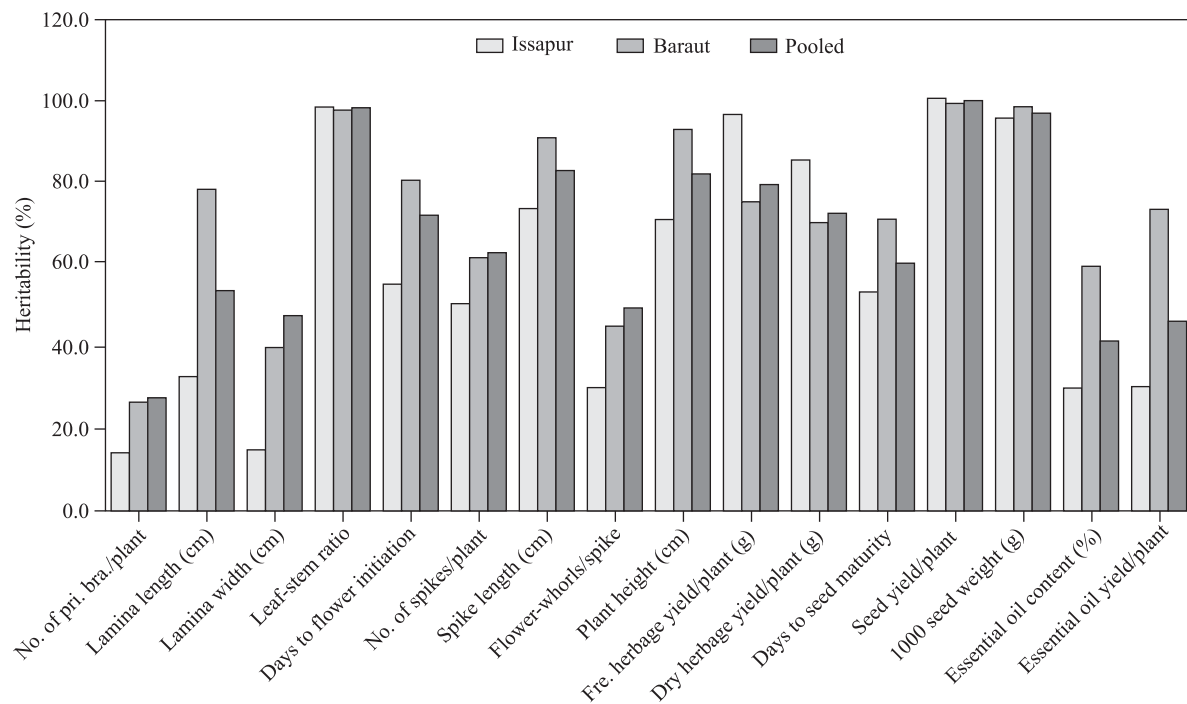


Fig. 3. Heritability (bs) in 30 accessions of basil

Genetic advance is also an important selection parameter. The estimates of genetic advance for various characters studied are presented in Table 1. Overall pooled analysis of the data of both the locations showed that the highest genetic advance was obtained in fresh herbage yield/plant (61.14). Seed yield/plant (21.34), followed by plant height (12.89), dry herbage yield/plant (12.47)

and number of spikes/plant (10.97) showed the moderate estimates of genetic advance. For remaining characters the genetic advance was low which ranged from 0.03 to 6.08. The details of the same are presented in Fig. 4.

The results of genetic advance as per cent of mean revealed that overall pooled analysis of the data for both the locations revealed that the highest genetic advance as

Table 1. Variability parameters for 16 characters in 30 basil germplasms

S.No.	Character(s)	Range	SEm $\pm$	GCV	PCV	Heritability (%)	Genetic advance	Genetic advance as % of mean
1.	No. of primary branches/plant	10.63–12.98	0.26	3.31	6.35	27.1	0.42	3.57
2.	Lamina length (cm)	4.42–5.89	0.12	6.44	8.52	53.0	0.48	9.74
3.	Lamina width (cm)	2.60–2.82	0.06	4.79	7.00	46.7	0.18	6.64
4.	Leaf-stem ratio	0.59–1.67	0.02	29.75	30.18	97.2	0.60	60.61
5.	Days to flower initiation	60.28–72.82	0.68	4.11	4.86	71.4	4.58	7.15
6.	No. of spikes/plant	54.55–82.18	2.12	9.65	12.20	62.6	10.97	15.73
7.	Spike length (cm)	10.55–23.91	0.63	19.73	21.80	81.9	6.08	36.76
8.	No. of flower-whorls/spike	10.85–15.28	0.30	5.77	8.27	48.7	1.04	8.29
9.	Plant height (cm)	44.95–81.70	1.36	12.82	14.22	81.3	12.89	23.81
10.	Fresh herbage yield/plant (g)	223.58–346.25	7.05	11.48	12.93	78.9	61.14	21.01
11.	Dry herbage yield/plant (g)	49.16–75.78	1.83	11.26	13.29	71.8	12.47	19.67
12.	Days to seed maturity	153.58–167.33	1.22	2.29	2.96	59.8	5.79	3.65
13.	Seed yield per plant	10.41–44.65	0.43	50.37	50.62	99.0	21.34	103.24
14.	1000 seed weight (g)	1.10–1.69	0.01	11.36	11.60	95.8	0.32	23.02
15.	Essential oil content (%)	0.14–0.23	0.01	11.46	17.98	40.6	0.03	16.67
16.	Essential oil yield/plant	0.39–0.71	0.03	12.98	19.26	45.4	0.10	18.87

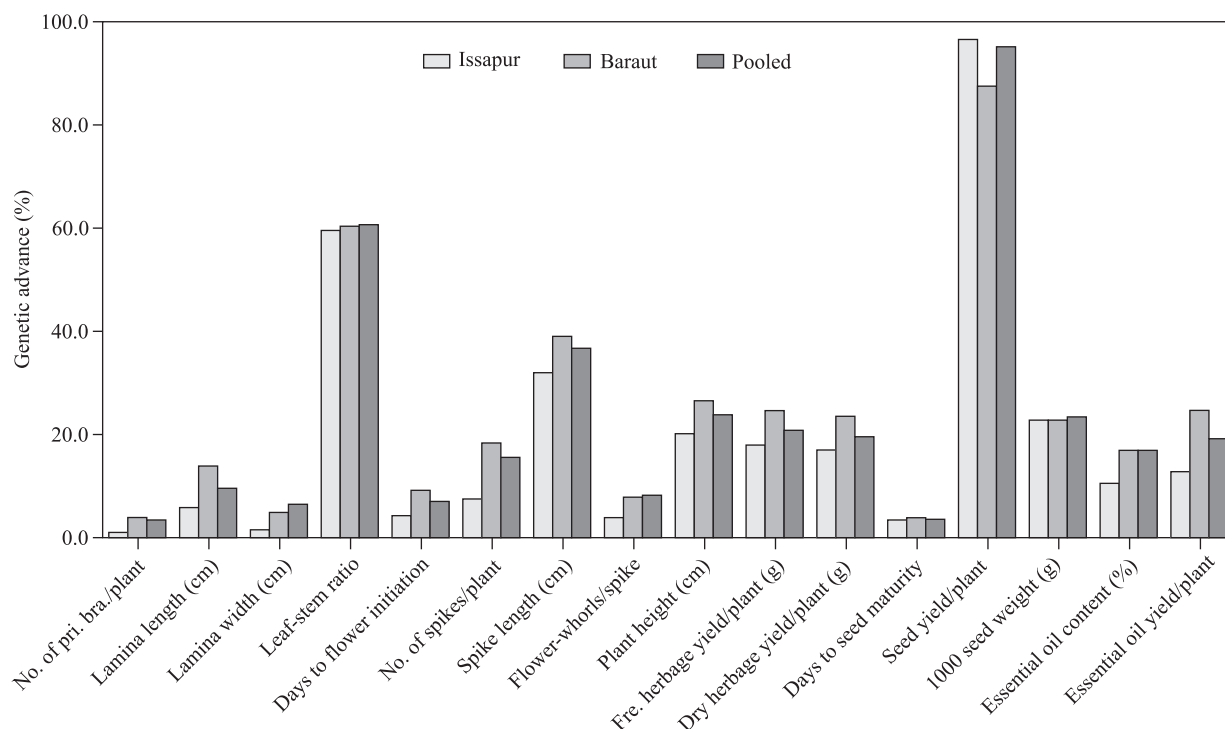


Fig. 4. Genetic advance (%) in 30 accessions of basil

per cent of mean was observed in seed yield/plant (103.29) followed by leaf-stem ratio (60.61). Moderate genetic advance as per cent of means were observed in spike length (36.76), plant height (23.81), 1000-seed weight (23.02), fresh herbage yield/plant (21.01), dry herbage yield/plant (19.67), essential oil yield/plant (18.87), essential oil content (16.67) and number of spikes/plant (15.73). Whereas low values of genetic advance as per cent of means were recorded for number of primary branches/plant (3.57), days to seed maturity (3.65), days to flower initiation (7.15), number of spikes/plant (8.29) and lamina length (9.74).

Thus, information regarding the variability, genotypic and phenotypic coefficient of variation, heritability and genetic advance would be useful in developing reliable selection indices. The desired variability for different agro-morphological traits along with phyto-chemical parameters have been identified for further improvement. As plant height, fresh herbage yield/plant and seed yield/plant recorded higher estimates for genetic heritability and genetic advance, selection for these traits would be more effective. These studies will be helpful and practical use to the plant breeders and to achieve the desired level of improvement in this important but neglected medicinal plant.

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References

- Burton, GW and EH DeVane (1953) Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.* **45**: 478–481
- Balyan SS and P Pushpangadan (1988) A study on the taxonomical status and geographical distribution of genus *Ocimum*. *PAFAI J.* **10(2)**: 13–19.
- Bhattacharjee SK, (1998) A Hand Book of Medicinal Plants. Pointer Pub., Jaipur, India, pp 241–242.
- Johnson HW, HF Robinson and RE Comstock (1955) Estimates of genetic and environmental variability in soybean. *Agron. J.* **49**: 314–318.
- MGrieve (1992) A Modern Herbal. RCN-ISBN/ISSN/BNB 1855012499, Tiger Books International London, pp 85–86.
- Pandey AK and AR Chowdhary (2002) Essential oil of *Ocimum basilicum* L. from Satara plateau of central India. *Indian Perfumer* **46(2)**: 131–134.
- Pushpangadan P and BL Bradu (1995) In: KL Chadha and Rajendra Gupta (eds) Advances in Horticulture-Vol. 11-Medicinal and Aromatic Plants: Malhotra Publishing House, New Delhi, India, pp 627–657.
- Verma PK, SN Gupta, M Khabiruddin and GD Sharma (1998) Genetic variability parameters for herb and oil yield in different *Ocimum* species. *Indian Perfumer* **42(1)**: 36–38.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXIth meeting held on May 18, 2010 at the National Bureau of Plant Genetic Resources, New Delhi, approved the registration of following 115 germplasm lines out of 206 proposals considered. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. AKAW-3717 (IC0582907; INGR10001), a Wheat (*Triticum aestivum* L.) Germplasm with Tolerance to Drought and Heat

NR Potdukhe and SG Bharad

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Nearly 22.5 m ha area is under bread and durum wheat in North-West, North-East and central India, where early or late heat stress or both affects wheat productivity. Stagnant wheat production in recent years is partly due to climatic factors including heat stress characterized by an increasing trend in average temperature during winter months (Rane *et al.*, 2000; Nagarajan 2005). With an objective of development of short duration temperature insensitive wheat varieties with tolerance to terminal heat, a cross between germplasm line HW-2035 and NI-5439 was performed at Wheat Research Unit, Dr Panjabrao Deshmukh Krishi Vidyapeeth (PDKV), Akola. Further generations of cross HW-2035 x NI-5439 were advanced as per pedigree selection breeding method. After stabilization of material, it was contributed in DHTSN during the

year 2006-07, to judge its performance under high temperature both at early and terminal growth stages and moisture stress throughout the crop period.

Morpho-agronomic Characteristics

Growth habit of the genotype AKAW-3717 is erect and coleoptiles, leaf sheaths and auricles are free from anthocyanine pigmentation. Flag leaf length and breadth is medium and it requires average 62 days for ear emergence. Waxiness on flag leaf sheath is strong and medium on leaf blade. Average plant height is 65 cm. Ear head length and density is medium with white colored awns of medium length. Amber colored grains are medium in size and are having about 38.0 g/1000 grain weight with semi-hard grain texture. Data on grain yield (g/plot), Morphological

Table 1. Grain yields (g/plot) performance, rank as revealed by pooled analysis

Rank	Genotype	Sagar	Hisar	Kanpur	Pune	Indore	Karnal	Kota	Bardoli	Dharwad	Dhanduka
A	19 th DHTSN, 2006-07										
1	HI-1544	333.4	511.0	192.9	551.1	—	—	—	—	—	66.5
2	AKAW-3717	364.9	374.3	214.4	591.9	—	—	—	—	—	61.1
	Gen. Mean	346.1	398.7	174.8	356.6	—	—	—	—	—	64
	CD at 5%	91.2	70.3	50.0	—	—	—	—	—	—	9.6
B	20 th DHTSN, 2007-08										
1	NI-5439	445.1	339.3	249.6	475.0	548.7	162.0	925.0	—	—	—
18	AKAW-3717	517.7	324.9	234.7	462.5	395.8	132.5	418.5	—	—	—
	Gen. Mean	358.6	230.2	229.1	424.8	385.0	139.4	594.5	—	—	—
	CD at 5%	87.3	63.2	127.1	121.0	91.6	Ns	60.1	—	—	—
C	21 st DHTSN, 2008-09										
1	AKAW-3717	440.0	430.0	129.0	208.0	335.5	456.1	410.0	395.0	368.0	—
2	HI-1564	440.0	322.5	117.5	218.0	253.5	471.0	457.5	400.0	272.0	—
	Gen. Mean	284.5	287.1	119.3	152.4	253.7	412.8	398.3	359.2	311.5	—
	CD at 5%	183.9	66.3	6.28	73.13	58.8	189.3	0	58.35	31.0	—

*Compiled and edited by: Anjali Kak and RK Tyagi, Division of Germplasm Conservation, National Bureau of Plant Genetic Resources, New Delhi-110 012

Table 2. Ancillary data of breeding trials NIVT-5A, 02-03 & 04-05 and AVT (RF-TS), 05-06

Character	Trial name& year	AKAW-3717	NI-5439	LOK-1	HW-2004	AKDW-2997-16	MACS-1967
Days to heading	NIVT-5A, 2002-03	111	105	103	104	—	—
	NIVT-5A, 2004-05	88	84	—	95	—	—
	AVT (RF), 2005-06	62	59	—	—	62	56
	Mean	87.0	83.0	103.0	99.5	62.0	56.0
Days to Maturity	NIVT-5A, 2002-03	154	151	144	155	—	—
	NIVT-5A, 2004-05	145	140	—	145	—	—
	AVT (RF), 2005-06	102	102	—	—	104	99
	Mean	134.0	131.0	144.0	150.0	104.0	99.0
Plant height (cm)	NIVT-5A, 2002-03	95	90	86	103	—	—
	NIVT-5A, 2004-05	89	84	—	104	—	—
	AVT (RF), 2005-06	65	66	—	—	60	65
	Mean	83.0	80.0	86.0	103.5	60.0	65.0
1000 Grain wt (g)	NIVT-5A, 2002-03	33	34	45	38	—	—
	NIVT-5A, 2004-05	26	26	—	35	—	—
	AVT (RF), 2005-06	38	38	—	—	41	49
	Mean	32.3	32.6	45.0	36.5	41.0	49.0

A: Amber; W: White; Ey: Easy; M: Medium; SO: Soft; SH: Semi hard; H: hard

Table 3. Reaction against rusts and KB diseases under field conditions (Artificial inoculations)

Varieties	Stem rust		Leaf rust				Stripe rust		KB (%)
	South		South		North		North		
	HS	ACI	HS	ACI	HS	ACI	HS	ACI	
NIVT-5A, 2002-03									
AKAW-3717	60S	22.3	60S	8.6	TS	0.8	80S	40.0	45.0
NI-5439	50S	26.3	70S	36.7	60S	23.6	80S	50.0	62.8
LOK-1	80S	29.0	80S	41.7	60S	18.7	80S	44.2	10.0
HW-2004	20MR	2.2	TMR	0.1	10MS	2.0	5S	1.2	13.0
INFECTOR	100S	63.3	100S	71.1	90S	74.3	80S	60.0	63.0
NIVT-5A, 2004-05									
AKAW-3717	50S	19.9	40S	8.4	10MS	1.3	100S	81.7	15.2
NI-5439	80S	30.9	60S	32.3	60S	21.7	100S	71.3	31.8
LOK-1	—	—	—	—	—	—	—	—	—
HW-2004	20MS	3.8	10MR	1.0	0	0.0	40S	10.0	50.8
INFECTOR	100S	74.3	100S	80.0	80S	78.3	100S	88.3	28.1
AVT (RF), 2005-06									
AKAW-3717	60S	28.0	20S	4.3	TS	0.1	80S	64.0	80.4
INFECTOR	80S	68.0	80S	58.8	80S	67.5	80S	52.0	76.0

R: Resistant; MR: Moderately resistant; MS: Moderately susceptible; S: Susceptible

Table 4. Quality characteristics in trials NIVT-5A, 02-03 & 04-05 and AVT (RF-TS), 05-06

S. No.	Quality characters	AKAW-3717			NI-5439		
		2002-03	2004-05	2005-06	2002-03	2004-05	2005-06
A	Grain characters						
	Texture	SO-SH	H	SO-SH	SO-SH	A-W	SO-SH
	1000 grain Wt (g)	33	38	38	37	34	38
	Grain colour	A	A	A	A	A-W	A
B	Quality characters						
	i) Protein content (%)	12	13	8.97	12.3	12.2	9.25
	ii) Grain appearance score	5.2	4.8	5.1	5.2	5.5	5.5
	iii) Sedimentation value (kg/hl)	43.5	49	48	45.1	47	52
	iv) Hectolitre weight (kg/ha)	77	76.4	80.4	74.8	76.4	81.2
	v) HMW (GLU-1 Score)	—	—	6	—	—	6

characters, reaction to rust and kernel bunt disease and quality characteristics is presented in Table 1, 2 & 3. Data source utilized is AICW&BIP Progress Reports 2002-03 to 2008-09.

The genotype AKAW-3717 developed at Wheat

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two replications and each genotype was raised on plots with 2 rows of 2 m row length with 30 cm space between two rows. The crop was sown with pre-sowing irrigation only when germination was likely to be affected by soil moisture deficit, no irrigation was provided after germination and the crop growth was dependent on stored soil moisture or rainfall.

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3. Atharga Kempu Jola (IC0584056; INGR10003), a Sorghum (*Sorghum bicolor*) landrace for Good Flaking

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References

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The DSR-GMN-41, DSR-GMN-42, DSR-GMN-46, DSR-GMN-52, DSR-GMN-58, and DSR-GMN-59, grain mould resistance lines were developed from crosses involving 8 grain mould susceptible parental B lines and 7 grain mould resistant germplasm lines by pedigree method. The F_1 s were raised at Parbhani, and F_2 and F_3 at AICSIP multi-locations. Over locations, three hundred F_3 selections were made and further evaluated (F_4) at three centers. The superior selections were advanced to F_6 and again evaluated at DSR. Superior performing lines for grain mold resistance were DSR-GMN-41, DSR-GMN-42, DSR-GMN-46, DSR-GMN-52, DSR-GMN-58, and DSR-GMN-59. The grain mold resistant lines, DSR-GMN-41, DSR-GMN-42, DSR-GMN-46, DSR-GMN-52 are derived from a cross between elite restorer Indore 12 and grain mold resistant line IS 25017. DSR-GMN-41 was selected at Akola, DSR-GMN-42 at Parbhani, DSR-GMN-46 at Surat, and DSR-GMN-52 at Hyderabad. DSR. DSR-GMN-58 is a derivative of

a cross between SRT26, grain mold tolerant line from Surat, and IS25017, a grain mold resistant source from Sudan. DSR-GMN-59 is derived from a cross, GMRP 9 $\times$ IS 25017, where GMRP 9 is a grain mold resistant variety from Parbhani, and IS 25017 a grain mold resistant genetic stock from Sudan. These lines in F_4 to F_6 were evaluated for grain mould resistance.

Morpho-agronomic Characteristics

380 segregants in F_4 were evaluated during 2006 in augmented design at three locations. The field grade score at physiological maturity ranged from 3.4 to 5.6 and field grade score at normal maturity ranged from 4.5 to 7.7. The resistant check, B 58586 scored 4.5 FGS at physiological maturity and normal maturity. The susceptible check, 296 B scored 5.0 at physiological maturity and 7.7 at normal maturity. During 2007, out of 23 derivatives, 12 were on par (scored 3.1 to 4.4) with resistant check, B 58586 (3.2 score). During 2008

Table1. Performance of superior derivatives in F₄ to F₆ for grain mould resistance

Generation-year	F ₄ - 2006											F ₅ - 2007			F ₆ - 2008	
	P	D	D-	D-	FG	FG	FG	FG	FG	FG	FG	FG	FG	FG	FG	FG
	H	F	PM	NM	S	S	S	S	S	S	S	S	S	S	S	S
					PM	PM	PM	PM	NM	NM	NM	NM	NM	NM	NM	NM
Entry	Av	Av	Av	Av	Coi	Hyd	Par	Av	Hyd	Par	Av	Hyd	Coi	Par	Av	Hyd
GMN 41	164	74	104	115	3.06	3.78	4.32	3.8	5.4	5.04	5.2	3	3.6	2.7	3.1	2
GMN 42	166	74	103	115	6.66	3.42	4.32	4.9	5.04	5.04	5	4	3.6	3	3.3	2.5
GMN 46	196	71	100	112	5.76	3.42	4.32	4.5	5.4	4.14	4.9	3	3.6	2.7	3.2	2
GMN 47	189	71	103	114	3.96	3.42	3.42	3.6	6.3	3.24	4.9	3	6.6	3.3	4.4	2
GMN 49	205	73	104	114	4.86	4.14	3.78	4.3	5.94	4.14	5	4	6	2.7	4.1	2
GMN 52	185	70	101	110	2.88	3.24	3.6	3.2	4.68	4.68	4.7	3	3.6	4.2	3.5	2.5
GMN 58	210	66	98	109	8.1	2.7	3.42	4.7	5.94	3.78	4.9	3	4.2	3	3.4	2.5
GMN 59	199	69	99	111	5.4	2.7	3.42	3.8	5.76	4.68	5.2	3	4.2	2.7	3.5	5.5
GMN 60	149	72	101	113	8.1	3.6	5.22	5.6	3.96	6.48	5.2	4	9	3	5.2	3
GMN 63	192	71	101	115	4.68	3.24	3.6	3.8	5.76	4.5	5.2	4	3.6	2.7	3.3	2
B 58586	167	77	100	112	3.42	5.58	4.5	4.5	3.78	5.22	4.5	4	3.6	2.7	3.2	2
296 B	179	79	103	115	6.3	2.16	6.84	5	7.92	7.56	7.7	9	6.6	8.4	8	7
CD (p=0.05)	95	26	39	44	1.62	3.42	3.42	2.7	5.4	3.24	4.3	1.2	1	0.8	1.2	2.9

PH = plant height (cm), DF= days to flowering, D-PM= days to physiological maturity, D-NM = days to normal maturity, FGS PM = field grade score physiological maturity, FGS NM = field grade score normal maturity, FGS = field grade score on the scale of 1 to 9 where 1 is highly resistant and 9 is highly susceptible, and AV = Average

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yellow grain; DSR-GMN-46 (GMN-46) is tall grain mould resistant line; DSR-GMN-52 (GMN-52) is grain mould resistant line having yellow white grain; DSR-GMN-58 (GMN-58) is tall grain mould resistant line with long panicle, DSR-GMN-59 (GMN-59) is grain mould resistant with circular grain shape

References

SS Ambekar, MY Kamtar, K Ganesamurthy, RB Ghorade, Usha Saxena, Pooranchand, BD Jadav, IK Das, TG Nageshwarara, N Seetharama and S Audilakshmi (2009) Breeding for grain mold resistance, *Jowar Samachar* 5(2): 7-8.

5. MS3054 A & B, MS3060 A & B, MS3061 A & B, MS3095 A & B, MS3143 A & B, MS3146 A & B, MS3183 A & B, MS3216 A & B, and MS3228 A & B (IC0584519-IC0584536; INGR10010-INGR10018), Sorghum (*Sorghum bicolor*) Male Sterile Lines with Superior Grain Yields

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developing these male sterile lines. The male sterile line MS3054 was developed from a cross between elite kharif MS line 27B and grain mold resistant line GM 97433; MS3060 developed from crossing two elite lines, 27 B and breeding line N 99; MS 3061 from a cross between 27 B and germplasm line IS 19305; MS3095 from crossing MS line 422 B and

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Generation-year	F ₄ - 2006											F ₅ - 2007			F ₆ - 2008	
	P	D	D-	D-	FG	FG	FG	FG	FG	FG	FG	FG	FG	FG	FG	FG
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					PM	PM	PM	PM	NM	NM	NM	NM	NM	NM	NM	NM
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References

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Table1. Performance of new MS lines for grain yield and ancillary data

Backcross no	Plant Height (cm)			Days to Flower			Panicle Length (cm)			No. of Primary branches			Grain Yield (g/plant)		
	2005	2006	AV	2005	2006	AV	2005	2006	AV	2005	2006	AV	2005	2006	AV
3054	211	182	196	75	75	75	20	34.6	27.5	58.7	50.48	54.6	54.5	126.7	90.6
3060	152	147	149	75	73	74	35	40.3	37.7	77.5	66.64	72.1	66.5	78.6	72.6
3061	171	166	169	68	70	69	30	32.3	31.1	64.5	57.44	61.0	66.5	75.6	71.1
3095	289	222	255	70	77	73.5	33	37.1	35.0	72.1	58.64	65.4	87.5	95.6	91.6
3143	163	159	161	78	78	78	22	29.7	25.9	72.7	55.36	64.0	63.3	81.4	72.4
3146	154	156	155	76	77	76.5	23	29.9	26.4	67.3	43.96	55.6	81.3	74.4	77.9
3183	160	156	158	72	74	73	25	30.1	27.6	63.7	46.32	55.0	66.3	76.3	71.3
3216	171	135	153	67	70	68.5	26	27.3	26.7	47	47.92	47.5	66	78.3	72.2
3228	188	173	181	72	72	72	25	25.9	25.6	59.4	55.52	57.5	65	78.3	71.7
296 B	134	130.83	133	76.8	76	76.4	31	33.5	32.1	101.6	61.05	81.3	50.8	57.0	53.9
CD (p=0.05)	70	67.5		3	3.1		5.3	5.2		19.3	26.1		18.2	23.0	

grain mould resistant line IS 25017. MS 3143 and MS3146 were developed from a cross between 463B and variety SPV 475. MS3183 was developed from a cross between AKMS 14 B and grain mold resistant line IS 25017; MS 3216 from a cross between grain mold resistant line SPGM 94009 and a variety SPV 1231 and MS 3228 from a multiple cross among MS line 2219 B, SPV 462 and IS 18475. Two hundred MS lines and checks were grown in augmented design during rainy season of 2005 and 2006 at DSR and were evaluated for plant height, days to flowering, panicle length, primary branches, panicle weight, and grain yield.

Morpho-agronomic Characteristics

The MS lines showed large variation for all the characters studied. MS3054 is a tall MS line with 196cm height and takes 75 days to flower. MS3060 a superior line with medium dwarf height (149 cm tall), medium late flowering (74 days) and has very long panicle (38 cm). MS3061 is medium in stature (169cm) and medium in flowering (69 days) and has long panicle (31cm). MS3095 is a very tall MS line(255 cm) and medium duration for flowering (74

days) (Table 1). The MS line has a long panicle (35 cm) and greyed yellow grain. MS 3143: MS line is medium tall (161 cm) and medium late duration type (78 days). MS 3146 is 155 cm tall plant and takes 77 days for flowering. MS3183 is medium in stature (158 cm), takes 73 days to flower and has medium length panicle (28cm) and short pedicel. MS3216 is of medium height (153 cm), and medium early for flowering (69 days). MS3228 is 181cm tall and takes 72 days for flowering with grain shape circular in dorsal view and elliptical in profile view.

MS3054 A & B, MS3060 A &B, MS3061, MS3095, MS3143 A & B, MS3146 A & B, MS3183 A & B, MS3216 A & B, and MS3228 showed significant superiority for grain yield over the check 296 B (Audilakshmi et al. 2009). MS3054 has 91 g/plant of grain yield; MS3060 has 73 g; MS3061 has 71 g; MS3095 yields 92 g; MS 3143, MS3216, and MS3228 yield 72 g; MS 3146 has 78 g; MS3183 yields 71 g/plant as compared to 54 g/plant of 296 B, check (Table 1).

Reference

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6. BANG – 4/5 (IC0569319: INGR10019), a Guar (*Cyamopsis tetragonoloba*) Germplasm with Branched as well as all Node Cluster Bearing Habit

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Guar [*Cyamopsis tetragonoloba* (L.) Taub.] is an annual drought hardy leguminous crop cultivated mainly in semi-arid and arid tracts of India for the galactomannan gum extracted from its endosperm. With

increasing constrain in the production of guar, breeders continually look for new and diverse germplasm with specific traits to enhance crop productivity. New plant types with unique characters and altered growth habit

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Backcross no	Plant Height (cm)			Days to Flower			Panicle Length (cm)			No. of Primary branches			Grain Yield (g/plant)		
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6. BANG – 4/5 (IC0569319: INGR10019), a Guar (*Cyamopsis tetragonoloba*) Germplasm with Branched as well as all Node Cluster Bearing Habit

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Guar [*Cyamopsis tetragonoloba* (L.) Taub.] is an annual drought hardy leguminous crop cultivated mainly in semi-arid and arid tracts of India for the galactomannan gum extracted from its endosperm. With

increasing constrain in the production of guar, breeders continually look for new and diverse germplasm with specific traits to enhance crop productivity. New plant types with unique characters and altered growth habit

will play an important role in improving the crop yield. A wide range of variability has been reported for several morphological characters in guar (Gopala Krishnan and Dwivedi, 2007). In the branched plant types namely erect branching (EB) and branching (B) (Hymowitz, 1963), the cluster bearing habit reported is either alternate/ irregular. But there have not been a single report on germplasm/ genotype possessing any type of branching behaviour producing clusters in every node (branched as well as all node cluster bearing habit in a single genotype).

For the first time, a unique guar genotype, BANG-4/5 (branched all node cluster bearing guar – 4/5; IC0569319), with branched as well as all node cluster bearing guar habit have been developed. This genotype was developed from a spontaneous mutant identified from the guar germplasm selection IC421844-4/P₁ (with basal branching as well as all node bearing habit) through further selection.

7. IC51174 - P₁ (IC0574580: INGR10020), a Guar (*Cyamopsis tetragonoloba*) Germplasm with Shortened Internode

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Guar [*Cyamopsis tetragonoloba* (L.) Taub.] is an annual drought hardy leguminous crop cultivated mainly in semi-arid and arid tracts of India. Guar breeders are in need of diverse germplasm with specific traits to enhance its productivity. New plant types with unique characters and altered growth habit will play an important role in improving the crop yield. A wide range of variability has been reported for several morphological characters in guar (Gopala Krishnan and Dwivedi, 2007). Normally, the unbranched (single stemmed) guar genotypes are tall and there have not been a single report on dwarf genetic stock in guar.

For the first time, a unique guar genotype, IC0574580, with dwarf plant habit and shortened internode (< 1.5 cm) has been developed. This genotype was isolated from a spontaneous mutant showing dwarf plant habit with shortened internodes

BANG - 4/5 is a photo-insensitive, branched as well as all node cluster bearing guar genotype possessing basal branching habit with four primary and four secondary branches and all node cluster bearing habit (both in main stem as well as branches). On an average, it produces 15 clusters in the main stem and 63 clusters/ plant. The mean number of pods/ plant of this genotype is 188.2 with an average per plant seed yield of 12.2 g. BANG-4/5 (IC0569319) produces higher number of clusters produced per plant, thereby improving the pods produced per plant as well as the yield. This genotype can be used in guar improvement programme for enhancing yield.

References

- Gopala Krishnan S and NK Dwivedi (2007) Genetic stocks of clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] – assessment and utilization. *J. Arid Legumes* **4**(2): 121-126.
- Hymowitz T (1963) Studies on guar – *Cyamopsis tetragonoloba* (L.) Taub. Ph.D. diss. Oklahoma State Univ., Stillwater, OK 74078, USA, pp 87-89.

in the guar germplasm, IC51174. This genotype is dwarf in stature with a mean plant height of 48.6 cm. The dwarf stature is due to shortened internodes (< 1.5 cm) compared to longer internode (> 2.5 cm) in normal guar genotypes. It is photo-insensitive, single stemmed (unbranched), broad leaved and are highly resistant to lodging due to compact growth habit and sturdy stem. They possess all node cluster bearing habit with higher number of clusters/ plant and pods/ cluster and as result, higher harvest index. This dwarf genetic stock of guar can be used in guar improvement for breeding high yielding input responsive, semi-dwarf varieties of guar.

Reference

- Gopala Krishnan S and NK Dwivedi (2007) Genetic stocks of clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] – assessment and utilization. *J. Arid Legumes* **4**(2): 121-126.

will play an important role in improving the crop yield. A wide range of variability has been reported for several morphological characters in guar (Gopala Krishnan and Dwivedi, 2007). In the branched plant types namely erect branching (EB) and branching (B) (Hymowitz, 1963), the cluster bearing habit reported is either alternate/ irregular. But there have not been a single report on germplasm/ genotype possessing any type of branching behaviour producing clusters in every node (branched as well as all node cluster bearing habit in a single genotype).

For the first time, a unique guar genotype, BANG-4/5 (branched all node cluster bearing guar – 4/5; IC0569319), with branched as well as all node cluster bearing guar habit have been developed. This genotype was developed from a spontaneous mutant identified from the guar germplasm selection IC421844-4/P₁ (with basal branching as well as all node bearing habit) through further selection.

7. IC51174 - P₁ (IC0574580: INGR10020), a Guar (*Cyamopsis tetragonoloba*) Germplasm with Shortened Internode

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Guar [*Cyamopsis tetragonoloba* (L.) Taub.] is an annual drought hardy leguminous crop cultivated mainly in semi-arid and arid tracts of India. Guar breeders are in need of diverse germplasm with specific traits to enhance its productivity. New plant types with unique characters and altered growth habit will play an important role in improving the crop yield. A wide range of variability has been reported for several morphological characters in guar (Gopala Krishnan and Dwivedi, 2007). Normally, the unbranched (single stemmed) guar genotypes are tall and there have not been a single report on dwarf genetic stock in guar.

For the first time, a unique guar genotype, IC0574580, with dwarf plant habit and shortened internode (< 1.5 cm) has been developed. This genotype was isolated from a spontaneous mutant showing dwarf plant habit with shortened internodes

BANG - 4/5 is a photo-insensitive, branched as well as all node cluster bearing guar genotype possessing basal branching habit with four primary and four secondary branches and all node cluster bearing habit (both in main stem as well as branches). On an average, it produces 15 clusters in the main stem and 63 clusters/ plant. The mean number of pods/ plant of this genotype is 188.2 with an average per plant seed yield of 12.2 g. BANG-4/5 (IC0569319) produces higher number of clusters produced per plant, thereby improving the pods produced per plant as well as the yield. This genotype can be used in guar improvement programme for enhancing yield.

References

- Gopala Krishnan S and NK Dwivedi (2007) Genetic stocks of clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] – assessment and utilization. *J. Arid Legumes* **4**(2): 121-126.
- Hymowitz T (1963) Studies on guar – *Cyamopsis tetragonoloba* (L.) Taub. Ph.D. diss. Oklahoma State Univ., Stillwater, OK 74078, USA, pp 87-89.

in the guar germplasm, IC51174. This genotype is dwarf in stature with a mean plant height of 48.6 cm. The dwarf stature is due to shortened internodes (< 1.5 cm) compared to longer internode (> 2.5 cm) in normal guar genotypes. It is photo-insensitive, single stemmed (unbranched), broad leaved and are highly resistant to lodging due to compact growth habit and sturdy stem. They possess all node cluster bearing habit with higher number of clusters/ plant and pods/ cluster and as result, higher harvest index. This dwarf genetic stock of guar can be used in guar improvement for breeding high yielding input responsive, semi-dwarf varieties of guar.

Reference

- Gopala Krishnan S and NK Dwivedi (2007) Genetic stocks of clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] – assessment and utilization. *J. Arid Legumes* **4**(2): 121-126.

8. IPA 16 F (IC0574574; INGR10021), a Pigeonpea (*Cajanus cajan*) Germplasm with Resistance to *Fusarium* Wilt, Donor for Resistance to Sterility Mosaic Disease of Pigeon Pea

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IPA 16 F has been registered for its resistance to most dreaded diseases of pigeonpea i.e. *Fusarium* wilt and sterility mosaic (Anonymous, 2005; 2006; 2007). It is a selection from pigeonpea germplasm line JKH/SSC-3/18. It has been developed following the selection method of breeding at Indian Institute of Pulses Research, Kanpur.

Morpho-agronomic Characteristics of IPA 16 F

Growth habit	Spreading
Plant type	Non-determinate
Stem colour	Green
Base flower colour	Yellow
Pattern of streaks	Medium sparse
Pod colour	Mixed (Green with black stripes)
Seed colour	Light brown
Days to 50% flowering	159
Days to 75% maturity	256
Plant Height (cm)	181
100 Seed weight (g)	12.1

Multilocal evaluation of IPA 16 F was carried out in Initial Varietal Trial (IVT Long duration pigeonpea) in 2005-06 and Advance Varietal Trial (AVT Long duration pigeonpea) in 2006-07 under AICRP on

Pigeonpea. In IVT it was evaluated at six locations and average yield was 1874 Kg/ha (Anonymous, 2006). In AVT it was evaluated at five locations and average yield was 1208 Kg/ha (Anonymous, 2007).

Associated Characters

IPA 16F is of long duration. Its resistance can be transferred through conventional breeding in popular varieties of long duration pigeonpea which are being grown in North East Plain Zone of India.

References

- Anonymous (2005) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 231p.
- Anonymous (2006) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.
- Anonymous (2006) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 43p.
- Anonymous (2007) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 255p.
- Anonymous (2007) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 52p.

9. IPA 8 F (IC0574575; INGR10022), a Pigeonpea (*Cajanus cajan*) Germplasm with Resistance to Sterility Mosaic Disease of Pigeon Pea

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(E-mail: farindra.singh@rediffmail.com)

IPA 8 F has been registered for its resistance to one of the important diseases of pigeon pea i.e. sterility mosaic (Anonymous, 2006, 2007, 2008). It is a selection from pigeon pea germplasm line ICP 13673. It has been developed following the selection method of breeding at Indian Institute of Pulses Research, Kanpur.

Morpho-agronomic Characteristics of IPA 8 F

Growth habit	Spreading
Plant type	Non-determinate
Stem colour	Green
Base flower colour	Yellow
Pattern of streaks	Medium sparse
Pod colour	Dark purple
Seed colour	Mottled
Days to 50% flowering	159
Days to 75% maturity	264
Plant Height (cm)	212.6
100 Seed weight (g)	12.3

8. IPA 16 F (IC0574574; INGR10021), a Pigeonpea (*Cajanus cajan*) Germplasm with Resistance to *Fusarium* Wilt, Donor for Resistance to Sterility Mosaic Disease of Pigeon Pea

F Singh, IP Singh, ND Majumder and PK Katiyar

Indian Institute of Pulses Research, Kanpur-208 024, Uttar Pradesh
(E-mail: farindra.singh@rediffmail.com)

IPA 16 F has been registered for its resistance to most dreaded diseases of pigeonpea i.e. *Fusarium* wilt and sterility mosaic (Anonymous, 2005; 2006; 2007). It is a selection from pigeonpea germplasm line JKH/SSC-3/18. It has been developed following the selection method of breeding at Indian Institute of Pulses Research, Kanpur.

Morpho-agronomic Characteristics of IPA 16 F

Growth habit	Spreading
Plant type	Non-determinate
Stem colour	Green
Base flower colour	Yellow
Pattern of streaks	Medium sparse
Pod colour	Mixed (Green with black stripes)
Seed colour	Light brown
Days to 50% flowering	159
Days to 75% maturity	256
Plant Height (cm)	181
100 Seed weight (g)	12.1

Multilocal evaluation of IPA 16 F was carried out in Initial Varietal Trial (IVT Long duration pigeonpea) in 2005-06 and Advance Varietal Trial (AVT Long duration pigeonpea) in 2006-07 under AICRP on

Pigeonpea. In IVT it was evaluated at six locations and average yield was 1874 Kg/ha (Anonymous, 2006). In AVT it was evaluated at five locations and average yield was 1208 Kg/ha (Anonymous, 2007).

Associated Characters

IPA 16F is of long duration. Its resistance can be transferred through conventional breeding in popular varieties of long duration pigeonpea which are being grown in North East Plain Zone of India.

References

- Anonymous (2005) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 231p.
- Anonymous (2006) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.
- Anonymous (2006) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 43p.
- Anonymous (2007) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 255p.
- Anonymous (2007) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 52p.

9. IPA 8 F (IC0574575; INGR10022), a Pigeonpea (*Cajanus cajan*) Germplasm with Resistance to Sterility Mosaic Disease of Pigeon Pea

F Singh, IP Singh, ND Majumder and PK Katiyar

Indian Institute of Pulses Research, Kanpur-208 024, Uttar Pradesh
(E-mail: farindra.singh@rediffmail.com)

IPA 8 F has been registered for its resistance to one of the important diseases of pigeon pea i.e. sterility mosaic (Anonymous, 2006, 2007, 2008). It is a selection from pigeon pea germplasm line ICP 13673. It has been developed following the selection method of breeding at Indian Institute of Pulses Research, Kanpur.

Morpho-agronomic Characteristics of IPA 8 F

Growth habit	Spreading
Plant type	Non-determinate
Stem colour	Green
Base flower colour	Yellow
Pattern of streaks	Medium sparse
Pod colour	Dark purple
Seed colour	Mottled
Days to 50% flowering	159
Days to 75% maturity	264
Plant Height (cm)	212.6
100 Seed weight (g)	12.3

Multi-locational evaluation of IPA 8 F was carried out in Initial Varietal Trial (IVT long duration pigeonpea) in 2005-06 and Advance Varietal Trial (AVT long duration pigeonpea) in 2006-07 under AICRP on Pigeonpea. In IVT it was evaluated at six locations and average yield was 2004 Kg/ha (Anonymous, 2006). In AVT it was evaluated at five locations and average yield was 965 Kg/ha (Anonymous, 2007).

Associated Characters

IPA 8F is of long duration. Its resistance can be transferred through conventional breeding in popular

varieties of long duration pigeonpea which are being grown in North East Plain Zone of India.

References

- Anonymous (2006) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.
- Anonymous (2006) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 43p.
- Anonymous (2007) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 255p.
- Anonymous (2007) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 52p.
- Anonymous (2008) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.

10. IPA 15F (IC0574576; INGR10023), a Pigeonpea (*Cajanus cajan*) Germplasm with Resistance to Sterility Mosaic Disease

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IPA 15 F has been registered for its resistance to one of the important diseases of pigeonpea i.e. sterility mosaic (Anonymous, 2006; 2007; 2008). It is a selection from pigeonpea germplasm line PBJ/SSC -2/33. It has been developed following the selection method of breeding at Indian Institute of Pulses Research, Kanpur.

IPA 15 F was only evaluated for its resistance to sterility mosaic disease and morpho-agronomic traits.

Associated Characters

IPA 15F is of long duration. Its resistance can be transferred through conventional breeding in popular varieties of long duration pigeonpea which are being grown in North East Plain Zone of India.

References

- Anonymous (2006) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.
- Anonymous (2007) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 255p.
- Anonymous (2008) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.

Morpho-agronomic Characteristics of IPA 15 F

Growth habit	Erect & Compact
Plant type	Non- determinate
Stem colour	Green
Base flower colour	Yellow
Pattern of streaks	Sparse
Pod colour	Mixed (Green with black stripes)
Seed colour	Cream
Days to 50% flowering	159
Days to 75% maturity	263
Plant Height (cm)	200
100 Seed weight (g)	12.6

11. IPA204 (IC0574577; INGR10024) a Pigeonpea (*Cajanus cajan*) Germplasm with Wilt Resistant line of Long-duration Pigeonpea

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Pigeonpea [*Cajanus cajan* (L.) Millsp] is the second most important grain legume after chickpea in India. The main concern, however, is stability in production,

which is highly affected by pigeonpea wilt especially in North-East Plains, Central and Peninsular India. The Disease is caused by a soil borne fungus, *Fusarium*

Multi-locational evaluation of IPA 8 F was carried out in Initial Varietal Trial (IVT long duration pigeonpea) in 2005-06 and Advance Varietal Trial (AVT long duration pigeonpea) in 2006-07 under AICRP on Pigeonpea. In IVT it was evaluated at six locations and average yield was 2004 Kg/ha (Anonymous, 2006). In AVT it was evaluated at five locations and average yield was 965 Kg/ha (Anonymous, 2007).

Associated Characters

IPA 8F is of long duration. Its resistance can be transferred through conventional breeding in popular

varieties of long duration pigeonpea which are being grown in North East Plain Zone of India.

References

- Anonymous (2006) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.
- Anonymous (2006) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 43p.
- Anonymous (2007) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 255p.
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- Anonymous (2008) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.

10. IPA 15F (IC0574576; INGR10023), a Pigeonpea (*Cajanus cajan*) Germplasm with Resistance to Sterility Mosaic Disease

F Singh, IP Singh, ND Majumder and PK Katiyar

Indian Institute of Pulses Research, Kanpur-208 024, Uttar Pradesh

(E-mail: farindra.singh@rediffmail.com)

IPA 15 F has been registered for its resistance to one of the important diseases of pigeonpea i.e. sterility mosaic (Anonymous, 2006; 2007; 2008). It is a selection from pigeonpea germplasm line PBJ/SSC -2/33. It has been developed following the selection method of breeding at Indian Institute of Pulses Research, Kanpur.

IPA 15 F was only evaluated for its resistance to sterility mosaic disease and morpho-agronomic traits.

Associated Characters

IPA 15F is of long duration. Its resistance can be transferred through conventional breeding in popular varieties of long duration pigeonpea which are being grown in North East Plain Zone of India.

References

- Anonymous (2006) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.
- Anonymous (2007) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 255p.
- Anonymous (2008) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.

Morpho-agronomic Characteristics of IPA 15 F

Growth habit	Erect & Compact
Plant type	Non- determinate
Stem colour	Green
Base flower colour	Yellow
Pattern of streaks	Sparse
Pod colour	Mixed (Green with black stripes)
Seed colour	Cream
Days to 50% flowering	159
Days to 75% maturity	263
Plant Height (cm)	200
100 Seed weight (g)	12.6

11. IPA204 (IC0574577; INGR10024) a Pigeonpea (*Cajanus cajan*) Germplasm with Wilt Resistant line of Long-duration Pigeonpea

AK Choudhary and IP Singh

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(E-mail: akiipr23@yahoo.com)

Pigeonpea [*Cajanus cajan* (L.) Millsp] is the second most important grain legume after chickpea in India. The main concern, however, is stability in production,

which is highly affected by pigeonpea wilt especially in North-East Plains, Central and Peninsular India. The Disease is caused by a soil borne fungus, *Fusarium*

Multi-locational evaluation of IPA 8 F was carried out in Initial Varietal Trial (IVT long duration pigeonpea) in 2005-06 and Advance Varietal Trial (AVT long duration pigeonpea) in 2006-07 under AICRP on Pigeonpea. In IVT it was evaluated at six locations and average yield was 2004 Kg/ha (Anonymous, 2006). In AVT it was evaluated at five locations and average yield was 965 Kg/ha (Anonymous, 2007).

Associated Characters

IPA 8F is of long duration. Its resistance can be transferred through conventional breeding in popular

varieties of long duration pigeonpea which are being grown in North East Plain Zone of India.

References

- Anonymous (2006) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.
- Anonymous (2006) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 43p.
- Anonymous (2007) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 255p.
- Anonymous (2007) Annual Report of AICRP on Long duration pigeonpea. Indian Institute of Pulses Research, Kanpur, 52p.
- Anonymous (2008) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.

10. IPA 15F (IC0574576; INGR10023), a Pigeonpea (*Cajanus cajan*) Germplasm with Resistance to Sterility Mosaic Disease

F Singh, IP Singh, ND Majumder and PK Katiyar

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(E-mail: farindra.singh@rediffmail.com)

IPA 15 F has been registered for its resistance to one of the important diseases of pigeonpea i.e. sterility mosaic (Anonymous, 2006; 2007; 2008). It is a selection from pigeonpea germplasm line PBJ/SSC -2/33. It has been developed following the selection method of breeding at Indian Institute of Pulses Research, Kanpur.

IPA 15 F was only evaluated for its resistance to sterility mosaic disease and morpho-agronomic traits.

Associated Characters

IPA 15F is of long duration. Its resistance can be transferred through conventional breeding in popular varieties of long duration pigeonpea which are being grown in North East Plain Zone of India.

References

- Anonymous (2006) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.
- Anonymous (2007) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 255p.
- Anonymous (2008) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, 239p.

Morpho-agronomic Characteristics of IPA 15 F

Growth habit	Erect & Compact
Plant type	Non- determinate
Stem colour	Green
Base flower colour	Yellow
Pattern of streaks	Sparse
Pod colour	Mixed (Green with black stripes)
Seed colour	Cream
Days to 50% flowering	159
Days to 75% maturity	263
Plant Height (cm)	200
100 Seed weight (g)	12.6

11. IPA204 (IC0574577; INGR10024) a Pigeonpea (*Cajanus cajan*) Germplasm with Wilt Resistant line of Long-duration Pigeonpea

AK Choudhary and IP Singh

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Pigeonpea [*Cajanus cajan* (L.) Millsp] is the second most important grain legume after chickpea in India. The main concern, however, is stability in production,

which is highly affected by pigeonpea wilt especially in North-East Plains, Central and Peninsular India. The Disease is caused by a soil borne fungus, *Fusarium*

udum. The incidence of wilt alone causes 20-25% yield losses in the North-East plains (Dhar and Reddy, 1999). The best way to deal with this disease is to grow cultivars with built-in resistance to the causal organism. None of the existing varieties and land races under cultivation in North-East plains appears to be resistant to wilt disease. This calls for development and release of resistant types to ensure stability of production in this zone. The present paper deals with a genotype IPA204 which has shown broad and stable resistance to the wilt pathogen besides having very good yield potential.

IPA204 was derived from a cross, Bahar x 'Ac 314-314' following pedigree method of selection. It has compact plant type and indeterminate growth habit. Plants are tall (1.75-2.0 m) with green stem colour. Standard (outer petal) is golden yellow without any streaks on either side. Pods are green with black stripes. Seeds are medium bold (12 g/100 seeds) and light brown in colour. Based on its agronomic performance in station trial at IIPR, Kanpur, it was put to AICRP (pigeonpea) initial varietal trial (IVT) for assessment of its performance over the ruling check varieties of long-duration pigeonpea such as Bahar, 'Narendra Arhar-1, and the like during the year 2004-05. Keeping its good performance in IVT (>5%

superiority over the best check), it was decided to assess its wilt reaction in wilt-sick nursery of AICRP on pigeonpea located in almost all pigeonpea-growing regions of the country. The wilt reaction of IPA204 was assayed at a total of 24 locations (3, 10, 5, and 6 locations during 2005-06, 2006-07, 2007-08, and 2008-09, respectively). At each location, it was replicated twice along with other test entries keeping an inter-row and plant-to-plant spacing at 75 cm and 20 cm, respectively. At each location, at least one susceptible check (such as Bahar, 'ICP 2376', etc.) was also put along with the test entries; however, the same check was not used at all the locations. Data on per cent plant mortality/replication were recorded at flowering, full podding, and harvesting stages. The mean per cent mortality has been presented in the Table 1.

It is obvious from Table 1 that mean plant mortality (%) in 'IPA204' ranged from 0.00 (at Badnapur during 2006-07) to 27.25 (at IIPR, Kanpur during 2008-09). The wilt reaction of this entry varied from resistant (16 locations) to moderately resistant (8 locations). In the North-East Plain Zone (Dholi, Faizabad and Kanpur) and Central India (Badnapur, Rahuri, Bharuch, Khargone and Akola), the wilt reaction was similar, that is, from resistant to moderately resistant. However, in

Table1. Wilt reaction of 'IPA204' in wilt-sick nursery at different locations

Year	Location	LSI	% infection (susceptible check)	% infection (IPA204)	Wilt reaction of IPA204
2005-06	Dholi	72.3	74.9 ('Bahar')**	6.1	Resistant*
	Badnapur	36.1	100.0 ('ICP 2376')	4.3	Resistant
	Rahuri	34.8	—	19.3	Moderately Resistant
2006-07	Rahuri	74.7	100.0 ('ICP 2376')	16.4	Moderately Resistant
	Bharunch	32.4	—	4.0	Resistant
	Khargone	25.0	67.0 ('ICP 2376')	5.8	Resistant
	Badnapur	45.4	100.0 ('ICP 2376')	0.0	Resistant
	ICRISAT	60.8	100.0 ('ICP 2376')	2.6	Resistant
	Warangal	32.1	63.1 ('ICP 2376')	6.1	Resistant
	Gulbarga	63.2	100.0 ('PT 221')	4.2	Resistant
	Dholi	49.1	90.0 ('Bahar')	12.0	Moderately Resistant
	Faizabad	41.6	100.0 ('Bahar')	6.0	Resistant
	Akola	44.3	—	13.0	Moderately Resistant
2007-08	Dholi	29.4	90.0 ('ICP 2376')	8.0	Resistant
	Gulbarga	39.2	100.0 ('ICP 2376')	7.6	Resistant
	Rahuri	45.4	100.0 ('ICP 2376')	8.3	Resistant
	Badnapur	30.7	93.5 ('ICP 2376')	19.4	Moderately Resistant
	ICRISAT	29.7	95.8 ('ICP 2376')	9.3	Resistant
2008-09	Badnapur	18.5	100.0 ('ICP 2376')	14.3	Moderately Resistant
	Dholi	20.8	80.7 ('ICP 2376')	10.3	Moderately Resistant
	Gulbarga	17.1	96.7 ('ICP 2376')	3.8	Resistant
	Rahuri	33.9	100.0 ('ICP 2376')	8.1	Resistant
	ICRISAT	25.6	100.0 ('ICP 2376')	4.8	Resistant
	IIPR, Kanpur	21.8	91.8 ('ICP 2376')	27.3	Moderately Resistant

*Disease reaction quantified on the basis of acceptable scale used by pathologists (resistant: up to 10% wilted plants; moderately resistant: >10 – 30% wilted plants)

**Susceptible check in parentheses

South India (ICRISAT, Warangal, and Gulbarga), the test entry showed exclusively resistant reaction during all the three years. Keeping its uniform and stable resistant reaction, it was recommended as potential donor for wilt resistance in the Annual Group Meet on Pigeonpea (2009).

References

- AICRP (2005) Annual Meeting on late pigeonpea. Indian Institute of Pulses Research, Kanpur, India, pp 1-8.
- AICRP (2005-06) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 190 p.
- AICRP (2006-07) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 195 p.

- AICRP (2007-08) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 185 p.
- AICRP (2008-09) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 184 p.
- AICRP (2009) Proceedings, Recommendations and Technical Programme of the Annual Group Meet of AICRP on Pigeonpea (25-27 May, 2009). Indian Institute of Pulses Research, Kanpur, India, 36 p.
- Dhar V and MV Reddy (1999) Disease management strategies for increasing pulses production. *Paper presented in the Brain Storming Meeting on Pulses Production* held at NBPGR, New Delhi, March 26-27, 1999.

12. IPA234 (IC0574578; INGR10025) a Pigeonpea (*Cajanus cajan*) Germplasm, with Resistance to Sterility Mosaic Disease

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Pigeonpea [*Cajanus cajan* (L.) Millsp.] suffers from a number of diseases, viz., *Phytophthora* blight, *Fusarium* wilt and sterility mosaic disease (SMD). SMD is caused by an unknown virus and spreads through a mite, *Aceria cajani*. This disease sometimes leads to total yield losses as affected plants do not flower and set pods at all. It accounts for 10-15% yield reduction in North-East Plain Zone (NEPZ) (UP and Bihar), Central Zone (CZ) (Maharashtra) and South Zone (SZ) (TN and Karnataka). The best way to deal with the problem of this disease is to breed lines with built-in resistance to the pathogen. This may ensure stability in pigeonpea production. The present paper deals with a genotype IPA234 which has shown broad and stable resistance to the SMD besides having very good yield potential.

IPA234, which belongs to late pigeonpea group, was derived from a cross, T-7 x WRP-1 following pedigree method of selection. The chief morphological and reproductive characteristics of this genotype include loose canopy, indeterminate growth habit, green stem colour, yellow standard (petal) colour, green pods with thin black stripes, light brown seed colour, medium plant height (165 cm), large seed (>10 g/100 seeds) and long maturity period (245 days). Based on its agronomic performance in station trial

at IIPR, Kanpur, it was put to AICRP (pigeonpea) for overall agronomic and pathological assessments over the ruling check varieties of long-duration pigeonpea. It was tested for resistance to SMD for the consecutive three years (2005-06, 2006-07 and 2007-08) at a total of 19 locations. At each location, it was replicated twice along with other test entries keeping an inter-row and plant-to-plant spacing at 75 cm and 20 cm, respectively. At each location, 'ICP8863' was used as the susceptible check. Data on mean per cent infection has been presented in the Table 1.

It showed resistance reaction at Dholi and Varanasi (NEPZ) and Rahuri (CZ) in all the three years. The SMD reaction in the South Zone was variable. Resistance, moderate resistance and susceptible reactions were observed at ICRISAT, Tamil Nadu and Bangalore, respectively during 2006-07 and 2007-08. It indicated the presence of three distinct variants of the virus in the SZ. In AICRP yield trials (IVT and AVT-I during 2006-07 and 2007-08, respectively), the grain yield of IPA234 was comparable to those of ruling check varieties, Bahar and Narendra Arhar-1. Therefore, this genotype IPA234 may be used as a donor for resistance to sterility mosaic disease especially in North East plains. Alternatively, it may be cultivated

Table1. SMD reaction of 'IPA234' in SMD nursery at different locations.

Year	Location	LSI	% infection (susceptible check)	% infection (IPA234)	SMD reaction of (IPA234)
2005-06	Dholi	27.2	72.3 ('ICP8863')**	10.0	Resistant*
	Varanasi	59.0	— ('ICP8863')	6.3	Resistant
	Rahuri	38.3	— ('ICP8863')	7.1	Resistant
2006-07	Dholi	65.8	100.0 ('ICP8863')	8.3	Resistant
	Varanasi	65.0	100.0 ('ICP8863')	0.0	Resistant
	Rahuri	52.5	— ('ICP8863')	2.4	Resistant
	Pant Nagar	65.7	— ('ICP8863')	0.0	Resistant
	ICRISAT	30.9	100.0 ('ICP8863')	0.0	Resistant
	Coimbatore	24.2	— ('ICP8863')	27.7	Moderately resistant
	Bangalore	77.5	100.0 ('ICP8863')	88.3	Susceptible
	Dholi	38.9	100 ('ICP8863')	7.7	Resistant
2007-08	Varanasi	41.0	100 ('ICP8863')	0.0	Resistant
	Rahuri	29.3	100 ('ICP8863')	9.2	Resistant
	ICRISAT	16.2	92.3 ('ICP8863')	4.2	Resistant
	Coimbatore	24.2	41.4 ('ICP8863')	25.0	Moderately resistant
	Bangalore	86.4	100 ('ICP8863')	84.5	Susceptible

*disease reaction quantified on the basis of acceptable scale used by pathologists (resistant: up to 10% infection; moderately resistant: >10 – 30% infection)

**Susceptible check in parentheses

in endemic areas (Bihar) just to minimize the risk of total yield loss.

References

- AICRP (2006) Annual Meeting on late pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 4 p.
- AICRP (2007) Annual Meeting on late pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 16p.

AICRP (2005-06) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 190 p.

AICRP (2006-07) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 198 p.

AICRP (2007-08) Annual Report of AICRP on Pigeonpea. Indian Institute of Pulses Research, Kanpur, India, 18 p.

13. JJK-2000-220 (IC0280837; INGR10026), French bean (*Phaseolus vulgaris*) Germplasm, with Long and Broad Poded Pole type habit

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This French bean (Pole type habit) germplasm IC 280837 was procured from Officer-In-Charge, NBPGR, Regional Station Vellanikkara, Trissur, Kerala. It was collected from village Alampatty, district Idukki of Kerala state. On the basis of single plant selection from bulk it was found promising for its long and broad pods used as dual purpose i.e. tender pods as vegetable and matured seeds as pulse.

Morpho-agronomic Characteristics

Being pole type habit, the plant height ranges from 185 cm-280 cm. Pods are long in size, smooth and broad. The pod length is 23 cm-25 cm and width is 1.5 cm-2.1 cm. Pod shape is flat, flower colour is white and seed colour is also bright white. The number of grains per pods are 5 to 9. The seed length and

width is 14.7 x 7.6 mm. 100 grain weight is 32-40 grams. The number of pods per plant are 18-30. The tender green pod yield per plant is 230 grain to 300 grains. The grain yield per plant is 50-75 g. The material was received in 2004 and it was evaluated during kharif 2005, 06 and 2007 alongwith a large number of exotic and indigenous bean germplasm at NBPGR, Regional Station Bhowali. Among all the germplasm lines as well as checks it was found superior to all. (Annual report 2006-07; Muneem *et al.*, 2009).

Associated Characters and Cultivated Practices

Generally it has been observed that white seeded beans are more prone to diseases like *Cercospora* leaf spot, Zonate leaf spot, Anthracnose, yellow

mosaic virus, mosaic virus and powdery mildew. This IC280837 was found continuously free from diseases as compare to checks and other lines. As the plants are quite large in height they can be used as green fodder for domestic cattle. The pods are also large in size and width they are also used by domestic cattle after shelling the grains. This germplasm can be grown successfully in Northern hills by the local

farmers, without using huge amount of fungicides and insecticides.

References

- Annual report (2006-07). NBPGR, Pusa Campus, New Delhi, 80 p.
- Muneem, K.C., P.S. Mehta, K.S. Negi and R.K. Mahajan (2009). Genetic diversity in climber French bean (*Phaseolus vulgaris* L.). *J. Arid Legumes* **6(2)**: 91-95.

14. NS/08/047 (IC0564627; INGR10027), a Linseed (*Linum usitatissimum*) Germplasm with High Oleic Acid Content in Seed (32.0%)

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Linseed or flax (*Linum usitatissimum* L.) belongs to the family Linaceae under the genus *Linum*, which is reported to have about 100 species distributed globally. Linseed is under cultivation since ancient times for its fibre and seed and occupies a prominent place among the oilseed crops owing to its various uses and special qualities. The seeds are a rich source of drying oil of edible nature and are the most potent source of omega-3 fatty acid, the desirable cholesterol for healthy living.

Oleic acid is a monounsaturated fatty acid naturally found in plant and animal products. It is an omega-nine fatty acid and considered as one of the healthiest sources of fat in the diet. Scientific research indicates that this healthy fat helps prevent a wide range of medical problems, including cardiovascular diseases, adrenoleukodystrophy, hypertension etc. Identification of linseed germplasm accessions with high oleic acid facilitates dietary supplementation of the fatty acid in the human nutrition through seed. Eighty four accessions of linseed collected from Andhra Pradesh and Maharashtra, India were analyzed for fatty acid composition on a gas chromatograph (Agilent 6890) equipped with a flame ionization detector (FID) on a split injector system. Oleic acid ranged from 18.1 - 32% with the local check varieties J-23-10 and RLC-6 recording 29.7% and 28.1%, respectively. From the literature (Nagaraj, 2009), the range of Oleic acid reported was between 16.53% and 27.10%. The linseed accession IC564627 collected from Gangawar, Nyalkal Mandal of Medak district, Andhra Pradesh found to contain high Oleic acid in the seed with

Table1. Morpho-agronomic Characteristics of linseed germplasm accession IC564627

Descriptor	Descriptor State
Plant growth habit	Bushy branching
Plant height (cm)	50.0
Flower size	Medium
Flower shape	Funnel form
Petal colour	Violet-blue
Petal aestivation	Semi-twisted
Stamen filament colour	Colour less
Anther colour	Blue
Capsule size	Medium
Shape of capsule tip	Pointed
100 seed weight (g)	0.78
Seed length (mm)	5.02
Seed width (mm)	2.61
Seed thickness (mm)	1.07
Oil content (%)	34
Palmitic acid (%)	5.9
Oleic acid (%)	32
Stearic acid (%)	8.2
Linoleic acid (%)	13.8
Linolenic acid (%)	39.5
Arachidic acid (%)	0.3
Behenic acid (%)	0.3

32.0% (Sivaraj *et al.*, 2009). The morpho-agronomic characteristics of the linseed accession IC564627 are given in the Table 1.

References

- Nagaraj G (2009) Oilseeds: properties processing, products and procedures. New India Publishing Company, New Delhi, 601p.
- Sivaraj N, N Sunil, SR Pandravada, V Kamala, Vinod Kumar, BVSK Rao, RBN Prasad and KS Varaprasad (2009) DIVA-GIS Approaches for diversity assessment of fatty acid composition in linseed, *Linum usitatissimum* L. germplasm collections from peninsular India. *J. Oilseeds Res.* **26**: 13-15.

mosaic virus, mosaic virus and powdery mildew. This IC280837 was found continuously free from diseases as compare to checks and other lines. As the plants are quite large in height they can be used as green fodder for domestic cattle. The pods are also large in size and width they are also used by domestic cattle after shelling the grains. This germplasm can be grown successfully in Northern hills by the local

farmers, without using huge amount of fungicides and insecticides.

References

- Annual report (2006-07). NBPGR, Pusa Campus, New Delhi, 80 p.
- Muneem, K.C., P.S. Mehta, K.S. Negi and R.K. Mahajan (2009). Genetic diversity in climber French bean (*Phaseolus vulgaris* L.). *J. Arid Legumes* **6(2)**: 91-95.

14. NS/08/047 (IC0564627; INGR10027), a Linseed (*Linum usitatissimum*) Germplasm with High Oleic Acid Content in Seed (32.0%)

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Linseed or flax (*Linum usitatissimum* L.) belongs to the family Linaceae under the genus *Linum*, which is reported to have about 100 species distributed globally. Linseed is under cultivation since ancient times for its fibre and seed and occupies a prominent place among the oilseed crops owing to its various uses and special qualities. The seeds are a rich source of drying oil of edible nature and are the most potent source of omega-3 fatty acid, the desirable cholesterol for healthy living.

Oleic acid is a monounsaturated fatty acid naturally found in plant and animal products. It is an omega-nine fatty acid and considered as one of the healthiest sources of fat in the diet. Scientific research indicates that this healthy fat helps prevent a wide range of medical problems, including cardiovascular diseases, adrenoleukodystrophy, hypertension etc. Identification of linseed germplasm accessions with high oleic acid facilitates dietary supplementation of the fatty acid in the human nutrition through seed. Eighty four accessions of linseed collected from Andhra Pradesh and Maharashtra, India were analyzed for fatty acid composition on a gas chromatograph (Agilent 6890) equipped with a flame ionization detector (FID) on a split injector system. Oleic acid ranged from 18.1 - 32% with the local check varieties J-23-10 and RLC-6 recording 29.7% and 28.1%, respectively. From the literature (Nagaraj, 2009), the range of Oleic acid reported was between 16.53% and 27.10%. The linseed accession IC564627 collected from Gangawar, Nyalkal Mandal of Medak district, Andhra Pradesh found to contain high Oleic acid in the seed with

Table1. Morpho-agronomic Characteristics of linseed germplasm accession IC564627

Descriptor	Descriptor State
Plant growth habit	Bushy branching
Plant height (cm)	50.0
Flower size	Medium
Flower shape	Funnel form
Petal colour	Violet-blue
Petal aestivation	Semi-twisted
Stamen filament colour	Colour less
Anther colour	Blue
Capsule size	Medium
Shape of capsule tip	Pointed
100 seed weight (g)	0.78
Seed length (mm)	5.02
Seed width (mm)	2.61
Seed thickness (mm)	1.07
Oil content (%)	34
Palmitic acid (%)	5.9
Oleic acid (%)	32
Stearic acid (%)	8.2
Linoleic acid (%)	13.8
Linolenic acid (%)	39.5
Arachidic acid (%)	0.3
Behenic acid (%)	0.3

32.0% (Sivaraj *et al.*, 2009). The morpho-agronomic characteristics of the linseed accession IC564627 are given in the Table 1.

References

- Nagaraj G (2009) Oilseeds: properties processing, products and procedures. New India Publishing Company, New Delhi, 601p.
- Sivaraj N, N Sunil, SR Pandravada, V Kamala, Vinod Kumar, BVSK Rao, RBN Prasad and KS Varaprasad (2009) DIVA-GIS Approaches for diversity assessment of fatty acid composition in linseed, *Linum usitatissimum* L. germplasm collections from peninsular India. *J. Oilseeds Res.* **26**: 13-15.

15. NS/08/102 (IC0564681; INGR10028), a Linseed (*Linum usitatissimum*) Germplasm as Source of High Oil Content in Seed (42.6%)

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Linseed or flax is a member of the genus *Linum* belonging to the family Linaceae. The crop is native to the region extending from the Mediterranean to India. India is one of the major countries of linseed cultivation with an annual production of about 1, 67, 000 metric tonnes. The dried seeds are a rich source of oil and omega-3 fatty acid, the desirable cholesterol for healthy living. Scientific research indicates that omega-3 which is a healthy polyunsaturated fatty acid prevents a wide range of medical problems, including cardiovascular diseases, depression, asthma and rheumatoid arthritis. Linseed oil is also used to bind wood dust, cork particles and other materials in manufacturing of Linoleum used for floor covering. It is used in wood putty and as a carrier in oil paints as well.

Given the increasing importance of linseed, to augment the germplasm, an exploration was conducted in parts of Andhra Pradesh and Maharashtra during March, 2008 which resulted in the collection of 84 accessions. These germplasm collections were characterized for their oil content using solvent extraction methods and fatty acid profile by gas chromatography. While the normal expression of oil content in linseed varies from 30-35% (Nagaraj, 2009) to 40-42% (Gill, 1989), a promising linseed germplasm accession (IC564681) with high oil (42.6%) and omega-3 content (54.8%) was identified from the germplasm (Sivaraj *et al.*, 2009).

The presence of high oil content and high omega-3 in a single genotype is indeed a significant finding having a bearing on the genetic improvement of this oilseed crop for the above two important traits and also for recommending it as a dietary supplement. This particular genotype which is characterized by

blue anthers which are very uncommon may also serve as a morphological marker for wilt resistance (Green, 1995) and this accession might be having natural resistance to wilt as well.

The morpho-agronomic description of linseed germplasm accession IC0564681 is as follows:

Descriptor	Descriptor State
Plant growth habit	Bushy branching
Plant height (cm)	54.6
Flower size	Medium (18 mm)
Flower shape	Funnel form
Petal colour	Light violet-blue
Petal aestivation	Semi-twisted
Stamen filament colour	Colour less
Anther colour	Blue
Capsule size	Bold (8.8 mm)
Capsule tip shape	Pointed
100-seed weight (g)	0.79
Seed length (mm)	4.92
Seed width (mm)	2.59
Seed thickness (mm)	1.05
Oil content (%)	42.6
Palmitic acid (%)	5.6
Stearic acid (%)	6.6
Oleic acid (%)	20.5
Linoleic acid (%)	12.1
Linolenic acid (Omega-3) (%)	54.8

References

- Gill KS (1989) *Linseed*. Indian Council of Agricultural Research, New Delhi, pp 300-316.
- Green AG (1995) Register of Australian oilseed cultivars *Linum usitatissimum* (L.) (linseed) cv. Wallaga. *Aus. J. Exp. Agri.* **35**: 120-120.
- G Nagaraj (2009) Oilseeds: properties, processing, products and procedures. New India Publishing Company, New Delhi, 601p.
- N Sivaraj, N Sunil, SR Pandravada, V Kamala, Vinod Kumar, BVSK Rao, RBN Prasad and KS Varaprasad (2009) DIVA-GIS Approaches for diversity assessment of fatty acid composition in linseed, *Linum usitatissimum* L. germplasm collections from peninsular India. *J. Oilseeds Res.* **26**: 13-15.

16. NRCGCS 77 (IC0582472; INGR10029), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBND (Peanut bud necrosis diseases), Stem Rot, Late Leaf Spot, Early Leaf Spot, Rust and *Alternaria* Leaf Blight

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NRCGCS 77 (INGR10029; IC0582472) was selected from advanced generation of cross (CT 7-1 x SB 11) × *A. diogeni*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has erect growth habit, produces 50% flowering in 29 days after sowing (DAS) and matures in 103 DAS during rainy season. The genotype produces an average pod yield of 109.7 g per square metre with 72% shelling out turn. Pods are slightly constricted, moderately beaked and deeply reticulated; mostly two seeded

with rose colour kernels. Kernels are medium in size with hundred kernel mass of 48 g and contain 50.5% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 2.8 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 15.1% for peanut bud necrosis disease (PBND) and 13.7% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

17. NRCGCS 85 (IC0582473; INGR10030), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBND (Peanut bud necrosis diseases), Stem Rot, Late Leaf Spot, Early Leaf Spot, Rust and *Alternaria* Leaf Blight

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NRCGCS 85 (INGR10030; IC0582473) was selected from advanced generation of cross (CT 7-1 x SB 11) × *A. kretschmeri*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has erect growth habit, produces 50% flowering in 25 days after sowing (DAS) and matures in 107 DAS during rainy season. The genotype produces an average pod yield of 84.3 g /m² with 74% shelling out turn. Pods are slightly constricted, moderately beaked and deeply reticulated; mostly two seeded

with rose colour kernels. Kernels are medium in size with hundred kernel mass of 45.6 g and contain 52% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 2.0 for early leaf spot and 3.0 for late leaf spot on a modified 9-point scale, and an incidence of 4.0% for peanut bud necrosis disease (PBND) and 8.0% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype can be used as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

18. NRCGCS 86 (IC0582474; INGR10031), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Late Leaf Spot, Early Leaf Spot, Rust and *Alternaria* Leaf Blight

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NRCGCS 86 (INGR10031; IC0582474) was selected from advanced generation of cross (CT 7-1 x SB 11) X *A. correntina*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has erect growth habit, produces 50% flowering in 26 days after sowing (DAS) and matures in 116 DAS during rainy season. The genotype produces an average pod yield of 84.5 g/m² with 73% shelling out turn. Pods are slightly constricted and moderately beaked as well as reticulated; mostly two seeded with

rose colour kernels. Kernels are small in size with hundred kernel mass of 32 g and contain 51.5% oil. The severity of foliar diseases in the genotype under field conditions are 2.0 for rust, 3.2 for early leaf spot and 3.8 for late leaf spot on a modified 9-point scale, and an incidence of 14.7% for peanut bud necrosis disease (PBNB) and 8.3% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

19. NRCG 14326 (INGR 10032; IC 0548192), NRCG 14336 (INGR 10033; IC 0582477), NRCG 14350 (INGR 10034; IC 0582478), NRCG 14409 (INGR 10035; IC 0582479), Groundnut (*Arachis hypogaea* L.) Germplasm, Spanish Bunch Germplasm Accessions with Fresh Seed Dormancy

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Groundnut is an important oilseed crop of India grown in about 5.0 million ha during *kharif* and 1.0 million ha in *rabi*-summer seasons. The crop has four botanical varieties, Spanish bunch (Subspecies *fastigiata* var. *vulgaris*), Valencia (Subspecies *fastigiata* var. *fastigiata*), Virginia bunch and Virginia runner (Subspecies *hypogaea* var. *hypogaea*). The Spanish and Valencia genotypes have short life cycle and non-dormant seeds while those of Virginia types have long life cycle and dormant seeds. In India, Spanish types are predominantly grown in semi-arid regions where the growing seasons are short or are grown in multiple cropping sequences. Untimely rains either in *kharif* or in *rabi*-summer seasons prior to

or immediately after harvest can cause seeds of Spanish and Valencia types to sprout *in situ* in the ground. In the semi-arid tropics, which account for 60% of the global production such situations are frequent and losses in yield and quality are substantial (Upadhyaya and Nigam, 1999). To avoid these losses during harvest it is essential to breed varieties having fresh seed dormancy up to 2-3 weeks duration. Before formulation of suitable breeding strategies, identification of sources of fresh seed dormancy are very essential. Reported sources of fresh seed dormancy especially among the Spanish bunch germplasm remain very few in literature.

18. NRCGCS 86 (IC0582474; INGR10031), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Late Leaf Spot, Early Leaf Spot, Rust and *Alternaria* Leaf Blight

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rose colour kernels. Kernels are small in size with hundred kernel mass of 32 g and contain 51.5% oil. The severity of foliar diseases in the genotype under field conditions are 2.0 for rust, 3.2 for early leaf spot and 3.8 for late leaf spot on a modified 9-point scale, and an incidence of 14.7% for peanut bud necrosis disease (PBNB) and 8.3% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

19. NRCG 14326 (INGR 10032; IC 0548192), NRCG 14336 (INGR 10033; IC 0582477), NRCG 14350 (INGR 10034; IC 0582478), NRCG 14409 (INGR 10035; IC 0582479), Groundnut (*Arachis hypogaea* L.) Germplasm, Spanish Bunch Germplasm Accessions with Fresh Seed Dormancy

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Groundnut is an important oilseed crop of India grown in about 5.0 million ha during *kharif* and 1.0 million ha in *rabi*-summer seasons. The crop has four botanical varieties, Spanish bunch (Subspecies *fastigiata* var. *vulgaris*), Valencia (Subspecies *fastigiata* var. *fastigiata*), Virginia bunch and Virginia runner (Subspecies *hypogaea* var. *hypogaea*). The Spanish and Valencia genotypes have short life cycle and non-dormant seeds while those of Virginia types have long life cycle and dormant seeds. In India, Spanish types are predominantly grown in semi-arid regions where the growing seasons are short or are grown in multiple cropping sequences. Untimely rains either in *kharif* or in *rabi*-summer seasons prior to

or immediately after harvest can cause seeds of Spanish and Valencia types to sprout *in situ* in the ground. In the semi-arid tropics, which account for 60% of the global production such situations are frequent and losses in yield and quality are substantial (Upadhyaya and Nigam, 1999). To avoid these losses during harvest it is essential to breed varieties having fresh seed dormancy up to 2-3 weeks duration. Before formulation of suitable breeding strategies, identification of sources of fresh seed dormancy are very essential. Reported sources of fresh seed dormancy especially among the Spanish bunch germplasm remain very few in literature.

Hence, a study was carried out to identify promising sources in summer 2008 and *kharif* 2008 in 64 diverse Spanish bunch germplasm accessions along with two Spanish bunch non-dormant check varieties, JL 24 and GG 2 for fresh seed dormancy under laboratory conditions. Significant differences were observed among the genotypes for days taken for complete germination and per cent of germination. Both the check varieties exhibited 100% germination within 4 weeks. Seeds of two accessions, NRCGs 14350

and 14409 did not germinate even after 60 days of incubation indicating the presence of long dormancy period while the two other accessions, NRCGs 14326 and 14336, exhibited a dormancy period up to 40 days. The oil content in these accessions was also high (about 50%) and matured around 115 days.

References

Upadhyaya HD and SN Nigam (1999) Inheritance of Fresh Seed Dormancy in Peanut. *Crop Sci.* **39**: 98-101.

20. NRCGCS 21 (IC0583387; INGR10036), Ground nut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, Early Leaf Spot

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NRCGCS 21 (INGR10036; IC0583387) was selected from advanced generation of cross CT7-1 x SBXI. This genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has erect growth habit, produces 50% flowering in 28 days after sowing (DAS) and matures in 114 DAS during rainy season. The genotype produces an average pod yield of 104.3g /m² with 73% shelling out turn. Pods are slightly constricted and moderately beaked; mostly two seeded with rose colour kernels.

Kernels are medium in size with hundred kernel mass of 85 g and contain 50% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.4 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 9.3% for peanut bud necrosis disease (PBNB) and 6.5% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis disease, stem rot, early leaf spot, rust, late leaf spot and *Alternaria* leaf blight.

21. NRCGCS 83 (IC0583388; INGR10037), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, Alternaria Leaf Blight

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NRCGCS 83 (INGR10037; ID-IC0583388) was selected from advanced generation of cross (CT7-1 × SB XI) × *A. diogeni*. The genotype was developed by pedigree

selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has erect growth

Hence, a study was carried out to identify promising sources in summer 2008 and *kharif* 2008 in 64 diverse Spanish bunch germplasm accessions along with two Spanish bunch non-dormant check varieties, JL 24 and GG 2 for fresh seed dormancy under laboratory conditions. Significant differences were observed among the genotypes for days taken for complete germination and per cent of germination. Both the check varieties exhibited 100% germination within 4 weeks. Seeds of two accessions, NRCGs 14350

and 14409 did not germinate even after 60 days of incubation indicating the presence of long dormancy period while the two other accessions, NRCGs 14326 and 14336, exhibited a dormancy period up to 40 days. The oil content in these accessions was also high (about 50%) and matured around 115 days.

References

Upadhyaya HD and SN Nigam (1999) Inheritance of Fresh Seed Dormancy in Peanut. *Crop Sci.* **39**: 98-101.

20. NRCGCS 21 (IC0583387; INGR10036), Ground nut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, Early Leaf Spot

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Kernels are medium in size with hundred kernel mass of 85 g and contain 50% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.4 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 9.3% for peanut bud necrosis disease (PBNB) and 6.5% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis disease, stem rot, early leaf spot, rust, late leaf spot and *Alternaria* leaf blight.

21. NRCGCS 83 (IC0583388; INGR10037), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, Alternaria Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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NRCGCS 83 (INGR10037; ID-IC0583388) was selected from advanced generation of cross (CT7-1 × SB XI) × *A. diogeni*. The genotype was developed by pedigree

selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has erect growth

Hence, a study was carried out to identify promising sources in summer 2008 and *kharif* 2008 in 64 diverse Spanish bunch germplasm accessions along with two Spanish bunch non-dormant check varieties, JL 24 and GG 2 for fresh seed dormancy under laboratory conditions. Significant differences were observed among the genotypes for days taken for complete germination and per cent of germination. Both the check varieties exhibited 100% germination within 4 weeks. Seeds of two accessions, NRCGs 14350

and 14409 did not germinate even after 60 days of incubation indicating the presence of long dormancy period while the two other accessions, NRCGs 14326 and 14336, exhibited a dormancy period up to 40 days. The oil content in these accessions was also high (about 50%) and matured around 115 days.

References

Upadhyaya HD and SN Nigam (1999) Inheritance of Fresh Seed Dormancy in Peanut. *Crop Sci.* **39**: 98-101.

20. NRCGCS 21 (IC0583387; INGR10036), Ground nut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, Early Leaf Spot

SK Bera¹, Vinod Kumar³, G Sunkad², AL Rathnakumar¹ and T Radhakrishnan¹

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Kernels are medium in size with hundred kernel mass of 85 g and contain 50% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.4 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 9.3% for peanut bud necrosis disease (PBNB) and 6.5% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis disease, stem rot, early leaf spot, rust, late leaf spot and *Alternaria* leaf blight.

21. NRCGCS 83 (IC0583388; INGR10037), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, Alternaria Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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NRCGCS 83 (INGR10037; ID-IC0583388) was selected from advanced generation of cross (CT7-1 × SB XI) × *A. diogeni*. The genotype was developed by pedigree

selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has erect growth

habit, produces 50% flowering in 28 days after sowing (DAS) and matures in 112 DAS during rainy season. The genotype produces an average pod yield of 96.9 g/m² with 75% shelling out turn. Pods have moderate constriction and beak; mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 44.0 g and contain 51% oil. The severity of foliar diseases in the genotype under field conditions

are 3.0 for rust and 5.0 for late leaf spot on a modified 9-point scale, and an incidence of 3.6% for peanut bud necrosis disease (PBNB) and 10.3% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

22. NRCGCS 124 (IC0583389; INGR10038), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, *Alternaria* Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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NRCGCS 124 (INGR10038; IC0583389) was selected from advanced generation of cross (CT7-1 x SBXI) x *A. kretschmetri*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has semi spreading (decumbent-3) growth habit, produces 50% flowering in 25 days after sowing (DAS) and matures in 112 DAS during rainy season. The genotype produces an average pod yield of 58.4 g/m² with 76% shelling out turn. Pods are moderately beaked and reticulated; mostly two seeded with rose colour kernels. Kernels

are medium in size with hundred kernel mass of 38 g and contain 48.5% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.5 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 8.7% for peanut bud necrosis disease (PBNB) and 13% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

23. NRCGCS 180 (IC0583390; INGR10039), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, *Alternaria* Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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NRCGCS 180 (INGR10039; IC0583390) was selected from advanced generation of cross J 11 x *A. cardenasii*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has spreading (decumbent-2) growth habit, produces 50% flowering in 35 days after sowing

(DAS) and matures in 123 DAS during rainy season. The genotype produces an average pod yield of 65.8 g/m² with 74% shelling out turn. Pods are prominently beaked and reticulated; mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 38.9 g and contain 51% oil. The severity of foliar diseases in the genotype under field conditions

habit, produces 50% flowering in 28 days after sowing (DAS) and matures in 112 DAS during rainy season. The genotype produces an average pod yield of 96.9 g/m² with 75% shelling out turn. Pods have moderate constriction and beak; mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 44.0 g and contain 51% oil. The severity of foliar diseases in the genotype under field conditions

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22. NRCGCS 124 (IC0583389; INGR10038), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, *Alternaria* Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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are medium in size with hundred kernel mass of 38 g and contain 48.5% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.5 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 8.7% for peanut bud necrosis disease (PBNB) and 13% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

23. NRCGCS 180 (IC0583390; INGR10039), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, *Alternaria* Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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(DAS) and matures in 123 DAS during rainy season. The genotype produces an average pod yield of 65.8 g/m² with 74% shelling out turn. Pods are prominently beaked and reticulated; mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 38.9 g and contain 51% oil. The severity of foliar diseases in the genotype under field conditions

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are 3.0 for rust and 5.0 for late leaf spot on a modified 9-point scale, and an incidence of 3.6% for peanut bud necrosis disease (PBNB) and 10.3% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

22. NRCGCS 124 (IC0583389; INGR10038), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, *Alternaria* Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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are medium in size with hundred kernel mass of 38 g and contain 48.5% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.5 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 8.7% for peanut bud necrosis disease (PBNB) and 13% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

23. NRCGCS 180 (IC0583390; INGR10039), Groundnut (*Arachis hypogaea*) Germplasm, a source of Resistance to PBNB (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Spot, *Alternaria* Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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NRCGCS 180 (INGR10039; IC0583390) was selected from advanced generation of cross J 11 x *A. cardenansii*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has spreading (decumbent-2) growth habit, produces 50% flowering in 35 days after sowing

(DAS) and matures in 123 DAS during rainy season. The genotype produces an average pod yield of 65.8 g/m² with 74% shelling out turn. Pods are prominently beaked and reticulated; mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 38.9 g and contain 51% oil. The severity of foliar diseases in the genotype under field conditions

are 2.0 for rust, 4.3 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 12.4% for peanut bud necrosis disease (PBND) and 2.5% for stem rot with almost immunity to *Alternaria*

leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

24. NRCGCS 222(IC0583391; INGR10040), Groundnut (*Arachis hypogaea*) Germplasm, a Source Resistance to PBND (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Blight, Early Leaf Spot and *Alternaria* Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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NRCGCS 222 (INGR10040; IC0583391) was selected from advanced generation of cross (C364×PBDR 25) × *A. kemfmercadoi*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has semi spreading (decumbent-3) growth habit, produces 50% flowering in 30 days after sowing and matures in 121 DAS during rainy season. The genotype produces an average pod yield of 49.8 g per square metre with 60% shelling out turn. Pods are highly reticulated and slightly constricted; mostly two seeded

with rose colour kernels. Kernels are medium in size with hundred kernel mass of 37.5 g and contain 45% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.0 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 12.4% for peanut bud necrosis disease and 9.9% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

25. NRCG-11846 (INGR10041; IC0583392), Groundnut (*Arachis hagenbeckii* Benth) Germplasm, with High Fodder Bio-Mass (2.4 ton/ha/year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Useful for Pasture Development, High Crude Fibre (31.2%) and Ash (11.7%) Contents

NRCG-11847 (INGR10042; IC0583393), Groundnut (*Arachis glabrata* Benth) Germplasm, with High Fodder Bio-Mass (3.8 Ton/Ha/Year), Suitable under Wasteland Conditions, Perennial in Nature; Useful for Pasture Development, High Protein Content (16.9%)

NRCG-17205 (INGR10045; IC0583396) Groundnut (*Arachis prostrata* Benth) Germplasm, with High Fodder Bio-Mass (3.6 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (14.2%) and Iron Content (0.7%).

are 2.0 for rust, 4.3 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 12.4% for peanut bud necrosis disease (PBND) and 2.5% for stem rot with almost immunity to *Alternaria*

leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

24. NRCGCS 222(IC0583391; INGR10040), Groundnut (*Arachis hypogaea*) Germplasm, a Source Resistance to PBND (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Blight, Early Leaf Spot and *Alternaria* Leaf Blight

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NRCGCS 222 (INGR10040; IC0583391) was selected from advanced generation of cross (C364×PBDR 25) × *A. kemfmercadoi*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has semi spreading (decumbent-3) growth habit, produces 50% flowering in 30 days after sowing and matures in 121 DAS during rainy season. The genotype produces an average pod yield of 49.8 g per square metre with 60% shelling out turn. Pods are highly reticulated and slightly constricted; mostly two seeded

with rose colour kernels. Kernels are medium in size with hundred kernel mass of 37.5 g and contain 45% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.0 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 12.4% for peanut bud necrosis disease and 9.9% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

25. NRCG-11846 (INGR10041; IC0583392), Groundnut (*Arachis hagenbeckii* Benth) Germplasm, with High Fodder Bio-Mass (2.4 ton/ha/year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Useful for Pasture Development, High Crude Fibre (31.2%) and Ash (11.7%) Contents

NRCG-11847 (INGR10042; IC0583393), Groundnut (*Arachis glabrata* Benth) Germplasm, with High Fodder Bio-Mass (3.8 Ton/Ha/Year), Suitable under Wasteland Conditions, Perennial in Nature; Useful for Pasture Development, High Protein Content (16.9%)

NRCG-17205 (INGR10045; IC0583396) Groundnut (*Arachis prostrata* Benth) Germplasm, with High Fodder Bio-Mass (3.6 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (14.2%) and Iron Content (0.7%).

are 2.0 for rust, 4.3 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 12.4% for peanut bud necrosis disease (PBND) and 2.5% for stem rot with almost immunity to *Alternaria*

leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

24. NRCGCS 222(IC0583391; INGR10040), Groundnut (*Arachis hypogaea*) Germplasm, a Source Resistance to PBND (Peanut bud necrosis diseases), Stem Rot, Tolerant to Late Leaf Blight, Early Leaf Spot and *Alternaria* Leaf Blight

SK Bera¹, G Sunkad², Vinod Kumar³, AL Rathnakumar¹ and T Radhakrishnan¹

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NRCGCS 222 (INGR10040; IC0583391) was selected from advanced generation of cross (C364×PBDR 25) × *A. kemfmercadoidi*. The genotype was developed by pedigree selection from interspecific progenies developed at the Cytogenetics Section, Directorate of Groundnut Research, Junagadh, Gujarat. The plant has semi spreading (decumbent-3) growth habit, produces 50% flowering in 30 days after sowing and matures in 121 DAS during rainy season. The genotype produces an average pod yield of 49.8 g per square metre with 60% shelling out turn. Pods are highly reticulated and slightly constricted; mostly two seeded

with rose colour kernels. Kernels are medium in size with hundred kernel mass of 37.5 g and contain 45% oil. The severity of foliar diseases in the genotype under field conditions are 3.0 for rust, 5.0 for early leaf spot and 4.0 for late leaf spot on a modified 9-point scale, and an incidence of 12.4% for peanut bud necrosis disease and 9.9% for stem rot with almost immunity to *Alternaria* leaf blight disease has been recorded. The genotype has been identified as donor for multiple disease resistance in groundnut for peanut bud necrosis diseases, stem rot, late leaf spot, rust and *Alternaria* leaf blight.

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NRCG-17205 (INGR10045; IC0583396) Groundnut (*Arachis prostrata* Benth) Germplasm, with High Fodder Bio-Mass (3.6 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (14.2%) and Iron Content (0.7%).

NRCG-17206 (INGR10046; IC0583397), Groundnut (*Arachis marginata* Gardner) Germplasm, with High Fodder Bio-Mass (3.2 ton/ha/year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (16.8%) and Iron Content (0.7%).

AL Rathnakumar¹, T Radhakrishnan¹, SK Bera¹, HB Lalwani¹, Nilesh Joshi² and Sugad Singh¹

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Groundnut haulms form one of the important sources of proteinaceous fodder for cattle especially among the resource poor farmers of the Semi-Arid-Tropics (SAT). The haulms of cultivated groundnut are fed as green or stored in haystacks and are often mixed with other fodder materials. In addition to the cultivated types, the vast reservoir of wild species of groundnut (1500 wild accessions) available around the world have potential to be used as a source of green or dry fodder. So far only very few of them have been evaluated for their fodder/forage potential (Cook and Crosthwaite, 1994).

Among the mostly utilized wild species of groundnut for fodder purposes, members of the section *Rhizomatosae*, and *Extranervosae* are more common in China, Africa and South America while in Australia few species of the section *Caulorhizae* have been released as forage varieties. These species are perennial and characterized by the presence of rhizomes (in case of *Caulorhizae* it is seeds) there by making the propagation easy.

Hence, a systematic evaluation has been carried out with four high biomass yielding perennial species of the section *Rhizomatosae* (*A. glabrata* and *A. hagenbeckii*; both are robust tetraploid species) and section *Extranervosae* (*A. marginata* and *A. prostrata*) for five fodder quality traits including biomass under wasteland conditions in the experimental farm area of Directorate of Groundnut Research, Junagadh, Gujarat. After four years of their establishment, the average dry matter yield (Table 1) was in the range of 2.4 ton/ha/

Table 1. Biomass yield and fodder quality in four promising wild *Arachis* species of the section *Rhizomatosae*

Wild Species	Biomass yield ton/ha/year	Leaf:twig ratio	Protein (%)	Ca (%)	Fe (%)
<i>A. hagenbeckii</i>	2.4	1:1.3	11.1	2.3	0.80
<i>A. glabrata</i>	3.8	1:1.3	16.9	2.6	0.50
<i>A. prostrata</i>	3.6	1:1.3	14.2	2.1	0.70
<i>A. marginata</i>	3.2	1:2.3	16.8	2.9	0.70

year (*A. hagenbeckii*) to 3.8 ton/ha/year (*A. glabrata*) followed by *A. prostrata* (3.6 ton/ha/year) in two cuttings indicating their potential as a source of fodder under wasteland conditions. In addition, these species produce dense and thick rhizomes (about 1.5 ton/ha/year), which act as a soil binder and thus indicating the usefulness in high rainfall regions and slopes to prevent soil erosion. The crude protein content (N content x 6.25) was the in the range of 11.1% (*A. hagenbeckii*) to 16.9%. (*A. glabrata*). Nutrients important for lactation in animals like Calcium (>2.0%) and iron (≥0.5%) were also high in these four species. Rumen microbes usually require a minimum of 7.0% of crude protein for effective digestion of the feed. The higher protein content coupled with high calcium and iron contents present in the above species indicated the nutritional superiority of the four species to be used as forage under wasteland conditions.

References

- Cook BG and IC Crosthwaite (1994). Utilization of *Arachis* species as forage. In: The Groundnut Crop: A scientific basis for improvement. J Smart (ed), Chapman and Hall, London, pp 624-663.

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NRCG-11847 (INGR10042; IC0583393), Groundnut (*Arachis glabrata* Benth) Germplasm, with High Fodder Bio-Mass (3.8 Ton/Ha/Year), Suitable under Wasteland Conditions, Perennial in Nature; Useful for Pasture Development, High Protein Content (16.9%)

NRCG-17205 (INGR10045; IC0583396) Groundnut (*Arachis prostrata* Benth) Germplasm, with High Fodder Bio-Mass (3.6 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (14.2%) and Iron Content (0.7%).

NRCG-17206 (INGR10046; IC0583397), Groundnut (*Arachis marginata* Gardner) Germplasm, with High Fodder Bio-Mass (3.2 ton/ha/year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (16.8%) and Iron Content (0.7%).

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NRCG-11847 (INGR10042; IC0583393), Groundnut (*Arachis glabrata* Benth) Germplasm, with High Fodder Bio-Mass (3.8 Ton/Ha/Year), Suitable under Wasteland Conditions, Perennial in Nature; Useful for Pasture Development, High Protein Content (16.9%)

NRCG-17205 (INGR10045; IC0583396) Groundnut (*Arachis prostrata* Benth) Germplasm, with High Fodder Bio-Mass (3.6 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (14.2%) and Iron Content (0.7%).

NRCG-17206 (INGR10046; IC0583397), Groundnut (*Arachis marginata* Gardner) Germplasm, with High Fodder Bio-Mass (3.2 ton/ha/year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (16.8%) and Iron Content (0.7%).

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NRCG-17206 (INGR10046; IC0583397), Groundnut (*Arachis marginata* Gardner) Germplasm, with High Fodder Bio-Mass (3.2 ton/ha/year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Binds Soil through Tough Rhizomes, High Protein Content (16.8%) and Iron Content (0.7%).

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26. NRCG-12035 (INGR 10043; IC 0583394), Groundnut (*Arachis appressipila* Krapov. and WC Gregory) Germplasm, with High Fodder Bio-Mass (1.8 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Seed Forming, Semi-Perennial; Suitable for Pasture Development, Protein Content (14.8%)

NRCG-12990 (INGR 10044; IC 0583395), Groundnut (*Arachis pintoii* Krapov and WC Gregory) Germplasm, with High Fodder Bio-Mass (2.7 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Protein Content (12.1%) and Iron Content (0.5%)

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The science of tropical forages is in its infancy in comparison with that of temperate forages. It spans around a period of little more than 50 years, during which commercial forage legumes have been dawn from may genera, the most widely planted probably coming from *Centrosema*, *Macroptilium*, *Stylosanthes* and *Desmodium* (Cook and Crosthwaite, 1994). However, the genetic potential of these and other genera including *Arachis*, has been only partly exploited. Considerable contribution of *Arachis* to the pasture lands of South America, the USA and Australia is well recognized and the most of the pasture lands is occupied by Rhizoma peanuts. However, evaluation of the seed forming species of other section is quite rare across the world.

Hence, two seed forming perennial species *A. pintoii* Krap. and Greg. of the section *Caulorhizae* and *A. appressipila* Krapov and WC Gregory of the section *Procumbentes* were evaluated along with eight other species under wasteland conditions in the experimental farm area of Directorate of Groundnut Research, Junagadh, Gujarat. After four years of establishment, *A. pintoii* was found to be superior only in respect of

Table1. Biomass yield and fodder quality in two promising seed forming wild *Arachis* species

Wild Species	Biomass Yield ton/ha/year	Leaf:twig ratio	Protein (%)	Ca (%)	Fe (%)
<i>A. appressipila</i> (NRCG 12035)	1.8	1:1.6	14.8	2.3	0.5
<i>A. pintoii</i> (NRCG 12990)	2.7	1:1.6	12.1	2.1	0.5

biomass yield (2.7ton/ha/year in two cuttings) while for crude protein content (14.8%) and Ca (2.3%) were found to be high in *A. appressipila*. For two other fodder quality traits, leaf: twig ratio (1:1.6) and Fe content (0.5%), there was no difference between these two species (Table 1). However, the species, *A. pintoii* has stoloniferous roots at the nodes and anchor very well in the soil. It also has the advantage of producing profuse and large seeds when compared with *A. appressipila*. These two species may be used in pasture development in wastelands

References

- Cook BG and IC Crosthwaite (1994) Utilization of *Arachis* species as forage. In: The Groundnut Crop: A scientific basis for improvement. J Smart (ed.), Chapman and Hall, London, pp 624-663.

26. NRCG-12035 (INGR 10043; IC 0583394), Groundnut (*Arachis appressipila* Krapov. and WC Gregory) Germplasm, with High Fodder Bio-Mass (1.8 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Seed Forming, Semi-Perennial; Suitable for Pasture Development, Protein Content (14.8%)

NRCG-12990 (INGR 10044; IC 0583395), Groundnut (*Arachis pintoii* Krapov and WC Gregory) Germplasm, with High Fodder Bio-Mass (2.7 Ton/Ha/Year), Suitable Even Under Wasteland Conditions, Perennial in Nature; Suitable for Pasture Development, Protein Content (12.1%) and Iron Content (0.5%)

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The science of tropical forages is in its infancy in comparison with that of temperate forages. It spans around a period of little more than 50 years, during which commercial forage legumes have been drawn from many genera, the most widely planted probably coming from *Centrosema*, *Macroptilium*, *Stylosanthes* and *Desmodium* (Cook and Crosthwaite, 1994). However, the genetic potential of these and other genera including *Arachis*, has been only partly exploited. Considerable contribution of *Arachis* to the pasture lands of South America, the USA and Australia is well recognized and the most of the pasture lands is occupied by Rhizoma peanuts. However, evaluation of the seed forming species of other section is quite rare across the world.

Hence, two seed forming perennial species *A. pintoii* Krap. and Greg. of the section *Caulorhizae* and *A. appressipila* Krapov and WC Gregory of the section *Procumbentes* were evaluated along with eight other species under wasteland conditions in the experimental farm area of Directorate of Groundnut Research, Junagadh, Gujarat. After four years of establishment, *A. pintoii* was found to be superior only in respect of

Table1. Biomass yield and fodder quality in two promising seed forming wild *Arachis* species

Wild Species	Biomass Yield ton/ha/year	Leaf:twig ratio	Protein (%)	Ca (%)	Fe (%)
<i>A. appressipila</i> (NRCG 12035)	1.8	1:1.6	14.8	2.3	0.5
<i>A. pintoii</i> (NRCG 12990)	2.7	1:1.6	12.1	2.1	0.5

biomass yield (2.7ton/ha/year in two cuttings) while for crude protein content (14.8%) and Ca (2.3%) were found to be high in *A. appressipila*. For two other fodder quality traits, leaf: twig ratio (1:1.6) and Fe content (0.5%), there was no difference between these two species (Table 1). However, the species, *A. pintoii* has stoloniferous roots at the nodes and anchor very well in the soil. It also has the advantage of producing profuse and large seeds when compared with *A. appressipila*. These two species may be used in pasture development in wastelands

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27. Mutant No. 1022 (IC0582890; INGR10047), Sesame (*Sesamum indicum* L.) Germplasm, with High Lignin and Improved Nutraceutical Traits

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Lignans such as sesamin, sesamlin and γ -tocopherol from sesame seeds play an important role in plant defense such as antifedant as well as potent antioxidants and insecticides. Sesamin is the most abundant lignan in sesame seed. It shows anti hypertensive, anti inflammatory and anti allergic effect (Jeng and Hou, 2005). This compound is also effective in preventing an increase in the serum triacylglycerol level following ethanol consumption in the rats (Akimoto, 1993). The cholesterol lowering effect of sesame has also been shown in humans (Hirata, 1996)

Induced mutagenesis with gamma radiation and chemical mutagen was employed in sesame (*Sesamum indicum* L.) to enhance the genetic variability for higher seed yield and seed quality components. Some of the isolated mutants for higher seed yield with improved test weight and colour were subjected for analysis of nutraceutical components.

ANOVA among the induced mutants indicated very highly significant variation between mutants and their interaction. The induced mutant lines were found to be promising for seed yield. Out of 49 mutants, top ten mutants were selected in the order of their merit for the lignan profiles are presented below.

Mutant No.1022 recorded significantly higher total lignan content of 14.23 g/kg as against the parent (5.79 g/kg), that accounts for 145.76% improvement over the parent, DS-1. Incidentally, the same mutant recorded high amount of sesamin (10.46 g/kg) which is an important and major lignan content as against

the parent DS-1 with 3.59 g/kg. The top four induced mutants (No.1022, 23, 191 and 983) recorded the total lignan content of more than double compared to the parent DS-1 (5.79 g/kg). These mutant lines can be further utilized in inter-mutant hybridization / recurrent irradiation for enhancing the lignan profiles for their better health benefit. Since, these mutant lines are having higher proportions of lignan they can be better exploited for their anti-diabetic and anti-hypertension benefits.

Table 1. Lignan profiles of selected induced mutant lines

Mutant lines	Sesamin (g /kg oil)	Sesamolin (g /kg oil)	γ -toco- pherol	Total
1022	10.46	3.18	0.59	14.23
23	9.15	3.77	0.62	13.54
191	9.13	2.66	0.77	12.56
983	8.32	2.98	0.55	11.85
365	8.03	2.34	0.54	10.91
383	7.15	2.53	0.72	10.40
949	7.56	1.90	0.62	10.08
946	6.34	3.13	0.57	10.04
699	6.42	2.68	0.53	9.63
5004	7.05	1.91	0.62	9.58
DS-1 (Parent)	3.59	1.68	0.52	5.79
Mean	5.44	1.92	0.58	—
CD (5%)	0.702	0.277	0.039	—

References

- Akimoto K (1993) Protective effect of sesamin against liver damage caused by alcohol or carbon tetra chloride in rodents. *Ann. Nutr. Meabol.* **37**: 218-224.
- Hirata I (1996) Hypocholesteromic effect of sesame lignan in humans. *Atherosclerosis.* **122**: 135-136.
- Jeng KCG and RCW Hou (2005) Sesamin and sesamolin: Natures therapeutic lignans. *Current Enzyme Inhibition.* **I**: 11-20.

28. NRC GS-1 (IC0582897; INGR10048), a Rapeseed (*Brassica napus*) Germplasm, with Early Flowering and Dwarf Plant Type

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Gobhi sarson (*Brassica napus*) is an introduction from European countries and basically a crop of long duration and is of high yield potential. However, in India, Indian

mustard is grown predominantly largely because of its inherent capacity to tolerate the drought stress. However, with the expansion of irrigation facilities, most of the

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28. NRC GS-1 (IC0582897; INGR10048), a Rapeseed (*Brassica napus*) Germplasm, with Early Flowering and Dwarf Plant Type

SS Meena, Rajbir Yadav, Arvind Kumar, VV Singh, KH Singh and AK Misra

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Gobhi sarson (*Brassica napus*) is an introduction from European countries and basically a crop of long duration and is of high yield potential. However, in India, Indian

mustard is grown predominantly largely because of its inherent capacity to tolerate the drought stress. However, with the expansion of irrigation facilities, most of the

mustard in India is now grown under irrigated condition and therefore, a plant type suited for irrigated condition can be a mean for further increase in yield potential of rapeseed-mustard. Beside, high yield potential of *Brassica napus*, it is fortunately resistant against all the available racial flora of white rust and also has high oil content. Keeping these into consideration, a number of varieties like GSL-1, GSL-2 and a hybrid Hyola- 401 was released for cultivation in Punjab and Himanchal Pradesh where winters are comparatively longer. These varieties and hybrid could not become popular largely because of their long duration and tall growth habit.

An inter-specific hybridization, programme, therefore, was initiated at NRCRM, Bharatpur, during 1999-2000 to introgress the desirable character of Gobhi sarson into Indian mustard and vice versa. From this hybridization, a dwarf and very early flowering genotype of *Brassica napus* was isolated, which was advanced to F₇ through selfing and a stable line is here proposed for registration.

It increases the yield potential in mustard by prolonging the reproductive phase in comparison to vegetative phase and the proposed line flowers in 32-35

days and maturing in 135-40 days is the right kind of donor. Beside this, it is dwarf in height and therefore can find favor with the farmers directly in the Himanchal Pradesh region.

The earlier registered germplasm by Teri Gaurav (Double low) is direct introduction and the selection from *Brassica napus*. The proposed line, however, is a product of inter-specific hybridization and therefore, likely to possess many advantageous traits of *Brassica juncea* and, therefore, likely to have more benefit by utilization in the breeding programme. Moreover, this can add to the very limited diversity available for plant height in the germplasm collection of *Brassica napus*. The detail of the genotype NRC-GS-1 is given below along with figures.

Characteristics	NRC GS-1	BEC 107	NRCG 11
Days to Flowering	32-35 (34)	45-49 (47)	55-65 (60)
Days to maturity	130-135 (138)	134-139 (135)	145-152 (149)
Plant height	70-80 (75)	123-135 (130)	144-151 (147)
Primary branches	3-4 (3.6)	5-7 (6.4)	4-5 (4.8)
Siliquae on main shoot	20-24 (22.8)	35-40 (38.900)	45-53 (49.6)
Seeds per siliquae	18-20 (18.9)	12-14 13.4)	19-21 (20.4)
1000-seed weight(g)	2.86	4.23	3.21
Oil content (%)	37.6	38.6	39.2

Figures in parentheses showing mean value.

29. NRCKR-304 (IC 0582898, INGR 10049), Mustard (*Brassica carinata*) Germplasm, with Early Maturity, Long Main Shoot and Bold Seed

VV Singh¹, Rajbir Yadav², Arvind Kumar³, SS Meena¹, KH Singh¹ and AK Misra⁴

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Karan Rai or Ethiopian mustard [*Brassica carinata* (A. Braun)] is a mustard crop suitable for rainfed and low moisture condition. A natural amphidiploid between *Brassica nigra* and *Brassica oleracea*, it is believed to be originated in Ethiopian high lands. Beside its tolerance to moisture stress, Karan rai is a reservoir of number of disease resistant genes to number of diseases prevalent in India like white rust, Alternaria blight and stem rot. Despite such advantages, this crop could not find favours with farmers largely because it is a very long duration crop along with other inherent defects like low test weight, short shoot length and long duration. Most of its agronomic features suit

rain fed conditions with uneven plant stand. However, in India rapeseed-mustard is now largely grown on conserved moisture with one life saving irrigation and therefore, the variety should possess the characteristics which suit this kind of agronomy.

At NRCRM, Bharatpur, an inter specific hybridization programme was therefore, initiated during 1999-2000 to genetically improve Karan rai by introgressing the high yielding agronomic traits of *Brassica juncea* in the genetic background of *Brassica carinata*. One of the released varieties of Indian mustard, namely Varuna was crossed with a germplasm line BPKR 13 of *Brassica carinata*. Segregant were advanced

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to F₇ generation and some stable lines of *Brassica carinata* were obtained which possesses some desirable characteristics such as long main shoot, bold seed, early duration and designated as NRCKR-304. This line is one step ahead of released Karan rai variety in many agronomic features and can act as donor for further improvement of *Brassica carinata* as well as *Brassica juncea*. The features of this stock are unique and no literature available to applicant shows these features.

Table 1. Salient features of NRCKR-304

Characteristics	NRCKR-304	Kiran (released variety of <i>Brassica carinata</i>)	Varuna (released variety of <i>Brassica juncea</i>)
Days to Flowering	43	84	48
Days to maturity	135	150	130
Plant height	163	170	155
Primary branches	6.4	9.8	5.2
Secondary branches	15.8	15.6	7.2
Fruiting zone length	107.8	52	70
Main shoot length	110	24	53
Siliquae on main shoot	40.2	24	40
Siliquae per plant	336	254	150
Seeds per siliquae	16.4	12.0	14.2
Thousand seed weight(g)	5.8	2.9	5.1

30. BPR-541- 4(IC0583386; INGR10050), Mustard (*Brassica juncea* L.) Germplasm, with High Water use Efficiency. Thermo-tolerance at Terminal Stage, Salinity Tolerance at Juvenile Stage

JS Chauhan¹, Maharaj Singh¹, KH Singh¹, Rajbir Yadav², AK Misra³, VV Singh¹, SS Meena¹, ML Meena¹ and YP Singh

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High temperature is the second most important stress next to drought, which affects crop plant at any time and imposes severe limitation on crop growth and development. Flowering is the most sensitive stage for high temperature damage probably due to vulnerability during pollen development, anthesis and fertilization leading to reduced crop yield (Hall, 1992). In India prevalence of high temperature stress at terminal stage of Indian mustard is inevitable in substantial acreage due to delayed sowing after rice and mixed /intercropping with wheat. No donor source having tolerance of high temperature stress during terminal stage has been available in Indian mustard. Strain BPR-541-4 (IC 0583448) was developed from the cross MDOC 8×PCR 7 following pedigree method of selection at Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur (Rajasthan) showed thermo-tolerance during terminal stage in the experiments conducted at Hisar, Kanpur and Ludhiana under AICRPRM during 2007-08 and 2008-09. Of the 6 locations (pooled over years), it showed consistently low (<20%) reduction in seed yield at 5 locations. It also showed tolerance to

saline conditions during juvenile stage in experiments conducted at Hisar, Karnal and Kanpur during 2007-08 and Hisar, Karnal, Kanpur and S.K.Nagar during 2008-09. The tolerance to salinity (12 dS/m) was characterized on the basis of per cent reduction in seedling emergence and dry weight. This germplasm showed less reduction in seedling emergence (< 10%) and dry weight (< 15%) at 4 out of 7 locations.

BPR 541-4 was also identified to possess high water use efficiency (WUE) during bolting and full flowering stage on the basis of lower $\Delta^{13}\text{C}$ (18.5%) than the check Varuna (21.1%) and Rohini (22.1%) under irrigated conditions and also higher seed yield/plant than Varuna (29.3%) and Rohini (12.7%). On the basis of gas exchange parameters, BPR-541-4 also showed 50.6% and 52.0% higher WUE over Varuna and Rohini, respectively, under irrigated conditions with 29.3% and 12.7% higher seed yield/plant. Under rainfed conditions it had 21.6% higher WUE and 24.3% higher yield than check RH-819. It is tall and has medium maturity, medium size seeds and high oil content (Table 1).

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JS Chauhan¹, Maharaj Singh¹, KH Singh¹, Rajbir Yadav², AK Misra³, VV Singh¹, SS Meena¹, ML Meena¹ and YP Singh

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saline conditions during juvenile stage in experiments conducted at Hisar, Karnal and Kanpur during 2007-08 and Hisar, Karnal, Kanpur and S.K.Nagar during 2008-09. The tolerance to salinity (12 dS/m) was characterized on the basis of per cent reduction in seedling emergence and dry weight. This germplasm showed less reduction in seedling emergence (< 10%) and dry weight (< 15%) at 4 out of 7 locations.

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Table1. Morphological characters of BPR-541-4

Plant height (cm)	200.0 (200–210)
Days to maturity	135.0 (130–145)
Primary branches/plant(no.)	7.7 (7–9)
Secondary branches/plant (no.)	11.7 (10–13)
Main shoot length (cm)	70.0 (65–73)
Siliquae on main shoot (no.)	41.4 (41–43)
Silique length (cm)	6.9 (5.6–7.0)
Seeds/silique (no.)	16.6 (15.8–17.2)
1000–seeds weight (g)	4.4 (4.2–4.6)
Total dry matter/plant (g)	52.2 (48–56)
Harvest index (%)	30.9 (28–33)
Oil content (%)	42.2 (41–43)
Protein content (%)	19.4 (19.2– 19.8)

Reference

Hall AE (1992) Breeding for heat tolerance. *Plant Breed. Rev.* **10**: 129-168.

31. BPR-543-2 (IC0583448; INGR10051), Mustard (*Brassica juncea* L.) Germplasm, with High Water Use Efficiency and Thermo-tolerance at Juvenile Stage

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Water use efficiency (WUE), ability of the plant to produce dry matter / unit of water is an important character especially under drought and also showed positive correlation with seed yield (Singh *et al.* 2007). No donor source for this character has been available in Indian mustard. The identified germplasm, BPR 543-2 (IC 0583386) was developed from the cross TM 2 x PCR 9202 following pedigree method of selection at Directorate of Rapeseed-Mustard, Sewar, Bharatpur (Rajasthan). It had 40% higher WUE ($\Delta^{13}\text{C} = 18.1\%$) during bolting and full flowering stage than check Varuna ($\Delta^{13}\text{C} = 21.1\%$) and Rohini ($\Delta^{13}\text{C} = 22.1\%$) with 23.2% higher seed yield/plant over Varuna and 7.4% over Rohini under irrigated conditions, while under rainfed conditions it showed 23.0% higher WUE ($\Delta^{13}\text{C} = 18.2\%$) over best check RH-819 ($\Delta^{13}\text{C} = 22.4\%$) with 10.6% higher seed yield. It showed consistently low seedling (< 20 %) mortality at high temperature ($45 \pm 1^\circ\text{C}$) during juvenile stage in the experiments conducted at Hisar, Kanpur, Ludhiana and Bharatpur under AICRPRM during 2007-08 and 2008-09 and also identified as tolerant of high temperature. It matured in 125 days

Table1. Morphological characters of BPR-543-2

Plant height (cm)	192 (100–195)
Days to maturity	125 (120–135)
Primary branches/plant(no.)	6.3 (6–7)
Secondary branches/plant (no.)	10.7 (9–12)
Main shoot length (cm)	76.7 (70–80)
Siliquae on main shoot (no.)	54.7 (51–58)
Silique length (cm)	6.5 (6.2–7.0)
Seeds/silique (no.)	15.8 (14.3–16.8)
1000–seeds weight (g)	4.7 (4.4–5.0)
Total dry matter/plant (g)	51.5 (48–55)
Harvest index (%)	30.8 (29–32)
Oil content (%)	41.8 (41–42)
Protein content (%)	19.9 (19–20.5)

with an average height of 192 cm. It had medium size seeds with high oil content (Table 1)

References

Singh M, JS Chauhan, MS Sheshashayee, M Udayakumar and A Kumar (2007) Isotope discrimination technique ($\delta^{13}\text{C}$): A possible selection criteria for drought tolerance in Indian mustard (*Brassica juncea* L.). In: Proc. 12th International Rapeseed Congress, Sustainable Development in Cruciferous oilseed Crops Production, Wuhan, China, March 25-30, pp 404-407.

Table1. Morphological characters of BPR-541-4

Plant height (cm)	200.0 (200–210)
Days to maturity	135.0 (130–145)
Primary branches/plant(no.)	7.7 (7–9)
Secondary branches/plant (no.)	11.7 (10–13)
Main shoot length (cm)	70.0 (65–73)
Siliquae on main shoot (no.)	41.4 (41–43)
Silique length (cm)	6.9 (5.6–7.0)
Seeds/silique (no.)	16.6 (15.8–17.2)
1000–seeds weight (g)	4.4 (4.2–4.6)
Total dry matter/plant (g)	52.2 (48–56)
Harvest index (%)	30.9 (28–33)
Oil content (%)	42.2 (41–43)
Protein content (%)	19.4 (19.2– 19.8)

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32. NRC106 (IC0582899, INGR10052) and IC210 (IC0582900; INGR10053), Soybean (*Glycine max*) Germplasm, Lines with High Oleic Acid Content and Early Maturity

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The fatty acid composition of conventional soybean cultivars shows 11% palmitic acid (C16:0), 3% stearic acid (C18:0), 23 % oleic acid (C18:1), 53% linoleic acid (C18:2) and 8% linolenic acid (C18:3). Poor oxidative stability of soybean oil has been ascribed to its high unsaturated fatty acids content. Susceptibility of a fatty acid molecule to oxidation increases with the increasing number of unsaturations. Oleic acid with only single double bond is the least susceptible fatty acid of three major unsaturated fatty acids viz. oleic acid, linoleic acid and linolenic acid. This has been substantiated by the study of Fatemi and Hammond (1980) which showed a ratio of 21.6:10.3:1 for the rate of oxidation for linolenic acid, linoleic acid and oleic acid. In vegetable oil industry, the oxidative stability is improved artificially by employing partial hydrogenation; however, this process is not only cost-ineffective but also results in the formation of trans fats, which are atherogenic and diabetogenic (Lichtenstein *et al.*, 2003). Therefore, globally, soybean genotypes with high oleic acid content are being searched and developed which can deliver oil which is oxidatively stable and hence obviates the need of process of partial hydrogenation (Kumar *et al.*, 2004).

At Directorate of Soybean Research, Indore, 2100 germplasm lines were screened for fatty acid profile under the AP Cess funded Scheme using gas chromatography. NRC106 a soybean germplasm line developed at Directorate of Soybean Research by selection from the germplasm line EPS472 was found to contain average oleic acid to the magnitude of 41.9 % over three years at Indore. The genotype is a determinate soybean plant with an average height of

40cm. Days-to-50% flowering and days-to-maturity was 38 and 86 days, respectively. Average number of pods/plant and seeds/pod were 35.3 and 2.65, respectively. Weight of 100 seeds was 11.72g and the yield potential of this genotypes is 21.0 qt/ha. Similarly, IC210, a soybean genotype, has also been zeroed in for high oleic acid content with the average value of 42.7% for this fatty acid over three consecutive years. The germplasm line, which is an indigenous collection, has a determinate plant type with an average height of 43 cm. Days-to-50% flowering and days-to-maturity were 37 and 84 days, respectively. Average number of pods per plant was 30.0, while average number of seeds per pod was 2.7. Weight of 100 seeds was 11.25 g. Agronomic trials at DSR, Indore showed a yield potential of 18.3 q per ha for this genotype. More importantly, both the genotypes were tolerant to any major insect-pest attack. The genotypes are of immense importance for vegetable oil industry as the oil extracted need not be partially hydrogenated for improved oxidative stability.

References

- Fatemi SH and Hammond EG (1980) Analysis of oleate, linoleate and linolenate hydroperoxides in oxidized ester mixtures. *Lipids* 15: 379-385.
- Kumar V, Rani A and Joshi OP (2004) Fatty acid profile of released cultivars of Indian soybean (*Glycine max*) with special reference to identification of comparatively low linolenic and high oleic acid cultivars. *Indian J. Agri. Res.* 74(7): 388-391.
- Lichtenstein AH, Erkkila, AT, Lamarche B, Schwab US, Jalbert SM and Ausman M (2003) Influence of hydrogenated fat and butter on CVD risk factors remnant like particles, glucose, and insulin, blood pressure and C reactive protein. *Atherosclerosis* 171: 97-103.

33. NRC101 (IC0582901; INGR10054) and NRC102 (IC582902; INGR10055), Soybean (*Glycine max*) Germplasm, Free from Kunitz Trypsin Inhibitor Polypeptide

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Kunitz trypsin inhibitor is an anti-nutritional factor present in soybean seed which limits the food uses of soybean. The anti-nutritional factor needs to be inactivated by heat treatment during processing. However, heat treatment insolubilizes the much-valued soy proteins and more importantly, can cause the loss of essential amino acids (Anderson 1992; Rio-Iriarte and Barnes 1996). Besides, the heat inactivation increases the cost of processing. Furthermore, in India, soybean is often recommended to mix with wheat (1:9) for making *chapati* flour. This necessitates the boiling of beans for best possible inactivation of kunitz trypsin inhibitor before grinding with wheat, which is an extra effort at household level and incurs 25% of energy cost at the industry level. The elimination of kunitz inhibitor at genetic level thus will be an important contribution for enhancement of soybean in food uses (Kumar *et al.*, 2010).

The authors have used an exotic germplasm accession PI542044 as the source of null kunitz inhibitor allele and transferred it to early duration popular cultivar Samrat. The selection of *ti* plants in the segregating generation was through SSR marker Satt 228. The homozygous recessive F_8 lines thus developed shows marked improvement in agronomic features over

unadapted germplasm parent. NRC101 and NRC102 flowered in 29 and 33 days and reached harvest maturity in 81 and 89 days, respectively. The yield of NRC101 and NRC102 is 19.5 and 21.9 q/ha, respectively, which is at par with the adapted parent Samrat. NRC101 has a semi-determinate plant-type with 35 cm plant height, while NRC102 has a determinate type of plant with plant height 33.5 cm. Germination percentage of NRC101 and NRC102 was found to be 91 and 82%, respectively. These lines will be very useful as a source of null kunitz inhibitor allele in improved agronomic background as pre-breeding lines. The germplasm lines developed can be very useful in the enhancement of soybean in food uses. Besides, both the genotypes possess the desirable trait of earliness.

References

- Anderson RL (1992) Effect of steaming on soybean proteins and trypsin inhibitors. *J Amer. Oil Chemists' Soc.* **69**: 1170-1176.
- Kumar V, Rani A and Chauhan G S (2010) Nutritional value of soybean. In: G Singh (ed.) *The Soybean: Botany, production and Uses*: CAB International, pp 375-403.
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34. NRC105 (IC0512375; INGR10056), Soybean (*Glycine max*) Germplasm – A Vegetable type

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Consumption of green seeds of soybean seeds at immature stage is an alternative mode of availing health benefits from soybean. The tender green seeds are a rich source of protein, energy, minerals, vitamins and antioxidative value (Rao *et al.*, 2010; Kumar *et al.*, 2010; Shanmugasundaram and Yan 2004) and can be cooked as vegetable similar to the tender seeds of

chick pea and green pea. There are special genotypes which can be used for vegetable purposes. The green seeds of these genotypes are different in taste from conventional soybean types. Vegetable soybean has been consumed in many South-East Asian countries since a long time. It is known as *edamame* in Japan, *mao dou* in China and *poot kong* in Korea,

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however, in India vegetable soybean is a relatively new concept (Kumar *et al* 2003). At Directorate of Soybean Research, soybean genotype NRC105 has been developed for vegetable purpose by selection from the segregating population of ACCGC99009-25-9-1-3GC95024-2-1xR75. The genotype reaches its picking stage of R6 i.e. when the pod cavity is completely filled and the pod shell not yet turned yellow (Fehr *et al* 1971) in 65 days after sowing. The green seeds shelled from the pods at R6 stage are sweet (8% sucrose content) and tender with 100 green seeds weight as high as 60.2g. The genetic potential of pod yield and green seed yield is 8.2 and 3.9 tonnes per ha, respectively.

The plant of NRC105 is determinate in growth with average height of 35.9 cm and flowers in 28 days. Average number of branches per plant, pods per plant and green seeds per pod were: 2-3, 21 and 2.7, respectively. The genotype attains complete maturity in 80 days with 100-seed weight of 33.0 g and an average yield of 16.0 qts/ha. Mature seeds give 82%

germination. The whole pods can be boiled with a pinch of salt and the green seeds can be consumed as snack or cooked similar to the green pea and chick pea at household level. Alternatively, the green seeds can be stored at -25 °C for later use.

References

- Fehr WR, CE Caviness, DT Burmood and Penington (1971) Development description of soybean, *Glycine max* (L) Mer. *Crop Sci.* **11**: 929-931.
- Kumar V, A Rani and OP Joshi (2003) Vegetable soybean: A concept yet to be developed in India. SOPA DIGEST May Issue 18-21.
- Kumar V, A Rani, AK Dixit, D Bhatnagar and GS Chauhan (2009) relative changes in tocopherols, isoflavones, total phenolic content and antioxidative activity in soybean seeds at different reproductive stages. *J Agric. Food Chem.* **57**: 2705-2710.
- Rao MSS, AS Bhagsari and AI Mohamed (2002) Fresh green seed yield and seed nutritional traits of vegetable soybean genotypes. *Crop Sci.* **42**: 1950-1958.
- Shanmugasundaram S and MR Yan (2004) *Proceeding of IV International Soybean Processing and Utilisation Conference Feb 29-March, 5*, pp 915-920.

35. CISA-2(GMS) (IC0538548; INGR10057), Cotton (*Gossypium arboreum*) Germplasm, a Spontaneous Sterile Mutant having Yellow Open Flower with Red Petal Spot and Green Plant Body

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CISA-2 – a spontaneous sterile mutant having yellow flower with red petal and green plant has been registered with Registration No. INGR10057 and National Identity No. IC 0538548. The new GMS line is having open flowering which facilitates easy crossing whereas the earlier reported lines have closed flowers which creates problem in crossing.

The original male sterile mutant plant was observed from the seed multilocation plot CISA-2 (*G. arboreum* race *bengalense*) at Central Institute for Cotton Research, Regional Station, Sirsa during 2000-01. It was maintained by its counter fertile plant having the same traits except sterility. During 2001-01 and 2002-03 its stability was studied. Genetic basis of character was studied in F₂ and BC₁ from cross between male sterile plant observed in CISA 2 and the fertile plant. After its confirmation the genetics

and gene identification was studied in detail by making crosses between identified male sterile plant of CISA 2 and of heterozygous male fertile plants of DS-5 (GMS) having genetic constitution aMS₁ams₁. The segregation ratio of 3:1 was observed and the Chi square test confirmed the 3:1 ratio. Therefore the new GMS line is governed by a different pair of allele named as 'ams₂ams₂' for complete male sterility condition and the heterozygous F₁(male fertile) is designated as aMS₂ams₂.

Among the cultivated cotton species, diploid cottons have wide adaptability and are relatively tolerant to biotic and abiotic stresses. Conventional *desi* hybrids have been developed and released for commercial cultivation; however, significant coverage under these hybrids has not been achieved. Conventional hybrid seed production in *G. arboreum* cotton is not feasible

however, in India vegetable soybean is a relatively new concept (Kumar *et al* 2003). At Directorate of Soybean Research, soybean genotype NRC105 has been developed for vegetable purpose by selection from the segregating population of ACCGC99009-25-9-1-3GC95024-2-1xR75. The genotype reaches its picking stage of R6 i.e. when the pod cavity is completely filled and the pod shell not yet turned yellow (Fehr *et al* 1971) in 65 days after sowing. The green seeds shelled from the pods at R6 stage are sweet (8% sucrose content) and tender with 100 green seeds weight as high as 60.2g. The genetic potential of pod yield and green seed yield is 8.2 and 3.9 tonnes per ha, respectively.

The plant of NRC105 is determinate in growth with average height of 35.9 cm and flowers in 28 days. Average number of branches per plant, pods per plant and green seeds per pod were: 2-3, 21 and 2.7, respectively. The genotype attains complete maturity in 80 days with 100-seed weight of 33.0 g and an average yield of 16.0 qts/ha. Mature seeds give 82%

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35. CISA-2(GMS) (IC0538548; INGR10057), Cotton (*Gossypium arboreum*) Germplasm, a Spontaneous Sterile Mutant having Yellow Open Flower with Red Petal Spot and Green Plant Body

OP Tuteja¹, SK Verma¹, D Monga¹ and P Singh²

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due to small size of the bud and weak peduncle and because of high wages of labour, short duration of flowering period. On the other hand, India became the pioneer country in the world in 1971 with the release of first hybrid H 4 of *G. hirsutum* cotton. The hybrid cotton technology as expected made a quantum increase in production and productivity in the country after the release of intra-hirsutum hybrids. The success in development of hybrids in *desi* cotton depends on availability of male sterile lines and good

combining parent that gives the standard heterosis over the available conventional hybrids. And also the hybrid seed production in *G. arboreum* cotton based on genetic male sterility (GMS) system is more convenient and useful than conventional system of hand emasculation and pollination. Reduction in cost of hybrid seed is also possible by the use of genetic male sterility. Therefore the male sterile line CISA-2(GMS) can be used commercially for production of hybrid seed in *G. arboreum* cotton.

36. ABGMS (CSHN) (IC 0584053; INGR 10058), Cotton (*Gossypium arboreum*) Germplasm, a Genetic Male Sterile Line of Cotton with Curved Stigma

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ABGMS is a genetic male sterile line belonging to race *Latifolium* of *G. hirsutum* cultivated species of cotton. It was developed through mutagen treatment of Abadhita variety at UAS, Dharwad followed by single plant selection and testing for stability of the characters (sterility and curved nature of the stigma) at CICR, Nagpur and UAS, Dharwad. Treatment of 10 kR of gamma rays in combination of 0.2 % ethyl methane sulfonate was the best combination. All the male sterile plants of this line possessed curved stigma.

Morpho-agronomic Characters

ABGMS is a compact plant type with short internodes, small to medium hairy, dark green leaves with one extra- floral nectary on mid rib. The flowers possess light yellow petals with yellow claws and 5 nectaries at the base of the petals. Stigma in sterile plants is

curved while it is straight in the male fertile plants. The bracteoles are free with 5-7 serrations and 2-3 nectaries. Bolls are oval shaped, medium size and densely pitted.

Associated Characters and Cultivation Practices

The curved nature of the stigma is beneficial for tenacity of high density of pollen grains. The unique feature is visible right from the bud stage thus helping in roguing out fertile plants at the early crop stage thereby helpful in maintaining the plant population in hybrid seed production plots.

The fibre quality of this line is very good with 2.5% span length of 26 mm, fibre strength of 21 g/tex at 3.2 mm gauge, ginning percentage of 36% and strength to length ratio of 0.81.

It is also tolerant to bollworm and white fly.

38. CINA - 333 (IC 0583996; INGR10059), Cotton (*Gossypium arboreum*) Germplasm, with High Seed Cotton Yield Potential, High Volume of Capsule/Boll and Long Claw of Petals

Punit Mohan¹, KR Kranthi¹, Harish Kumbhalkar¹ and Anjali Kak²

¹ Central Institute for Cotton Research, Post Bag No. 2, Post Shankar Nagar, Nagpur-440 010, Maharashtra

² National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

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CINA-333 (High Seed Cotton Yield cultivar of *Gossypium arboreum*, race-Bengalense) has been developed at Central Institute for Cotton Research, Nagpur through pedigree method of breeding. Cultivar CINA-333 has

been evaluated in National Evaluation Trial of All India Coordinated Cotton Improvement Project (AICCIP) in 2005-06 at North, Central and South Zones, respectively. The cultivar CINA-333 recorded the highest Seed Cotton

due to small size of the bud and weak peduncle and because of high wages of labour, short duration of flowering period. On the other hand, India became the pioneer country in the world in 1971 with the release of first hybrid H 4 of *G. hirsutum* cotton. The hybrid cotton technology as expected made a quantum increase in production and productivity in the country after the release of intra-hirsutum hybrids. The success in development of hybrids in *desi* cotton depends on availability of male sterile lines and good

combining parent that gives the standard heterosis over the available conventional hybrids. And also the hybrid seed production in *G. arboreum* cotton based on genetic male sterility (GMS) system is more convenient and useful than conventional system of hand emasculation and pollination. Reduction in cost of hybrid seed is also possible by the use of genetic male sterility. Therefore the male sterile line CISA-2(GMS) can be used commercially for production of hybrid seed in *G. arboreum* cotton.

36. ABGMS (CSHN) (IC 0584053; INGR 10058), Cotton (*Gossypium arboreum*) Germplasm, a Genetic Male Sterile Line of Cotton with Curved Stigma

Suman Bala Singh¹, AM Badigannavar², IS Kategiri², BM Khadi² and KR Kranthi¹

¹ Central Institute of Cotton Research, PBNo-2, PO-Shankar Nagar, Nagpur-440 010, Maharashtra

²University of Agricultural Sciences, Dharwad-580 005, Karnataka

(E-mail: sumanbalasingh2005@yahoo.com)

ABGMS is a genetic male sterile line belonging to race *Latifolium* of *G. hirsutum* cultivated species of cotton. It was developed through mutagen treatment of Abadhita variety at UAS, Dharwad followed by single plant selection and testing for stability of the characters (sterility and curved nature of the stigma) at CICR, Nagpur and UAS, Dharwad. Treatment of 10 kR of gamma rays in combination of 0.2 % ethyl methane sulfonate was the best combination. All the male sterile plants of this line possessed curved stigma.

Morpho-agronomic Characters

ABGMS is a compact plant type with short internodes, small to medium hairy, dark green leaves with one extra- floral nectary on mid rib. The flowers possess light yellow petals with yellow claws and 5 nectaries at the base of the petals. Stigma in sterile plants is

curved while it is straight in the male fertile plants. The bracteoles are free with 5-7 serrations and 2-3 nectaries. Bolls are oval shaped, medium size and densely pitted.

Associated Characters and Cultivation Practices

The curved nature of the stigma is beneficial for tenacity of high density of pollen grains. The unique feature is visible right from the bud stage thus helping in roguing out fertile plants at the early crop stage thereby helpful in maintaining the plant population in hybrid seed production plots.

The fibre quality of this line is very good with 2.5% span length of 26 mm, fibre strength of 21 g/tex at 3.2 mm gauge, ginning percentage of 36% and strength to length ratio of 0.81.

It is also tolerant to bollworm and white fly.

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combining parent that gives the standard heterosis over the available conventional hybrids. And also the hybrid seed production in *G. arboreum* cotton based on genetic male sterility (GMS) system is more convenient and useful than conventional system of hand emasculation and pollination. Reduction in cost of hybrid seed is also possible by the use of genetic male sterility. Therefore the male sterile line CISA-2(GMS) can be used commercially for production of hybrid seed in *G. arboreum* cotton.

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Morpho-agronomic Characters

ABGMS is a compact plant type with short internodes, small to medium hairy, dark green leaves with one extra- floral nectary on mid rib. The flowers possess light yellow petals with yellow claws and 5 nectaries at the base of the petals. Stigma in sterile plants is

curved while it is straight in the male fertile plants. The bracteoles are free with 5-7 serrations and 2-3 nectaries. Bolls are oval shaped, medium size and densely pitted.

Associated Characters and Cultivation Practices

The curved nature of the stigma is beneficial for tenacity of high density of pollen grains. The unique feature is visible right from the bud stage thus helping in roguing out fertile plants at the early crop stage thereby helpful in maintaining the plant population in hybrid seed production plots.

The fibre quality of this line is very good with 2.5% span length of 26 mm, fibre strength of 21 g/tex at 3.2 mm gauge, ginning percentage of 36% and strength to length ratio of 0.81.

It is also tolerant to bollworm and white fly.

38. CINA - 333 (IC 0583996; INGR10059), Cotton (*Gossypium arboreum*) Germplasm, with High Seed Cotton Yield Potential, High Volume of Capsule/Boll and Long Claw of Petals

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been evaluated in National Evaluation Trial of All India Coordinated Cotton Improvement Project (AICCIP) in 2005-06 at North, Central and South Zones, respectively. The cultivar CINA-333 recorded the highest Seed Cotton

Yield in South Zone and ranked first in that zone. CINA-333 has been evaluated for Yield Potential and Fibre Quality Traits in Technology Mission on Cotton (TMC MM-1.1) in North, Central and South Zone respectively. The cultivar CINA-333 possesses high numbers of bolls with high volume. The Fruiting bodies/capsules/bolls were originated at very closer distance on sympodial branch. However, the above designated trait cannot be classified under cluster fruiting habit of the genetic stock. Because, fruiting bodies/bolls are not initiated/developed from a single initiation point. As the development of fruiting bodies at a closer distance and plants also retains the high number of bolls upto the maturity, it leads to high seed cotton yield. The genetic stock CINA-333

possesses the following economic characters viz, Average seed cotton yield (125 g/plant), Average boll weight (3.2 to 3.5 g.), Ginning outturn (35.7%), Seed Index (8.2 g.), Lint Index (3.8 g). The fibre properties parameter of the genetic stock CINA-333 are as under.

Staple length (mm)	: 28.5
Uniformity Ratio (%)	: 50.0
Micronaire (µg/inch)	: 4.2
Fibre bundle strength (g/tex)	: 20.3

1. The cultivar CINA- 333 can be utilized in breeding programme for development of high yielding varieties/ hybrids of arboreum cotton.
2. Long claw of petals can be used as a marker trait.

38. SLL-33 (IC 0583997; (INGR10060), Cotton (*Gossypium hirsutum*) Germplasm, with Single Leaf Lobe A Marker Trait

Punit Mohan¹, KR Kranthi¹, Anjali Kak² and BR Rode¹

¹ Central Institute for Cotton Research, Post Bag No. 2, Post Shankar Nagar, Nagpur-440 010, Maharashtra

² National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

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Single leaf lobe is a marker character. Semi and deeply palmate leaf in *Gossypium hirsutum* are classified as okra type similar to the okra plant *Abelmosches esculentus*. However, single leaf lobe with rudimentary accessory lobe has been classified in super okra in *Gossypium*. The Genetic Stock SLL-33 single leaf lobe is having lacinate, sharp shaped without rudimentary accessory lobe. The above designated trait is evolved from super okra leaf lobe and stability of trait was recorded over generations. The genetic stock SLL -33 possesses the following economic characters viz, Average seed cotton yield

(58.3 g/plant), Average boll weight (3.7 g), Ginning outturn (35.7%), Seed Index (8.2 g.), Lint Index (3.8 g). The fibre properties are as under.

Staple length (mm)	: 27.3
Uniformity Ratio	: 58
Micronaire	: 4.7
Fibre bundle strength (g/tex)	: 21.9

Single leaf lobe is a stable marker character and can be utilized in breeding programme for development of varieties and hybrids with unique traits and can be identified easily at morphological level from other varieties and hybrids.

39. YPLL-29 (IC 0583998; INGR10061), Cotton (*Gossypium hirsutum*) Germplasm, with Yellow Pigmented Leaf Lobe a Marker Trait

Punit Mohan¹, KR Kranthi¹, Anjali Kak² and BR Rode¹

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The cultivars/germplasm lines of red or pigmented plant body and leaf lobe are available in *G. hirsutum*, *G. barbadense*, *G. arboreum*, and *G. herbaceum* species. However, the yellow pigmented leaf lobe are

not available in the above four species of *Gossypium*. The yellow pigmentation in genetic stock YPLL-29 appears in the nascent leaf primordial at the time of entry of reproductive phase of the above designated

Yield in South Zone and ranked first in that zone. CINA-333 has been evaluated for Yield Potential and Fibre Quality Traits in Technology Mission on Cotton (TMC MM-1.1) in North, Central and South Zone respectively. The cultivar CINA-333 possesses high numbers of bolls with high volume. The Fruiting bodies/capsules/bolls were originated at very closer distance on sympodial branch. However, the above designated trait cannot be classified under cluster fruiting habit of the genetic stock. Because, fruiting bodies/bolls are not initiated/developed from a single initiation point. As the development of fruiting bodies at a closer distance and plants also retains the high number of bolls upto the maturity, it leads to high seed cotton yield. The genetic stock CINA-333

possesses the following economic characters viz, Average seed cotton yield (125 g/plant), Average boll weight (3.2 to 3.5 g.), Ginning outturn (35.7%), Seed Index (8.2 g.), Lint Index (3.8 g). The fibre properties parameter of the genetic stock CINA-333 are as under.

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Fibre bundle strength (g/tex)	: 20.3

1. The cultivar CINA- 333 can be utilized in breeding programme for development of high yielding varieties/ hybrids of arboreum cotton.
2. Long claw of petals can be used as a marker trait.

38. SLL-33 (IC 0583997; (INGR10060), Cotton (*Gossypium hirsutum*) Germplasm, with Single Leaf Lobe A Marker Trait

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Single leaf lobe is a stable marker character and can be utilized in breeding programme for development of varieties and hybrids with unique traits and can be identified easily at morphological level from other varieties and hybrids.

39. YPLL-29 (IC 0583998; INGR10061), Cotton (*Gossypium hirsutum*) Germplasm, with Yellow Pigmented Leaf Lobe a Marker Trait

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not available in the above four species of *Gossypium*. The yellow pigmentation in genetic stock YPLL-29 appears in the nascent leaf primordial at the time of entry of reproductive phase of the above designated

Yield in South Zone and ranked first in that zone. CINA-333 has been evaluated for Yield Potential and Fibre Quality Traits in Technology Mission on Cotton (TMC MM-1.1) in North, Central and South Zone respectively. The cultivar CINA-333 possesses high numbers of bolls with high volume. The Fruiting bodies/capsules/bolls were originated at very closer distance on sympodial branch. However, the above designated trait cannot be classified under cluster fruiting habit of the genetic stock. Because, fruiting bodies/bolls are not initiated/developed from a single initiation point. As the development of fruiting bodies at a closer distance and plants also retains the high number of bolls upto the maturity, it leads to high seed cotton yield. The genetic stock CINA-333

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Uniformity Ratio (%)	: 50.0
Micronaire (µg/inch)	: 4.2
Fibre bundle strength (g/tex)	: 20.3

1. The cultivar CINA- 333 can be utilized in breeding programme for development of high yielding varieties/ hybrids of arboreum cotton.
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Micronaire	: 4.7
Fibre bundle strength (g/tex)	: 21.9

Single leaf lobe is a stable marker character and can be utilized in breeding programme for development of varieties and hybrids with unique traits and can be identified easily at morphological level from other varieties and hybrids.

39. YPLL-29 (IC 0583998; INGR10061), Cotton (*Gossypium hirsutum*) Germplasm, with Yellow Pigmented Leaf Lobe a Marker Trait

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not available in the above four species of *Gossypium*. The yellow pigmentation in genetic stock YPLL-29 appears in the nascent leaf primordial at the time of entry of reproductive phase of the above designated

genetic stock. The appearances of yellow pigment in leaves are maintained upto harvesting stage. The stability and uniformity of yellow pigmentation characters in leaf is of perpetual nature and it was observed over generations by the repeated course of sowing. The genetic stock YPLL-29 possesses the following economic characters viz, Average seed cotton yield (28.9 g/plant), Average boll weight (2.3 g), Ginning outturn (36.9%), Seed Index (6.5 g), Lint Index (3.5 g) and Boll Volume upto (17.6 cc). The genetic stock

YPLL-29 possesses the following fibre properties.

Staple length (mm)	: 26.3
Uniformity Ratio	: 58.0
Micronaire	: 4.9
Fibre bundle strength (g/tex)	: 17.6

The genetic stock YPLL-29 yellow pigmented leaf lobe (Marker character) can be used in breeding programme for development of varieties/hybrids, which can be identified and distinguished from other cultivars of *Gossypium* at morphological level.

40. CSLL-59 (IC 0583999; INGR 10062), Cotton (*Gossypium hirsutum*) Germplasm, with Cup Shaped Leaf Lobe a Marker Trait

Punit Mohan¹, KR Kranthi¹, Anjali Kak² and BR Rode¹

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The Genetic Stock CSLL-59 (*Gossypium hirsutum*, race: *Latifolium*) possesses 3-5 lobed palmately broad cup shaped leaf. At flowering stage the peripheral region of leaf lobe gradually lead to vertical growth. The central portion of leaf lobe maintained the horizontal shape. Consequently the central lobe of leaf develop a depression and zone of elongation forming a cup like shape. The cup shape leaf lobe is unique and novel marker character and stable over generations. The above genetic stock possesses the economic characters viz., Average seed cotton yield (32.9 g/plant), Average boll weight (3.5 g), Ginning outturn (36.8%), Seed Index (10.4 g), Lint Index (5.8 g), Boll volume upto (21.2

cc). The fibre properties parameter of the genetic stock CSLL-59 are as under.

Staple length (mm)	: 19.5
Uniformity Ratio	: 53
Micronaire	: 6.6
Fibre bundle strength (g/tex)	: 15.3

Cup shape leaf lobe is a marker trait and can be utilized in breeding programme for development of promising distinct varieties and hybrids with specific unique traits. The cup shape leaf lobes are unique, novel and distinct character. Therefore, further investigations are needed to study reactions to pests and diseases.

41. PT-2 (INGR 10063; IC 0584318), Shisham (*Dalbergia sissoo* Roxb.) Germplasm with Straightness of Main Stem with Few and Small Secondary Branches

K Gupta, SP Ahlawat, RV Kumar and A Datta

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(E-mail: vkgup@rediffmail.com)

Shisham is known internationally as a premier timber species of rose wood genus generally, shisham has spreading type canopy which suppress yield of lower storey crops significantly in agroforestry system as well as reduce the price of wood. At National Research Centre for Agroforestry (NRCAF), Jhansi, efforts were made to select germplasm which have straight bole with high wood volume for better return

in agroforestry system as well as in pure plantation. To achieve the goal survey was made in January 1994 of Bundelkhand region for selection of plus trees and to collect their seeds. Selection was made on the basis of straightness, fast growth and clear bole height. Total 35 collections were made. Out of collected germplasm, 12-month old seedlings of 14 plus trees, two composites and one selection of

genetic stock. The appearances of yellow pigment in leaves are maintained upto harvesting stage. The stability and uniformity of yellow pigmentation characters in leaf is of perpetual nature and it was observed over generations by the repeated course of sowing. The genetic stock YPLL-29 possesses the following economic characters viz, Average seed cotton yield (28.9 g/plant), Average boll weight (2.3 g), Ginning outturn (36.9%), Seed Index (6.5 g), Lint Index (3.5 g) and Boll Volume upto (17.6 cc). The genetic stock

YPLL-29 possesses the following fibre properties.

Staple length (mm)	: 26.3
Uniformity Ratio	: 58.0
Micronaire	: 4.9
Fibre bundle strength (g/tex)	: 17.6

The genetic stock YPLL-29 yellow pigmented leaf lobe (Marker character) can be used in breeding programme for development of varieties/hybrids, which can be identified and distinguished from other cultivars of *Gossypium* at morphological level.

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41. PT-2 (INGR 10063; IC 0584318), Shisham (*Dalbergia sissoo* Roxb.) Germplasm with Straightness of Main Stem with Few and Small Secondary Branches

K Gupta, SP Ahlawat, RV Kumar and A Datta

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YPLL-29 possesses the following fibre properties.

Staple length (mm)	: 26.3
Uniformity Ratio	: 58.0
Micronaire	: 4.9
Fibre bundle strength (g/tex)	: 17.6

The genetic stock YPLL-29 yellow pigmented leaf lobe (Marker character) can be used in breeding programme for development of varieties/hybrids, which can be identified and distinguished from other cultivars of *Gossypium* at morphological level.

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41. PT-2 (INGR 10063; IC 0584318), Shisham (*Dalbergia sissoo* Roxb.) Germplasm with Straightness of Main Stem with Few and Small Secondary Branches

K Gupta, SP Ahlawat, RV Kumar and A Datta

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Shisham is known internationally as a premier timber species of rose wood genus generally, shisham has spreading type canopy which suppress yield of lower storey crops significantly in agroforestry system as well as reduce the price of wood. At National Research Centre for Agroforestry (NRCAF), Jhansi, efforts were made to select germplasm which have straight bole with high wood volume for better return

in agroforestry system as well as in pure plantation. To achieve the goal survey was made in January 1994 of Bundelkhand region for selection of plus trees and to collect their seeds. Selection was made on the basis of straightness, fast growth and clear bole height. Total 35 collections were made. Out of collected germplasm, 12-month old seedlings of 14 plus trees, two composites and one selection of

Haryana Agricultural University, Haryana were planted along with control in two sites (cultivated land and degraded land) at Central Farm of NRCAF, Jhansi. Data on straightness was recorded on 5 point scaling (1= highly crooked, 5 = maximum straight) at the age of 2.5 years and visually observed upto 9.5 years. Data on tree height and diameter at breast height were recorded at the age of 9.5 years. Bole volume was calculated as per volume equation.

Morpho-agronomic Characteristics

PT-2, selected near Saprar Dam, tehsil Mahuranipur, district Jhansi, is highly straight germplasm. This progeny obtained 3.59 and 4.42 score out of 5 at site I (cultivated land) and site II (degraded land), respectively (Table 1). While local race obtained 2.12 and 2.00 score in two sites, respectively. Percentage superiority in term of straightness was 69 and 121 at two sites, respectively. Wood volume estimated at the age of 9.5 year. PT-2 is 69% and 67% superior over

Table 1. Straightness scoring of clean bole of PT-2 at 2.5 years age

Year check	PT-2	Check variety	% increase over
1998 at site I	3.59	2.12	69.34
1998 at site II	4.42	2.00	121.00

Table 2. Bole volume (m³ha⁻¹) of PT-2 at 9.5 years age

Year	PT-2	Check variety	% increase over check
1998 at site I	43.44	25.71	68.96
1998 at site II	20.59	12.31	67.26

local at site I and site II, respectively (Table 2)

Associated Characters and Cultivated Practices

Besides this, branches are short and less compared to local race. Crown is cylindrical, butt and pockets are absent. Bark is semi-smooth with shallow longitudinal fissures and dark in colour.

PT-2 is promising germplasm of shisham in Agroforestry system to obtain more return from the system as a whole.

42. NS/2009/042 (IC0571819; INGR10064), Bottle gourd (*Lagenaria siceraria* L.) Germplasm, a Rare and Unique Bottle Gourd Accession with Spindle Shaped Fruits with Hard Durable Rind

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Bottle gourd (*Lagenaria siceraria* L.) is one of the popular cucurbitaceous vegetable crops grown in India and other parts of the world. The bottle gourd is a warm season crop and grows best in tropical humid climate. Andhra Pradesh is endowed with rich genetic diversity in bottle gourd especially with varied fruit shape and size. While the immature fruits are used as a vegetable by the general population, the dried fruit shells of suitable shape and size apt for different household purposes are in extensive use exclusively by the tribal communities. The extent of available diversity for fruit shape in bottle gourd in India and elsewhere is reported in literature. During a collection mission undertaken in February 2009 in the Telangana region of Andhra Pradesh, the survey team stumbled upon a bottle gourd landrace of rare occurrence in Nagaram, Parakala Mandal of Warangal district having spindle shaped fruits. This landrace vernacularly referred as *Anapakaya/ Sorakaya* (Sivaraj *et al.*, 2009) has been

assigned a collector number NS/2009/042 and an indigenous collector number IC571819.

The morpho-agronomic description is as follows: An annual, monoecious climber with robust, longitudinally furrowed stem, hairy, gland dotted; tendrils bifid; leaves 20-25 cm long, petiole with two glands at joints, lamina ovate with cordate base, dentate, lobed; flowers solitary axillary, calyx tube campanulate, petals 5, free, white, woolly, 3-5 × 2.5-4.0 cm; male flowers on long peduncles, filaments 3, free, anthers white; female flowers on short robust peduncles, stigma-3, bifid. Fruit exhibits a unique spindle shape with hard durable rind (5.2 mm thickness). Other fruit and seed characters of the germplasm accession are: fruit length (33.0 cm), fruit circumference (51.0 cm), fruit width (25.3 cm), seed length (17.3 mm), seed width (6.3 mm) and 100-seed mass (13.5 g). Seeds are many, compressed, whitish grey in colour. Young fruits are green in colour turning to yellow and then to grey on maturity. The general

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42. NS/2009/042 (IC0571819; INGR10064), Bottle gourd (*Lagenaria siceraria* L.) Germplasm, a Rare and Unique Bottle Gourd Accession with Spindle Shaped Fruits with Hard Durable Rind

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recommended package of practices for bottle gourd could be followed for cultivation of this particular accession as well.

References

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Sivaraj N, SR Pandravada, V Kamala, N Sunil and KS Varaprasad (2009) IC 571819 – A unique bottle gourd with spindle-shaped fruits. *ICAR News* **15(4)**: 4.

43. Coll. No. V 90/P-92 (IC266417; INGR10065), a Black pepper (*Piper nigrum* L.) Germplasm with Oval Shaped Berries

Latha M, KC Velayudhan, VS Sujatha, C Rajalakshmi, S Mani and Z Abraham

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Black pepper (*Piper nigrum* L.) with a monocentric origin in a limited geographic area lying in tropical region with high rainfall on the western slopes and plateau region of southern Western Ghats has a short history as a crop but has longer commercial history as a forest produce. Cultivar diversity is richest in Kerala followed by Karnataka. Around hundred cultivars have been reported from southern region of India. IC266417, collected from Ithikkara, Kollam, Kerala, India, a member of race-1 (*Kariyilanchi*) is registered for its unique oval shaped berries. The collections were divided subjectively into two races (race-1 and race-2) based on two associated characters such as berry shape and pace of colour change in ripening berries. On the basis of berry shape and the time taken for berry colour change in ripening berries, two distinct cultivar groups such as oval and spherical berry bearing types were identified. The size of berry varied in both cultivar groups. The first group hailing from southern Kerala contained seven accessions with oval berries, more pronounced and uniform yellow colour of mature berries and uniformly larger berries. The large berry size is commercially a useful character. The second group included ninety six

accessions with round berry, less uniform yellow colour in mature berries and with highly varying berry size from small to large. This group is uniformly distributed all over in the pepper growing areas in Kerala and Karnataka and as wild in forest areas. The two races identified were named as '*Kariyilanchi*' for race-1 and '*Karimunda*' for the race-2 as these were representative common cultivars of black pepper in the region. Among these two races, race 2 is more common than race-1. The accession IC266417 is characterized by climbing plant growth habit, polymorphic branching type with production of many runners, glabrescent stem, horizontal lateral branches, ovate-elliptic leaves, wavy leaf margin, campylodromous leaf venation pattern, leaf hairs present all over, absence of leaf scales, flowers sessile and arranged free on spikes, filiform, less compact, glabrescent and fragrant spikes with medium sized berries turning slowly from green to red on maturity. The vine is 150 cm high, spike length 7.1 cm, 3 spikes/lateral branch, 24 spikes/vine, 5 bisexual flowers/spike, total berry weight 204 g, dry weight of berry 28.19%, 100 berry weight 10.75 g and volume 10.75 g.

44. YCMS-12A (IC0583131; INGR10066), a Sweet Pepper (*Capsicum annuum*) Germplasm with Male Sterility (Genetic), Bell Shaped Fruits and Non-Pungent Background

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Male sterile plants of hot pepper (ms-12) were obtained from PAU, Ludhiana in 2007 and planted at experimental

farm of IARI, Regional Station, Katrain. This line contains ms-509 gene (Pochard, 1970) which is recessive nuclear

recommended package of practices for bottle gourd could be followed for cultivation of this particular accession as well.

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farm of IARI, Regional Station, Katrain. This line contains ms-509 gene (Pochard, 1970) which is recessive nuclear

gene controlling male sterility. The sterile plants were crossed with a number of lines of sweet pepper and a paprika variety viz., KtPl-19. An organoleptic comparison for pungency was carried out. It was found that one cross viz., ms-12 X Yellow Capsicum was the least pungent among the array of crosses. The second filial generation (F_2) seed of this cross was obtained by selfing. The F_2 generation was grown in glasshouse and screened for male sterility with help of microscopic test for pollen viability using acetocarmine stain. Out of 261 plants 63 were found to be male sterile. These sterile plants were pollinated with pollen of Yellow Capsicum (the recipient parent). Upon fruit setting an organoleptic test was again carried out to identify non-pungent plants if any. A total of 6 non-pungent plants were isolated out of which 3 plants bore bell shaped 3-4 lobed fruits and 3 plants had conical fruits. One of the 3 plants with bell shaped fruits had greener and larger fruits with greater resemblance with the recurrent parent. This single plant was used for further maintenance of male sterility in bell pepper background. This plant is now being maintained with the recurrent parent i.e., Yellow Capsicum since 2007. Two crops were taken each year, one in open field during summers and another in glass house during winters.

Morpho-agronomic characters

The plants bear a total of 14-16 pendant dark green 3-4 lobed fruits with an average weight of 70-75g. The average height of the plants is 45-55 cm. Plants possess moderate branching habit. In 2009 it was

found that enough bee visit is there on flowers and each plant produces on an average more than 2500 seed amounting to more than 7 g seeds/plant, thus presenting a good prospect of hybrid seed production without deploying human labour for emasculation and pollination.

Associated Characters and Cultivation Practices

The fruits turn yellow on ripening, therefore, this line can be used for breeding hybrids with coloured fruits. The line is moderately tolerant to water logging and resistant to fusarium wilt. The nursery is sown in March in hills and transplanted to main field in May. It comes to flowering after 40-45 days of transplanting and first harvesting can be done after 65 days of transplanting. Ripened or coloured fruits can be harvested after 85 days of transplanting. Crop duration is longer and yield is higher under protected cultivation. The male sterile line can be multiplied using tissue culture technique also.

References

- Breuil G and E Pochard (1975) Hybrid seed production in the pepper 'Lamuyo-INRA' with the male sterile mutant *ms 509*. *Ann Amelior Plant (Paris)* **25**: 399-409.
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45. IIHGR-5, IIHR-84-7-11 (IC0584125; INGR10067), a Gladioli (*Gladiolus grandiflorous*) Germplasm with floret colour: (Based on R.H.S. colour chart) Purple-violet (82.C) having Red-Purple (72.B) margin with Yellow-Green (154.D) blotch

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46. IIHRG-9, IIHR-87-7-11 (IC0584126; INGR10068), a Gladioli (*Gladiolus grandiflorous*) Germplasm with Floret Colour: (Based on RHS Colour chart) Yellow (4.C) having Yellow (6.C) Lower Lip with Red (39.A) blotch

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47. IIHRG-10, IIHR-87-22-1 (IC0584127; INGR10069), a Gladioli (*Gladiolus grandiflorous*) germplasm, with Resistance to *Fusarium* Wilt Disease cause by *Fusarium oxysporum* f.sp.*gladioli* race 1. Floret colour: (Based on R.H.S. Colour Chart) Red (46.D) having Red (45.B) margin and White line on tepals with Yellow (2.C) blotch

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48. IIHRP-2-28-1 (IC0584135; INGR10070) and IIHRP-3-18-2 (IC0584136; INGR10071) Rose (*Rosa hybrida*) Germplasm, with Shining Foliage, Unique Bicolor consisting Vermillion Red Shading towards Orient Pink; Less Thorns, Straight Stalk of Cut Flower Quality, Light Pink Flowers with Pointed Bud and High Centre

Tejaswini and Dhananjay MV

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Rose is the most admired and adored aristocratic flower in India. Even before the entry of cut flower industry rose was being cultivated in public and private gardens. Present day commercial cultivation of cut roses is dependent upon varieties being imported from well established commercial breeders of temperate countries. Rose breeding program in India was concentrated on aesthetic appeal of flowers. With the expanding commercial cultivation of roses, the rose breeding objectives in India has shifted from garden roses to commercial cut flowers. Rose breeding program at Indian Institute of Horticulture Research, has resulted several progenies that are being evaluated for various desired characters. With the commercial cultivation of roses, it is essential to protect important lines developed in breeding program and needs to be safeguarded by registration.

IIHRP-2-28-1: In flower crops color combinations of flower and foliage adds to the aesthetic value of a genotype. IIHRP-2-28-1 was selected particularly for its aesthetic value with attractive flower color along with glossy foliage. It is a selected seedling from half sib progeny population of Folklore. This particular genotype is of importance as it has exhibited good yield capacity and with less number of thorns that are important features for cut flowers. Attractive

Table 1. Colours of selected genotypes on various petal parts according to RHS colour chart

Genotype	Front	Back	Tip	Centre	Basal	Colour group
IIHRP-2.28.1	41B	56C	41B	41B	158C	Red&Purple
IIHRP-3.18.2	155B	155B	155B	155B	155B	White

Table 2. Morphological characters of selected rose genotypes of IIHR in comparison with commercial varieties

Lines/ varieties	Stalk length	Bud length	Flower length	Flower width	Pedicle length	Petal Number
IIHRP-2.28.1	61.6	3.8	4.7	9.8	5.9	43.6
IIHRP-3.18.2	57.6	4.7	5.0	10.7	10.1	35.1
Carvetty	50.1	3.8	4.4	8.6	7.1	20.0
Diplomat	71.0	4.3	4.6	10.0	9.3	33.2
First Red	50.9	3.4	3.6	7.4	7.1	29.9
Konfetty	59.4	3.4	3.6	8.0	5.6	26.2
CD @5%	0.7	0.6	0.7	1.5	2.3	16.0
CV	0.6	12.8	8.4	13.4	15.5	16.5

Table 3. Number of thorns on various selected rose lines in comparison with commercial varieties (Thorns/10cm stalk)

Lines/ Varieties	Thorns (big)	Thorns (small)
IIHRP-3.18.2	0.8	0.0
IIHRP-2.28.1	2.0	0.0
Carvetty	4.0	4.4
Diplomat	10.6	8.0
First red	4.6	0.0
Konfetty	7.2	0.0
CD @5%	4.9	21.0

flower color and shining foliage with good branching pattern would make it a good option for production of pot plants that can be taken for interior as well as for landscape ornamental value.

Flowers of IIHRP-2-28-1 are bicolor and attractive. The advanced breeding line of rose IIHRP-2-28-1 is registered with NBPGR, with a registration number INGR no. 10070 for its unique bicolor consisting vermilion red shading towards orient pink with dark green glossy foliage. Flowers are born in clusters with long stalk. Flowers are of medium size with

a flower bud length of 4.50-5 cm, with number of petals ranging from 35 to 40.

IIHRP-3-18-2: It is a selection from induced mutants of the variety 'Dr. GS Randhwa' at 80 Gy. IIHRP-3-18-2 was selected for its straight stalk and less thorns. It has exhibited high yield capacity along with qualities of cut flower. Attractive pink colored flower with pointed buds makes it viable for its potential utility as a cut flower. IIHRP-3-18-2 is registered with NBPGR, for its straight stalk and less thorns with the registration number, INGR No. 10071.

50. IIHRP-13 (IC0574579; INGR10072) Rose (*Rosa hybrida*) Germplasm with Fragrance and Field Tolerance to Thrips

Tejaswini, Dhananjay MV, Jansi Rani B and RN Bhat

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Thrips (*Scriptothrips dorsalis*) have become a major production constraint in rose cultivation. Characteristic feature of rose fragrance is being lost in modern varieties. IIHRP-13 is a fragrant rose line registered for its unique characteristics of fragrance and field tolerance to thrips. Salient characteristic features of the genotypes are i) The genotype has field tolerance to thrips and fragrance ii) IIHRP-13 was found promising for cultivation in open field for loose flower purpose (Table 1) iii) It has red colored fragrant flowers (RHS colour chart 61 C) under red purple category.

Rose breeding program at IIHR concentrates on developing varieties for commercial production having pest tolerance. As an outcome of this breeding program, out of several advanced lines developed, IIHR P-13 has been identified as superior genotype for higher yield over the ruling checks with filed tolerance to thrips. It has all the desired traits for cultivation in

open field. IIHRP-13 is a selection from half sib progenies of rose variety 'Red Chief'.

Screening for thrips was done in polyhouse condition during maximum infestation under highest threshold level of thrips incidence. The accessions were scored in 1-10 scale, with 1 being highly resistant and 10 as highly susceptible based on severity of thrips damage. IIHRP-13 along with other advanced lines and two commercial varieties namely First Red and Grand gala as checks were scored for damage on various plant parts and also for whole plant.

Based on different plant parts of rose screened for resistance to thrips, *S.dorsalis*, IIHRP-13 showed significantly lower damage with reference to leaves (2.33), buds (2.66) and flowers (1.33). IIHRP-13 was considered to be field tolerant to thrips and with fragrant red flowers its registered as a valuable genetic stock.

Table1. Pooled means for yield and related characters

Genotypes	Plant height (cm)	No. of branches	Flower length (cm)	Flower diameter (cm)	Number of petals	Shelf life (days)	Pinch flower yield/plant/year
Wobourn Gold	77.4	4.87	4.41	8.29	25.89	4.70	123.2
IIHRP-15	83.7	5.31	4.02	6.44	23.33	5.33	136.6
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Mulla Hybrid	93.7	4.19	5.72	11.14	54.56	3.78	52
Sophia Laurens	112.5	3.91	5.31	8.89	40.44	3.11	52
CD@5%	6.023	0.73	0.38	0.53	2.64	0.57	8.62
CD@1%	8.44	1.02	0.53	0.75	3.70	0.80	12.1

gene controlling male sterility. The sterile plants were crossed with a number of lines of sweet pepper and a paprika variety viz., KtPl-19. An organoleptic comparison for pungency was carried out. It was found that one cross viz., ms-12 X Yellow Capsicum was the least pungent among the array of crosses. The second filial generation (F_2) seed of this cross was obtained by selfing. The F_2 generation was grown in glasshouse and screened for male sterility with help of microscopic test for pollen viability using acetocarmine stain. Out of 261 plants 63 were found to be male sterile. These sterile plants were pollinated with pollen of Yellow Capsicum (the recipient parent). Upon fruit setting an organoleptic test was again carried out to identify non-pungent plants if any. A total of 6 non-pungent plants were isolated out of which 3 plants bore bell shaped 3-4 lobed fruits and 3 plants had conical fruits. One of the 3 plants with bell shaped fruits had greener and larger fruits with greater resemblance with the recurrent parent. This single plant was used for further maintenance of male sterility in bell pepper background. This plant is now being maintained with the recurrent parent i.e., Yellow Capsicum since 2007. Two crops were taken each year, one in open field during summers and another in glass house during winters.

Morpho-agronomic characters

The plants bear a total of 14-16 pendant dark green 3-4 lobed fruits with an average weight of 70-75g. The average height of the plants is 45-55 cm. Plants possess moderate branching habit. In 2009 it was

found that enough bee visit is there on flowers and each plant produces on an average more than 2500 seed amounting to more than 7 g seeds/plant, thus presenting a good prospect of hybrid seed production without deploying human labour for emasculation and pollination.

Associated Characters and Cultivation Practices

The fruits turn yellow on ripening, therefore, this line can be used for breeding hybrids with coloured fruits. The line is moderately tolerant to water logging and resistant to fusarium wilt. The nursery is sown in March in hills and transplanted to main field in May. It comes to flowering after 40-45 days of transplanting and first harvesting can be done after 65 days of transplanting. Ripened or coloured fruits can be harvested after 85 days of transplanting. Crop duration is longer and yield is higher under protected cultivation. The male sterile line can be multiplied using tissue culture technique also.

References

- Breuil G and E Pochard (1975) Hybrid seed production in the pepper 'Lamuyo-INRA' with the male sterile mutant *ms 509*. *Ann Amelior Plant (Paris)* **25**: 399-409.
- Csillery G, L Uncini and A Moor (1987) Cross-pollination experiments with bees in Italy and Hungary. *Capsicum Newsl.* **6**: 30-32.
- Pochard E (1970) Obtaining three new male sterile mutants of pepper (*C. annuum*) through application of mutagens on monoploid material. *Eucarpia* (Versailles, France). pp. 93-95.
- Woong Yu L (1985) Inheritance of cytoplasmic male sterility in pepper (*Capsicum annuum* L.). Kyung Hee University, South Korea. *M.Sc. Thesis*, pp 1-43.

45. IIHGR-5, IIHR-84-7-11 (IC0584125; INGR10067), a Gladioli (*Gladiolus grandiflorous*) Germplasm with floret colour: (Based on R.H.S. colour chart) Purple-violet (82.C) having Red-Purple (72.B) margin with Yellow-Green (154.D) blotch

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46. IIHRG-9, IIHR-87-7-11 (IC0584126; INGR10068), a Gladioli (*Gladiolus grandiflorous*) Germplasm with Floret Colour: (Based on RHS Colour chart) Yellow (4.C) having Yellow (6.C) Lower Lip with Red (39.A) blotch

T Manjunatha Rao, T Janakiram, SS Negi, MV Dhananjaya, Sangama and D Vamana Naik

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- 47. IIHRG-10, IIHR-87-22-1 (IC0584127; INGR10069), a Gladioli (*Gladiolus grandiflorous*) germplasm, with Resistance to *Fusarium* Wilt Disease cause by *Fusarium oxysporum f.sp.gladioli* race 1. Floret colour: (Based on R.H.S. Colour Chart) Red (46.D) having Red (45.B) margin and White line on tepals with Yellow (2.C) blotch**

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Rose is the most admired and adored aristocratic flower in India. Even before the entry of cut flower industry rose was being cultivated in public and private gardens. Present day commercial cultivation of cut roses is dependent upon varieties being imported from well established commercial breeders of temperate countries. Rose breeding program in India was concentrated on aesthetic appeal of flowers. With the expanding commercial cultivation of roses, the rose breeding objectives in India has shifted from garden roses to commercial cut flowers. Rose breeding program at Indian Institute of Horticulture Research, has resulted several progenies that are being evaluated for various desired characters. With the commercial cultivation of roses, it is essential to protect important lines developed in breeding program and needs to be safeguarded by registration.

IIHRP-2-28-1: In flower crops color combinations of flower and foliage adds to the aesthetic value of a genotype. IIHRP-2-28-1 was selected particularly for its aesthetic value with attractive flower color along with glossy foliage. It is a selected seedling from half sib progeny population of Folklore. This particular genotype is of importance as it has exhibited good yield capacity and with less number of thorns that are important features for cut flowers. Attractive

Table 1. Colours of selected genotypes on various petal parts according to RHS colour chart

Genotype	Front	Back	Tip	Centre	Basal	Colour group
IIHRP-2.28.1	41B	56C	41B	41B	158C	Red&Purple
IIHRP-3.18.2	155B	155B	155B	155B	155B	White

Table 2. Morphological characters of selected rose genotypes of IIHR in comparison with commercial varieties

Lines/ varieties	Stalk length	Bud length	Flower length	Flower width	Pedicle length	Petal Number
IIHRP-2.28.1	61.6	3.8	4.7	9.8	5.9	43.6
IIHRP-3.18.2	57.6	4.7	5.0	10.7	10.1	35.1
Carvetty	50.1	3.8	4.4	8.6	7.1	20.0
Diplomat	71.0	4.3	4.6	10.0	9.3	33.2
First Red	50.9	3.4	3.6	7.4	7.1	29.9
Konfetty	59.4	3.4	3.6	8.0	5.6	26.2
CD @5%	0.7	0.6	0.7	1.5	2.3	16.0
CV	0.6	12.8	8.4	13.4	15.5	16.5

Table 3. Number of thorns on various selected rose lines in comparison with commercial varieties (Thorns/10cm stalk)

Lines/ Varieties	Thorns (big)	Thorns (small)
IIHRP-3.18.2	0.8	0.0
IIHRP-2.28.1	2.0	0.0
Carvetty	4.0	4.4
Diplomat	10.6	8.0
First red	4.6	0.0
Konfetty	7.2	0.0
CD @5%	4.9	21.0

flower color and shining foliage with good branching pattern would make it a good option for production of pot plants that can be taken for interior as well as for landscape ornamental value.

Flowers of IIHRP-2-28-1 are bicolor and attractive. The advanced breeding line of rose IIHRP-2-28-1 is registered with NBPGR, with a registration number INGR no. 10070 for its unique bicolor consisting vermilion red shading towards orient pink with dark green glossy foliage. Flowers are born in clusters with long stalk. Flowers are of medium size with

a flower bud length of 4.50-5 cm, with number of petals ranging from 35 to 40.

IIHRP-3-18-2: It is a selection from induced mutants of the variety 'Dr. GS Randhwa' at 80 Gy. IIHRP-3-18-2 was selected for its straight stalk and less thorns. It has exhibited high yield capacity along with qualities of cut flower. Attractive pink colored flower with pointed buds makes it viable for its potential utility as a cut flower. IIHRP-3-18-2 is registered with NBPGR, for its straight stalk and less thorns with the registration number, INGR No. 10071.

50. IIHRP-13 (IC0574579; INGR10072) Rose (*Rosa hybrida*) Germplasm with Fragrance and Field Tolerance to Thrips

Tejaswini, Dhananjay MV, Jansi Rani B and RN Bhat

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(E-mail: tejaswini@ihr.ernet.in)

Thrips (*Scriptothrips dorsalis*) have become a major production constraint in rose cultivation. Characteristic feature of rose fragrance is being lost in modern varieties. IIHRP-13 is a fragrant rose line registered for its unique characteristics of fragrance and field tolerance to thrips. Salient characteristic features of the genotypes are i) The genotype has field tolerance to thrips and fragrance ii) IIHRP-13 was found promising for cultivation in open field for loose flower purpose (Table 1) iii) It has red colored fragrant flowers (RHS colour chart 61 C) under red purple category.

Rose breeding program at IIHR concentrates on developing varieties for commercial production having pest tolerance. As an outcome of this breeding program, out of several advanced lines developed, IIHR P-13 has been identified as superior genotype for higher yield over the ruling checks with field tolerance to thrips. It has all the desired traits for cultivation in

open field. IIHRP-13 is a selection from half sib progenies of rose variety 'Red Chief'.

Screening for thrips was done in polyhouse condition during maximum infestation under highest threshold level of thrips incidence. The accessions were scored in 1-10 scale, with 1 being highly resistant and 10 as highly susceptible based on severity of thrips damage. IIHRP-13 along with other advanced lines and two commercial varieties namely First Red and Grand gala as checks were scored for damage on various plant parts and also for whole plant.

Based on different plant parts of rose screened for resistance to thrips, *S.dorsalis*, IIHRP-13 showed significantly lower damage with reference to leaves (2.33), buds (2.66) and flowers (1.33). IIHRP-13 was considered to be field tolerant to thrips and with fragrant red flowers its registered as a valuable genetic stock.

Table1. Pooled means for yield and related characters

Genotypes	Plant height (cm)	No. of branches	Flower length (cm)	Flower diameter (cm)	Number of petals	Shelf life (days)	Pinch flower yield/plant/year
Wobourn Gold	77.4	4.87	4.41	8.29	25.89	4.70	123.2
IIHRP-15	83.7	5.31	4.02	6.44	23.33	5.33	136.6
Red Chief	80.8	5.26	5.69	8.33	31.00	5.55	52
IIHRP-13	111.9	5.15	5.02	8.62	34.56	4.78	82
Mulla Hybrid	93.7	4.19	5.72	11.14	54.56	3.78	52
Sophia Laurens	112.5	3.91	5.31	8.89	40.44	3.11	52
CD@5%	6.023	0.73	0.38	0.53	2.64	0.57	8.62
CD@1%	8.44	1.02	0.53	0.75	3.70	0.80	12.1

flower color and shining foliage with good branching pattern would make it a good option for production of pot plants that can be taken for interior as well as for landscape ornamental value.

Flowers of IIHRP-2-28-1 are bicolor and attractive. The advanced breeding line of rose IIHRP-2-28-1 is registered with NBPGR, with a registration number INGR no. 10070 for its unique bicolor consisting vermilion red shading towards orient pink with dark green glossy foliage. Flowers are born in clusters with long stalk. Flowers are of medium size with

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open field. IIHRP-13 is a selection from half sib progenies of rose variety 'Red Chief'.

Screening for thrips was done in polyhouse condition during maximum infestation under highest threshold level of thrips incidence. The accessions were scored in 1-10 scale, with 1 being highly resistant and 10 as highly susceptible based on severity of thrips damage. IIHRP-13 along with other advanced lines and two commercial varieties namely First Red and Grand gala as checks were scored for damage on various plant parts and also for whole plant.

Based on different plant parts of rose screened for resistance to thrips, *S.dorsalis*, IIHRP-13 showed significantly lower damage with reference to leaves (2.33), buds (2.66) and flowers (1.33). IIHRP-13 was considered to be field tolerant to thrips and with fragrant red flowers its registered as a valuable genetic stock.

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Sophia Laurens	112.5	3.91	5.31	8.89	40.44	3.11	52
CD@5%	6.023	0.73	0.38	0.53	2.64	0.57	8.62
CD@1%	8.44	1.02	0.53	0.75	3.70	0.80	12.1

In India, Rose (*Rosa hybrida*) is one of the major flower crops grown in open field cultivation. Commercially rose is cultivated for its flowers and for production of rose oil, rose water, attar and gulkand. Thrips (*Scriptothrips dorsalis*) has become a major production constraint in rose cultivation. With the development of new rose varieties, characteristic feature of rose fragrance is being lost in modern varieties. Rose breeding program at Indian Institute of Horticulture Research has focused objective in combining biotic resistance with attractive color and fragrance. As an outcome of on going rose breeding projects at our institute, a promising line IIHRP-13 has been identified having moderate resistance to thrips and with fragrant flowers. IIHRP-13 is a selection from half sib progenies of rose genotype Red Chief. Evaluation of the genotype in open field and poly house has indicated moderate resistance to thrips. This line has been registered with NBPGR, New Delhi, as a valuable genetic stock with a registration number INGR No. 10072.

Screening for thrips was done in polyhouse condition during maximum infestation under highest threshold level of thrips incidence. The accessions were scored in 1-10 scale, with 1 being highly resistant and 10 as highly susceptible based on severity of thrips damage. IIHRP-13 along with other advanced lines and two commercial varieties namely First Red and Grand gala as checks were scored for damage on various plant parts and also for whole plant. Based

Table 2. Evaluation of IIHRP-13 in comparison with commercial varieties for thrips incidence

Advanced line	Damage Rating		
	Leaves	Buds	Flowers
IIHRP-13	2.33 (1.52)	2.66 (1.62)	1.33 (1.14)
First Red	5.66 (2.38)	5.66 (2.38)	2.66 (1.62)
Grand gala	7.00 (2.82)	8.00 (2.82)	4.33 (2.06)
CV (%)	9.5	11.12	13.09
CD at 0.05%	0.15	0.19	0.16

on different plant parts of rose screened for resistance to thrips, *S.dorsalis*, IIHRP-13 showed significantly lower damage with reference to leaves (2.33), buds (2.66) and flowers (1.33). The genotype has yield potential of 80-100 flowers per plant per year

Salient Features of IIHRP-13

1. The genotype is moderately resistant to thrips. (Table 2)
2. It has red colored fragrant flowers. (RHS color chart No. 61 C under Red Purple group)
3. Suitable for open field cultivation with multiple utility as short stalk cut flower and loose flower.
4. With good seed setting ability IIHRP-13 is a valuable genetic stock in breeding program for incorporating fragrance and thrips resistance.
5. It is Hybrid Tea rose, with medium height and flowers of medium size borne as a solitary flower.

51. NRCO-42 (IC0574581; INGR10073), a Orchid (*Dendrobium* hybrid) Germplasm Phalaenopsis Type Hybrid, Broad and Flat Petals, Purple Colour and Big Size Flower

Ramgopal Devadas¹, SP Das², Pema C Bhutia³, P Khatiwara¹, Kesang Lachungpa³, P Subba³, RC Upadhyaya¹, RP Medhi¹ and D Barman¹

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India is largely depending on Southeast Asian countries for importing new *Dendrobium* hybrids for domestic cut flower marketing and commercial exports. The only synthesized *Dendrobium* hybrid in India, *D. "A. Abraham"* was developed by Tropical Botanical Garden and Research institute (TBGRI), Kerala in 1986 using *D. 'Ng Eng Cheow'* and *D. 'Tay Swee*

Keng' as parents (Gupta *et al.*, 2004). In order to fulfill the marketing requirements, the introduction of new variants and hybrids with new characters is invariably required that also helps indirectly to reduce the threatening pressure on their wild species and related genera. A new *Dendrobium* hybrid, NRCO-42 is developed using *Dendrobium* "Emma White"

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CD at 0.05%	0.15	0.19	0.16

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and *Dendrobium* “Pompadour” as female and male parents respectively. The crossing and *in-vitro* rising of progeny was performed during 2003-04 and flowering obtained in 2007-08 was evaluated. This double hybrid flowered with features of moth type *Dendrobium* (*D. phalaenopsis*-cane type) with bigger petals, overlapping petals and sepals (unlike *D. nobile*-cane types) and purple colored (RHS N78A) having whitish shade at base. Plants grow semi-erect and having slightly stout pseudo-stems (1.5 cm). Leaves – 3-7, narrow elliptic, 12-19 cm length, 2.5-2.9 cm width. Inflorescence – 22 to 28 cm long emerges from top portion of pseudo-stem with un-branched raceme. The flower size (6.9 cm x 7.7 cm), dorsal sepal size (4 cm x 1.8 cm), lateral sepal size (4.4 cm x 2 cm), petal size (4.4 cm x 3.8 cm) of the new hybrid, showed superiority over both the parents and check cultivar (*D. “A. Abraham”*). Colour enrichment of hybrid over male parent could be due to the parentage of the hybrids used in crossing program and their pedigree record (Devadas *et al.*, 2009) and purple floral pigments of flower color of *D. “Pompadour”* were reported due to the presence of two rare anthocyanins (cyanidin 3-(6-malonylglucoside)-7,3'-di(6-sinapyglucoside) and demalonyl derivative and other flavonol glycosides (Williams *et al.*, 2002). More numbers of flowers are recorded in female parent, *D. “Emma White”* than F_1 hybrid. The color of lip throat and column was whitish pink and white respectively in F_1 hybrid, and purple and deep purple with creamy white anther cap in check cultivar (*D. “A. Abraham”*) respectively helped as phonological markers for recoding differences. Side lobes of lip in new hybrid (NRCO-42) were semi-arching over column, unlike broadly open in male parent and semi open in female parent. Pedigree record

of both the parents indicated that the *D. phalaenopsis*, a native species to Australia and New Guinea was used extensively in development of modern hybrids of moth type (or) double humped *Dendrobiums*. This new hybrid (*D. phalaenopsis*-cane type cultivar) has preference over *D. nobile*-cane type cultivars, due to ever green nature with long branching flowering inflorescence, unlike flowers attached to canes, epiphytic and pendulous in latter case. More over, this hybrid can be used as cut flower, unlike *D. nobile*-cane type cultivars and related species of Asiatic origin (India, Southern China & Burma) that show semi-deciduous nature after flowering and require cool winter phase and cannot be used as cut flowers. This hybrid (NRCO-42) is adjudged as best paper in poster presentation for during ‘National Conference of Floriculture for Livelihood and Profitability’, 16-19 March, 2009 at IARI, New Delhi. All the characters described support the novelty in the new *D. phalaenopsis*-cane type *i.e.*, moth type hybrid, NRCO-42.

The efforts and dedication of Late Dr V Nagaraju, Ex-Principal Scientist (Horticulture), for raising the progeny is highly remembered and acknowledged.

References

- Gupta V, K Anjali, AB Chaudhary and AK Singh (2004) *Dendrobium* ‘A Abraham’ (INGR No. 030094; National identity IC No. 401584). In: News from Orchid Centres, NBPGR, Pusa Campus. *Orchid News* **20**: 5-6.
- Devadas R, P Khatiwara, D Barman and SP Das (2009) Breeding *Dendrobium phalaenopsis*-cane type hybrid in India: NRCO-42 (*Den. ‘Emma White’* x *Den. ‘Pompadour’*). *Indian J. Genet.*, **69**(3): 237-242.
- Williams CA, J Greenham, JB Harborne, JM Kong, LS Chia, NK Goh, N Saito, K Toki and F Tatsuzawa (2002) Acylated anthocyanins and flavonols from purple flowers of *Dendrobium* cv. ‘Pompadour’. *Biochem. Syst. Eco.* **30**: 667-675.

52. UHFHYP-I (IC0582480; INGR10074), UHFHYP-II (IC0582481; INGR10075) and UHFHYP-III (IC0582482; INGR10076), St. John’s Wort (*Hypericum perforatum*) Germplasm with Semi-Erect, Oblong Lanceolate Leaf; Erect-Oblong Leaf; Prostrate (Decumbent) Obovate Leaf

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Hypericum perforatum (St John’s Wort), locally known as Bassant and Dendhu in Hindi is chiefly valued as an antidepressant (Newall *et al.*, 1924) attributed chiefly

due to the active content hypericin present in almost all parts of the plant (Grieve, 1992). Besides, the herb is also used as an astringent, expectorant, diuretic

and *Dendrobium* “Pompadour” as female and male parents respectively. The crossing and *in-vitro* rising of progeny was performed during 2003-04 and flowering obtained in 2007-08 was evaluated. This double hybrid flowered with features of moth type *Dendrobium* (*D. phalaenopsis*-cane type) with bigger petals, overlapping petals and sepals (unlike *D. nobile*-cane types) and purple colored (RHS N78A) having whitish shade at base. Plants grow semi-erect and having slightly stout pseudo-stems (1.5 cm). Leaves – 3-7, narrow elliptic, 12-19 cm length, 2.5-2.9 cm width. Inflorescence – 22 to 28 cm long emerges from top portion of pseudo-stem with un-branched raceme. The flower size (6.9 cm x 7.7 cm), dorsal sepal size (4 cm x 1.8 cm), lateral sepal size (4.4 cm x 2 cm), petal size (4.4 cm x 3.8 cm) of the new hybrid, showed superiority over both the parents and check cultivar (*D. “A. Abraham”*). Colour enrichment of hybrid over male parent could be due to the parentage of the hybrids used in crossing program and their pedigree record (Devadas *et al.*, 2009) and purple floral pigments of flower color of *D. “Pompadour”* were reported due to the presence of two rare anthocyanins (cyanidin 3-(6-malonylglucoside)-7,3'-di(6-sinapyglucoside) and demalonyl derivative and other flavonol glycosides (Williams *et al.*, 2002). More numbers of flowers are recorded in female parent, *D. “Emma White”* than F_1 hybrid. The color of lip throat and column was whitish pink and white respectively in F_1 hybrid, and purple and deep purple with creamy white anther cap in check cultivar (*D. “A. Abraham”*) respectively helped as phonological markers for recoding differences. Side lobes of lip in new hybrid (NRCO-42) were semi-arching over column, unlike broadly open in male parent and semi open in female parent. Pedigree record

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due to the active content hypericin present in almost all parts of the plant (Grieve, 1992). Besides, the herb is also used as an astringent, expectorant, diuretic

and in pulmonary and urinary troubles (Anonymous, 1959). St John's Wort oil (*oleum hyperici*), prepared by infusing fresh flowers in olive oil is used externally in the treatment of wounds, sores and swellings. It is distributed in Europe, North Africa, Siberia, West Asia, Temperate western Himalayas from Kashmir to Kumaon (Blatter, 1984). In Himachal Pradesh, it grows in shady and damp forests of Shimla and Kullu in sporadic patches (Collett, 1971).

This species is under cultivation in Germany, East Europe, Austria, Italy, France, Chile and USA (Franke *et al.*, 1999). In India, the herb is not under cultivation. For commercial cultivation to succeed, there would be need of better yielding strains which require complete understanding of its natural variability, breeding system and morphological markers associated with better strains. This is more so with regard to DUS (distinctiveness, uniformity and stability) criteria that have emerged in varietal/strain identification and also important in the context of IPR.

Morpho-Agronomic Characteristics

After extensive explorations in Himachal Pradesh, three distinct plant types based on morphological features in *Hypericum perforatum* were identified under ICAR AINRP on M&AP's center at Dr. Y.S.Parmar University of Horticulture & Forestry, Nauni-Solan. The chief diagnostic traits of these three plant types are presented in Table 1. These morphological features have been found to be stable after successive generations. Inbred seeds of these lines breed true and produce homogenous progeny.

Associated Characters and Cultivation Practices

Studies on the reproductive biology have revealed that the species is highly self compatible and pure lines can be produced through inbred seed. This apparently is the reason why the selected morphotypes breed true to type when raised through inbred seeds. These distinct and stable morphological traits can be used in varietal development programmes conforming to the DUS criteria.

Table 1. Distinguishing characteristics of the three identified morphotypes in *Hypericum perforatum*

Morphotypes	Morphological characters				
	Habit	Leaf shape	Flowering duration	50% flowering*	Leaf length/breadth ratio
(L/B)					
UHFHYP-I (IC0582480; above INGR10074)	Semi erect	Oblong lanceolate	100 days	3 rd week of June	3.00 and of June
UHFHYP-II (IC0582481; INGR10075)	Erect	Oblong	123 days	2 nd week of June	~2.25
UHFHYP-III (IC0582482; INGR10076)	Prostrate (decumbent)	Obovate	77 days	4 th week of June	~1.75

*Under Nauni/ Solan (1300m at msl) conditions

It is a sexually propagated species and nursery sowing should be done in November/December. Seedlings are ready for transplantation in the month of February /March.

Investigations are continuing at Dr. Y.S.Parmar University of Horticulture & Forestry, Nauni-Solan to assess the comparative performance in respect of total biomass yield and hypericin content with a view to develop a high yielding stain ensuring perpetuation of the characteristic morphological features of the selected strain which shall be helpful in strain identification, thus fulfilling the major requirement of DUS criteria.

References

- Anonymous (1959) Wealth of India: Dictionary of Indian raw material and Industrial products Vol. V., New Delhi, CSIR, pp154-156.
- Newall N, Coral A, Anderson and Linda A (1924) Chromosome numbers in the genus *Hypericum* *Hereditas* 5: 378-382.
- Grieve M (1992) Modern Herbal: Medicinal, Culinary and cosmetic properties. Tiger Book International London, pp138-139.
- Blatter E (1984) Beautiful flowers of Kashmir. International Book Distributors, Dehra Dun, pp 54-55.
- Collett Henry (1971) Flora Simlensis: Hand Book of flowering plants of Shimla and the Neighbourhood. 3rd edn. W. Thacker and Company, London, 56 p.
- Franke R, Schenk R and Bauermann U (1999) Variability in *Hypericum perforatum* L. breeding lines. *Acta Horti.* **502**: 167-172.

53. DMR 7 (IC0584583; INGR10077), Maize (*Zea mays* L.) Germplasm with Flint Grain, Productivity and Resistance to Pink Borer

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Pink borer tolerant population named WNZPBTL 2 was developed at Directorate of Maize Research to derive resistant inbred lines. This population was subjected to inbreeding followed by ear-to-row selection. Every generation was screened under artificial epiphytotic conditions against Pink borer. After 8 generations of continuous inbreeding, a uniform inbred line was developed which was named as DMR 7 and this inbred was resistant to pink borer.

The four year data with respect to Pink borer reaction revealed that the line has shown consistently very high level of resistance against the susceptible check CM300. The mean leaf injury for Pink borer in DMR 7 ranged from 2.5 to 3.3 against the check

CM 300 (6.2-8.2). Thus can be utilized as a source of stable resistance against this insect for development of insect free hybrids as the source of resistance to this insect are rarely available.

The line was evaluated for various morphological traits for three seasons i.e. from 2007-2009 at Hyderabad and DMR, Delhi. Based on this data, it reveals that the line has late maturing height with medium sized cob length. It takes 56 days for anthesis and 59 days to silk during kharif season. It has sparse tassel branches. The grain row arrangement is straight and has very attractive yellow flint grain colour. Different quality parameters revealed that DMR 7 contains >12% protein and >70% starch.

54. DMR 15 (IC0584584; INGR10078), Maize (*Zea mays* L.) Germplasm with Flint Grain, Productivity, Good Combining Ability, Attractive Grain Colour and Temperate Origin

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DMR 15 was derived from NC 262 (temperate material). Tropicalized plant from NC 262 material was subjected to inbreeding followed by ear-to-row selection. The inbreeding was done at Hyderabad and Delhi. The productive ears with desirable traits were selected in each generation and after 7 generations of inbreeding, this line became uniform.

Different morphological traits studied in three seasons at Hyderabad and DMR, Delhi in kharif reveals that DMR 15 is late maturing and has short plant height (99cm). It yields 2.5 ton/ha in Kharif. It takes 60 days for flowering and 64 days to silk. It has sparse tassel branches. The grain row arrangement is irregular and has very attractive yellow flint grain colour.

55. DMR 16 (IC0584585; INGR10079), Maize (*Zea mays* L.) Germplasm with Flint Grain, Productivity, Good Combining Ability, Long Cob, Attractive Grain Colour and Temperate Origin

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DMR 16 was derived from NC 390 (temperate material). Tropicalized plant from NC 262 material

was subjected to inbreeding followed by ear-to-row selection. The inbreeding was done at Hyderabad and

53. DMR 7 (IC0584583; INGR10077), Maize (*Zea mays* L.) Germplasm with Flint Grain, Productivity and Resistance to Pink Borer

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Pink borer tolerant population named WNZPBTL 2 was developed at Directorate of Maize Research to derive resistant inbred lines. This population was subjected to inbreeding followed by ear-to-row selection. Every generation was screened under artificial epiphytotic conditions against Pink borer. After 8 generations of continuous inbreeding, a uniform inbred line was developed which was named as DMR 7 and this inbred was resistant to pink borer.

The four year data with respect to Pink borer reaction revealed that the line has shown consistently very high level of resistance against the susceptible check CM300. The mean leaf injury for Pink borer in DMR 7 ranged from 2.5 to 3.3 against the check

CM 300 (6.2-8.2). Thus can be utilized as a source of stable resistance against this insect for development of insect free hybrids as the source of resistance to this insect are rarely available.

The line was evaluated for various morphological traits for three seasons i.e. from 2007-2009 at Hyderabad and DMR, Delhi. Based on this data, it reveals that the line has late maturing height with medium sized cob length. It takes 56 days for anthesis and 59 days to silk during kharif season. It has sparse tassel branches. The grain row arrangement is straight and has very attractive yellow flint grain colour. Different quality parameters revealed that DMR 7 contains >12% protein and >70% starch.

54. DMR 15 (IC0584584; INGR10078), Maize (*Zea mays* L.) Germplasm with Flint Grain, Productivity, Good Combining Ability, Attractive Grain Colour and Temperate Origin

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DMR 15 was derived from NC 262 (temperate material). Tropicalized plant from NC 262 material was subjected to inbreeding followed by ear-to-row selection. The inbreeding was done at Hyderabad and Delhi. The productive ears with desirable traits were selected in each generation and after 7 generations of inbreeding, this line became uniform.

Different morphological traits studied in three seasons at Hyderabad and DMR, Delhi in kharif reveals that DMR 15 is late maturing and has short plant height (99cm). It yields 2.5 ton/ha in Kharif. It takes 60 days for flowering and 64 days to silk. It has sparse tassel branches. The grain row arrangement is irregular and has very attractive yellow flint grain colour.

55. DMR 16 (IC0584585; INGR10079), Maize (*Zea mays* L.) Germplasm with Flint Grain, Productivity, Good Combining Ability, Long Cob, Attractive Grain Colour and Temperate Origin

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DMR 16 was derived from NC 390 (temperate material). Tropicalized plant from NC 262 material

was subjected to inbreeding followed by ear-to-row selection. The inbreeding was done at Hyderabad and

Delhi. The productive ears with desirable traits were selected in each generation and after 7 generations of inbreeding, this line became uniform.

Different morphological traits studied in three seasons at Hyderabad and DMR, Delhi reveals that DMR 16 is a late maturing line and takes 64 days

for flowering and 68 days for silk emergence during kharif season. It has short plant height (85cm) with medium sized cob length. The line yields 2.3 ton/ha in Kharif. It has sparse tassel branches and the grain row arrangement is straight. It has very attractive yellow flint grain colour with cap.

56. DMR 17 (IC0584586; INGR10080), Maize (*Zea mays* L.) Germplasm with Flint Grain, Productivity, Good Combining Ability, Attractive Grain Colour and Temperate Origin

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DMR 17 was derived from NC 418 (temperate material). Tropicalized plant from NC 418 material was subjected to inbreeding followed by ear-to-row selection. The inbreeding was done at Hyderabad and Delhi. The productive ears with desirable traits were selected in each generation and after 7 generations of inbreeding, this line became uniform.

Based on different morphological traits studied in three seasons at Hyderabad and DMR, Delhi, it shows that DMR 17 is a late maturing line. It has short plant height (85cm) and yields 2.1 ton/ha in Kharif. It takes 57 days to flower and 60 days for silk emergence. It has dense tassel branches and the grain row arrangement is straight. It has very attractive yellow flint grain colour.

57. HKI C-322 (IC0584587; INGR10081), Maize (*Zea mays* L.) Germplasm with Medium Duration White, Flint Grain, Productivity, Strong Plant and Dark Green Leaves

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HKI C-322 is medium maturing white maize inbred line derived from single cross hybrid HM 2. The hybrid was subjected to 7 generations of inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal and a uniform inbred line was developed.

Different morphological traits studied in three seasons at winter nursery, Hyderabad and DMR,

Delhi reveals that HKI C-322 has short plant height (106cm) with dark green leaves. It takes 58 days to flower and 63 days to silk during kharif. The grain yield is >2.5ton/ha. It has sparse tassel branches. The grain row arrangement is irregular and has white flint grain colour. Different quality parameters reveals that it contains >11% protein and >70% starch.

Delhi. The productive ears with desirable traits were selected in each generation and after 7 generations of inbreeding, this line became uniform.

Different morphological traits studied in three seasons at Hyderabad and DMR, Delhi reveals that DMR 16 is a late maturing line and takes 64 days

for flowering and 68 days for silk emergence during kharif season. It has short plant height (85cm) with medium sized cob length. The line yields 2.3 ton/ha in Kharif. It has sparse tassel branches and the grain row arrangement is straight. It has very attractive yellow flint grain colour with cap.

56. DMR 17 (IC0584586; INGR10080), Maize (*Zea mays* L.) Germplasm with Flint Grain, Productivity, Good Combining Ability, Attractive Grain Colour and Temperate Origin

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DMR 17 was derived from NC 418 (temperate material). Tropicalized plant from NC 418 material was subjected to inbreeding followed by ear-to-row selection. The inbreeding was done at Hyderabad and Delhi. The productive ears with desirable traits were selected in each generation and after 7 generations of inbreeding, this line became uniform.

Based on different morphological traits studied in three seasons at Hyderabad and DMR, Delhi, it shows that DMR 17 is a late maturing line. It has short plant height (85cm) and yields 2.1 ton/ha in Kharif. It takes 57 days to flower and 60 days for silk emergence. It has dense tassel branches and the grain row arrangement is straight. It has very attractive yellow flint grain colour.

57. HKI C-322 (IC0584587; INGR10081), Maize (*Zea mays* L.) Germplasm with Medium Duration White, Flint Grain, Productivity, Strong Plant and Dark Green Leaves

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HKI C-322 is medium maturing white maize inbred line derived from single cross hybrid HM 2. The hybrid was subjected to 7 generations of inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal and a uniform inbred line was developed.

Different morphological traits studied in three seasons at winter nursery, Hyderabad and DMR,

Delhi reveals that HKI C-322 has short plant height (106cm) with dark green leaves. It takes 58 days to flower and 63 days to silk during kharif. The grain yield is >2.5ton/ha. It has sparse tassel branches. The grain row arrangement is irregular and has white flint grain colour. Different quality parameters reveals that it contains >11% protein and >70% starch.

58. HKI MBR-139-2 (IC0584588; INGR10082), Maize (*Zea mays* L.) Germplasm with Medium Duration, White Flint Grain, Good Combining Ability and Dark Green Leaves

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HKI MBR-139-2 is medium maturing white maize inbred line derived from HKI-139 (yellow maize). The line was subjected to of inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal. After 7 generations of continuous inbreeding, the line became uniform.

The line was evaluated for various morphological traits for three seasons i.e. from 2007-2009 at

Hyderabad and DMR, Delhi. Based on this data, it reveals that the line has medium plant height (130cm) with medium sized cob length. It takes 69 days for flowering and 72 days for silk emergence in Kharif. It yields >2.0 ton/ha depending upon weather conditions. It has sparse tassel branches with medium dark green leaves. The grain row arrangement is straight and has white flint grain colour.

59. HKI 5072-2-BT (IC0584589; INGR10083), Maize (*Zea mays* L.) Germplasm with High Tryptophan, Medium Duration, Yellow, Flint, Attractive Grain Colour and Dark Green Leaves

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HKI 5072-2-BT is QPM line derived from DMRQPM-5072 (QPM line). The line was subjected to inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal. After 7 generations of continuous inbreeding, a medium maturing inbred line was developed.

Different morphological traits were studied in three seasons i.e. from 2007-2009 at winter nursery, Hyderabad and DMR, Delhi. Based on this data, it

reveals that HKI 5072-2-BT has short plant height (95cm) with medium sized cob length. The leaves are dark green in colour. The line takes 58 days for flowering and 62 days for silk emergence during kharif. It has dense tassel branches. The grain row arrangement is straight and the Anthocyanin colour of glume is dark purple. It has yellow flint grain with cap. The line contains high levels of lysine and tryptophan.

60. DMRQ – 107 (IC0584590; INGR10084), a Maize (*Zea mays* L.) Germplasm with High Tryptophan, Medium, Yellow, Flint, Good Combining Ability and Thin Cob

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DMRQ-107 is QPM line derived from CLQRCYQ-47-B (QPM line). The line was subjected to inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi. After 7 generations of

continuous inbreeding, medium maturing inbred line was derived.

Different morphological traits were studied in three seasons i.e. from 2007-2009 at winter nursery,

58. HKI MBR-139-2 (IC0584588; INGR10082), Maize (*Zea mays* L.) Germplasm with Medium Duration, White Flint Grain, Good Combining Ability and Dark Green Leaves

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HKI MBR-139-2 is medium maturing white maize inbred line derived from HKI-139 (yellow maize). The line was subjected to of inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal. After 7 generations of continuous inbreeding, the line became uniform.

The line was evaluated for various morphological traits for three seasons i.e. from 2007-2009 at

Hyderabad and DMR, Delhi. Based on this data, it reveals that the line has medium plant height (130cm) with medium sized cob length. It takes 69 days for flowering and 72 days for silk emergence in Kharif. It yields >2.0 ton/ha depending upon weather conditions. It has sparse tassel branches with medium dark green leaves. The grain row arrangement is straight and has white flint grain colour.

59. HKI 5072-2-BT (IC0584589; INGR10083), Maize (*Zea mays* L.) Germplasm with High Tryptophan, Medium Duration, Yellow, Flint, Attractive Grain Colour and Dark Green Leaves

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HKI 5072-2-BT is QPM line derived from DMRQPM-5072 (QPM line). The line was subjected to inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal. After 7 generations of continuous inbreeding, a medium maturing inbred line was developed.

Different morphological traits were studied in three seasons i.e. from 2007-2009 at winter nursery, Hyderabad and DMR, Delhi. Based on this data, it

reveals that HKI 5072-2-BT has short plant height (95cm) with medium sized cob length. The leaves are dark green in colour. The line takes 58 days for flowering and 62 days for silk emergence during kharif. It has dense tassel branches. The grain row arrangement is straight and the Anthocyanin colour of glume is dark purple. It has yellow flint grain with cap. The line contains high levels of lysine and tryptophan.

60. DMRQ – 107 (IC0584590; INGR10084), a Maize (*Zea mays* L.) Germplasm with High Tryptophan, Medium, Yellow, Flint, Good Combining Ability and Thin Cob

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DMRQ-107 is QPM line derived from CLQRCYQ-47-B (QPM line). The line was subjected to inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi. After 7 generations of

continuous inbreeding, medium maturing inbred line was derived.

Different morphological traits were studied in three seasons i.e. from 2007-2009 at winter nursery,

Hyderabad and DMR, Delhi. Based on this data, it reveals that DMRQ-107 has medium plant height ((146 cm) with medium sized cob length. The line flowers in 60 days during kharif. It has dense tassel

branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is spiral and has very attractive yellow dent grain with cap. The line contains high levels of protein (>11%) and tryptophan (>0.70%).

61. Win Sweet Corn (WSC 1) (IC0584591; INGR10085), a Maize (*Zea mays* L) Germplasm with High Sugar and Yellow Shrunken Grain

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WSC 1 is sweet corn line derived from Win Orange Sweet Corn (composite variety). The line was subjected to 7 generations of inbreeding followed by ear-to-row selection at Hyderabad and Directorate of Maize Research, Delhi. After 7 generations of continuous inbreeding, a uniform inbred line was developed which was early maturing in nature.

Different morphological traits studied in three seasons reveals that WSC 1 has short plant height

(95.5 cm) with medium sized cob length. It takes 60 days for flowering and 62 days for silk emergence depending upon weather conditions. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is irregular and has very attractive yellow dent grain colour. WSC 1 contains high level of sugar and TSS (25.3%).

62. DMSC-1 (IC0584592; INGR10086), a Maize (*Zea mays* L) Germplasm with High Sugar and Yellow Shrunken Grain

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DMSC-1 is an early maturing, sweet corn line derived from MUS MADHU (sweet corn) after 7 generations of inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi.

Studies on different morphological traits reveal that DMSC-1 has short plant height (120 cm) with medium sized cob length. It takes 57 days for flowering and

61 days for silk emergence in kharif. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is straight and has very attractive yellow dent grain colour. The line contains high levels of sugar with TSS value of 16.2%.

Hyderabad and DMR, Delhi. Based on this data, it reveals that DMRQ-107 has medium plant height ((146 cm) with medium sized cob length. The line flowers in 60 days during kharif. It has dense tassel

branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is spiral and has very attractive yellow dent grain with cap. The line contains high levels of protein (>11%) and tryptophan (>0.70%).

61. Win Sweet Corn (WSC 1) (IC0584591; INGR10085), a Maize (*Zea mays* L) Germplasm with High Sugar and Yellow Shrunken Grain

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WSC 1 is sweet corn line derived from Win Orange Sweet Corn (composite variety). The line was subjected to 7 generations of inbreeding followed by ear-to-row selection at Hyderabad and Directorate of Maize Research, Delhi. After 7 generations of continuous inbreeding, a uniform inbred line was developed which was early maturing in nature.

Different morphological traits studied in three seasons reveals that WSC 1 has short plant height

(95.5 cm) with medium sized cob length. It takes 60 days for flowering and 62 days for silk emergence depending upon weather conditions. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is irregular and has very attractive yellow dent grain colour. WSC 1 contains high level of sugar and TSS (25.3%).

62. DMSC-1 (IC0584592; INGR10086), a Maize (*Zea mays* L) Germplasm with High Sugar and Yellow Shrunken Grain

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Studies on different morphological traits reveal that DMSC-1 has short plant height (120 cm) with medium sized cob length. It takes 57 days for flowering and

61 days for silk emergence in kharif. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is straight and has very attractive yellow dent grain colour. The line contains high levels of sugar with TSS value of 16.2%.

63. DMSC-6 (IC0584593; INGR10087), a Maize (*Zea mays* L) Germplasm with High Sugar and Yellow Shrunken Grain

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DMSC-6 is an early maturing, sweet corn line derived from MUS MADHU (sweet corn) after 7 generations of inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi.

Studies on different morphological traits reveal that DMSC-6 has medium plant height (100 cm) with medium sized cob length. It takes 58 days for

flowering and 60 days for silk emergence during kharif. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is irregular and has very attractive yellow dent grain colour. The line contains high levels of sugar with TSS value of 15.6%.

64. DMS-201 (IC0584594; INGR10088), a Maize (*Zea mays* L) Germplasm with High Sugar and Yellow Shrunken Grain

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DMS-201 is sweet corn line derived from CP Golden Sweet 3. The line was subjected to 7 generations of inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi and a uniform line was derived which was early maturing.

Studies on different morphological traits reveal that DMS-201 has short stature plant height (104

cm) with medium sized cob length. The line takes 59 days for flowering and 61 days for silk emergence during kharif. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is straight and has very attractive yellow dent grain colour. The line contains high levels of sugar with TSS value of 18.2%.

65. DMS-203 (IC0584595; INGR10089), a Maize (*Zea mays* L) Germplasm with High Sugar and Yellow Shrunken Grain

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DMS-203 is sweet corn line derived from Single cross hybrid [NSS 2W 9301A (sh2sh2) × Sweet corn]. The hybrid was subjected to 7 generations of inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi and a uniform line was derived

Studies on different morphological traits reveal that DMS-203 is an early maturing line. It has short

plant height (116 cm) with medium sized cob. The line flowers in 55 days in kharif. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is straight and the Anthocyanin colour of glume is light purple. It has very attractive yellow dent grain colour. The line has high levels of sugar with TSS value of 26.1%.

66. DMS-206 (IC0584596; INGR10090), a Maize (*Zea mays* L) Germplasm with High Sugar and Yellow Shrunken Grain

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DMS-206 is sweet corn line derived from Single cross hybrid (WSC1 x MUS MADHU). The hybrid was subjected to 7 generations of inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi and a uniform early maturing inbred line was derived.

Studies on different morphological traits reveal that DMS-206 has short plant height (91 cm) with

medium sized cob length. The line flowers in 57 days during kharif. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is straight and has very attractive yellow dent grain colour. The line contains high levels of sugar with TSS value of 21.3%.

67. DMS-207 (IC.No. 0584597; INGR No. 10091), a Maize (*Zea mays* L) Germplasm with High Sugar, Yellow Shrunken Grain and Thin Cob

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DMS-207 is sweet corn line derived from CUBA 378. The line was subjected to 7 generations of inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi and a uniform line was derived which was early maturing.

Studies on different morphological traits reveal that DMS-207 has short plant height (85 cm) with medium

sized cob length. It takes 59 days for flowering and 63 days to silk during kharif. It has dense tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is straight and has very attractive light yellow dent grain colour. The line contains high levels of sugar with TSS value of 18.3%.

68. DMS-208 (IC0584598; INGR10092), a Maize (*Zea mays* L) Germplasm with High Sugar, Yellow Shrunken Grain and Long Cob

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DMS-208 is sweet corn line derived from CUBA 379. The line was subjected to 7 generations of inbreeding followed by ear-to-row selection at winter nursery, Hyderabad and DMR, Delhi and a uniform inbred line was derived which was early maturing in nature.

Different morphological traits were studied in three seasons i.e. from 2007-2009 at winter nursery, Hyderabad and DMR, Delhi. Based on this data, it reveals that

DMS-208 has short plant height (98 cm) with medium sized cob length during kharif. The line takes 65 days to flower and 69 days to silk. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is straight and has very attractive light yellow dent grain colour. The line contains high levels of sugar with TSS value of 25.8%.

69. HKI PC-4B (IC0584599; INGR10093), a Maize (*Zea mays* L) Germplasm with High Popping, Medium Duration and Good Pollinator

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HKI PC-4B popcorn inbred line was derived from LMC 4 collected from local market of Karnal (Haryana). LMC 4 was subjected to 7 generations of inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal and a uniform line was derived.

Different morphological traits studied in three seasons at Hyderabad and DMR, Delhi reveals that HKI

PC-4B is medium maturing and has short plant height (108 cm) with medium sized cob length. The line takes 50 days to flower and 53 days to silk during kharif. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is straight. It has very attractive yellow flint grain colour. The line has 100% popping trait.

70. HKI PCBT-3(IC0584600; INGR10094), a maize (*Zea mays* L) Germplasm with High Popping, Early and Good Pollinator

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HKI PCBT-3 is popcorn line, derived from LMC 3 collected from local market of Karnal (Haryana). LMC 3 was subjected to 7 generations of inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal and a uniform line was derived which was early maturing in nature.

Different morphological traits studied in three seasons at Hyderabad and DMR, Delhi reveals that

HKI PCBT-3 is a hard endosperm, short grain, high popping trait line. It has short plant height with medium sized cob length. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is irregular and has very attractive yellow flint grain colour. The line has 100% popping trait.

71. HKI -6 (IC0584601; INGR10095), a Maize (*Zea mays* L) Germplasm with High Oil Content and Yellow Flint Grain

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HKI-6 is high oil line derived from high oil Shahad population (SHD-1ER6). The population was subjected to inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal. After 7 generations of continuous inbreeding, a uniform line was derived which was early maturing in nature.

The line was evaluated for various morphological traits for three season i.e. from 2007-2009 at Hyderabad

and DMR, Delhi. Based on this data, HKI-6 has short plant height with medium sized cob length. It takes 58days for anthesis and 64days for silk emergence depending on different weather conditions. It has sparse tassel branches and a good pollen shedder, which is a merit of good pollen parent. The grain row arrangement is irregular. It has very attractive yellow flint grain colour. The line contains high levels of protein and oil.

72. HKI-1 (T) (IC0584602; INGR10096), a Maize (*Zea mays* L) Germplasm with High Oil Content and Yellow Flint Grain

S Dass, Dharam Pal, JC Mehla and KS Dhanju

Chaudhary Charan Singh Haryana Agricultural University, RRS, Uchani, Karnal, Haryana

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HKI-1(T) is high oil line derived from from Talar (high oil). The line was subjected to 7 generations of inbreeding followed by ear-to-row selection at CCS HAU, Uchani, Karnal and a uniform late maturing line was derived named as HKI-1(T).

Different morphological traits studied in three seasons at winter nursery, Hyderabad and DMR, Delhi

reveals that HKI 1-(T) has short plant height (100cm). It takes 53 days for flowering and 56 days for silk emergence in kharif. It has sparse tassel branches. The grain row arrangement is straight. It has very attractive yellow flint grain colour. Different quality parameters revealed that it contains high levels of protein (13.12%) and oil (6.31%).

73. HS-491 (IC0566222; INGR10097), a Wheat (*Triticum aestivum*) Germplasm with Good Biscuit Quality

Sanjay Kumar, Dharam Pal, DK Bhatnagar, Rashmi Bhatnagar, RK Gupta, D Mohan and Sewa Ram

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74. UP 2698 (IC0573852; INGR10098), a Wheat (*Triticum aestivum*) Germplasm with High Protein (12.8%)

RS Rawat, JP Jaiswal, Swati, Anil Kumar, DP Saini and Sohan Pal

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UP 2689, an elite wheat genetic stock, which was tested in the name of UP 2689, has been registered as an unique germplasm vide registration number INGR: 09122 (IC 0573852), which has given an average protein content of 13 per cent in North Eastern Plains Zone (NEPZ) where in general low protein content is reported in the wheat varieties. Hence this genetic stock will be useful as a donor for developing the wheat varieties with high protein content. High protein content is one of the most important quality parameters which is required not only for mitigating the malnutrition but also for the production of better quality bread and other value added products. Wheat is staple crop of India and development of variety with high protein is essentially required.

UP 2689, a spring wheat (*Triticum aestivum* L.) is derived from the cross UP2382/DLRSN-5 and developed through pedigree breeding method. It was evaluated in All India Coordinated Wheat & Barley Improvement Project (ICAR) in the year 2005-06 in NIVT-3 and in 2006-07 in AVT-IR-LS-TAS in North Eastern Plains Zone (NEPZ). In late sown conditions, it has given an average yield of 39.2 q/ha in NIVT-3 and 28.5 q/ha in AVT on NEPZ.

In addition to high protein content its thousand grain weight 39 g is also acceptable. It has shown high resistance to brown rust and also possesses Sr2 complex. Its ear size is large with dense spikelets, ears are in club shaped with white colour, outer glumes are glabrous. Anthocyanin pigmentation is

72. HKI-1 (T) (IC0584602; INGR10096), a Maize (*Zea mays* L) Germplasm with High Oil Content and Yellow Flint Grain

S Dass, Dharam Pal, JC Mehla and KS Dhanju

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In addition to high protein content its thousand grain weight 39 g is also acceptable. It has shown high resistance to brown rust and also possesses Sr2 complex. Its ear size is large with dense spikelets, ears are in club shaped with white colour, outer glumes are glabrous. Anthocyanin pigmentation is

absent in the coleoptiles while it is medium on leaf sheath auricle at flag leaf stage. The average plant height is 83 cm having thick culm and dark green

leaves. This genetic stock flowers in 74 days, matures in about 108 days, produces amber and hard grains. The thousand grain weight of UP 2689 is 39 gm.

75. PU 06-14 (IC0570262; INGR 10099), PU 06-23 (IC0570264; INGR 10100), PU 06-24 (IC0570265; INGR 10101), PU 06-19 (IC0570267; INGR 10102), PU 06-20 (IC0570268; INGR 10103), PU 06-21 (IC0570269; INGR 10104), Blackgram (*Vigna mungo*) Germplasm, with High Iron, Zinc, Protein Content, High Resistance to MYMV (Mung Bean Yellow Mosaic Virus)

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exhibited transgressive segregation for one or more quality traits. The details are given in Table 1. The lines were developed under AICRP on MULLaRP at G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India.

Mungbean Yellow Mosaic Virus (MYMV) is economically the most important disease of blackgram and resistance to MYMV is essentially required in the cultivars to sustain their high yield potential over long period of time. Enhancement of protein content in the cultivars is important to combat the growing malnutrition problems, particularly in the Indian subcontinent where grain legumes constitute chief source of dietary protein in the predominantly vegetarian diets of people. The germplasm lines INGR 10099 to 10104 derived from mungbean x blackgram wide cross will be useful to breeders for developing biofortified, disease resistant and high yielding cultivars of blackgram (Singh and Khulbe, 2009).

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Table 1. Salient agro-morphological characteristics of mungbean lines derived from BDYR-1 x DPU 88-31 wide cross

Character	PU 06-14 (INGR 10099)	PU 06-23 (INGR 10100)	PU 06-24 (INGR 10101)	PU 06-19 (INGR 10102)	PU 06-20 (INGR 10103)	PU 06-21 (INGR 10104)	Pant U-35	BDYR-1	DPU 88-31
Days to first flowering	43.7	42.7	41.0	43.7	40.7	44.3	37.3	33.0	44.0
Days to 50% flowering	46.7	46.0	46.7	46.7	44.7	47.7	42.3	37.0	48.0
Days to first pod maturity	62.7	62.0	63.7	63.0	63.0	63.0	62.7	56.3	63.0
Plant height (cm)	73.0	64.0	68.7	70.0	62.0	67.7	83.0	64.0	74.0
Clusters/plant.)	20.0	20.7	10.7	16.3	11.7	21.3	15.3	8.7	14.0
Pods/cluster	2.0	2.7	3.3	3.7	3.0	2.7	3.7	3.3	2.7
Pods per plant	49.0	52.0	28.7	38.7	36.3	57.7	53.3	27.0	45.3
Seeds/pod	6.0	5.0	4.3	5.0	6.7	6.3	6.7	10.0	6.7
100-seed weight (g)	3.9	4.1	4.2	4.1	4.1	4.0	4.4	4.06	4.37
Yield/plant (g)	34.1	37.6	20.3	23.4	26.2	44.9	47.5	34.3	46.4
Seed colour	Black	Black	Black	Black	Black	Black	Black	Shining green	Black
MYMV incidence (1-9)	1.0	1.0	1.0	1.0	1.0	1.0	1.0	7.0	1.0
Protein content (%)	23.10	23.10	24.56	26.50	26.25	26.70	24.50	22.10	22.30
Iron (mg/100 g sample)	11.53	11.29	12.05	6.85	7.59	7.70	8.80	7.15	7.92
Zinc (mg/100 g sample)	2.62	3.11	4.11	2.78	3.11	2.82	3.45	3.19	2.98

and Opportunities, held during 3-5 November 2007 at the Indian Institute of Pulse Research, Kanpur, 228 p.

Singh DP, Singh BB and Gupta Sanjeev (2009) Genetic enhancement for yield and quality improvement in *Vigna* species. In: International Conference on Grain Legumes : *Quality Improvement, Value Addition and Trade*, held during

February 14-16, 2009 at the Indian Institute of Pulse Research, Kanpur, pp 16-17.

Singh DP and Khulbe RK (2009) Urdbean breeding. In: *Pulse Research at Pantnagar (2000-2009)*. DP Singh (ed). GB Pant University of Agriculture and Technology, Pantnagar-263145, Uttarakhand, India, pp 11-17.

76. BDN 2004-4 (IC0573418; INGR10105), a Pigeonpea (*Cajanus cajan* L. Millsp.) Germplasm with Open Flower and Obcordate Leaf

DK Patil, SS Kakde, KR Kamble and VK Gite

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Pigeonpea (*Cajanus cajan* L. Millsp.) has a typical papilionaceous flower ensuring self pollination, a certain amount of entomophilous cross pollination does occur (Saxena *et al.*, 1990). Basically the self-pollination occurs in the bud before the petal opens, when the petals are open insect pollination may take place (Van der Maesen, 1986). Natural out crossing has a potential role in hybrid Pigeonpea research. Thus an open flower mutant can be effectively utilized for the development of exclusively cross pollinating Pigeonpea. This desirable trait can be effectively transferred in CMS line and agronomical suitable genotype can be developed after inheritance study.

During *kharif* 2004-05, a kind of mutant action is found to have in the population of cultivated species of *Cajanus cajan* in the genotype BDN-

2003-2 at Agril. Research Station, Badnapur, MS (Marathwada Agricultural University, Parbhani) i. e. BDN 2004-4.

Morpho-agronomic Characteristics

The pigeonpea flower is irregular (zygomorphic) consisting of five petals, a standard, two wings and two petals fused together to form a keel which encloses anthers and stigma. The genotype BDN 2004-4 is a natural mutant possessing characteristic flower having free keel petals, symmetrical wings and normal standard petal having yellow colour. The boat-shaped keels were split dorsally exposing the reproductive parts to the environment. Such open flowers encourage cross pollination as the pollinating agents such as honey bees have free access to pollen grains liberated after bursting of anthers and the stigma. Another feature

Table 1. Salient agro-morphological characteristics of mungbean lines derived from BDYR-1 x DPU 88-31 wide cross

Character	PU 06-14 (INGR 10099)	PU 06-23 (INGR 10100)	PU 06-24 (INGR 10101)	PU 06-19 (INGR 10102)	PU 06-20 (INGR 10103)	PU 06-21 (INGR 10104)	Pant U-35	BDYR-1	DPU 88-31
Days to first flowering	43.7	42.7	41.0	43.7	40.7	44.3	37.3	33.0	44.0
Days to 50% flowering	46.7	46.0	46.7	46.7	44.7	47.7	42.3	37.0	48.0
Days to first pod maturity	62.7	62.0	63.7	63.0	63.0	63.0	62.7	56.3	63.0
Plant height (cm)	73.0	64.0	68.7	70.0	62.0	67.7	83.0	64.0	74.0
Clusters/plant.)	20.0	20.7	10.7	16.3	11.7	21.3	15.3	8.7	14.0
Pods/cluster	2.0	2.7	3.3	3.7	3.0	2.7	3.7	3.3	2.7
Pods per plant	49.0	52.0	28.7	38.7	36.3	57.7	53.3	27.0	45.3
Seeds/pod	6.0	5.0	4.3	5.0	6.7	6.3	6.7	10.0	6.7
100-seed weight (g)	3.9	4.1	4.2	4.1	4.1	4.0	4.4	4.06	4.37
Yield/plant (g)	34.1	37.6	20.3	23.4	26.2	44.9	47.5	34.3	46.4
Seed colour	Black	Black	Black	Black	Black	Black	Black	Shining green	Black
MYMV incidence (1-9)	1.0	1.0	1.0	1.0	1.0	1.0	1.0	7.0	1.0
Protein content (%)	23.10	23.10	24.56	26.50	26.25	26.70	24.50	22.10	22.30
Iron (mg/100 g sample)	11.53	11.29	12.05	6.85	7.59	7.70	8.80	7.15	7.92
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DK Patil, SS Kakde, KR Kamble and VK Gite

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During *kharif* 2004-05, a kind of mutant action is found to have in the population of cultivated species of *Cajanus cajan* in the genotype BDN-

2003-2 at Agril. Research Station, Badnapur, MS (Marathwada Agricultural University, Parbhani) i. e. BDN 2004-4.

Morpho-agronomic Characteristics

The pigeonpea flower is irregular (zygomorphic) consisting of five petals, a standard, two wings and two petals fused together to form a keel which encloses anthers and stigma. The genotype BDN 2004-4 is a natural mutant possessing characteristic flower having free keel petals, symmetrical wings and normal standard petal having yellow colour. The boat-shaped keels were split dorsally exposing the reproductive parts to the environment. Such open flowers encourage cross pollination as the pollinating agents such as honey bees have free access to pollen grains liberated after bursting of anthers and the stigma. Another feature

in this variant was the obcordate leaf structure. The plant had trifoliate leaf reduced in shape with short petiole as compared to the normal pigeonpea plant. The leaflet apices were protruded inwards to the mid rib. However, the venation was prominent and normal. The plant had short stature as compared to the normal plant of the genotype.

This mutant was stabilized and crossed with normal plant to study the inheritance of open flower and leaf structure during *Kharif* 2005-06. Such types of cases were reported by Singh *et al.* (1942), Kajjari (1956) and Patil (1959).

For inheritance study, the crosses were made between an open flower mutant having obcordate leaf type and normal plant. All F_1 s had normal flower and normal leaf. However in F_2 segregation from these cross showed the ratio of 3:1 i.e. Normal flower:

Open flower. Similarly for leaf structure, obcordate leaf structure the ratio is 3:1 i.e. Normal leaf: obcordate leaf, which indicates the simple monogenic inheritance with the recessive gene which govern the character of open flower and obcordate leaf.

References

- Kajjari NB (1956) A new mutation in *Cajanus cajan* Millsp. *Curr. Sci.* **25**: 333.
- Patil, JA (1959) A mutation in *Cajanus cajan* (Linn.). Millsp. *Poona Agricultural College Magazine* **49**: 264
- Saxena, KB, L Singh and MD Gupta (1990) Variation for natural out-crossing in Pigeonpea. *Euphytica* **46**: 143-148.
- Singh DN, RK Bansal, and SP Mital (1942) *Cajanus obcordifolia* Singh—a new species of *Cajanus*. *Indian J. Agric. Sci.* **12**: 779-784.
- Van der Maesen, LJG (1986) *Cajanus* DC and *Atylosia* W and A (Leguminosae). *Agricultural University Wageningen Papers* 85-4 (1984). Agricultural University, Wageningen, the Netherlands, 225-4.

77. BDN 2004-4A & B (IC0573419; IC0573420; INGR10106), a Pigeonpea (*Cajanus cajan* L. Millsp.) Germplasm, CMS based BDN 2004A and B Male Sterile Open Flower Mutant

DK Patil, KR Kamble, SS Kakde and VK Gite

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During *kharif* 2004-05, a kind of mutant action is found to have in the population of cultivated species of *Cajanus cajan* in the genotype BDN-2003-2 at Agril. Research Station, Badnapur, M.S. (Marathwada Agricultural University, Parbhani). This mutant is successfully converted into male sterile background

with the cytoplasm of *C. scarabaeoides*. (BDN 2004A & B).

Morpho-agronomic Characteristics

The pigeonpea flower is irregular (zygomorphic) consisting of five petals, a standard, two wing petals and two petals fused together to form a keel which encloses anthers and stigma. This natural mutant had characteristic flower having free keel petals, symmetrical wings and normal standard petal possessing yellow colour. The boat-shaped keels were split dorsally exposing the reproductive parts to the environment. Such open flowers encourage cross pollination as the pollinating agents such as honey bees, have free access to pollen grains liberated after bursting of anthers and the stigma. Another feature in this variant was the obcordate leaf structure. The plant had trifoliate leaf reduced in shape with short petiole as compared

in this variant was the obcordate leaf structure. The plant had trifoliate leaf reduced in shape with short petiole as compared to the normal pigeonpea plant. The leaflet apices were protruded inwards to the mid rib. However, the venation was prominent and normal. The plant had short stature as compared to the normal plant of the genotype.

This mutant was stabilized and crossed with normal plant to study the inheritance of open flower and leaf structure during *Kharif* 2005-06. Such types of cases were reported by Singh *et al.* (1942), Kajjari (1956) and Patil (1959).

For inheritance study, the crosses were made between an open flower mutant having obcordate leaf type and normal plant. All F_1 s had normal flower and normal leaf. However in F_2 segregation from these cross showed the ratio of 3:1 i.e. Normal flower:

Open flower. Similarly for leaf structure, obcordate leaf structure the ratio is 3:1 i.e. Normal leaf: obcordate leaf, which indicates the simple monogenic inheritance with the recessive gene which govern the character of open flower and obcordate leaf.

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- Van der Maesen, LJG (1986) *Cajanus* DC and *Atylosia* W and A (Leguminosae). *Agricultural University Wageningen Papers* 85-4 (1984). Agricultural University, Wageningen, the Netherlands, 225-4.

77. BDN 2004-4A & B (IC0573419; IC0573420; INGR10106), a Pigeonpea (*Cajanus cajan* L. Millsp.) Germplasm, CMS based BDN 2004A and B Male Sterile Open Flower Mutant

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with the cytoplasm of *C. scarabaeoides*. (BDN 2004A & B).

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The pigeonpea flower is irregular (zygomorphic) consisting of five petals, a standard, two wing petals and two petals fused together to form a keel which encloses anthers and stigma. This natural mutant had characteristic flower having free keel petals, symmetrical wings and normal standard petal possessing yellow colour. The boat-shaped keels were split dorsally exposing the reproductive parts to the environment. Such open flowers encourage cross pollination as the pollinating agents such as honey bees, have free access to pollen grains liberated after bursting of anthers and the stigma. Another feature in this variant was the obcordate leaf structure. The plant had trifoliate leaf reduced in shape with short petiole as compared

to the normal pigeonpea plant. The leaflet apices were protruded inwards to the mid rib. However, the venation was prominent and normal. The plant had short stature as compared to the normal plant of the genotype.

The plant is successfully converted into sterile cytoplasm (CMS base male sterility) to take the advantage of open flower for easy pollination and

to facilitate easy seed production to minimise the cost.

References

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- Van der Maesen, LJG (1986) *Cajanus DC and Atylosia W. & A.* (Leguminosae). *Agricultural University Wageningen Papers* 85-4 (1984). Agricultural University, Wageningen, the Netherlands, 225-4.

78. MTS-37 (IC 0418452; INGR 10107), a Mungbean (*Vigna radiata*) Germplasm, with Highest Seed Weight (9.43 g/100seed)

NK Dwivedi and S Gopala Krishnan

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A wide range of variability has been reported for several morphological characters in mungbean germplasm. The range of variability for 100-seed weight in Indian mungbean germplasm varies from 0.8 g to 6.8 g (Bisht *et al.* 1998). The variability for seed weight in the world mungbean collection at AVRDC, Taiwan ranges from 2.65 g to 7.75 g per 100 seeds (Andreas W. Ebert, AVRDC, Personal communication). Among the 73 mungbean varieties released in India since 1936, only two cultivars namely Pusa Vishal and SMBL 668 have been found to possess large seeds (>5 g) (Katiyar *et al.* 2008). IC 418452 is an unique extra bold seeded germplasm with highest 100-seed weight (>9.0 g) recorded till date among all the mungbean germplasm accessions collected and characterized in India.

A mungbean accession IC418452 (Collector No. MTS-37) collected from North Andaman (Andaman and Nicobar Islands) was characterized during *kharif* 2004 at NBPGR Regional Station, Jodhpur in an Augmented Block Design. It was observed to possess unusually extra bold seeds with 100 seed weight of more than 9.0g (Dwivedi and Gopala Krishnan, 2009). This germplasm accession was further evaluated during *kharif* 2005 for validation of the trait. During *kharif* 2008, an experiment was conducted in Randomized Block Design with twenty three accessions of bold seeded mungbean germplasm accessions possessing 100-seed weight of more than 6.0 g along with

M1319B, Pusa Vishal and Pusa 105 as checks. Among all twenty three accessions of mungbean evaluated, IC418452 recorded the highest 100-seed weight of 9.43 g compared to that of the three checks which had 100-seed weight less than 6.00 g.

IC418452 has semi-erect growth habit and attains a height of 40–60 cm. Flowering is synchronous and it flowers in 43–45 days. The hypocotyls colour is purple. Leaves are trifoliate, alternate and intermediate green in colour. The terminal leaf is large and the leaflets are entire. The plant is pubescent with central branching pattern. The flower colour is greenish yellow. The raceme position is indeterminate. Mature pods are brownish black, densely pubescent and possess 11–13 seeds/pod. Seeds are drum shaped and dull green in colour. It has an average 100-seed weight of 9.43 g. It has 2–3 primary branches with 9–10 clusters per plant. IC415482 produces an average seed yield of 16.52g per plant compared to the 16.94 g in Pusa Vishal. A photograph comparing the seeds of extra bold seeded germplasm accession IC418452 with that of cultivars namely M1319B, Pusa Vishal and Pusa 105 is given below:

Seed size is an important character in mungbean since large seed has an advantage of having higher stored energy supply and also has good consumer preference. The extra bold seeded mungbean genotype IC418452 can be utilized in developing improved mungbean cultivars with bold seeds and higher yield.

to the normal pigeonpea plant. The leaflet apices were protruded inwards to the mid rib. However, the venation was prominent and normal. The plant had short stature as compared to the normal plant of the genotype.

The plant is successfully converted into sterile cytoplasm (CMS base male sterility) to take the advantage of open flower for easy pollination and

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78. MTS-37 (IC 0418452; INGR 10107), a Mungbean (*Vigna radiata*) Germplasm, with Highest Seed Weight (9.43 g/100seed)

NK Dwivedi and S Gopala Krishnan

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Seed size is an important character in mungbean since large seed has an advantage of having higher stored energy supply and also has good consumer preference. The extra bold seeded mungbean genotype IC418452 can be utilized in developing improved mungbean cultivars with bold seeds and higher yield.

In addition, it can be utilized in mapping QTLs (genes) for seed weight in mungbean.

References

Bisht IS, RK Mahajan and DP Patel (1998) The use of characterization data on establish the Indian Mungbean Core Collection and Assessment of Genetic Diversity. *Genet.*

Resour. Crop Evol., **45**:127-133.

Dwivedi, NK and S Gopala Krishnan (2009) IC418452 – A unique extra bold seeded germplasm accession of mungbean [*Vigna radiata* (L.) Wilczek] *J. Arid Legumes* **6** (2): 77-79.

Katiyar, PK, GP Dixit and BB Singh (2008) Morphological characterization of greengram (*Vigna radiata*) varieties and stability testing. *Indian J. Agri. Sci.* **78**(5):439-444.

79. PRB-2006-5 (IC573439; INGR10108), a Mustard (*Brassica juncea*) Germplasm, with Bold Seed

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PRB-2006-5 is an Indian-mustard (*Brassica juncea* L. Czern. & Coss.) strain registered for seed boldness with national identity, IC0573439 and registration number INGR10108. It was developed from a three-way cross “(Kranti×LPIPS-2)×BSIPS-11” by pedigree selection. Among its parents Kranti is a high yielding widely adapted variety but its small seeds have generally been a deterrent for its wide acceptance by its growers. LPIPS-2 is a long siliquae (>4 cm) and BSIPS-11 is a bold seeded selection developed through pedigree selection following hybridization between medium bold × bold seeded strains.

It was tested in the coordinated Initial Varietal Trial-Mustard (Timely sown) under AICRP on Rapeseed-Mustard at 16 locations across zones during Rabi 2007-08 (AICRP on Rapeseed-Mustard, 2008). On the basis of average over locations in IVT-Mustard, PRB-2006-5 registered the boldest seeds averaging 6.10 g/1000-seeds which were 16.86 and 37.70% higher than national

checks Varuna and Kranti respectively. Its boldest seed were produced at Morena location in zone-III (7.90 g/1000 seeds). The seeds of PRB-2006-5 are brown with 39.52% oil and 20.89% protein. Being an improved genetic stock it is high yielding (1949 kg/ha) and at par with varieties Varuna (1838 kg/ha) and Kranti (2014 kg/ha) besides having extra bold seeds.

It is medium maturing genotype (135 days) being numerically at par with that of Varuna (134 days) and Kranti (133 days). PRB-2006-5 is being used as potential genetic donor in mustard breeding programme for improving the seed size-an important seed yield component in mustard besides other traits.

References

AICRP (Rapeseed-Mustard) 2008 Annual Progress Report. National Research Centre on Rapeseed-Mustard, Bharatpur-321 303, Rajasthan, pp 37-41.

80. PCL8 (IC0563952; INGR10109), a Linseed (*Linum usitatissimum*) Germplasm, with High Yield Coupled with Resistance against Major Diseases

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Development of high yielding multiple diseases resistant varieties has been thrust areas of linseed breeding. PCL 8 – a derivative of cross (RL 993 × Ayogi) × Ayogi

was handled through pedigree method of breeding at Project Coordinating Unit (Linseed), CSA University of Agriculture and Technology, Campus, Kanpur.

In addition, it can be utilized in mapping QTLs (genes) for seed weight in mungbean.

References

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79. PRB-2006-5 (IC573439; INGR10108), a Mustard (*Brassica juncea*) Germplasm, with Bold Seed

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checks Varuna and Kranti respectively. Its boldest seed were produced at Morena location in zone-III (7.90 g/1000 seeds). The seeds of PRB-2006-5 are brown with 39.52% oil and 20.89% protein. Being an improved genetic stock it is high yielding (1949 kg/ha) and at par with varieties Varuna (1838 kg/ha) and Kranti (2014 kg/ha) besides having extra bold seeds.

It is medium maturing genotype (135 days) being numerically at par with that of Varuna (134 days) and Kranti (133 days). PRB-2006-5 is being used as potential genetic donor in mustard breeding programme for improving the seed size-an important seed yield component in mustard besides other traits.

References

AICRP (Rapeseed-Mustard) 2008 Annual Progress Report. National Research Centre on Rapeseed-Mustard, Bharatpur-321 303, Rajasthan, pp 37-41.

80. PCL8 (IC0563952; INGR10109), a Linseed (*Linum usitatissimum*) Germplasm, with High Yield Coupled with Resistance against Major Diseases

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(E-mail: pclinseed@rediffmail.com)

Development of high yielding multiple diseases resistant varieties has been thrust areas of linseed breeding. PCL 8 – a derivative of cross (RL 993 × Ayogi) × Ayogi

was handled through pedigree method of breeding at Project Coordinating Unit (Linseed), CSA University of Agriculture and Technology, Campus, Kanpur.

In addition, it can be utilized in mapping QTLs (genes) for seed weight in mungbean.

References

Bisht IS, RK Mahajan and DP Patel (1998) The use of characterization data on establish the Indian Mungbean Core Collection and Assessment of Genetic Diversity. *Genet.*

Resour. Crop Evol., **45**:127-133.

Dwivedi, NK and S Gopala Krishnan (2009) IC418452 – A unique extra bold seeded germplasm accession of mungbean [*Vigna radiata* (L.) Wilczek] *J. Arid Legumes* **6** (2): 77-79.

Katiyar, PK, GP Dixit and BB Singh (2008) Morphological characterization of greengram (*Vigna radiata*) varieties and stability testing. *Indian J. Agri. Sci.* **78**(5):439-444.

79. PRB-2006-5 (IC573439; INGR10108), a Mustard (*Brassica juncea*) Germplasm, with Bold Seed

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PRB-2006-5 is an Indian-mustard (*Brassica juncea* L. Czern. & Coss.) strain registered for seed boldness with national identity, IC0573439 and registration number INGR10108. It was developed from a three-way cross “(Kranti×LPIPS-2)×BSIPS-11” by pedigree selection. Among its parents Kranti is a high yielding widely adapted variety but its small seeds have generally been a deterrent for its wide acceptance by its growers. LPIPS-2 is a long siliquae (>4 cm) and BSIPS-11 is a bold seeded selection developed through pedigree selection following hybridization between medium bold × bold seeded strains.

It was tested in the coordinated Initial Varietal Trial-Mustard (Timely sown) under AICRP on Rapeseed-Mustard at 16 locations across zones during Rabi 2007-08 (AICRP on Rapeseed-Mustard, 2008). On the basis of average over locations in IVT-Mustard, PRB-2006-5 registered the boldest seeds averaging 6.10 g/1000-seeds which were 16.86 and 37.70% higher than national

checks Varuna and Kranti respectively. Its boldest seed were produced at Morena location in zone-III (7.90 g/1000 seeds). The seeds of PRB-2006-5 are brown with 39.52% oil and 20.89% protein. Being an improved genetic stock it is high yielding (1949 kg/ha) and at par with varieties Varuna (1838 kg/ha) and Kranti (2014 kg/ha) besides having extra bold seeds.

It is medium maturing genotype (135 days) being numerically at par with that of Varuna (134 days) and Kranti (133 days). PRB-2006-5 is being used as potential genetic donor in mustard breeding programme for improving the seed size-an important seed yield component in mustard besides other traits.

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80. PCL8 (IC0563952; INGR10109), a Linseed (*Linum usitatissimum*) Germplasm, with High Yield Coupled with Resistance against Major Diseases

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was handled through pedigree method of breeding at Project Coordinating Unit (Linseed), CSA University of Agriculture and Technology, Campus, Kanpur.

Table1. Disease Reactions of linseed genotype PCL 8 in Uniform disease nursery trial (UDN Natural)

Entry	Alternaria blight (0–5 Scale*)													Overall rating
	Berhampore		Faizabad		Jashipur	Kangra	Kanke	Kaul	Kota	Ludhiana	P.C.Unit	Raipur		
	L	B	L	B								L	B	
PCL 8	1	29.8	1	10.0	0	23.3	2	0	4	27.5	2	1	12.41	MR
Sheela (RC)	3	26.1	2	15.0	1	23.6	1	0	–	20.7	2	1	20.22	MR
Chambal (SC)	3	12.5	3	20.5	4	—	2	0	–	22.5	3	–	13.24	MS

Entry	Powdery mildew (0–5 Scale*)							Overall rating
	Kota	Mauranipur	Nagpur	Jashipur	Raichur	Raipur		
PCL 8	3	1	0	0	2	0		R
Kiran (RC)	–	1	1	0	2	1		R
Chambal (SC)	–	4	5	0	5	5		HS

Entry	Rust (0–5 Scale*)				Overall rating
	Kangra	Kanke	Berhampore		
PCL 8	1	1	1		R
Surabhi (RC)	0	1	1		R
Chambal (SC)	5	2	1		HS

L = Leaf; B= Bud; RC = Resistant Check; SC= Susceptible check

1 = 0 to 10% area of leaves/plant infection (R),
 2 = 10.1 to 25% area of leaves/plant infection (MR),
 3 = 25.1 to 50% area of leaves/plant infection (MS),
 4 = 50.1 to 75% area of leaves/plant infection (S),
 5 = Above 75% area of leaves/plant infection (MS)

Source: Annual Report (Linseed), 2006–07, pp: 162–163.

(0–5 Scale*)

0 = No disease or free,

PCL 8 was screened under natural condition of uniform disease nursery trial during *rabi* 2006-07 and found to be resistant to rust, powdery mildew and moderately resistant *Alternaria* blight which are the major diseases of economic importance (Table 1).

It is a blue flowered variety with disc shape flower and semi-twisted aestivation. PCL 8 belongs

to medium maturity group (139 days) and can gain a height up to 70cm. Its seed colour is light brown and medium sized seed contains 38.93 per cent oil.

PCL 8 recorded mean seed yield of 1359 kg/ha in initial varietals trial conducted under irrigated condition at 20 locations during *rabi* 2006-07.

81. CMSA-line & B-line (IC0570071 & IC0570261; INGR10110), a Carrot (*Dacus carrota* L.) Germplasm, Petaloid Type Stable Male Sterile Line of Asiatic Carrot

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Male sterility is a noble tool in the hands of plant breeders for their usefulness in hybrid seed production of crop plants. The male sterility in temperate type carrot has been available since long (Thompson, 1962 and Morelock, 1974). There are two main sources of cms identified in carrots: I) Petaloid and carpeloid CMS system which was found in wild stocks of carrot where, stamens get modified to petals (Munger, 1953) or to carpels (Linke *et al.*, 2003). II) Brown anther

type CMS, where, anthers get dried and deformed due to degeneration found by Welch and Grimbail, 1947 in cv. Tendersweet. Newer sources for both types of CMS have been found in the recent years. However, there are no reports of male sterile lines in Asiatic carrot.

Studies were conducted at Plant Biotechnology Center, Rajasthan Agricultural University, Bikaner to isolate male sterile line (s) from the local carrot

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Chambal (SC)	3	12.5	3	20.5	4	—	2	0	–	22.5	3	–	13.24	MS

Entry	Powdery mildew (0–5 Scale*)							Overall rating
	Kota	Mauranipur	Nagpur	Jashipur	Raichur	Raipur		
PCL 8	3	1	0	0	2	0		R
Kiran (RC)	–	1	1	0	2	1		R
Chambal (SC)	–	4	5	0	5	5		HS

Entry	Rust (0–5 Scale*)				Overall rating
	Kangra	Kanke	Berhampore		
PCL 8	1	1	1		R
Surabhi (RC)	0	1	1		R
Chambal (SC)	5	2	1		HS

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type CMS, where, anthers get dried and deformed due to degeneration found by Welch and Grimbail, 1947 in cv. Tendersweet. Newer sources for both types of CMS have been found in the recent years. However, there are no reports of male sterile lines in Asiatic carrot.

Studies were conducted at Plant Biotechnology Center, Rajasthan Agricultural University, Bikaner to isolate male sterile line (s) from the local carrot

material collected from the local markets. Some male sterile plants were identified in a seed lot of 'ameri red' cultivar, a local cultivar from Amer region, Jaipur, Rajasthan, India. Sterile plants were noticed for their grossly different umbel morphology. The umbels were devoid of petals and looked sepaloid. The close microscopic examination revealed absence of anthers. In order to recover seeds and establish nature of sterility, different pollination methods (selfing, hand pollination and open pollination) were applied. The plants raised from crossed seed showed complete sterility in next generation.

All of the plants (about 100 from each type of cross) raised from these crosses showed complete sterility over three generations in crosses with different populations while seed set completely failed on selfing. No segregation on crossing with various populations suggests cytoplasmic nature of the male sterility under study. Moreover, the recovery of sterile plants from crosses with various populations involving more than 5 plants each in addition to from open pollination suggests non-availability of restorers for it. However, being a root crop this type of male sterility may efficiently be used for commercial hybrid production in carrot.

Plants of CMS lines obtained in different backgrounds and in its original genotype were otherwise normal growing. However, cross with var. super red (CR 27) produced genotypes with most desirable type root characters resembling to its recurrent parent and was further evaluated and maintained in abundance. The CMS line developed in the back ground of CR 27 was named as PK/RA CR-27S against the male fertile line CR27F. The sterile cytoplasm PK/RA CR-27S and its male counter part CR27F has been provided with national identity, IC-570071 and IC 0570261 respectively by NBPGR, New Delhi.

The major morphological characters of PK/RA CR-27S (Sterile cytoplasm) are as follows: Root Length: 20 ± 2.6 cm., Root girth: 11.6 ± 1.79 , Days to

maturity: 100 ± 7.3 , Medium self core, Juicy and sweet, Smooth, Cylindrical tapering, Dark red colored roots, Plant height (cm): 58.6 ± 6.4 , No. of primary branches: 6.3 ± 0.55 , No. of secondary branches: 10.3 ± 1.13 , No. of umbel/plant: 15 ± 1.4 , Umbel size (L×W) cm²: 41.6 ± 2.6 etc. The cultivation practice is similar like ordinary Asiatic carrots.

In the present CMS system whole umbel look green. This could be a newer class of male sterility. The CMS system reported could be of great importance to resolve genetic and molecular mechanism differentiating carpeloid/sepaloid and brown anther type CMS systems of carrot in addition to their use in hybrid seed production. This is critical as the inheritance of cms has not been considered simple and has not been completely resolved. Both types of cms are dominant and may be determined by triplicated nuclear genes, one dominant (M), the two recessive (t and l), which interact with sterile cytoplasm (Morelock, *et al.*, 1996). Maternally inherited defects in the formation of male flower organs leading to cytoplasmic male sterility (CMS) indicate an involvement of mitochondrial genes in the control of flower formation.

References

- Thompson DJ (1962) Studies on inheritance of male sterility in carrot (*Daucus carota*). *Proc. Am. Soc. Hort. Sci.* **78**:332-338.
- Morelock TE (1974) Influence of cytoplasmic source on expression of male sterility in carrot. PhD Thesis, Univ. of Wisconsin, Madison, USA.
- Munger HM (1953) In carrots and related vegetable umbelliferae by Rubatzky VE, Quiros CF and Simon PW. CABI pub, CAB, International Wallingford, Oxon, UK, 57p.
- Linke B, T Nothnagel and T Borner (2003) Flower development in carrot CMS plants: Mitochondria affect the expression of MADS box genes homologous to GLOBOSA and EFICIENS. *The Plant Journal* **34**: 27-37.
- Welch JE and EL Grimball (1947) Male sterility in carrot. *Science* **106**: 594.
- Morelock TE, PW Simon and CE Peterson (1996) Wisconsin wild: another petaloid male sterile cytoplasm for carrot. *Hort. Sci.* **31**: 887-888.

82. Coll. No. 002/FI No. 002 or Gauri-UBKVM-1 (IC0569192; INGR10111), a Nepalese Kutki (*Picrorhiza scrophulariiflora*) Germplasm with High Picroside Content

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The Nepalese Kutki (*Picrorhiza scrophulariiflora* (Pennell), *Scrophulariaceae*, is an endangered small herbaceous plant found in the sub-alpine as well as alpine zone of the eastern Himalayas comprising Sikkim, Nepal and China (Bantawa *et al.*, 2009a). The rhizomes are used in Tibetan and Chinese traditional medicines to treat various ailments such as liver disorders, fever, asthma, jaundice and have pharmaceutical value for hepatoprotective, immunomodulator and antiasthmatic activities. Rhizomes of mature plants collected from various locations of the eastern Himalayan region of Indo-China border were characterized morphologically

and analyzed chemically by TLC, HPLC to determine the content of marker compounds, namely picroside I and II. Amidst the genotypes, one genotype Gauri-UBKVM-1 was found to contain highest amount of total picroside (7.33% dw) (Table 1). The same genotype was multiplied by micropropagation and distributed to the tribal of Sikkim for sustainable conservation (Bantawa *et al.*, 2009b, Bantawa *et al.*, 2010a, Bantawa *et al.*, 2010b).

Characteristics: Long, thick rhizome, Irhizome with higher dry weight, the picroside content is highest and it is easy to propagate.

Table1. Morphological descriptions and Picroside I and II contents in rhizomes

Name of the gerplasm	Rhizome			Picroside I (%)	Picroside II (%)	Total (%)
	Diameter(cm)	Length (cm)	Dry weight (g/rhizomes)			
Gauri-UBKVM-1	0.7 ± 0.12	11.89 ± 0.4	2.12 ± 0.31	2.21 ± 0.56	5.12 ± 0.12	7.33 ± 0.68
Data (mean ± SE) pooled from three independent experiments						

83. Coll. No. SL No. 005/FL No. 008 or Shankar-UBKVM-2 (IC0569193; INGR10112), an Indian Winter Green (*Gaultheria fragrantissima*) Germplasm with High Essential Oil Content

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Indian Wintergreen (*Gaultheria fragrantissima* Wall. (Ericaceae) is a small woody evergreen perennial plant, found in hilly terrain of north-eastern India including Indo-Nepal as well as Indo-Bhutan territories at an altitude between 1,800 to 2,500 m and also in Nilgiri, Palani hills of Travancore at an altitude above 1,500m in Western Ghats of India (Bantawa and Mondal , 2008). The genus *Gaultheria* comprises about 200 species which are native to a wide geographical areas ranging from Andes, North America, Australia

and nearby islands to eastern Asia and Himalayas. Out of the 12 species found in India, two belong to north-eastern India and seven species are found in Darjeeling-Sikkim Himalayas and rest three is available in Western Ghats of South India. This oil is popular as anti-inflammatory, antiseptic and soothing to the digestive system. The oil of wintergreen is an effective remedy for rheumatic, cellulites treatment and arthritic problems and it relieves flatulence and colic. The oil is also used as a flavouring agent (confectionaries,

82. Coll. No. 002/FI No. 002 or Gauri-UBKVM-1 (IC0569192; INGR10111), a Nepalese Kutki (*Picrorhiza scrophulariiflora*) Germplasm with High Picroside Content

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herbal tea, tooth paste, etc.) in perfuming industries and as condiments. Traditionally the leaves are used to treat headaches, aching muscles and sore throat. The oil of wintergreen is well document to have fungicidal properties. Leaves of mature plants collected from various locations of the eastern Himalayan region of Indo-China border were analyzed by steam distillation which resulted to identify an elite line (Shankar-UBKVM-2) containing 1.79% essential oil, of which 98% was methyl salicylate as determined by gas chromatography.

References

Bantawa P and TK Mondal (2008) Population studies of *Gaultheria fragrantissima* Wall. In Darjeeling district of West Bengal. *Nat. Prod. Rad.* 7: 68-73

Bantawa P, SK Ghosh, S Moitra, PD Ghosh and TK Mondal (2009a) Studies on dwindling population of *Picrorhiza scrophulariiflora* Pennell. (Scrophulariaceae): its status and conservation threats in Sikkim Himalayas, India. *Bio. Biodiver. Bioavail.* 3(1):15-22

Bantawa P, O SahaRoy, PD Ghosh and TK Mondal (2009b) Effect of Bavistin and adenine sulphate on shoot multiplication of *Picrorhiza scrophulariiflora* Pennell: an endangered medicinal plant of Indo-China Himalayan regions. *Plant Tissue Cult. Biotech.* 19(2): 237-245.

Bantawa P, SK Ghosh and TK Mondal (2010a) *In vitro* regeneration of a medicinal plant Nepalese Kutki (*Picrorhiza scrophulariiflora*) Pennell. *Biol. Planta.* (Accepted)

Bantawa P, SK Ghosh, P Bhandari, B Singh, PD Ghosh, PS Ahuja and TK Mondal (2010b) Micropropagation of an Elite Line of *Picrorhiza scrophulariiflora*, Pennell, an Endangered High Valued Medicinal Plant of the Indo-China Himalayan Region *Med Aroma. Plant Biotech.* (In press)

84. NRCO-Coll-77 (IC0566525; INGR10113), a Red Vanda (*Renanthera imschootiana*) Germplasm, with Red Colour Flower, Open Broad Sepals. Endemic to North-East

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Attractiveness, exotic nature, and shelf life of flowers play a major role in ornamental floriculture. Sometimes, rarity of these species also makes them almost novel, but popularity in disguise makes them more vulnerable due to over exploitation and leading even extinction in its own natural habitat. It is the common phenomenon currently occurring to Orchids, especially those listed under threatened and endangered category. *Renanthera imschootiana* Rolfe., known as 'red vanda' classified as an ally to Vanda group (Rao, 1997), comes under such category from north-east India. It is the only one species belonging to the genus *Renanthera*, found endemic to Manipur, Mizoram and Nagaland that are the part of the Indo-Burma mega bio-diversity hot spot. Enlistment of this species in Appendix-I, CITES (Convention on International Trade in related Endangered Species of Wild Fauna and Flora) during 1975 and prohibition of all species of orchids from exports as per 'Foreign Trade Development and Regulation Act, 1992' in India had much relevance for strengthened protective measures for conserving our rich orchid diversity. This species collected during

1998-99 at Imphal, Manipur with help rendered from ICAR RC NEHR, Manipur Centre was currently conserved at NRC for Orchids, Pakyong, Sikkim (Altitude 1,300 MSL) under the capacity as NAGS (National Active Germplasm Site) for Orchids. Apart from morphological characterization, its true breeding value of the accession was also assessed for effective utilization in genetic enhancement programmes. The accession, being monopodial epiphyte, the growth in terms of height was recorded from 35 cm to > 58 cm in a span of eight years (1999-2007). Stem is stout with leaves linear in shape measuring 7.8 cm x 1.6 cm with approx 14 numbers (per se). Generally the inflorescence is un-branched raceme, but in the year 2007-08 the branching of raceme was also noticed, with a recorded length of 38.2 cm. The flower size measures 4.7 cm x 2.9 cm. The species is peculiarly characterized with short (1.7 cm) and lanceolate shaped dorsal sepal and broader and free lateral sepals with a length of 2.8 cm. The red-purple (RHS-60A), the dominant color of the flower (lateral sepal & lip) and petals were colored grayed orange (RHS-164C)

herbal tea, tooth paste, etc.) in perfuming industries and as condiments. Traditionally the leaves are used to treat headaches, aching muscles and sore throat. The oil of wintergreen is well document to have fungicidal properties. Leaves of mature plants collected from various locations of the eastern Himalayan region of Indo-China border were analyzed by steam distillation which resulted to identify an elite line (Shankar-UBKVM-2) containing 1.79% essential oil, of which 98% was methyl salicylate as determined by gas chromatography.

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Bantawa P and TK Mondal (2008) Population studies of *Gaultheria fragrantissima* Wall. In Darjeeling district of West Bengal. *Nat. Prod. Rad.* 7: 68-73

Bantawa P, SK Ghosh, S Moitra, PD Ghosh and TK Mondal (2009a) Studies on dwindling population of *Picrorhiza scrophulariiflora* Pennell. (Scrophulariaceae): its status and conservation threats in Sikkim Himalayas, India. *Bio. Biodiver. Bioavail.* 3(1):15-22

Bantawa P, O SahaRoy, PD Ghosh and TK Mondal (2009b) Effect of Bavistin and adenine sulphate on shoot multiplication of *Picrorhiza scrophulariiflora* Pennell: an endangered medicinal plant of Indo-China Himalayan regions. *Plant Tissue Cult. Biotech.* 19(2): 237-245.

Bantawa P, SK Ghosh and TK Mondal (2010a) *In vitro* regeneration of a medicinal plant Nepalese Kutki (*Picrorhiza scrophulariiflora*) Pennell. *Biol. Planta.* (Accepted)

Bantawa P, SK Ghosh, P Bhandari, B Singh, PD Ghosh, PS Ahuja and TK Mondal (2010b) Micropropagation of an Elite Line of *Picrorhiza scrophulariiflora*, Pennell, an Endangered High Valued Medicinal Plant of the Indo-China Himalayan Region *Med Aroma. Plant Biotech.* (In press)

84. NRCO-Coll-77 (IC0566525; INGR10113), a Red Vanda (*Renanthera imschootiana*) Germplasm, with Red Colour Flower, Open Broad Sepals. Endemic to North-East

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Attractiveness, exotic nature, and shelf life of flowers play a major role in ornamental floriculture. Sometimes, rarity of these species also makes them almost novel, but popularity in disguise makes them more vulnerable due to over exploitation and leading even extinction in its own natural habitat. It is the common phenomenon currently occurring to Orchids, especially those listed under threatened and endangered category. *Renanthera imschootiana* Rolfe., known as 'red vanda' classified as an ally to Vanda group (Rao, 1997), comes under such category from north-east India. It is the only one species belonging to the genus *Renanthera*, found endemic to Manipur, Mizoram and Nagaland that are the part of the Indo-Burma mega bio-diversity hot spot. Enlistment of this species in Appendix-I, CITES (Convention on International Trade in related Endangered Species of Wild Fauna and Flora) during 1975 and prohibition of all species of orchids from exports as per 'Foreign Trade Development and Regulation Act, 1992' in India had much relevance for strengthened protective measures for conserving our rich orchid diversity. This species collected during

1998-99 at Imphal, Manipur with help rendered from ICAR RC NEHR, Manipur Centre was currently conserved at NRC for Orchids, Pakyong, Sikkim (Altitude 1,300 MSL) under the capacity as NAGS (National Active Germplasm Site) for Orchids. Apart from morphological characterization, its true breeding value of the accession was also assessed for effective utilization in genetic enhancement programmes. The accession, being monopodial epiphyte, the growth in terms of height was recorded from 35 cm to > 58 cm in a span of eight years (1999-2007). Stem is stout with leaves linear in shape measuring 7.8 cm x 1.6 cm with approx 14 numbers (per se). Generally the inflorescence is un-branched raceme, but in the year 2007-08 the branching of raceme was also noticed, with a recorded length of 38.2 cm. The flower size measures 4.7 cm x 2.9 cm. The species is peculiarly characterized with short (1.7 cm) and lanceolate shaped dorsal sepal and broader and free lateral sepals with a length of 2.8 cm. The red-purple (RHS-60A), the dominant color of the flower (lateral sepal & lip) and petals were colored grayed orange (RHS-164C)

with shade. The petals were observed smaller with a length of 1.3 cm and spotted. The lip size recorded 0.6 cm x 0.2 cm having presence of callus. The throat and column are in yellow color (RHS-8A). The flowering traits like spike initiation, flower bud initiation, days to 1st flower opening and days to 1st flower withering showed consistency, except number of raceme branches and number of flowers. Broader lateral sepals with attractive dominant red-purple/crimson colour and grayed orange with reddish spots

of petals in center of flower, having medium range vase life of 23.7 days have high breeding value of this accession for developing new hybrid derivatives at both national and international level.

References

- Rao AN (2000) Some important Indian orchids for breeding and Planting purposes. In: *Souvenir & Abstracts of 'National seminar on Developemntal biology and Commercialization of Orchids' and Orchid Show on 12-13th April, 1997 at Gangtok, Sikkim*, p7.

85. Selection IIHR-1 (IC0568708; INGR10114), Selection IIHR-2 (IC0568709; INGR10115), Chrysanthemum (*Dendranthema grandiflora*) Germplasm, with Early and Off Season Flowering, Suitable for Pot and Garden Use; Early and Off Season Flowering, Suitable for Pot and Garden Use

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Chrysanthemum is the second largest cut flower grown all over the globe. It is one of the most popular and commercial flower crops grown in India. In India large flowered varieties are grown as cut flower and used for interior decoration and for exhibition purposes. While small flowered varieties are also grown as flower and used for making garland, wreaths, 'veni', religious offerings and for bedding and potting purposes. Small flowered varieties are commercially grown in Tamil Nadu, Karnataka and Maharashtra (Poonam and Ashokkumar, 2007).

Fifteen chrysanthemum varieties have been developed at Indian Institute of Horticultural Research, Bangalore. Recently, efforts have been made to breed early and off-season varieties suitable for Bangalore conditions. Varieties for earliness in germplasm collection were strengthened from different sources. Two open pollinated seedlings, IIHR-1 (Pink Seedling) IIHR-2 (Brown seedling) from early flowering Punjab Gold (PAU, Ludhiana) were found to be promising. These were multiplied by vegetative propagation through rooted cuttings.

Characteristic Features of New Selections

IIHR-1 (Pink Seedling): This early flowering selection produces flowers in about 62.92 days in July-Sept.

Plants are dwarf (about 24.14 cm) with yellow green and medium leaves. Flowers are semi double with attractive pink (Purple 75 B) colour and are small-sized (about 3 cm in diameter). Average number of flowers per plant is 318.54 (Table 1)

IHR-2 (Brown Seedling): This early flowering selection produces flowers in about 68.02 days in July-Sept. Plants are dwarf (about 32.43 cm) with yellow green and medium leaves. Flowers are semi double with attractive brown (Grayed Orange 172 A) colour and are small-sized (about 4.84 cm in diameter). Average number of flowers per plant is 135.26 (Table 1)

Cultivation

It is multiplied by suckers and cuttings. After flowering, stems are cut back just above the ground. This induces formation of side suckers that are separated from mother plants and planted in the sand bed. Well-rooted suckers are directly transplanted to well drained red soil. Chrysanthemum is sensitive to waterlogging. Its transplanting is done during March-April under Bangalore like conditions.

Add 20-25 tonnes of well rotten farmyard manure, 125 kg N, 400 kg P₂O₅ and 200 kg K₂O in a hectare. Well-rooted suckers/cuttings are planted in beds following a spacing of 30 cm × 30 cm.

with shade. The petals were observed smaller with a length of 1.3 cm and spotted. The lip size recorded 0.6 cm x 0.2 cm having presence of callus. The throat and column are in yellow color (RHS-8A). The flowering traits like spike initiation, flower bud initiation, days to 1st flower opening and days to 1st flower withering showed consistency, except number of raceme branches and number of flowers. Broader lateral sepals with attractive dominant red-purple/crimson colour and grayed orange with reddish spots

of petals in center of flower, having medium range vase life of 23.7 days have high breeding value of this accession for developing new hybrid derivatives at both national and international level.

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Characteristic Features of New Selections

IIHR-1 (Pink Seedling): This early flowering selection produces flowers in about 62.92 days in July-Sept.

Plants are dwarf (about 24.14 cm) with yellow green and medium leaves. Flowers are semi double with attractive pink (Purple 75 B) colour and are small-sized (about 3 cm in diameter). Average number of flowers per plant is 318.54 (Table 1)

IHR-2 (Brown Seedling): This early flowering selection produces flowers in about 68.02 days in July-Sept. Plants are dwarf (about 32.43 cm) with yellow green and medium leaves. Flowers are semi double with attractive brown (Grayed Orange 172 A) colour and are small-sized (about 4.84 cm in diameter). Average number of flowers per plant is 135.26 (Table 1)

Cultivation

It is multiplied by suckers and cuttings. After flowering, stems are cut back just above the ground. This induces formation of side suckers that are separated from mother plants and planted in the sand bed. Well-rooted suckers are directly transplanted to well drained red soil. Chrysanthemum is sensitive to waterlogging. Its transplanting is done during March-April under Bangalore like conditions.

Add 20-25 tonnes of well rotten farmyard manure, 125 kg N, 400 kg P₂O₅ and 200 kg K₂O in a hectare. Well-rooted suckers/cuttings are planted in beds following a spacing of 30 cm × 30 cm.

Table1. Quantitative and qualitative characters of IIHR-1 and IIHR-2

Variety	IIHR-1 (Pink Seedling)	IIHR-2 (Brown seedling)	Punjab Gold	SEm±	CD @ 5%
Plant height (cm)	24.14	32.43	35.51	0.31	1.22
Plant Spread (cm)	32.97	37.7	33.62	0.3	1.18
No. of Lateral branches	18.80	22.01	18.01	0.09	0.39
Days taken to flowering	62.92	68.02	74.49	0.24	0.95
No. of flowers/plant	318.54	135.26	132.99	0.56	2.21
Size of flowers (cm)	2.95	4.84	6.75	0.05	0.21
Average weight of flowers (g)	0.53	1.51	2.49	0.03	0.12
Yield (gms/plant)	156.62	191.48	325.75	0.69	2.71

Table2. Qualitative characters of IIHR-1 and IIHR-2

Variety	IIHR-1 (Pink Seedling)	IIHR-2 (Brown seedling)	Punjab Gold
Flower colour	Purple 75 B*	Grayed Orange 172 A*	Yellow 12 A*
Disc presence	Prominent	Prominent	Not prominent
Flower type	Semidouble	Semidouble	Double
Economic use	Pot & garden use	Pot & garden use	Pot & garden use

*As per RHS Colour Chart

Another dose of 125 kg N/ha is given at the time of first pinching and 125 kg N/ha is given at the time of first pinching and 125 kg N one month after pinching. Irrigate once or twice in a week depending upon soil and weather conditions.

If foliage first turns yellow and dark brown with blackened margins, spray with Dithane M-45 or Kavach at 0.2%. Powdery mildew disease can be easily identified by powdery growth on leaves. Spraying of wettable sulphur 3 g/litre or Bavistin 2

g/litre helps control it. Aphids sucking the sap on leaves and causing discoloration of petals can be controlled by spraying of Demeton S-Methyl 0.05% (Metasystox 2 ml/litre). Caterpillars feeding on leaves and flowers are checked by spraying of neem oil 4 ml/litre.

References

Poonam and A Kumar (2007) Garden Beauty – A promising chrysanthemum cultivar for garden decoration. *J. Ornamental Hort.* 10:165-168.

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