Role of On-farm/*In situ* Conservation and Underutilized Crops in the Wake of Climate Change*

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Traditionally farmers use diverse crops, trees and wild plant species, livestock and aquatic species to sustain/enhance their livelihood. The use of diverse species and varieties enhances their adaptability and resilience capacity to changing environmental and economic conditions. Genetic diversity is a key element in farmers' livelihood strategies particularly in areas under high ecological, climatic and economic stresses and risks. Global food security has become increasingly dependent on a limited number of varieties of a few major crops and in the wake of climate change, such a situation makes farmers more vulnerable with regard to their nutrition and income security. This paper aims to discuss the conceptual framework of on-farm/*in situ* conservation in adapting and mitigating climate change through an integrated system of diversified food production and land use. The role of on-farm/in situ conservation of crops is discussed along with its complementary advantages over *ex situ* conservation. Empowerment of farming communities is essential for effective *in situ*/on-farm conservation as the process encourages local level decision making on management of genetic resources. The paper also highlights community-based biodiversity management as a methodology to realize *in situ*/on-farm conservation through strengthening farmer seed systems, and promoting climate resilient integrated home garden production systems, especially underutilized crop species and carbon rich farming that support climate change actions. Implementation of biodiversity management approaches will require conducive policy environment in order to be truly effective and sustainable. Some relevant recommendations on how to best proceed towards a viable *in situ*/on - farm conservation system are also proposed.

Keywords: Agrobiodiversity, Climate change, Farmers' seed system, *In situ* conservation, Integrated farming system, On-farm conservation, Underutilized crops

Introduction

The Convention on Biological Diversity (CBD) within its broader framework defines two conservation strategies: *ex situ* conservation and *in situ* conservation. UNEP (1992) defined *in situ* conservation as "the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticated and cultivated species, in the surroundings where they have developed their distinctive properties". These definitions and related strategies applied to the field of agricultural biodiversity require their blending with the use dimension in order to be translated into practices and realize the effective linking of conservation with farmers' livelihoods. *In situ*/on farm conservation (often just referred to as 'on farm conservation') refers to the maintenance of cultivated plants (often in association with their wild relatives that may be present in the same field) which are conserved in the very place where they developed their present-day characteristics (Altieri and Merrick, 1987; Brush, 1995; Jarvis and Hodgkin, 2000) and where they continue to evolve thanks to the work of farmers (Frankel *et al.*, 1975). On-farm conservation is thus a highly dynamic form of plant genetic resources (PGR) management, which allows the processes of both natural and human selection to continue to act in the production system. On-farm conservation is therefore generally used to describe the dynamic management process by which farmers maintain traditional crop varieties that were developed in their local conditions and that they continue to modify thanks to their management practices and crop selection efforts. Thus, the conservation of specific genotypes becomes a secondary objective to the continuation of the processes that allow the material to evolve and change over time (Jarvis and Hodgkin, 2000).

The potential threat that the loss of genetic diversity poses to the world's food fuelled the so called PGR conservation movement which started in the early 1970s with the establishment of IBPGR (now Bioversity

*Paper presented in the National Symposium on Recent Global Developments in the Management of Plant Genetic Resources, NBPGR, New Delhi, India,17-18 December 2009

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International) and which has led insofar to the creation of 1740 *ex situ* storage collections (called also gene banks) around the world (Pistorius 1997; Fowler and Hodgkin 2004; Bioversity 2009; FAO 2010). While this form of conservation remains no doubt practical and useful, especially for immediate use in plant breeding, it has major drawbacks in terms of effectiveness with regard to the use of stored material (not easily accessible by farmers). Serious concerns are also arising from the fact that they freeze the natural evolutionary process and in so doing limit the adaptive capacities of genetic resources to climate change. Furthermore, *ex situ* collections are more vulnerable to mismanagement (e.g. cases of genetic shifts, genetic drifts during rejuvenation activities or the spread of seed-borne pathogens due to poor plant quarantine practices). But *ex situ* conservation is also an expensive endeavor whether we are dealing with seed (orthodox seed crops) in cold stores or with vegetative material (field genebanks necessary for crops with recalcitrant seeds and clonally propagated species). With regard to on farm conservation, apart from allowing evolution to continue, this method contributes as well to the conservation of diversity at all levels (landscape, ecosystem, among and within species) and it is therefore highly strategic. It does also contribute to empower the farmers to better exercise control over their crop genetic resources, major biological and livelihood assets. Another major advantage of on farm conservation is related to its conduciveness in safeguarding the traditional knowledge associated to biodiversity which is an integral part of peoples' social and cultural identity (CUBIC, 2000), and which is fundamental for celebrating and appreciating crop diversity today and in the future. Lastly, on farm conservation is a powerful instrument to allow the implementation of benefit sharing as recommended by the CBD which has in fact recognized the continued maintenance of traditional varieties on-farm as an essential component of sustainable agricultural development (UNEP 1992).

Challenges

Since the time that the Convention on Biological Diversity provided a general framework for *ex situ* and *in situ* conservation strategies, most agencies dealing with plant genetic resources conservation have been facing the dilemma of how to implement in practical terms *in situ* conservation of agricultural biodiversity. The major challenges faced to achieve this end are centered around the following:

i) lack of a clear understanding of the scientific basis of *in situ* conservation of agricultural biodiversity and how it can be practically implemented on the ground,

ii) difficulty in changing the mindset of current PGR institutional set up to work closer with farmers and communities,

iii) rationale of identifying the least cost conservation areas

iv) difficulties in identifying sustainable incentive mechanisms to support on farm conservation and

v) obstacles when trying to canvass policy support to empower the communities in diversity rich areas for community based management of agricultural biodiversity.

What makes these challenges particularly complex is the fact that they are highly interlinked and dependent upon a mix of socio-cultural, economic and political factors, making on-farm conservation not a purely technical intervention (as is the case in *ex situ* conservation) but a much more complex social and collective-action type of endeavour.

Central to these issues, is the recognition that if crop genetic resources (including landraces) are to be conserved successfully and sustainably on-farm, such an outcome should be the result of farmers' production activities directed to improve his/her livelihood ("*conservation through use*"). This means that on-farm conservation efforts must be carried out within the framework of farmers' livelihood needs, and for that reasons, the mobilization of support to on farm conservation need to be conceived and designed within the broader objective of creating a more enabling environment for agricultural development in its various aspects. So far, rich local crop diversity is maintained in those regions where the private value of local landraces and public value of genetic diversity are high (Smale *et al*., 2004). Given the current globalization trends and market environments, it would be difficult to maintain valuable local crop genetic resources unless these are made economically attractive and competitive in the market through consistent interventions along the value chain from the selection of improved varieties, to enhanced cultivation practices, value addition and marketing as well as socio-cultural, educational and public awareness efforts.

One of the often-cited disadvantages of on-farm conservation is the difficulty experienced by plant breeders in accessing material that is maintained by farmers. This is mainly because the on-farm conservation efforts to date have not been mainstreamed or linked to national PGR efforts. Although *ex situ* and *in situ*/on- farm conservation methods are highly complementary measures, their interdependency has only very rarely been put into practice. Depending upon the available resources and government commitment, selection of on-farm conservation sites should consider two broad guidelines: a) identification of the least cost conservation site, and b) potentiality of "win-win" situation in terms of livelihood gains and ecological costs for the site. The least cost on-farm conservation will occur in those sites that are highly ranked in terms of public benefits (richness and evenness of genetic diversity) and where the private benefit that farmers obtain from growing genetically diverse varieties is the greatest. The economic concept that farmers' varieties embodies both (i) 'private' values in the harvest the farmer enjoys, either directly as food or feed, or indirectly through the cash obtained by selling the seed/grain and purchasing other items, and (ii) 'public' values in its contribution to the genetic diversity from which future generations of farmers and consumers will also benefit (Smale *et al*., 2004). The crop genetic resources which have both low farmer utility (current private value) and public value will be difficult to conserve on-farm unless public interventions are made for adding benefits.

Those crop genetic resources important zones (CGR-IZs) which have both high private value (direct use) and high public value (rich genetic diversity of CGR) are considered potential sites for on-farm conservation of agricultural biodiversity. Since there is a trade-off between livelihood gains and ecological costs, on-farm conservation programmes should aim to achieve "win-win" situation by balancing livelihood gains with conservation costs (Umashaankar *et al*., 2004). This requires community based approaches that empower farmers and rural institutions in better appreciating the value of on-farm conservation, take greatest advantage of genetic resources maintained on-farm and play a leading role in decision making in the management of this biodiversity at the local level. The actions such as public awareness, education, participatory plant breeding, value addition of local products and policy support through local institutions are very important for realizing on-farm conservation in a sustainable manner. Two options can be considered in providing benefits; the first through participatory plant breeding, and the second through public awareness, better marketing, and policy incentives (Gauchan *et al.*, 2003). The first option is to seek improved quality, disease resistance, high yield, better taste, and other preferred traits through breeding, seed networks and modified farming systems. The second option includes adding value to local crop genetic resources so that the demand for the material or some derived products may be increased. These diverse options will emerge when the communities, researchers, and developmental institutions are directly involved in the management of traditional knowledge and genetic resources for biodiversity-based livelihood and income generation. This is only possible if the local capacity of farming communities and institutions are strengthened for making appropriate decisions and for being able to take up effectively also important tasks including the documentation and monitoring of local crop diversity (Sthapit *et al.*, 2008).

To date, the organizations engaged in the promotion of conservation of plant genetic resources for food and agriculture (PGRFA) are facing the dilemma of how to strengthen capacity of communities and rural institutions for best implementing *in situ* conservation on-farm. Since the farmers and their social networks play a key role in maintaining dynamic process of evolution, selection and adaptation of useful diversity in the changing climate, it is important to understand that on-farm conservation is a constantly changing complex system of relations between people, plants, animals, other organisms and the environment, continuously challenged by new problems. In such a condition, the broader is the diversity employed on- farm, the more resilient will be the production system (Jarvis *et al.*, 2007). And this statement is particularly meaningful within a climate changing context. To that respect, therefore, the deployment of *in situ*/on- farm sustainable conservation and use of neglected and underutilized species (NUS) represent a very strategic component of community-based adaptation strategies (Padulosi *et al.* 2009). Functional partnerships between multi-sectoral institutions and community based organizations will be then fundamental to pursue such a strategy (Rojas *et al.*, 2009).

In response to these challenges, Bioversity International (formerly known as International Plant Genetic Resources Institute (IPGRI) and its national

partners launched an international research effort, 'Strengthening the scientific basis of on-farm conservation of agricultural biodiversity on-farm' in eight countries in 1995 to understand four basic questions (Jarvis *et al*., 2004, 2007):

- What is the amount and distribution of the genetic diversity maintained by farmers over space and time?
- What are the processes/methods used, consciously or unconsciously, to maintain the genetic diversity on-farm?
- Who maintains genetic diversity within a community and how?
- What factors influence farmers' decisions on maintaining traditional varieties?

Understanding the above mentioned questions provides the scientific knowledge needed not only to manage crop genetic resources on-farm, but also to develop options for better livelihoods and income that provide incentive for conservation efforts.

Impact of Climate Change in Agriculture and Livelihoods

The Fourth Assessment (AR4) of the Intergovernmental Panel on Climate Change (IPCC) provides an overview of recent scientific understanding on climate change (IPCC, 2007). Climate models are only predictable means to predict global future climate. Although 21 global climate models (GCM) give different scenarios based upon atmospheric science, chemistry, physics, biology and astrology. In general, as per the IPCC predictions, the global temperatures are likely to increase by 1.1-6.4ºC from 1990 to 2100 though the speed at which the temperature will rise is still debated (IPCC, 2001; 2002). The water availability in humid tropics and high latitude areas will increase due to 20-30% increase predicted in annual precipitation whereas in sub-tropical regions, the water availability will decrease as the region will receive less rain and/or untimely rains and therefore will be subjected to more frequent droughts. Sea levels are likely to rise in the range of 22-34 cm between 1990 and 2080s, thereby affecting lives of communities in coastal countries. The IPCC also predicted that Hindu Kush Himalayan climate will undergo an increase of 5-6ºC in atmospheric temperature as well as 20-30 % increase in precipitation. This coupled with glacial retreat and loss of snow cover on mountains will lead to unpredictability of seasons and monsoons in South Asia. Suitability for grain production will decrease more rapidly in regions with sandy soils than in regions with clay or medium soils, as the temperature increases (Zullo Junior *et al*., 2006). Furthermore, there is likelihood of higher frequency of extreme events such as cyclones, typhoons and hurricanes, floods and landslides, prolonged drought, etc.

Although there are lots of debates and disagreements in these predictions, the scientific community agree on the following common understanding: 1) climate change is already happening and will happen in future, 2) some regions will get hotter, some places dryer and others wetter, 3) there will be more variability and therefore, great uncertainties in agriculture, 4) the suitability of species/genotypes changes in both positive and negative directions, and finally 5) lack of knowledge on what will happen in some regions due to lack of data and information (Jarvis *et al.*, 2008a; 2008b).

In spite of what has been published in the abundant recent literature on this topic, the implications of climate change in agriculture are still a bit vague as these are based upon modeling and predictions. Lobell *et al*. (2008) carried out an analysis of climate risks for crops in 12 food insecure regions to identify adaptation priorities, based upon statistical crop models and climate projections for 2030 from 20 GCM models. The results indicated that South Asia and Southern Africa are the two regions that, without sufficient adaptation measures, are likely to suffer with negative impacts on several crops that are important to large food insecure human populations. Using the A2 scenario of the IPCC's NCAR and CSIRO models, International Food Policy Research Institute (IFPRI) studied the impact of climate change in agriculture in the time frame of 2000 - 2050. The report also suggests that South Asia will be particularly hard hit by climate change as the crop productivity of almost all crops is predicted to face the greatest decline in that region (IPCC, 2007). Higher temperatures eventually reduce yields of desirable crops while encouraging weed and pest proliferation. Although there will be gains in some crops in some regions of the world, particularly in developed countries in the North, the overall impacts of climate change on agriculture are expected to be negative, thereby threatening the global food security.

There is established evidence that climate change is already affecting biodiversity and will continue to do so. The Millennium Ecosystem Assessment (2005) report estimated that by the end of this century, the climate change will be the driver of biodiversity loss.

IPCC reports predicted that many species will be extinct from the ecosystems which will have profound impact on ecosystem functioning and services (i.e. provisioning, regulating, supporting and cultural) because of increase in global average temperature. There will also be an adverse effect on the species component of biodiversity (Rao, 2009) which include: i) changes in distribution pattern (Jarvis *et al*., 2008a), ii) increased extinction rates, iii) changes in reproduction timings, iv) changes in length of growing seasons for plants, v) changes in plant community composition, and vi) changes in ecosystems. These factors will result in significant changes in farming practices and genetic resources that are currently being used. Coping with these new realities will involve the use of agricultural biodiversity in innovative ways to provide adaptability and resilience in the face of changing and variable environments.

Role of *in situ* On-farm Conservation in the Context of Climate Change

In the debate on climate change and agriculture, the role of *in situ* conservation and on-farm management of agricultural biodiversity is seldom discussed with the attention it deserves. The various climate change predictions made it clear that many regions around the globe are going to witness the change in various ways. In such a situation, it is important to consider whether such changes will affect on-farm management of cultivated landraces and their wild relatives. Jarvis_*et al*.(2008a; 2008b) used current and projected future climate data for ~2055, and a climate envelope species distribution model to predict the impact of climate change on the wild relatives of groundnut (*Arachis hypogea*), potato (*Solanum tuberosum*) and cowpea (*Vigna unguiculata*). They reported that wild groundnuts were the most affected group among three spp, with 24-31 (depending on the migration scenario) of 51 species projected to go extinct and their distribution area, on an average, expected to be reduced by 85-94 %, depending on the migration scenario, over the next 50 years. In terms of species extinction, cowpea appeared to be the least affected by the climate projections on these three crops studied, although, according to other studies almost half of the natural distribution area of wild *Vigna* species (that is, not just wild *Vigna unguiculata*) is also expected to be lost by the middle of this century due to climate change (Anonymous 2007). These results suggest that there is an urgent need to identify and effectively conserve crop wild relatives that are at risk due to climate change. On the other hand, there are many reports indicating that the new strains of pathogens and pests (e.g. Ug99 strain of stem rust in wheat; bacterial fire blight in apples; new strain rice blast, etc.) are emerging which need landraces and wild relatives as sources of resistance genes (Qualset and Shands, 2005). Due to climate change, it is difficult to predict which new pest or pathogen will develop or how will be the rainfall next year, but agricultural biodiversity can be used - as always farmers do-to have a set of crop varieties in farming systems to increase the options to buffer against unpredictable changes (Holger *et al*., 2004). This requires access to a wide range of portfolio of local crop diversity at the hand of community for countering these threats. This explains why on-farm conservation can play critical role in future as well to solve emerging problems.

Genetic diversity which is currently underutilized may become more attractive to farmers as a result of climate change. Many neglected and underutilized species which are currently maintained through *in situ* conservation on-farm could be the important crops for the future. Their adaptability, plasticity and resilience to stresses provide farmers with needed coping strategies to confront with climate changes. Because of changes in shift in rainfall pattern and temperature deviations from normal, community based management of a wide portfolio of plant and animal genetic diversity is required to allow adaptive capacity. The suitability of current crop genotypes to local conditions will change in both positive and negative ways, depending upon the crop and region, but will affect many production systems. The processes of *in situ*/on-farm management of agricultural biodiversity carried out by millions of farmers in the world have developed a range of genetic diversity that helps to diversifying incomes and livelihoods of people in such changing situations. On-farm management of genetic diversity has traditionally allowed farmers to cope with adversity and this process will continue to serve that function in future too.

Climate variability and risk has always been a part of agriculture, and farmers have developed many ways of managing that risk. From farmers perspective, climate change is not seen in terms of major disasters such as floods or drought or hurricanes, but rather as increased uncertainty such as shift in onset of rain at planting time or end of rain at harvesting time; some years bring excessive rainfall while others are very dry, with a greater irregularity within and between two annual rainy seasons.

Such uncertain weather is directly affecting crop production and income of farmers. It is difficult to assume that current research system has capacity to develop a set of technologies and suitable varieties that match the needs of changing climate scenario.

The maintenance and use of a wide diversity of crops, trees and livestock are the livelihoods and survival strategies of rural farming communities throughout the world but the speed of climate change is reported to be much higher than that required for landraces to evolve and adapt for changing climatic environments. Hence, the plasticity of genetic resources will remain important for such situations. Pigliucci (2001) defines phenotypic plasticity as a "property of a genotype to produce different phenotypes" as a response to different environments. There is already a lot of debate in the scientific community (Scheiner, 1993; Via, 1993; Via *et al*., 1995; Pigliucci, 1996, 1998) about whether phenotypic plasticity (phenotypic variation due to environment) is an evolving trait, which can be adaptive, neutral or maladaptive (Alpert and Simms, 2002), or a by-product variation due to other plant responses. Regardless of the debate, it can be agreed that phenotypic plasticity can be a useful paradigm or framework to understand the interactions of genetics, development, ecology and evolution (DeWitt and Scheiner, 2004).

In order to understand the role of *in situ*/on-farm conservation of agricultural biodiversity in the wake of climate change, it is also important to understand how communities have been using diverse types of plants and animals in integrated production systems to adapt and cope with climate change effects. There are two ways: first, seed selection by farmers over seasons exerts selection pressure on populations of genotypes through the criteria used by the farmers to select the seeds and through the environment (Harlan, 1992). Second, new genetic diversity is introduced into the farmer's seed system through the introduction of new varieties or new selection and introgression of genes from hybridization with wild species or varieties. New varieties enter the farmer seed system through social seed network and exchange of seeds with other farmers, seed from local markets or from the project or commercial enterprises (Sthapit and Rao, 2009; Almekinders & Louwaars, 2002). This system is very dynamic and integrated to cope with all kinds of pressures. The common strategies used by farmers and communities to manage vulnerability caused by climate change are listed in following points:

- Maximize the use of NUS as genetic resource base (buffer) for managing adversity and to cope up with changing climate scenario
- Capitalize/ maximize the use of diverse-ecosystems, and species diversity integrated farming system (such as home gardens, livestock, aquaculture, perennials, bee keeping etc)
- Maintain intra-specific diversity to cope with environmental and economic adversity (e.g. maintain richness in staple crops to cope with vulnerability)
- Adopt farmer-to-farmer seed/planting materials exchange system (informal seed system) as a social seed network to ensure local level community based adaptation strategies and enhance access to locally adapted genetic resources for unpredictable climatic situations
- Farmer selection from available or introduced or introgressed diversity to adapt local situation

Neglected and Underutilized Species as a Buffer for Climate Change

Another interesting traditional practice is that indigenous farming communities in the most vulnerable areas such as Sub-Sahara Sahelian regions, Andean mountains, Himalayan high mountain ecosystem, maintain portfolios of species of neglected and underutilized species, animal breeds and farm trees as risk aversion or adversity management practices. Mixed farming and mixed cropping are common practices to address such uncertainties. In home gardens of East Java, a portfolio of emergency root crops (e.g. *Amorphophallus campanulatus*, *Colocacia* spp, *Dioscorea* spp, *Manihot* spp. etc.) is found to buffer food supply chain during climatic adversity. Many such examples were also reported in Chepang indigenous community of Nepal (Sthapit *et al.*, 2008; Aryal *et al.* 2009). Although policy makers and the media highlight the impact of extreme events such as hurricane, floods and drought, the farmers are worried from rainfall and temperature patterns moving outside the regular variability ranges. The impact of such local variation and uncertainty is the low farm productivity and income of farmers and there are not immediate technological solutions available to farmers as the speed of these changes is difficult to be controlled with the current research and development system.

Despite the general notion that NUS are neglected for specific socioeconomic reasons, the role of these species traditionally used by indigenous farming

communities, becomes extremely important to reduce risks and adapt to adversities caused by climate changes. The neglected and underutilized crop genetic resources are very vital for sustainable agriculture (Eyzaguirre *et al.*, 1999; Bhag Mal, 2007). Traditionally, these species contribute significantly to the well being and livelihoods of the rural households. Many of these species are well adapted to stress conditions of extreme environments and hence form part of the sustenance farming systems. Many underutilized species occupy important niches, adapted to risky and fragile conditions of rural communities and have a comparative advantage in marginal lands as they can withstand stress. They also contribute to the diversity and stability of agro-ecosystems and are potential crops for the diversification of agriculture. These species often play a strategic role in fragile ecosystems such as those of arid and semi-arid lands, mountains, steppes and tropical forests. Most of the these crops do not require high inputs and can be successfully grown in marginal, degraded and wastelands with minimal inputs and at the same time can contribute to increased agricultural production, enhanced crop diversification and improved environment and have the potential to contribute useful genes to breed better varieties capable of withstanding and sustain the climate change scenario (Bhag Mal and Joshi, 1991; Bhag Mal, 1993, 1994, 2007, Padulosi *et al.*, 2009).

The genetic resources of many of these important species are being lost through rapid destruction of natural habitats especially in the tropics. The State of the World Report II on PGRFA (FAO 2009) depicted a very worrying situation with regard to conservation and use of agricultural biodiversity and highlighted that very limited efforts are on record to curb the genetic and cultural erosion taking place on-farm and severely affecting the sustenance of local crops and varieties. Furthermore, the international policy instruments such as the Global Crop Diversity Trust are currently focusing on crops of Annex. 1 of the International Treaty on Plant Genetic resources, thus excluding *de facto* a large number of other important species including potential underutilized crops from being properly safeguarded, conserved and promoted for effective use. Hence, more and concerted efforts are needed to support *in situ*/on-farm conservation and sustainable use of neglected and underutilized species.

An Integrated Faming System to Climate Change Adaptation

It is a fact that agricultural biodiversity is an important part of the climate change management strategies being developed by indigenous people and rural communities but is not adequately recognized and the knowledge of how, when and what agricultural biodiversity has been used to cope with climate change is scattered and not well documented. Most rural areas have always experienced climate variability, and farmers have always had to cope with a degree of uncertainty in relation to the local weather. They maximize the wide range of ecosystem available in the landscape they live, their production systems are integrated with crops, animals, fisheries, perennial fruits and trees around homestead or at the vicinity to rivers, lakes and forests and maintain portfolios of varieties of staple crops for managing adversity. There is interdependence within the system which is designed to spread risk and vulnerability to stochastic events. In the past, the production system with greater diversity, or which was successfully integrated with livestock or orchard, was often less vulnerable to sudden changes, and showed higher levels of resilience. Farming systems with perennial fruit trees for example, coconut, mango, mangosteen, durian, jackfruit, etc. not only provide options for household food supply but also constantly maintain and develop their root and biomass and associated carbon (Scherr and Sthapit, 2009) while providing vegetative cover for soils whereas livestock provide cash to meet emergency needs. Livestock was never really mentioned in the climate change debate until 2007, when FAO reported that livestock produces 14.5% of all greenhouse gases. If the livestock are effectively integrated into ecological farming by small holder farmers, they have potential to mitigate some of the adverse effects of climate change and also offer options for coping strategies to farmers.

Similar to carbon credits, agrobiodiversity conservation credits (ACC) could be awarded to farmers who nurture wild and cultivated agrobiodiversity in their fields, who adopt agrobiodiversity or carbon friendly farming practices, such as no-tillage, using higher residue cover crops and rotations, decrease the use of fossil based fertilizer or pesticides, convert marginal crop land to trees or grass residue management, high-biomass crop rotation and cover crops or integrated home garden system, perennial grasses for pastures, rotational grazing, etc. In order to meet the restrictions on greenhouse gas emissions, industries need to buy "carbon credits," essentially paying another for storing carbon to offset the excess it is releasing to the air. This requires strong

policy support to implement such incentives.

Similar to the concept of reducing emissions from deforestation (REDD) and Avoided Deforestation (AD) for developing countries, agrobiodiversity conservation could potentially seek to be compensated through agrobiodiversity conservation credits (ACC) for saving genetic diversity for current and future food security and for providing valuable ecosystem services. Potentially, it can be used both as an adaptation and mitigation tool that will earn back money for the people who nurture and care for it.

Agrobiodiversity conservation credits might be just the answer to addressing pressing conservation challenges faced by farmers and scientists alike. The concept of agrobiodiversity conservation credits (ACC) has to demonstrate the full costs and benefits of the maintenance and use of agrobiodiversity in agricultural landscapes to the different stakeholders involved. This valuation must go beyond the present and future financial benefits of the marketable products of biological resources to include those of the ecosystem services that they provide. These credits could be traded or paid for maintenance.

Farmer Seed System

The traditional knowledge/practices and local genetic resources play a key role in farmers and community's capacity to adapt to climate change. Farmers' ability to cope with impact of climate change will be strengthened if the research and development institutions can build upon the traditional knowledge and practices of farmer seed and germplasm management systems. This requires strengthening their social seed networks and policy supports that promote farmer-to-farmer seed exchange system. Traditional or social or informal seed systems are maintained through the interactions of economic, social and cultural institutions that ensure availability of planting materials. Individual farmers search, select and keep their own locally adapted seeds and breeding stocks but practice social forms of exchange, including gifts, barter and sales that deploy agricultural biodiversity across landscapes and communities. In the context of climate variability and risk of crop failure in a local condition, communities with strong social seed networks are better equipped to cope with the effect of climate change compared to communities with weak and disturbed social seed networks (Subedi *et al.,* 2003; Paudel *et al.*, 2008). In many traditionally managed agro-ecosystems, local populations of domesticated crops maintain a high level of genetic diversity by the function of migration and re-colonization (sink-source) of meta-populations (van Dusen, 2003, Hastings and Harrison, 1994). It was observed that local varieties suffered from climate variability can re-colonize their populations (in terms of area and number of growers) by simple way of seed/planting materials flow that takes place from farmer to farmer networks. Commercially and centrally planned seed companies and government institutions have difficulty to predict climatic unpredictability and plan for seed provision that needed for diverse types of small farmers. In fact, on-farm conservation/management of wide range of crops, trees and animals play key role to buffer such situation and provide access to locally adaptive materials and sustain livelihoods. Farmer seed system allows the dynamic change that characterized crop landrace systems-open, decentralized genetic systems that are constantly evolving to fit farmers' needs and environmental changes-could help in coping with the uncertainty generated by climate change in agriculture (Bellon, 2010).

Strengthening Farmers' Capacity through R&D to Cope with Climate Change

In order to strengthen the capacity of farmers, it is essential to consolidate the roles of farmers as conservers, promoters of diversity and dynamic innovators by enabling policy environment for on-farm management, farmer innovation and strengthening farmers' seed systems coupled with scientific capacity building of these communities. The community biodiversity management (CBM) approach integrates knowledge and practices with social systems; local rules of institutions drive it (Sthapit *et al.,* 2006; Sthapit *et al.,* 2008ab). This approach can be realized by empowering communities and their institutions from the outset, building upon an analysis of sustainable livelihood assets for reducing poverty and social injustice. The key element is to institutionalize local level decision-making. As an integrated conservation and development approach, CBM reinforces the capacity of farming or user communities and their institutions. The focus is on increasing decision-making power and securing community access to and control over the resources required for community biodiversity management. The key elements of CBM include: (i) knowledge about biodiversity and associated landscapes, (ii) social systems facilitating maintenance and exchange of their genetic resources, (iii) local institutions that support and govern local management and access to biodiversity, (iv) technologies, processes and practices

that add value to local genetic resources, (v) local financial resources such as group savings and credits to ensure continuity, and (vi) necessary linkages to appropriate institutions which will sustain the access to livelihood assets.

CBM is a process-led approach and builds on farming/user communities' existing capacities and committed policy support. Empowerment of farmer communities is a precondition for effective *in situ* conservation of PGRFA. The experiences under Bioversity's global on-farm project amply demonstrated that community based biodiversity management facilitates the process of community empowerment and local decision making for collective action and therefore, the process that supports farmers decision making in management of genetic diversity is considered as a proxy methodology to realize *in situ*/on-farm conservation of PGRFA and this can be achieved by consolidating the role and capacity of farmers and their rural institutions. This approach is not easy for those people who work in genebank as they are used to control all decisions as per the need of *ex situ* system. In contrast, this mindset has to be changed in case of implementing on-farm work and many researchers find this challenging for current PGR conservation organizations as the institutions have to develop new kind of partnership with key and legitimate actors of on-farm management. PGR institutions that worked with community based organizations had been able to do this effectively by defining clear roles and responsibilities of different actors. During CBM process, all actors can find their respective role to cultivate partnership in research and development.

CBM is a methodology comprised of a number of steps and a set of practices that suit to the particular context (Sthapit *et al*., 2006). These include: i) enhancing community awareness, ii) understanding local biodiversity, social networks and institutions, iii) capacity building of community institutions, iv) setting up of institutional working modalities, v) consolidating community roles in planning and implementation, vi) establishing a CBM Trust Fund (payment system for community conservation efforts), vii) community monitoring and evaluation, and viii) social learning and scaling up for community collective action

This process allows farmers to gain scientific insights of knowledge related to climate change scenarios, access to new varieties and technologies and blend or integrate into their own traditional knowledge and farming system to cope with new problems and always finding new ways to deal with them. This allows the communities to be prepared against unpredictable nature of climate and socioeconomic environments.

Conclusions

Climate change represents a major threat to agrobiodiversity. However, agricultural biodiversity should be a key component of climate change adaptation strategies. One of the ways in which climate change negatively affects agriculture is to change the growing conditions and thus making the current practices and varieties ill-suited in the changed context.

Farmers may not have the capacity and facility to predict climatic variability before crop seasons or which new pest or pathogen will develop or how the rain will fall during the crop season. However, they can and do use a set of crop varieties in agricultural production systems to increase options to buffer against an unpredictable change. In this context, agricultural biodiversity has the potential to provide immediate cropping alternatives as well as genetic materials for the further development of stress tolerant varieties. The role of NUS as a buffer for climate change should be further strengthened and promoted. Crop diversification integrated with livestock/fisheries/forestry in a landscape for carbon rich farming and to cope with livelihood vulnerability needs to be also adequately supported.

Strengthening farmer seed systems of ranges of neglected crop species and other associated biodiversity promote open, dynamic and integrated genetic system to cope with climate change at the local level through: i) Community based conservation actions (e.g. seed fairs, diversity kits, community based register (CBR), community seed banks, community based seed production schemes) to improve access of materials and knowledge and their exchange, and ii) grassroots breeding, participatory variety selection and participatory plant breeding to develop farmer's skill and capacity in selection in the changing context. This is only possible if farmer's role as conserver and promoter of diversity and dynamic innovator is consolidated by strengthening farmer's seed system and agronomic practices and compensated/rewarded for the services of conservation.

Farmer's ability to search for new adaptive diversity, selection of new traits and exchange of selected materials with friends and relatives are key adaptive strategies for climatic adversity. While the international community

is responding to climate change threat by lending increased support to *ex situ* conservation, very little is done to support evolutionary breeding process i.e. on-farm/*in situ* conservation where the largest amount of the world's local crop diversity is maintained for immediate use. Therefore, it is extremely important to understand the (very poorly known) situation regarding the *in situ*/on farm conservation of agrobiodiversity (including NUS), mapping out species distribution and their threats, documenting who maintains/exchanges both diversity and associated traditional knowledge and how these materials and knowledge flows from farmer-to-farmer. All these data will be essential to guide local institutions and governments to develop suitable strategies for monitoring the impact of climate change over time and act in time to reduce negative impact on agrobiodiversity and livelihood of the people depending on it. It is therefore of utmost importance that greater research thrust is given on:

- Strengthening capacity of the community to maximize use of genetic diversity to adapt to climate change
- Integrating diverse crops, trees, livestock and aquatic species (including NUS) to enhance adaptability and resilience capacity to changing environmental conditions
- Establish monitoring and early warning systems for NUS in the context of greater interventions in support of in situ/on- farm conservation of local biodiversity (including the introduction of 'Red Lists' for cultivated crops);
- Promote greater access and exchange of diversity of underutilized (including expansion of Annex I list of the Treaty on PGRFA) as a critical element in support of crop diversification strategies.

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Plant Genetic Resources for Improvement of Rust Resistance in Wheat (*Triticum aestivum* L.)

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Plant genetic resources are most vital for developing high yielding rust resistant cultivars and orienting breeding strategies to cope with the threat posed by rust pathogens in wheat improvement programme. HS 424, developed from a cross [CPAN3004 x HPW(DL) 30 x HS 286], following pedigree method of breeding was resistant against prevalent pathotypes of leaf and stem rusts. It has also shown mean grain yield superiority over check varieties in All India Coordinated wheat trials during 2000-01 and 2001-02. HS 431, a selection from CIMMYT breeding material has shown seedling resistance against leaf and stem rust pathotypes prevalent in India. It carries single recessive gene pair for conferring resistance against 121R63-1 pathotype of leaf rust. WBM 1587 and WBM 1591 were found to be resistant against most virulent pathotype 46S119 of stripe rust. Diversification of germplasm with these genetic stocks of rust resistance and involving them in hybridization would prove useful in wheat improvement programme of India.

Key Words: Germplasm, Inheritance, Rust resistance

Introduction

The wheat crop is attacked by three different types of rusts (leaf rust, stripe rust and stem rust) all over the world and cause significant loss to the wheat production every year. Developing varieties with diverse rust resistance genes and their strategic deployment in different agro-climatic zones would help in arresting the spread of rusts in major wheat growing areas of the country. About 41 potentially useful genes are known to condition resistance against stripe rust pathotypes and about 61 leaf rust resistance (*Lr*) genes providing resistance world over have been documented (McIntosh, 2008). There are still a large number of undocumented genes which are effective and useful to provide durable rust resistance. However, *Lr*9 and *Lr*19 providing resistance against all the pathotypes of leaf rust got new virulences (Nayar *et al*., 2003; Bhardwaj *et al*., 2005) designated as 121R127 and 253R31, respectively. Recently, a pathotype virulent on *Lr* 28 has also been identified (Bhardwaj SC, Personal communication). The evolution of stripe rust pathotypes, 46S119 and 78S84 has rendered varieties carrying *Yr*9 susceptible in India. These newly evolved pathotypes of rusts have created threat to the wheat varieties grown in almost all the zones of the country. Therefore, identifying rust resistance sources effective against virulent pathotypes of rust, provides opportunities to the plant breeders for incorporating viable genes into germplasm pools and permit the system to release the cultivars carrying diverse resistance genes. The research reported in this paper is a step in this direction.

Materials and Methods

Seedlings of genetic stocks were inoculated with uredospores of rust pathotypes and infection type (IT) was recorded as per the method suggested by Stakman *et al*. (1962). The seedlings showing infection type 0; (naught fleck); (fleck) and; 1 were regarded as resistant whereas 3 and 4 were graded as susceptible. In order to study the inheritance of leaf rust resistance against pathotype 121R63-1 conferred by the test stock, 'HS 431' was crossed with susceptible landrace 'Agra local'. The material comprised of parents, F_1 and F_2 generations of this cross were scored and classified for resistance and susceptible reaction. The c^2 test was used to test the goodness of fit of expected ratios in segregating population. The observations on morpho–agronomic traits were recorded as per the descriptors suggested in All India Coordinated Research Project.

Results and Discussion

Response of genetic stocks against different pathotypes of stem, leaf and stripe rusts is presented in Table 1, 2 and 3. All the four genetic stocks as described under have been registered by the Plant Registration Committee of Indian Council of Agricultural Research.

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Table 1. Seedling reaction of genetic stocks against different pathotypes of stem rust

Genotype	Year of testing	Stem rust pathotypes														
		79G 31	203G 15	75G 5	24G 5	5G 19	10G 13	62G 29	62G 69-1	19G 35	38G 18	33G 3	37G 19	7G 11	53G 1	7G 43
HS 424	2000-01	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
	2001-02	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
	2002-03	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
	2003-04	R	R	R	R	R	R	R	R	R	R	-	R	R	-	R
	2004-05	R	R	R	-	-	R	R	R	R	R	R	R	R	R	R
	2005-06	R	R	R	-	R	R	R	R	R	R	R	R	R	R	R
HS 431	2001-02	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
	2002-03	R	S	R	R	R	R	R	R	R	R	R	MIX	R	R	R

R = Resistant, S = Susceptible, MIX = Mix reaction

Table 2. Seedling reaction of genetic stocks against different pathotypes of leaf rust

Genotype	Year of testing	Leaf rust pathotypes																		
		1 R 5	49 R 37	69 R 13	5 R 13	45 R 31	109 R 63	109 R 31-1	125 R 23-1	121 R 63-1	121 R 53-1	121 R 127	25 R 31	109 R 23	21 R 31-1	21 R 55	5 R 9	45 R 35	57 R 27	93 R 15
HS 424	2000-01	R	R	R	R	R	R	R	R	R	R	R	-	R	R	R	R	R	R	R
	2001-02	R	R	R	R	R	R	R	R	R	R	R	-	R	R	R	R	R	R	R
	2002-03	R	R	R	R	R	R	R	R	R	R	R	-	R	R	R	R	R	R	R
	2003-04	R	R	R	R	R	R	R	R	R	R	R	-	R	R	R	R	-	R	R
	2004-05	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
	2005-06	R	R	R	-	R	R	R	R	R	R	-	R	-	R	R	R	R	R	R
HS 431	2001-02	-	R	R	MIX	R	R	R	MIX	R	MIX	R	-	R	R	MR	R	R	R	R
	2002-03	R	R	R	R	R	R	R	R	R	R	R	-	R	R	-	R	R	R	R

R = Resistant, MR = Moderately resistant, MIX = Mix reaction

Table 3. Seedling reaction of genetic stocks against virulent pathotypes of stripe rust

Genetic stock	Year of testing			
	2004-05	2005-06	2006-07	2007-08
WBM 1587	;	;C	;	;
WBM 1591	0;	0;	NR	0;

Infection type : naught fleck (0;) = immune, fleck (;) = very resistant,; C = Chlorotic fleck, NR = not recorded

***HS 424 (INGR 08006)*:** This genetic stock was developed from a cross CPAN 3004/HPW(DL)30/ HS286 following pedigree method of breeding. It has shown consistent seedling resistance against all the pathotypes of stem and leaf rusts (DWR, 2005). It has light green foliage at boot stage, 105 cm average plant height, parallel ear shape, brown ear colour and the crop matures in 165 days under northern hills condition. The grains of this stock are amber, soft with ovate shape and 41g thousand grain weight. HS 424 has shown mean yield superiority over all the checks in All India Coordinated Wheat Trials during 2000-01 and 2001-02.

***HS 431 (INGR 08007)*:** The genetic stock, HS 431 [V 81623 x (BUC x PVN)], a selection from CIMMYT breeding material has shown seedling resistance against stem (except 203G15) and leaf rust pathotypes prevalent in India. HS 431 has shown adult plant resistance with maximum ACI (Average coefficient of infection) 5.3 against leaf rust and maximum ACI 5.4 against stem rust (DWR Report 2002). It has purple coleoptile, 103 cm average plant height, parallel ear shape, brown ear with medium awns and matures in 163 days under northern hills condition. Grains are dark amber, semi-hard with oblong shape and 45 g thousand grain weight. HS 431 has shown mean yield superiority over all the checks in All India Coordinated Wheat Trials under AVT-Timely Sown Irrigated Condition of Northern Hills Zone during 2001-02 and 2002-03.

***WBM 1587 (INGR 07009*:** The genetic stock, WBM 1587 (MILAN/SHA), a selection from CIMMYT breeding material has shown seedling resistance against most virulent pathotype 46S119 of stripe rust. Average plant height is 108 cm. Flag leaf, leaf sheath, ear and peduncle are waxy, clavate ear shape with white colour and short awns. It matures in 142 days under northern hills condition. The grains of this stock are amber, semi-hard with ovate shape and 40 g thousand grain weight.

***WBM 1591 (INGR 07010)*:** WBM 1591 [(PYN x BAU x MILAN)], a selection from CIMMYT breeding material

Table 4. Seedling reaction in parents, F_1 and F_2 generations of a cross (HS 431XAL) against leaf rust pathotype 121R63-1

Parent /Cross	ITP/F_1	Number of F_2 seedlings		Total	$\chi^{2(3:1)}$	Probability
		R	S			
HS 431	R	-	-	-	-	-
Agra local (AL)	S	-	-	-	-	-
HS 431 X AL	S	-	-	-	-	-
HS 431 X AL (2005-06)	-	29	102	131	0.57	0.45
HS 431 X AL (2006-07)	-	30	100	130	0.25	0.62
(Pooled)	-	59	202	261	0.80	0.37

P= Parent, R= Resistant, S= Susceptible, IT= Infection Type,

has shown consistent seedling resistance against most virulent pathotype 46S119. Average plant height is 100 cm. Flag leaf, leaf sheath, ear and peduncle are waxy, tapering ear shape with short awns and white ear colour. It matures in 160 days under northern hills condition. The grains of this stock are amber, semi-hard with oblong shape and 38 g thousand grain weight.

***Inheritance of Rust Resistance*:** The test stock, HS 431 showed distinct resistant seedling reaction to the pathotype 121 R63-1, whereas Agra local (landrace) showed high infection type. The cross HS 431 × Agra local showed susceptible reaction in F_1 and F_2 seedlings of this cross showed a segregation of 59 resistant and 202 susceptible with good fit to the expected ratio of 1R : 3S, suggesting the presence of single recessive gene pair for the inheritance of leaf rust resistance against the pathotype 121R63-1 (Table 4). The genetic stock, HS 424 was found to possess monogenic dominant control of inheritance against pathotype 121R63-1 (Datta *et al*., 2007). Based on infection data, inheritance study, morphological – marker genetic linkage and molecular marker analyses, it was indicated that HS 424 carries gene combination of *Lr*24+*Lr*26+*Sr*2+*Sr*24+*Sr*31+*Yr*9 genes. The genetic stocks, WBM 1587 and WBM 1591 reported to possess two dominant complementary genes for controlling the inheritance of resistance against stripe rust pathotype 46S119 (Kumar and Dharam Pal, 2006). Besides, resistance against 46S119, the genetic stock, WBM 1587 is also reported to carry single dominant gene pair for controlling inheritance of resistance against 78S84 pathotype of stripe rust (Dharam Pal *et al*., 2008). Diversification of germplasm with these genetic stocks of rust resistance and involving them in hybridization would prove useful in wheat improvement programme of India.

Acknowledgement

We thank Dr SC Bhardwaj, DWR Regional Station, Flowerdale, Shimla, for giving his valuable comments to improve the manuscript.

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Interspecific Derivatives for Widening the Genetic Base of Groundnut

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One hundred and fifteen interspecific derivatives of groundnut developed at National Research Centre for Groundnut, Junagadh (Gujarat) were evaluated along with checks in augmented design for yield and yield related traits under field conditions. The analysis of variance for quantitative traits revealed wide genetic diversity for biological yield, pod yield, kernel yield, hundred-kernel mass, harvest index and shelling out-turn. Two genotypes NRCGCS 268 and NRCGCS 269 recorded significantly higher hundred-kernel mass than the check variety, TKG 19A. Genotypes NRCGCS 257 and NRCGCS 277 were tolerant to multiple foliar diseases recording less than 4.0 disease severity of early leaf spot, late leaf spot and rust on a modified 9-point scale. Eight genotypes were found promising for oil content with more than 50% oil. The promising interspecific derivatives identified for various quantitative traits would help in broading the genetic base of groundnut.

Key Words: *Arachis hypogaea*, Foliar disease, Groundnut, Interspecific derivative, Oil content

Introduction

Groundnut (*Arachis hypogaea* L.) is the principal oilseed crop in India accounting for more than 25% of the total area under oilseeds. Though India accounts for the largest area under groundnut, it does not contribute much to the global production and trade due to low productivity, which is further compounded by fluctuations resulting from abiotic and biotic stresses in the rainfed production system. Development of the genotypes endowed with tolerance to different abiotic and biotic stresses along with high reproductive potential continues to be the major objective in groundnut improvement programmes. The success of improvement programme depends on the extent of variability available for desirable traits. Hence, to create wide genetic variability, interspecific crosses were made and they were evaluated for yield attributes, resistance to major foliar diseases like leaf spots and rust, and the oil content.

Materials and Methods

One hundred and fifteen groundnut interspecific derivatives were used in the experiment. Derivatives are progenies of crosses between J11 × *A. cardenasii*, J11 × *A. duranensis*, J11 × *A. kretschmeri*, J11 × *A. correntina*, J11 × *A. oteroi*, J11 × *A. stenosperma* and J11 × *A. diogoi* at National Research Centre for Groundnut (NRCG), Gujarat. Cultivar J11 is a Spanish bunch (erect type) groundnut (*A. hypogaea*) and used as ovule parent in all cross combinations. J11 produces higher number of cross pods than other cultivars while used in interspecific crosses (unpublished data generated by the author) and are resistant to *Aspergillus flavus*, the causal organism of aflatoxin contamination in groundnut. These were evaluated along with two Virginia bunch (TKG 19A and GG 20) and three Spanish bunch (TAG 24, GG 2 and JL 24) groundnut (*A. hypogaea*) varieties used as checks in Augmented Block Design distributed in five blocks in experimental farm of NRCG during rainy season 2006. Each entry was sown in three lines of five meters bed following standard crop management practices. The data were recorded on various qualitative traits namely biological yield/10 plant (BY), pod weight/10 plant, kernel weight/10 plant, harvest index (HI), shelling out-turn, hundred kernel mass (HKM) and the oil content. The severity of major foliar diseases, *viz*., early leaf spot (ELS), late leaf spot (LLS) and rust, arising from natural inoculums sources was recorded from 80-90 days old crop using modified 9-point scale (Subrahmanyam *et al*., 1995). Data were analysed using augmented design II. Range, mean and standard deviation were calculated for quantitative traits following standard statistical procedures.

Results and Discussion

Interspecific derivatives are generally characterized based on distinguishable pheonological and agro-morphological traits. Derivatives comprising both Spanish (erect) and Virginia bunch (semi-spreading) habit group showed good early plant vigour. The analysis of variance for quantitative traits revealed good amount of genetic diversity in the population for biological yield/10 plants, pod yield/10 plants, kernel yield/10 plants, hundred-

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kernel mass, harvest index and shelling out-turn (Table 1). A wide range of variation in HKM, pod weight, kernel weight, shelling out-turn, oil content, resistance to leaf spot and rust diseases in cultivated groundnut was also reported by Reddy and Gupta (1992), Khurram *et al.* (1998) and Salara and Gowda (1998). This indicates wide variation existing in cultivated groundnut for these traits. Block effect was significant and adjusted statistically as per augmented design. Checks used in the experiment differed significantly for biological yield/10 plant, pod yield/10 plants, kernel yield/10 plant, HKM, harvest index and shelling out-turn. Variability estimates indicated that a wide range of variations was available in the population confirming the positive transgression for trait of interest and the entries out yielded for various traits beyond the best check (Table 2). Biological yield/10 plants of the population ranged from 92-529 g with an average of 280 g. Segregants with higher biological yield/10 plants indicated the introgression of traits from wild parent having perennial creeping habit with large volume of foliage. Though twelve genotypes recorded biological yield more than 400 g, only NRCGCS-241 recorded significantly higher biological yield over the best check (505.2 g) (Table 2 and 5). Pod weight varied from 27-162 g with an average of 76.2 g. Frequency distribution showed that majority of genotypes could be grouped into the class of 51-100 g for pod weight. A few positive extreme segregants were available in the population, may be due to introgression of less pod bearing and smaller pod size characters of both wild pollen parent as well as pistil parent, J-11. However, two genotypes NRCGCS-241 and 242 significantly out-yielded than the best check (147.5 g) for pod yield. Singh and Singh (1998) also observed high variation for pod yield per plant and HKM. Kernel weight varied from 12-93.2 g with an average of 45 g. Unlike the pod weight, majority of the genotypes of population could be grouped into three classes (16-35, 36-45, and 46-55) for kernel weight with a continuous variation distributed in 8 classes. The genotypes, NRCGCS-241, 242, 253 and 296 produced significantly higher kernel weight than the check. HKM of the population varied from 11.5-61.2 g with a mean of 31.0 g. HKM of the majority of the entries grouped into four classes (21-25, 26-30, 31-35, 36-40). Unlike the kernel weight, HKM of the population showed continuous variation and distributed in 8 classes with few promising trnasgressive segregants. Two of which (NRCGCS-268 and 269) recorded significantly higher HKM than the best check (49.2 g). The continuous variation observed for biological yield, kernel weight and HKM could be due to the introgressive hybridisation of both wild and cultivated forms and subsequent selection under varying intensities of selection pressure (Oka *et. al.*, 1959).

Harvest index of the population ranged from 5.7-27 % with comparatively low mean value (16.0%). Harvest index of the population distributed in 5 classes of which, class 16-20 accommodated maximum numbers

Table 1. Analysis of variance for different traits of groundnut

Source	df	Mean sum of squares					
		BY/10 plants (g)	Pod wt./10 plants (g)	Kernelwt./10 plants (g)	HKM (g)	HI (%)	Shellingout-turn (%)
Blocks (b)	4	21842.00**	3326.05**	588.98**	80.48**	25.86**	270.16**
Genotypes (e)	119	10452.77**	1044.59**	340.35**	91.54**	20.28**	67.37**
Checks (c)	4	101878.9**	6999.16**	1655.06**	403.27**	13.35**	169.25**
Varieties (v)	114	7649.19**	892.62**	296.47**	72.14**	21.70**	77.41**
Check vs. varieties	1	35643.34**	5449.25**	83.78	1056.09**	113.55**	1484.73**
Error	28	394.37	50.90	26.72	7.54	2.43	11.39

df = degree of freedom; ** =significant at 1%

Table 2. Variability in quantitative characters of test genotypes

	Range	Mean	Best value	SE of the varieties in the same block	SE of the varieties in the in the different block	SE of the check varieties and & check
BY/10 plant (g)	92.0 -529.0	280.8	505.2	30.76	28.08	23.07
Pod wt./10 plant (g)	27.0 -162.0	76.2	147.5	11.05	10.09	8.28
Kernel wt./10 plant (g)	12.0 - 93.2	45.0	76.2	8.00	7.31	6.00
HKM (g)	11.5 - 61.2	31.1	49.2	4.25	3.88	3.19
HI (%)	5.7 - 27.0	16.0	18.8	2.41	2.20	1.81
Shelling out-turn (%)	31.0 - 75.0	60.0	61.6	5.22	4.77	3.92

BY= Biological yield, HKM= 100 kernel mass, HI= Harvest index

Table 3. Frequency distribution of quantitative characters

BY/10 pl. (g)		PodWt./10 pl. (g)		KernelWt./10 pl. (g)		HKM (g)		HI (%)		Shellingout-turn (%)	
Class	Freq.	Class	Freq.	Class	Freq.	Class	Freq.	Class	Freq.	Class	Freq.
1-100	1	1- 25	0	1-15	1	1-15	2	1- 5	0	1- 15	0
101-150	2	26-50	24	16-35	36	16-20	10	6-10	16	16-35	1
151-200	15	51-100	67	36-45	29	21-25	18	11-15	27	36-45	8
201-250	29	101-125	12	46-55	22	26-30	22	16-20	51	46-55	23
251-300	25	126-150	9	56-65	12	31-35	30	21-25	19	56-65	53
301-350	22	151-200	3	66-75	7	36-40	17	26-30	2	66-75	30
351-400	9	201-225	0	76-85	5	41-45	12	31-35	0	76-85	0
400-529	12	226-250	0	85-93	3	45-61	4	36-40	0	86-95	0

Table 4. Variability estimates of foliar diseases and oil content

Particulars	Disease severity (1-9 scale)			
	Early leaf spots	Late leaf spots	Rust	Oil content (%)
Range	4.17-8.67	3.67-8.67	2.67-8.50	44.0-54.0
Mean	7.76	7.49	7.00	49.95
Check	8.7	8.7	8.5	50.00
SD	0.89	1.01	1.06	1.98
CV %	11.52	13.43	15.16	3.97

of genotypes followed by class 11-15. In spite of lower HI of the population, twenty genotypes significantly surpassed the highest value of check (18.8) and the two genotypes (NRCGCS-297 and 304) were promising. Shelling out-turn of the population ranged from 31-75%, with the population mean of 60%. Majority of the genotypes grouped in the class 56-65 followed by the class 66-75 for shelling out-turn. Twenty-nine genotypes recorded significantly higher shelling out-turn than best check (61.6%), of which NRCGCS-357, 355, 301, 323 and 279 were promising recording more than 73% shelling out turn. Mathur *et al.* (1997) reported that shelling out-turn is most stable character in groundnut and can be used as selection criteria. Scoring of genotypes and checks against major foliar diseases *viz*., ELS, LLS and rust revealed high disease severity (8.50-8.67) under natural field conditions (Table 4). Singh and Singh (1997) also reported high disease pressure under field conditions among checks. Two genotypes NRCGCS-257 and 277 showed resistance to multiple foliar diseases recording low disease severity (<5) against ELS, LLS and rust (Table 5). These two genotypes could be utilized in developing multiple disease resistant groundnut varieties. Vasanthi and Naidu (1998) has also reported resistance to multiple diseases indicating that these three foliar diseases have fair amount of positive association if they are not tightly linked and can be incorporated in a single background by a single breeding effort.

The oil content of the population ranged from 44-54% with the population mean of 50%. The genotypes, NRCGCS-269, 254, 273, 297, 237, 243, 251 and 266 recorded more than 52% oil content and can be utilized for developing high oil content cultivars (Table 5). Promising genotypes identified for different quantitative traits can find their way into future breeding programmes.

Table 5. Promising breeding lines of groundnut for various traits

Character	Genotypes
BY/10 plant (g)	NRCGCS-241
Pod wt./10 plant (g)	NRCGCS-241, 242
Kernel wt./10 plant (g)	NRCGCS-241, 242, 245, 253, 264, 268, 280, 296
HKM (g)	NRCGCS-268, 269
HI (%)	NRCGCS-242, 305, 286, 296, 309, 338, 253, 266, 273, 356, 298, 260, 342, 357, 287, 264, 291, 289, 304, 297
Shelling out-turn (%)	NRCGCS-351, 290, 328, 314, 346, 345, 298, 322, 340, 321, 338, 260, 248, 342, 356, 297, 298, 325, 291, 319, 304, 320, 294, 306, 357, 355, 301, 323, 279
ELS (< 5 grade)	NRCGCS-277, 303, 311, 257
LLS (< 5 grade)	NRCGCS-257, 311, 303, 277
Rust (< 5 grade)	NRCGCS-277, 257, 256, 242, 243, 306
Oil content (%)	NRCGCS-269, 254, 273, 297, 237, 243, 251, 266

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Relative Efficiency of Experimental Designs in Evaluation of Plant Genetic Resources

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An experiment was conducted in a Reinforced Alpha Design (RAD) with 50 accessions and 5 control treatments of tomato during the *Rabi* season of 2006. The data on 9 distinct descriptors namely, plant height, primary branches, flower clusters per plant, flowers per cluster, days to first fruit set, fruits per plant, fruit weight per plant, locules per fruit and pericarp thickness were recorded on 12 randomly selected plants per accession. The designs, namely, Completely Randomized Design, Randomized Block Design and Augmented Block Design were derived from RAD. A comparison of the relative efficiency of these four designs revealed that in plant genetic resources evaluation for identification of promising material in case of insufficient seed quantity, one should adopt a two phase strategy using reinforced alpha design. During phase I (first year), when sufficient seed quantity is not available, one replication of reinforced alpha design may be used. During phase II (second year), the second replication of the design may be deployed.

Key Words: Augmented block design, Evaluation, Reinforced alpha design, Relative efficiency, Tomato

Introduction

In plant genetic resources evaluation, the germplasm is assembled either through explorations or introductions from exotic sources, and exchange programmes etc. Germplasm curator generally comes across situations when he has to test or evaluate the performance of the new germplasm/superior selections etc. with the existing released varieties (control treatments). Normally, the seed quantity of newly collected material is very limited in comparison to check varieties. Augmented Block Design (ABD) suggested by Federer (1956) has been extensively used by the germplasm evaluators for testing the new lines with the check varieties. Hence, an appropriate and efficient experimental design is required to handle such a situation. Relative efficiencies of some of the incomplete block designs have been compared with data on uniformity trials (Gomez, 1969; Johnson and Murphy, 1943; Sarma *et al*., 1985; Zuber, 1942). In the present investigation, the efficiency of experimental designs, *viz*., Completely Randomized Design (CRD), Randomized Block Design (RBD), Reinforced Alpha Design (RAD), and ABD used in evaluation of germplasm material have been compared. For this purpose, the experiment was laid in RAD and other designs were derived from it.

Materials and Methods

A total of 50 accessions and 5 controls of tomato from diverse eco-geographical regions were grown during the *Rabi* season of 2006 at NBPGR Experimental Farm, Issapur, New Delhi. The accessions were grown in 6 row plots of 2.25 m length with a row spacing of 60 cm and plant spacing of 45 cm in an Reinforced Alpha Design. The material was grown in 2 replications with 5 blocks each of size 15 in each replication. Each block contained 10 accessions and 5 controls, *viz.*, Pusa Upkar, Pusa Sheetal, Pusa Ruby, Pusa Gaurav and Pusa Early Dwarf. One could have used an alpha design for 55 treatments. Since, the interest in the present study is in making test vs. control treatment comparisons, therefore, RAD comprised 2 replications with each 50 accessions with 10 blocks of size 10 each and each of the 5 control treatments were added in each of the blocks of the RAD (Table 1). Thus, each accession was replicated twice and each control was replicated 10 times. Data were recorded for a set of 9 distinct descriptors, *viz.*, plant height, primary branches, flower clusters per plant, flowers per cluster, days to first fruit set, fruits per plant, fruit weight per plant, locules per fruit and pericarp thickness on 12 randomly selected plants per accession. The following three designs were derived from RAD.

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Completely Randomised Design (CRD): Each of the 50 accessions being replicated 2 times and the controls 5 times each.

Randomised Block Design (RBD): Each of the 50 accessions replicated 2 times and the controls replicated equal number of times in 2 replications, *i.e.*, 10 times each.

Augmented Block Design (ABD): One hundred treatments (2 times same set of 50 accessions) being laid out in 10 blocks and 5 controls being randomized in each block.

The randomization was done as per procedure of RAD and not as per the derived design. Therefore, the designs can not be analyzed as derived designs. However, for the sake of illustration purpose of use of RAD in reducing the experimental error and increasing the precision of treatment comparisons, the data was analyzed from experiments as per respective experimental designs. For a detailed discussion on alpha design, a reference may be made to Prasad *et al*. (2007), Prasad *et al.* (2008) and http://www.iasri.res.in/design/Alpha/Home.htm.

The data were subjected to statistical analysis for the corresponding design. The amount of information obtained from a design D is $(n_e+1)/ (n_e+3)s_e^2$ with n_e and s_e^2 representing the error degrees of freedom and the corresponding error mean square (Fisher, 1947). Then the relative efficiency of design D_1 with another design D_2 is the ratio of amounts of information in D_1 to D_2. When the treatment differences were significant for a descriptor, number of accessions superior to the best check and the number of pairs of treatment combinations having significant differences were determined. In ABD, for determining significant pairs of accessions, we have considered set 1 comprised first five blocks of replication 1 and set 2 comprised five blocks of replication 2. The significant pairs of accessions were determined in each set. The common pair of accessions between set 1 and 2 is reported.

For computing the number of significant comparisons among all possible pairs of treatment combinations, 2 critical differences between pair of treatments (i) accessions being replicated 2 times, and (ii) accession and control were computed in CRD and RBD. In ABD, 3 critical differences were computed, *viz.* (i) between 2 accessions occurring in the same block, (ii) between 2 accessions occurring in different blocks, and (iii) between an accession and control (Federer, 1956). The breeder is normally interested in identifying accessions superior to best control variety.

In ABD, while performing the analysis of variance, sum of squares for treatments was adjusted for block effects and blocks sum of squares was unadjusted. In addition, when treatment differences and block differences were significant, treatment means (other than control varieties) were adjusted for the block effects before making comparison between treatments.

Results and Discussion

All the accessions differed significantly (Table 2) for all the descriptors in all the designs except for number of locules per plant and pericarp thickness in CRD, RBD, and RAD. Replications were effective in controlling the error variation for primary branches, flower clusters per plant, days to first fruit set, fruits per plant, fruit weight per plant, locules per fruit and pericarp thickness in RBD and RAD. This resulted in increasing the efficiency of the design and more numbers of significant pair of treatment combinations in RBD over CRD. But there was more or less no change in number of treatments superior to the control variety. In RAD, blocks within replication were significant in controlling the error variation for all descriptors except plant height. Further, in ABD, 10 effective blocks were formed. This resulted in significant block effects and also more efficiency for ABD over RBD.

The relative efficiency (RE) of RAD ranged from 106.82%-354.63% over CRD and 104.5%-353.99% over RBD (Table 3). The RE of RAD was considerably higher than ABD for all the descriptors except for plant height and number of flowers per cluster. However, it was nearly same for primary branches and flower clusters per plant. The RE of ABD was considerably higher than CRD and RBD for all the descriptors except for fruit weight per plant and pericarp thickness where it was nearly similar. The RE of RBD over CRD was just above 100% for all the descriptors.

The number of significant pairs of treatments were the highest for primary branches (480), days to first fruit set (403), and fruit weight per plant (1064) in RAD and for plant height (672), flower clusters per plant (715), flowers per cluster (618), fruits per plant (492), and locules/fruit (5) in ABD (Table 4). The numbers of significant pairs in CRD and RBD were approximately equal for different descriptors. In RAD, the numbers of superior accessions over control were 23, 8, 18, 4,

Table 1. Layout of Reinforced Alpha Design (RAD) parameters: (v=50, b=10, k=10, r=2)

					Replication 1					
Block 1	50 (EC29627)	5 (EC742)	10 (EC29969)	15 (EC6486)	20 (EC3736)	25 (EC3815)	30 (EC32614)	35 (EC7345)	40 (EC32276)	45 (EC34480)
Block 2	1 (EC2585)	6 (EC35373)	11 (EC35257)	16 (EC13574)	21 (EC13274)	26 (EC2491)	31 (EC35242)	36 (EC5888)	41 (EC2699)	46 (EC4955)
Block 3	2 (EC35265)	7 (EC23528)	12 (EC16343)	17 (EC3366)	22 (EC35203)	27 (EC7785)	32 (EC32019)	37 (EC1087)	42 (EC35240)	47 (EC31767)
Block 4	3 (EC1191)	8 (EC35244)	13 (EC2653)	18 (EC33203)	23 (EC35236)	28 (EC8822)	33 (EC35272)	38 (EC14181)	43 (EC1753)	48 (EC8630)
Block 5	4 (EC2990)	9 (EC35382)	14 (EC5424)	19 (EC32577)	24 (EC32271)	29 (EC7371)	34 (EC27885)	39 (EC16368)	44 (EC35216)	49 (EC8590)
					Replication 2					
Block 6	50 (EC29627)	6 (EC35373)	12 (EC16343)	18 (EC33203)	24 (EC32271)	25 (EC3815)	33 (EC35272)	37 (EC1087)	44 (EC35216)	46 (EC4955)
Block 7	1 (EC2585)	7 (EC23528)	13 (EC2653)	19 (EC32577)	20 (EC3736)	26 (EC2491)	34 (EC27885)	38 (EC14181)	40 (EC32276)	47 (EC31767)
Block 8	2 (EC35265)	8 (EC35244)	14 (EC5424)	15 (EC6486)	21 (EC13274)	27 (EC7785)	30 (EC32614)	39 (EC16368)	41 (EC2699)	48 (EC8630)
Block 9	3 (EC1191)	9 (EC35382)	10 (EC29969)	16 (EC13574)	22 (EC35203)	28 (EC8822)	31 (EC35242)	35 (EC7345)	42 (EC35240)	49 (EC8590)
Block10	4 (EC2990)	5 (EC742)	11 (EC35257)	17 (EC3366)	23 (EC35236)	29 (EC7371)	32 (EC32019)	36 (EC5888)	43 (EC1753)	45 (EC34480)

Note: Text within parenthesis indicates accession number

Table 2. Analysis of variance for different descriptors in tomato

Source					Plant height (cm)				No. of primary branches			
	CRD	RBD	RAD	ABD	CRD	RBD	RAD	ABD	CRD	RBD	RAD	ABD
	Degrees of freedom				Mean square				Mean square			
Treatments	54	54	54	104	1293.75**	1293.75**	1293.75**	2002.03**	9.68**	9.68**	9.68**	775.11**
Blocks/replication	-	1	1	9	-	541.99	541.99	2512.42**	-	27.52**	27.52**	11.50**
Blocks within replications	-	-	8	-	-	-	257.17	-	-	-	10.84**	
Error	95	94	86	36	177.31	173.43	165.64	81.41	4.63	4.39	3.79	4.03
Source	No. of flower clusters per plant				No. of flowers per cluster				Days to first fruit set			
	CRD	RBD	RAD	ABD	CRD	RBD	RAD	ABD	CRD	RBD	RAD	ABD
	Mean square				Mean square				Mean square			
Treatments	179.24**	179.24**	179.24**	807.22**	2.83**	2.83**	2.83**	2.22**	38.32**	38.32**	38.32**	87.49**
Blocks/replication	-	1351.5**	1351.5**	77.82	-	0.01	0.01	964.49**	-	149.83**	149.83**	1060.25**
Blocks within replications	-	-	315.84**		-	-	1.47**	-	-	-	43.63**	
Error	92.02	78.63	56.56	50.83	0.56	0.56	0.48	0.31	16.32	14.90	12.23	13.31
Source	No. of fruits per plant				Fruit weight per plant (g)				No. of locules per fruit			
	CRD	RBD	RAD	ABD	CRD	RBD	RAD	ABD	CRD	RBD	RAD	ABD
	Mean square				Mean square				Mean square			
Treatments	2.30**	2.30**	2.30**	823.59**	153.02**	153.02**	153.02**	708.25**	0.22	0.22	0.22	776.37**
Blocks/replication	-	4.57**	4.57**	0.72**	-	23.05*	23.05*	58.47**	-	3.13**	3.13**	0.62**
Blocks within replications	-	-	1.4**	-	-	-	172.62**	-	-	-	0.62**	
Error	0.35	0.30	0.20	0.22	19.83	19.79	5.58	21.27	0.23	0.20	0.16	0.16
Source	Pericarp thickness (mm)											
	CRD	RBD	RAD	ABD								
	Mean square											
Treatments	0.004	0.004	0.004	1017.60**								
Blocks/replication	-	0.012*	0.012*	0.002								
Blocks within replications	-	-	0.01**	-								
Error	0.003	0.003	0.002	0.003								

*: P<=0.05; **: P<=0.01; CRD: Completely Randomized Design; RBD: Randomized Block Design; RAD: Reinforced Alpha Design; ABD: Augmented Block Design

Table 3. Relative efficiency of ddesigns

Design A versus Design B	Plant height (cm)	No. of primary branches	No. of flower clusters / plant	No. of flowers/ cluster	Days to first fruit set	No. of fruits/ plant	Fruit weight/ plant (g)	No. of locules/ fruit	Pericarp thickness (mm)
RAD vs. CRD	106.82	121.91	162.35	116.42	133.16	175.00	354.63	143.45	149.68
RAD vs. RBD	104.50	115.61	138.76	116.45	121.60	150.00	353.99	124.76	149.72
RAD vs. ABD	50.64	92.60	92.60	66.54	112.13	113.34	392.76	103.04	154.56
ABD vs. RBD	206.36	149.85	149.85	174.99	108.44	132.09	90.13	121.09	96.87
ABD vs. CRD	210.94	175.32	175.32	174.96	118.75	154.08	90.29	139.22	96.85
RBD vs. CRD	102.22	117.00	117.00	99.98	109.51	116.64	100.18	114.98	99.98

CRD: Completely Randomized Design; RBD: Randomized Block Design; RAD: Reinforced Alpha Design; ABD: Augmented Block Design

Table 4. Numbers of pairs of treatment combinations having significant differences and the number of significant pair of accessions superior to the best control variety

Design	Plant height (cm)	No. of primary branches	No. of flower clusters/ plant	No. of flowers/ cluster	Days to first fruit set	No. of fruits/ plant	Fruit weight/ plant (g)	No. of locules/ fruit	Pericarp thickness (mm)
CRD-A	625	280	230	233	343	431	747	–	–
CRD-B	9	1	6	1	0	3	1	–	–
RBD-A	631	292	272	233	372	398	746	–	–
RBD-B	9	1	9	1	0	3	1	–	–
AD-A	672	480	361	289	403	460	1064	–	–
AD-B	23	8	18	4	0	7	2	–	–
ABD-A	892	412	715	618	399	492	916	5	0
ABD-B	11	0	6	0	0	2	1	0	0

A: Refers to the number of significant pairwise comparisons among all possible treatment combinations; B: Refers to number of accessions superior to the best control variety

7 and 2 for plant height, primary branches, flower clusters per plant, flowers per cluster, fruits per plant, and fruit weight per plant, respectively. These were substantially higher in RAD for all the descriptors in comparison to other designs where as these were almost same for ABD (11, 0, 6, 0, 2 and 1), RBD (9, 1, 9, 1, 3 and 1), CRD (9, 1, 6, 1, 3 and 1) for plant height, primary branches, flower clusters per plant, flowers per cluster, fruits per plant, and fruit weight per plant, respectively.

The above study suggests that in plant genetic resources evaluation for identification of promising material, when sufficient seed quantity is not available, one should adopt a two phase strategy through the use of Reinforced Alpha Design. During phase I (first year), in case of insufficient seed quantity, one replication of Reinforced Alpha Design may be used. During phase II (second year), the second replication of the design may be deployed. However, a preliminary knowledge about the potential superior germplasm, promising, over the control treatment can be had from the data of first year. The analysis of this data can be performed in an ABD. In situations, when sufficient seed quantity is available, the experimenter should use an RAD and RBD should be discouraged.

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Genetic Variation and Character Association in F_6 Progenies of Interspecific Crosses between *Brassica juncea* and *B. carinata*

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One Hundred F_6 progenies of inter-specific crosses between *B. juncea* × *B. carinata* with 4 check varieties were evaluated in an Augmented Randomized Block Design with five blocks to study genetic variation and character association between yield and yield contributing traits. High heritability values accompanied with high genetic advance were observed for fruiting zone length (58%, 31%), number of siliquae/plant (63%, 33%) and seed yield/plant (75%, 97%). The seed yield/plant showed positive and significant correlation coefficient with plant height (0.364), number of siliquae/plant (0.242), number of seeds/siliqua (0.586). Progenies, 06-727, 06-729 and 06-754 exhibited significant superiority over the best check for seed yield, suggesting their use in crossing programme to throw desirable segregants for abiotic stresses.

Key Words: ***Brassica juncea, Brassica carinata*, Character association, Genetic variation, Heritability, Mustard**

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & coss] is an annual, *rabi* oilseed crop and possesses unique position by virtue of its high oil content. About 34 per cent of the cropped area in the semi-arid region under this crop is rainfed. Depending on planting time and winter rain, the crop is exposed to water stress at one or more phonological stages when stored water becomes depleted (Kumar, 2001). This calls for screening and development of drought tolerant genotypes. On the other hand, tropical origin of *B. carinata* may allow it to tolerate high temperature during the reproductive period better than the other species and possess genes for drought tolerance, which may be transferred to genetic background of adaptive varieties of Indian mustard. Therefore, assessment of genetic variation among the progenies obtained from interspecific hybridization is expected to identify high yielding progenies with greater tolerance to stresses.

Materials and Methods

The material for present investigation consisted of 100 selected F_6 progenies of 4 crosses of *B. juncea* × *B. carinata*. These progenies were evaluated at Research farm of DRMR, Bharatpur during *rabi* 2006-07 in an Augmented Randomized Block Design with five blocks. Each block consisted of 20 progenies and 4 check varieties namely, Varuna, RH-819, Kiran and PBR-97. In each block, progenies and check varieties were randomized and allotted to each plot. Each plot was having two rows of 3 m length with 30 cm x 10 cm spacing. The crop was kept un-irrigated except one pre-sowing irrigation. Ten plants were randomly selected from each plot to record the data on plant height, primary branches per plant, fruiting zone length, siliquae on main shoot, number of siliquae per plant, number of seeds per siliqua, seed yield per plant, 1000-seed weight and oil content. Analysis of variance was performed as per the method suggested by Federer (1956). GCV, PCV, heritability, genetic advance and correlation coefficient were calculated as per standard procedure. Rating of progenies for reaction to *Alternaria* blight and white rust was done as per scale given by Conn *et al.* (1990).

Results and Discussion

The analysis of variance revealed that significant amount of variability was present in the progenies for most of the characters under study except primary branches per plant, main shoot length and 1000-seed weight (Table 1). This suggests that the material has adequate variability and response to selection may be expected in the breeding programme for seed yield per plant. Estimates of genotypic and phenotypic coefficient of variations (Table 2) showed that the phenotypic variances were higher than genotypic variance indicating the role of environmental factors on character expression. The variance of various characters was compared on the basis of coefficient of variation. It was observed that seed yield per plant followed by number of siliquae per plant exhibited higher estimates

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Table 1. Mean squares for different characters of F_6 progenies in interspecific crosses between *Brassica juncea* × *B. carinata*

Source of variation	d.f	Plant height (cm)	Fruiting zone length (cm)	Number of primary branches per plant	Main shoot length (cm)	Number of siliquae on main shoot	Number of siliquae per plant	Number of seed per siliqua	Seed yield per plant (g)	1000-seed weight (g)	Oil content (%)
Treatment (c+g)-1	103	308.39**	245.28*	1.27	98.78	49.55	688.33*	2.52**	91.5**	0.32	2.78**
Check (c-1)	3	1437.2**	2175.82**	6.67**	1057.94**	129.21	4502.52**	14.07**	117.02*	2.75**	9.72
Progenies (g-1)	99	230.75*	189.14*	1.1	61.45	47.44**	530.66*	1.67*	90.69**	0.23	2.56**
Check vs Progenies	1	4609.2**	14.27	1.83	916.97**	19.27	4854.91**	51.5**	95.2**	1.48**	3.52*
Error (b-1)	12	61.24		78.26	0.6	55.54	20.27	194.94	0.72	22.31	0.21
0.62 (c-1)											

Table 2. Overall mean value of progenies, their range, genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance as percentage of mean for different characters of F_6 progenies of interspecific crosses between *Brassica juncea* × *B. carinata*

Characters	Mean	Range	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Heritability in broad sense (%)	Genetic advance as percentage of mean
Plant height (cm)	120.6	85.7-168.20	10.79	12.59	73	18.94
Fruiting zone length (cm)	53.9	14.6-80.90	19.53	25.51	58	30.48
*Number of primary branches per plant	5.1	2.3-9.2	–	–	–	–
*Main shoot length (cm)	41.3	15.76-69.64	–	–	–	–
Number of siliquae on main shoot	31	10.7-46.60	16.95	22.18	57	26.05
Number of siliquae per plant	91.6	45.7-137.30	20	25.14	63	32.63
Number of seeds per siliqua	11.7	7.5-16.05	8.33	11.04	56	12.74
Seed yield per plant (g)	15.1	2.7-37.80	54.76	63.07	75	97.43
*1000-seed weight (g)	3.6	2.1-5.27	–	–	–	–
Oil content (%)	40.6	36.3-44.07	3.43	3.95	75	6.09

* As mean sum of squares were non-significant for these characters, genetic parameters were not calculated

of genotypic as well as phenotypic coefficient of variation. These findings are similar to earlier reports of Shalini *et al*. (2000) and Pant and Singh (2001). The heritability estimates were of higher magnitude (>50%) for all the characters, where as high heritability values accompanied with high genetic advance were observed for fruiting zone length (58%, 31%), number of siliquae per plant (63%, 33%) and seed yield per plant (75%, 97%). Similar results of high heritability and high genetic advance for these characters were earlier reported by Uddin *et al.* (1995). This indicates that selection will be more effective in the present material for these characters.

Genotypic phenotypic correlation coefficients were worked out among different pairs of characters including seed yield per plant (Table 3). The seed yield per plant showed positive and significant correlation coefficient with plant height (0.364), number of siliqua/plant (0.242), number of seeds per siliqua (0.586). Similar significant and positive correlations of yield with these characters have been earlier reported by Kardam and Singh (2005). Among the various inter relationships between remaining traits, fruiting zone length showed significant positive association with primary branches per plant (0.276), main shoot length (0.219) and siliquae on main shoot (0.287). The other important associations noted are significant and positive association of number of siliquae on main shoot and number of siliquae/plant with main shoot length. However, number of seeds per siliqua had negative association with fruiting zone length, number of primary branches per plant and 1000-seed weight. Oil content also showed negative association with these characters. Adams (1967) reported that negative correlation arises in response to competition between developmentally flexible components. Based on above study, it can be concluded that characters, which exhibited positive association with seed yield, are important characters and should be considered in selection programme. Progenies were also assessed for their reaction to *Alternaria* blight and white rust. However, present material could not be differentiated for biotic stresses as all entries rated between 0 to 1 scale which may be due to low selection pressure of diseases.

Table 3. Correlation coefficient on the basis of unadjusted values (phenotypic level) and adjusted values (genotypic level) between different characters of F_6 progenies of interspecific crosses between *Brassica juncea* x *B. carinata*

Characters		Plant height (cm)	Fruiting zone length (cm)	Primary branches per plant	Main shoot length (cm)	Siliquae on main shoot	Siliquae per plant	Seeds per siliqua	Seed yield per plant (g)	1000-seed weight (g)
Fruiting zone length (cm)	P	0.119								
	G	0.257								
Number of primary branches per plant	P	0.209*	0.276**							
	G	0.244	0.345							
Main shoot length (cm)	P	0.151	0.219*	0.053						
	G	0.228	0.442	0.483						
Number of siliquae on main shoot	P	(-)0.028	0.287**	0.117	0.332*					
	G	0.056	0.384	0.204	0.523					
Number of siliquae per plant	P	0.234*	0.143	0.073	0.200*	0.242*				
	G	0.214	0.129	0.054	0.181	0.208				
Number of seeds per siliqua	P	0.199	(-)0.001	(-)0.384**	0.105	0.183	0.299**			
	G	0.038	(-)0.158	(-)0.377	(-)0.101	0.003	0.255			
Seed yield per plant (g)	P	0.364**	0.141	(-)0.162	0.075	0.175	0.242*	0.586**		
	G	0.332	0.209	(-)0.113	0.141	0.203	0.231	0.431		
1000-seed weight (g)	P	0.186	0.173	0.276**	0.061	(-)0.018	(-)0.051	(-)0.191	0.151	
	G	0.268	0.322	0.258	0.406	0.116	(-)0.040	(-)0.262	0.324	
Oil content (%)	P	0.034	(-)0.073	(-)0.246*	0.002	0.110	0.103	0.298**	0.235*	-0.108
	G	0.039	(-)0.049	(-)0.291	(-)0.099	0.077	0.101	0.276	0.278	0.0492

*Significant at p=0.05, ** Significant at p= 0.01

Ten best progenies on the basis of performance were selected (Table 4). The progenies, 06-727, 06-729 and 06-754 were significantly superior to the best check for seed yield and also high in oil content (%). Hence, it is suggested that these progenies be tested in multi-locational trials and also be used in hybridization programme to develop high yielding varieties for drought situations after stabilization.

Table 4. Evaluation data on best ten progenies along with parents and checks for seed yield and its components

Progenies	Seed yield/ plant (g)	Oil content (%)	Plant height (cm)	Fruiting zone length (cm)	Number of primary branches	Main shoot length (cm)	Number of siliquae on main shoot	Number of siliquae per plant	Number of seed per siliqua	1000-seed weight (g)
06-727**	37.8	42.5	164.2	76.9	6.1	48.7	23.1	122.8	15.8	4
06-729**	36.8	44.07	125.2	64.7	5.1	45.3	38.4	106.4	12.6	4.4
06-754**	35.6	42.8	116.2	48.3	3.6	38.2	28.5	109.2	14.0	3.2
06-828	29.9	42.4	156.4	30.1	7.1	69.6	31.6	115.7	13.5	4.8
06-751	29.7	41.7	110.2	47.1	4.4	29.4	25.2	88.1	13.3	3.3
06-796	28.3	41.3	138.4	70.7	5.8	56.9	36.7	107.1	14.3	4.3
06-812	27.8	41.8	118.4	53.6	4.8	41.3	42.5	64.7	12.5	4.5
06-789	26.9	38.0	130.7	78.6	9.2	39.6	33.4	125.5	9.7	4.1
06-757	26.7	41.6	98.2	54.5	3.5	32.7	27.1	85.6	15.0	2.7
06-793	26.3	39.7	127.4	69.5	5.4	53.3	31.6	58.7	12.3	3.9
Check/Parents										
RH 819	12.6	41.2	120.6	39.9	4.2	34.3	25.9	72.6	12.7	3.8
PBR 97	19.6	41.4	127.6	65.8	5.1	51.4	37.3	95.8	12.4	4.0
KIRAN	7.9	39.3	159.0	78.5	7.0	15.8	29.6	137.3	12.9	3.0
VARUNA	12.3	38.6	141.6	34.8	5.6	33.8	34.5	129.1	16.0	4.8
CD# (5%)	12.5	2.03	20.2	22.8	2.0	19.21	11.6	35.9	2.19	1.2

#Between check varieties and progenies, ** Significantly superior than the best check

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A Taxonomic Revision of the Genus *Momordica* L. (Cucurbitaceae) in India

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The genus *Momordica* L. is revised for India. Six species are recognized: *M. balsamina* L., *M. charantia* L., *M. dioica* Roxb., *M. sahyadrica* Joseph & Antony, *M. subangulata* Blume [ssp. *renigera* (G. Don) WJ de Wilde] and *M. cochinchinensis* (Lour.) Spreng. *M. dioica* sensu stricto comprises delicate forms with evening anthesis and intensely musky scented flowers, distributed in low elevation areas in Western Ghats, peninsular and central India. Stout forms with day anthesis and large showy flowers occurring in mid and high elevation Western Ghats are separated as a new species (*M. sahyadrica* Joseph & Antony). North eastern elements, presently treated under *M. dioica*, are placed under *M. subangulata* ssp. *renigera*. *M. macrophylla* Gage has been placed in synonymy with *M. cochinchinensis*. Presence *M. denudata* (Thwaites) CB Clarke in India is doubtful in the absence of valid herbarium specimens or field collections from the reported localities. Generic and specific descriptions, key to species, and notes on distribution, habitat and ecology are also provided.

Key Words: Distribution, Ecogeography, *Momordica*, Systematics, Taxonomy

Introduction

The genus *Momordica* L., best known for the bitter gourd, derives its name from Latin 'mordeo' (momordi=to bite) in allusion to the jagged seeds as though bitten (Drury, 1864), ironically though the type genus (*M. balsamina* L.) do not follow this generic character. It belongs to the tribe Joliffieae Schrad. of Cucurbitaceae (Jeffrey, 1980) and is a native of the Paleotropics (Robinson and Decker-Walters, 1997). Besides their importance as wild relative of bitter gourd, they also have direct utility as nutritious vegetables and multipurpose medicinal plants.

Generic and species descriptions (along with keys in some cases) are found in various monographic and floristic treatises (Linnaeus, 1753; 1754; Willdenow, 1805; Blume, 1826; Seringe, 1828; Roxburgh, 1832; Wight and Arnot, 1834; Thwaites, 1864; Hooker, 1871; Clarke, 1879; Trimen, 1894; Cooke, 1903; Gamble, 1919; Keraudren, 1975; Chakravarty, 1982; Jeffrey, 1980; 2001; de Wilde and Duyfjes, 2002). It got a prominent mention in Rheede's *Hortus Malabaricus* (Vol. 8, 1688), the oldest regional flora for any part of the world, with descriptions and plates of four entities. Many of the provincial (regional), state and district floras in India also provide a small description of various *Momordica* species (Duthie, 1903; Prain, 1903; Gage, 1908; Kanjilal *et al*., 1938; Santapau, 1953; Mathew, 1983; Saldhana, 1985; Narasimhan and Sharma, 1991; Deshpande *et al*., 1993; Singh *et al*., 2002, to cite a few). Often, descriptions of dioecious *Momordica* species in national and district floras are based on insufficient herbarium material and the descriptions of morphological features of some species are incorrect or incomplete (Joseph, 2005). A perusal of the herbarium sheets lodged in major herbaria in India reveals innumerable instances of incomplete labelling and misidentification.

Inter-specific diversity in the genus *Momordica* in India has been estimated differentially by different workers. Chakravarty (1982) in Fascicles of Cucurbitaceae recognized seven species under the genus in India. Jeffrey (1980; 2001) recognized only five species occurring in the Indian subcontinent. According to de Wilde and Duyfjes (2002), ten species are reported in South East Asia, of which six each occur in Malaysia and India, where *M. balsamina* L., *M. charantia* L., *M. subangulata* Blume [(ssp. *renigera* (G. Don) WJ de Wilde)] and *M. cochinchinensis* (Lour.) Spreng. are common. Many of the regional and provincial checklists and inventories are also replete with instances of wrong species identification and erroneous distribution data. This is perhaps understandable as many of these works are essentially bibliographic enumerations rather than taxonomic revisions. As evident, there is no clarity and consensus in the inter-specific taxonomy of the genus in India and the botanical names and common names are often used incorrectly or interchangeably (Joseph, 2005; Joseph *et al*., 2006).

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The classification of *Momordica* most widely used in the Indian context is that of Chakravarty (1982). However, it does not address the distinct entities of dioecious *Momordica*, which as per his identified specimens, are all *M. dioica*. His study does not specifically identify or cite *M. subangulata* specimens even though he broadly stated their distribution in Western Ghats of Karnataka and Maharashtra. Similarly, there are no reports of field collection or spotting of *M. denudata* (Thwaites) CB Clarke from Kerala and *M. cochinchinensis* from Tamil Nadu, other than his statement in Fascicles of Cucurbitaceae (1982). He has retained separate taxon status for *M. macrophylla* Gage, as distinct from *M. cochinchinensis*, for the unlobed nature of the leaves. In fact, heterophylly is observed in all dioecious species and hence, leaf shape may not be a reliable character in distinguishing species in this group. The descriptions are incomplete like many other previous treatments in the sense either male or female plant could not be studied and the fruit and seed morphology details are often scanty. Perennial nature of the plant and its tuber morphology do not find a place in his treatment. Moreover, he ignored important traits such as anthesis time, nectar guides on petals and ridged nature of the fruit. The morphological features of the flower, which is very striking within the dioecious group representing lower elevations and arid belt, mid and high elevation Western Ghats and North Eastern Hills, were not taken into account while devising the key. Jeffrey (1980) rightly stated longitudinally alate or ridged fruits as the key character for *M. subangulata* and purple-blotched petals are very specific to *M. subangulata* and *M. cochinchinensis*.

Subsequent to Chakravarty's Fascicles, there has been no critical appraisal of the genus in India, though Kumar and Pandey (2002) have made a taxonomic study of the genus. However, it did not vary substantially from that of Chakravarty (1982) and reported the same number of species and distribution in India. This has prompted an in depth study of the morphological variability present in the genus across the country and a taxonomic revision based on herbarium and field study.

Materials and Methods

As part of the ecogeographic study of the genus, the first author visited the major national Herbaria in India, *viz*., Botanical Survey of India, Calcutta (CAL), BSI Southern Circle, Coimbatore (MH); BSI Western Circle, Pune (BSI); BSI Arid Zone Circle, Jodhpur (BSIJO); BSI Eastern Circle, Shillong (BSISH); St. Joseph's College, Tiruchirapalli (RHT); BSI, A&N Circle, Port Blair (PBL); Agharkar Research Institute, Maharashtra Association for the Cultivation of Science, Pune (AHMA); St. Xavier's College, Bombay (BLAT); National herbarium of cultivated plants, NBPGR, New Delhi, (NHCP); Kerala Forest Research Institute, Trichur (KFRI); Tropical Botanical Garden and Research Institute, Trivandrum (TBGT) and University of Calicut, Calicut (CALI), and studied about 700 herbarium sheets (including type specimens) from India, Sri Lanka, Myanmar, Bangaladesh, Philippines, Malaysia and Africa. For brevity, only a handful of geographically representative and historical sheets are enumerated in the specimen citation. To supplement the herbarium information, the entire stretch of Western Ghats besides specific sites in Deccan plateau, Central India, Andaman Islands and North East India were surveyed for collection of germplasm and ecological data. All the taxa were studied in the field (in the wild) between 2003 and 2006, and collections made for herbarium and field planting.

Taxonomic treatment

Momordica L.

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Type: *Momordica balsamina* L.

Climbers, annual or perennial; glabrous or pubescent. ***Leaves*** simple, entire or lobed, or (sub) pedately 3-5 (12-15 in African) foliate. ***Tendrils*** simple, unbranched. ***Flowers*** medium to large, monoecious or dioecious, sometimes ± zygomorphic, petals imbricate, off-white, cream or yellow. ***Male flowers*** solitary or in short loose pseudo-racemes, each flower stalk with a persistent hooded bract; pedicels short or long, receptacle-tube short, cupular or saucer shaped; calyx lobes entire or scarious, adnate at base; petals 5, free, entire, 1-3 with an incurved scale inside at the base-receptacle juncture; stamens 3, anthers one 1-thecous, two 2-thecous, filaments very short, free, inserted at the mouth of the receptacle tube; thecae usually coherent, connective sometimes swollen; pistillode absent. ***Female flowers*** solitary, in axils, also with a conspicuous or rudimentary bract; calyx narrow; petals as in the male; ovary oblong-fusiform, ribbed, warty or soft papillose; ovules mostly

many, horizontal; stigma 3-lobed; staminodes absent. ***Fruit*** ovoid-ellipsoid or fusiform, fleshy, ornamented with soft spines, warts or tubercles and ridges, irregularly or regularly 3-valved, dehiscent. ***Seeds*** many, enclosed in orange red sarcotesta (aril), small or large, flattened or turgid on faces, smooth or sculptured, margins often undulate and dentate.

Distribution: Throughout India

Uses: The genus *Momordica* is unique in the sense that all are medicinal plants and vegetables. *M. charantia* is a cultivated and wild gathered vegetable. *M. dioica* and *M. sahyadrica* are extensively gatherd for tender fruit vegetable purpose and tubers are medicinal. Ethnobotanical uses of thsee taxa in Western Ghats are reported (Joseph and Antony, 2008). *M. subangulata* subsp. *renigera* and *M. ccochinchinensis* are cultivated for their fruits used as vegetables. *M. balsamina* is a medicinal plant and famine vegetable in Rajasthan.

Taxonomic notes: The genus as treated here has only six valid species, which can be grouped under two heads: *M. charantia* L. and *M. balsamina* L. representing the monoecious group and *M. dioica* Roxb., *M. sahyadrica* Joseph & Antony, *M. cochinchinensis* (Lour.) Spreng., and *M. subangulata* Blume [(ssp. *renigera* (G. Don) W.J.J.deWilde)] representing the dioecious group. Crossability relationships and chromosome number also support the natural of this grouping (Table 1).

The genus, as circumscribed here, do not include *M. cymbalaria* Fenzl [*Luffa cymbalaria* Fenzl ex Naud.= *M. tuberosa* (Roxb.) Cogn.], though few workers still treat it under *Momordica* as in de Wilde and Duyfjes (2002). Hooker (1871) removed it from *Luffa* (where Roxburgh placed it) and placed it under *Momordica* because of its simple tendrils (Clarke, 1879) and Chakravarty (1982) rightly restored it to *Luffa* (as *Luffa tuberosa* Roxb.). Our observations of live specimens from Tamil Nadu asserted its distinctness from *Momordica* for flowers being white, fruit a dry dehiscent one with fibrous mesocarp on ripening, scanty, white seed aril with no pulp and fruits not showing any colour change on ripening. All the six valid species treated here have fleshy scarlet-red fruits and fleshy red aril, which are adaptations for bird dispersal. Besides, the monoecious species have basic chromosome number n=11 and the dioecious group has n=14, whereas *M. cymbalaria* (*Luffa cymbalaria* Fenzl ex Naud.) has the basic number n=8.

Key to species

1a. Germination epigeal, annual, taproot non-tuberous, plants monoecious, nectary in male flowers not closed with scales, fruits muricate or tubercled.

2a. Bracts of male flowers about the middle or below the middle of the flower stalk; fruits small or large, softly tubercled or muricate with long broken ridges; seeds thick, flat on surface, margins edged, thick on sides, broadly rectangular, no distinction between chalazal or micropylar ends, ends sub tridentate, heavily or feebly sculptured. ***M. charantia***

2b. Bracts of male flowers at the apex of the peduncle; fruits small, distantly soft tubercled, no bumps or ridges; seeds very thin, sides not thick, margins not wedged, broadly ovate round with tapering micropylar end, ends roundish, finely pitted and feebly sculptured. ***M. balsamina***

1b. Germination hypogeal, perennial, taproot tuberous, plants dioecious, nectary of the male flowers closed with prominent scales, fruits echinate.

Table 1. Distinguishing characters in the sub generic grouping

Character	Monoecious	Dioecious
Basic chromosome no.	n=11	n=14
Germination	Epigeal	Hypogeal
Perennation	Annual, non-tuberous	Perennial-tuberous taproot
Fruit surface	Muricate-tubercled	Echinate-soft papillate
Seed sides	Rectangular, squarish	Cog wheel, round, oval, stellate
Seed colour	Brown-yellow	Black or grey
Leaf shape	Angular	Roundish
Male flower bract position	Mid way or towards axis- not protective	Just below the flower-protective
Male flower calyx	Broad, touching each other, protecting the nectary	Narrow, spaced and less protection to the nectary
Male flower nectary	Open from above	Closed by corolla scales
Relative size of ♂ and ♀ flowers (corolla)	♂ flowers larger than ♀	Of equal size

3a. Petals (3 inner) with black purple blotch, male calyx -hypanthium saucer shaped.

4a. Leaf cordate, unlobed, margins dentate, petiole eglandular, male calyx blackish purple, broad, tip round-oval, fruits faintly or prominently ridged, softly echinate, seeds medium sized, pitted on surface, rectangularly cog wheel shaped.

M. subangulata

4b. Leaf unlobed or shallowly 3 lobed, margins undulate, petiole gland dotted (6-12 bead like structures, often the lamina base also), male calyx green, broad, tip triangular, fruits with short conical projections, seeds large, smooth on surface, hexa-octagonal, subtridentate on ends.

M. cochinchinensis

3b. Petals without purple blotch, male calyx-hypanthium cup shaped.

5a. Anthesis in the early morning, flowers large showy, bright yellow, feebly scented, male calyx blackish purple, sepals of male flower broad, tip oval, round or scarious.

M. sahyadrica

5b. Anthesis in the evening, flowers small, pale yellow, intensely musky scented, male calyx whitish yellow, sepals of male flower narrow acute.

M. dioica

1. *M. balsamina* L. 1753, Sp. Pl.: 1009; Ser. 1828, in A. DC., Prodr. 3: 311; Wight et Arn. 1834, Prodr. Fl. Ind. Orient. 1: 348; CB Clarke 1879, in Hook. f., Fl. Brit. India 2: 617; Cooke 1903, Fl. Pres. Bomb. 1: 529; Duthie 1903, Fl. Upper Gang. Pl. 1: 370; Chakrav. 1959, Rec. Bot. Surv. India 17, 1: 90, p.p.; id. 1982, in SK Jain *et al*., Fasc. Fl. India 11: 88; C. Jeffrey 1980, Kew Bull.34: 790, p.p; id. 2001, in Hanelt, Mansf. Encyl. Agric. Hort. 3: 1523; de Wilde and Duyfjes 2002, Bot. zhuarn. 87(3): 134.

Slender trailing herb, 1.5-3.0 m high, annual; subglabrous; monoecious; ***Stems*** round, internodes 5.5-6 cm; tendrils delicate, 11-13 cm long, basal 1-1.5 cm uncoiled. ***Leaves*** 3-5 (-7)-lobed to c. halfway or more, subcircular in outline, 4-6 cm dia., base cordate with a cuneate petiole-blade juncture, apex mucronate, lobes rhomboid, margins acutely 3-7 lobulate; petiole 1-4 cm long, slender, puberulous. ***Flowers*** solitary. ***Male flowers*** 2-3 cm across, bigger than in female; peduncles slender (2-) 3-5 cm long; bract subapical, suborbicular, up to 0.6 x 0.5 cm, pale green, filmy, cordate at base, margins finely dentate; pedicel 0.3-0.4 cm long, ± pubescent; receptacle-tube cup-shaped (obconical), upto 0.2 mm long; sepals ovate, up to 0.7 x 0.3 mm, obtuse, faint green or pale cream, pubescent; petals obovate, 1-1.3 x 0.7-0.9 cm, pale yellow to creamish-yellow with green sub-parallel veins and undulate margins, scales in 2 petals only; filaments up to 0.2 mm long, inserted on the rim of the receptacle tube, anthers up to 1.2-1.8 mm long, ± coherent at base only; thecae bright yellow, disc inconspicuous by deep orange coloured nectary, open from above. ***Female flowers*** 1.7-1.8 cm across; peduncles 0.2-0.3 cm long; pedicels 0.4-0.6 cm long; bract small; calyx minute, thread like, thin, recurved; petals 0.8 × 0.8 cm, pale yellow to creamish-yellow with green sub parallel veins and undulate margins; ovary ovoid to fusiform, shortly rostrate, 5-7 mm long, ± pubescent, finely remotely warty in rows, style short, slender, whitish yellow. ***Fruits*** broadly ovoid-ellipsoid, bulged at middle, 2.5-3.5 (4.0) cm long, 1.8-2.0 cm in circumference and stalk 1-2 cm long, shortly rostrate, ashy-olive green with 2-3 white tubercles in lines across the whole length of fruits, bumps (murication in interspace between ridges) absent; fruits turning orange and later scarlet red on ripening; pericarp thin. ***Seeds*** 3-5, covered by deep red sarcotesta, ovate oblong, compressed, 8.5-9.5 × 5.9-6.2 mm, and margins finely grooved, crenulate; testa grey or light brown, delicately verrucose.

Type: South Africa, Naal River, Burke 81 (K)

Specimens examined: India, Rajasthan, Jodhpur: Birai dam site, 26 August 1977, AN Singh 4398 (BSIJO); Jhurjhunun: on the way to Jaosrapur, 29 September 1994, PJ Parmer 12379 (BSIJO); Pali: Samaji ka gudda, near Kantol, 305 m, 20 August 1975, BV Shetty 1825 (CAL, BSIJO); Ajmer: Pachkund, 20 March 1959, SK Jain 49685 (BSI); Gujarat, Mehasana: Pushpavati river banks, 90 m, 26 July 1977, V Singh 5462 (CAL, BSIJO); Bharuch, 20 October 1957, PS Tour 25878 (BSI); Nakhatrana, 15 September 1969, RSO Raghavan 114827 (BSI); Jodhpur, Kailana lake road, 24 September 2003, K Joseph John 3880 RHK.

Distribution: Rajasthan, Gujarath, Haryana, and adjoining arid North Western plains. Not known from South India or Western Ghats. It cannot naturalize in the heavy monsoon climate and obviously South India is far outside its natural range (geographically and in its climatic amplitude). The lone report of its occurrence in South India (from Aryankavu, Kollam District of Kerala) by Subramanian (1970) is based on wrong identification

of collection 77,286 (accession no. 35124 of BSI, Pune, originally identified as *M. balsamina* on 1.xii.1961 and subsequently determined as *M. dioica* on 22.x.1962). Hence, the enumeration of *M. balsamina* in the floristic diversity of Kerala (Sasidharan, 2004; Nayar *et al.*, 2006) does not stand valid.

Vernacular names: Barakarela (Rajasthan), Karelo-jangro (Sindhi).

Habitat and Ecology: Disturbed habitats in semi-arid and arid tropics, roadsides, farm borders and fences on medium heavy soils with slightly alkaline pH. *Prosopis cineraria* (L.) Druce was found to be the associated vegetation.

Taxonomic notes: The species is allied to *M. charantia* var. *muricata* and other African taxa for leaf lobing and dissection. Flowers are very distinct; the female flower is always smaller than the male flower and male flower has red nectar guides**.**

2. *M. charantia* L. 1753, Sp. Pl.: 1009; Willd 1805, Sp. Pl. 4: 602; Blume 1826, Bijdr.: 927; CB Clarke 1879, in Hook. f. Fl. Brit. India 2: 616; Cooke 1903, Fl. Pres. Bomb.1: 528; Duthie 1903, Fl. Upper Gang. Pl. 1: 369; Prain 1903, Beng. Pl. 1: 521; Gamble 1919, Fl. Pres. Madr. 3: 532; Kanjilal *et al*., 1938, Fl. Assam 2: 330; Chakrav. 1959, Rec. Bot. Surv. India 17, 1: 88; id.1982, in SK Jain *et al.*, Fasc. Fl. India 11: 89, f. 8-10; Backer 1963, in Backer et Bakh.f., Fl. Java I:299; Keraudren 1975, in Aubrev. et JF Leroy, Fl. Camb., Laos, Vietnam, 15:42; C. Jeffrey 1980, Kew Bull. 34: 789, p.p; id. 2001, in Hanelt, Mansf. Encyl. Agric. Hort. 3: 1523-24; de Wilde & Duyfjes 2002, Bot. zhuarn. 87 (3): 135; *M. muricata* Willd., 1805, Sp. Pl. 4: 602; *M. charantia* var. *muricata* (Willd.) Chakrav. 1982, in SK Jain *et al.*, Fasc. Fl. India 2: 92, f. 1-7; *M. charantia* L. var. *abbreviata* Ser. 1828, in DC. Prodr. 3: 311.

Annual, slender climber, 2-4 m high, scarcely to densely pubescent (tender parts wooly), monoecious. ***Leaves*** usually deeply palmately 5-9 lobed, reniform to orbicular or sub orbicular in outline, 2.5-8 x 4-10 cm, cordate at base, acute or acuminate at apex, lobes ovate or obovate, narrowed at base, margins sinuate to undulate, mucronate; petioles 1.5-5 cm long. ***Flowers*** solitary, pubescent; petals yellow. ***Male flower*** stalks slender with bract midway or towards base; peduncle 2-5 cm long; bract reniform, 5-11 mm diam., green, with mucronate apex and margins entire; pedicel 2-6 cm long; receptacle-tube cup-shaped, 2-4 mm long and 2-3 mm wide; sepals ovate-elliptic, 4-6 x 2-3 mm, pale green, touching each other and protecting the corolla tube; petals obovate, 10-20 x 7-15 mm, mucronate at apex, scales 2; filaments 1.5-2 mm long, inserted in the throat of the receptacle tube; anthers coherent; disc shortly cup shaped, c. 1.5 mm diam. ***Female flower*** peduncle 1-6 cm long; bract 1-9 mm diameter; pedicel 1-8 cm long; sepals narrow, oblong-lanceolate, 2-5 mm long; petals smaller than or equal to that in male, 7-10 mm long; ovary fusiform, narrowly rostrate, 5-11 x 2-3 mm, muricate, tuberculate or longitudinally ridged; style c. 2 mm long; nectary 3, at stylar base. ***Fruits*** pendulous, stalk 2-8 cm long; fruit discoid, ovoid, ellipsoid to oblong or blocky, often narrowed at ends, sometimes finely rostrate, 3-20 x 2-5 cm, white or green turning orange on maturity, soft tuberculate with 8-10 broken or continuous ridges, splitting from base into 3 irregular valves. ***Seeds*** 5-30, squarish rectangular, ends subtridentate, faces compressed, sculptured, 5-9 x 3-6mm, margins grooved; testa brown or black.

Type*:* Plate 10 in Rheede's *Hort. Mal. Ind.* 8. 1688 (*M. charantia* var. *muricata*) **Lectotype:** from a plant cultivated at Hartekamp, Netherlands (*M. charantia*)

Specimens examined: India, Gujarat, Bharuch: Broach river bank, 4 November 1955, GL Shah Shah 6311 (BLAT); Rajkot: Rajkot jilla park, H Santapau 16915 (BSI); Kerala, Palakkad: Silent valley, Panthenthode border, 1,100 m, 21 August 1982, T Sabu SV 10680 (CALI); Anamuli hill slopes, 300 m, 13 October 1979, NC Nair 64604 (CAL); Travencore, Quilon, 11 November 1913, M Rama Rao 2189 (CAL); Tamil Nadu, Tiruchirappally, Kudamuruti, 65 m, 30 March 1984, KM Mathew RHT 29973 (RHT); Rajasthan, Ganganagar: Raisingh nagar, 250 m, 14 November 1976, *GP Roy* 3,875 (CAL); Sikkim, West District: Singtam, 1,500ft, 12 May1967, MC Mazumdar 174 (CAL); Gangktok, G King 187 (CAL); Assam, Lakhimpur: Ranga reserve forest, 23 November 1957, G Panigrahy 11,500 (CAL); Andaman & Nicobar: Car Nicobar Islands, Kakana, 18. September 1976, NG Nair 4438 (CAL); Andhra Pradesh, Cuddappa, July 1885, JS Gamble s.n. (CAL); Maharashtra, Bombay: Mazgaon hill, February 1925, *AC Ackland* ack 491(BSI); Karnataka,Uttar Kannad: Yellapur, 20 October 1883, WA Talbot 4814 (BSI); Tumkur: Maralu bavi, 15 October 1978, KP Srinath KFP2749 (CAL)

Distribution: Large fruited forms cultivated all over

India as vegetable and small wild forms occur in forest pockets across Western Ghats and beyond in Eastern Ghats, Chhattisgarh (Bastar), Jharkhand and almost all over Central and South India.

Common and vernacular names: Bittergourd (Eng.), Uchchhe, Oochya, Oochi (Beng.), Jangli karela (Hindi, Mar.), Gidda hagala (Kan.), Kadu hagali (Tulu), Kattu pavaka (Mal.), Pavuka, Chinna paval (Tam.), Tulsi karela (Oriya).

Ecology: The species has wider adaptability as evidenced by herbarium records. It grows from sea level to 1700 m in sub-Himalayas and from arid Rajasthan to cool climate in high ranges of Western Ghats. A range of soil types from river alluvium to red laterite, black cotton and clay loam has been recorded. By far, this is the most adaptable taxa in the genus.

Taxonomic notes: Chakravarty has made a distinction between large and small-fruited forms, the former being *M. charantia* var. *charantia* (cultivated type) and the latter *M. charantia* var. *muricata* (wild type). However, citing the Plate 10 in Rheede (1688) as Type, he has described the small-fruited cultivated form ('Uchchhe' of West Bengal), as *M. charantia* var. *muricata*. Even then, this is not shown in the determinavit slips in any of the herbaria in India even though most of the *M. charantia* sheets belong to the small-fruited wild category. Often, herbarium labels refer to them as escapes from cultivation. The cultivated form is generally large fruited. The small-fruited types occur wild in nature often as a component of primary and secondary forests or as weeds in agro ecosystems. The small fruited types are variously described as *M. charantia* var. *abbreviata* Ser., *M. muricata* Willd. and *M. charantia* var. *muricata* (Willd.) Chakrav. by various workers in different areas of its distribution.

Key to the varieties

Vines robust, branches few, leaves large, fruits bulged, 5-30 cm, weighing 30-400 g, seeds large, flat subtridentate, brown, senescence early, cultivated

M. charantia var. ***charantia***

Vines thin, leaves small to medium, fruits small, 3-9 cm, 5-15 g, seeds small to medium, flat, subtridentate, brown, white, black or mottled, senescence late, wild or rarely cultivated

M. charantia var. ***muricata***

3. *M. dioica* Roxb. ex.Willd. 1805, Sp. Pl. 4: 605; Ser. 1828, in A. DC., Prodr. 3: 312; Roxb. 1832, Fl. Ind. 3: 709; Wight et Arn. 1834, Prodr. Fl. Ind. Orient.: 348; Wight 1841, Icon. Plant. Ind. Orient.: t. 505, 506; Thwaites 1859, Enum. Pl. Zeyl.: 126; CB Clarke 1879, in Hook. f., Fl. Brit. Ind. 2: 617; Trimen 1894, Handb. Fl. Ceylon 2: 249; Cooke 1903, Fl. Pres. Bomb. 1: 529; Duthie 1903, Fl. Upper Gang. Pl. 1: 370; Gamble 1919, Fl. Madras 1: 532; Chakrav. 1959, Rec. Bot. Surv. India 17: 91, p.p.; id. 1982, in SK Jain *et al*., Fasc. Fl. India 11: 94, pp; C Jeffrey 1980, Kew Bull. 34: 790, p.p.; id. 2001, in P. Hanelt, Mansf. Encyl. Agric. Hort. 3: 1522; KM Mathew 1983, Fl. Tamilnadu Carnatic 3: 648; de Wilde & Duyfjes 2002, Bot. zhuarn. 87(3): 142-144.

A dioecious vine, climbing up to 3-10 m high; the tap root perennial (up to 5 years), tuberous, fusiform in first year, subsequently getting elongated and bulged, rarely branched below, 9-18 x 6-11 cm, weighing between 180 to 350 g, occasionally up to 800 g. ***Stems*** slender, the internodes 3-8 cm long, cylindric, nodes in the mature basal region, quadragonal. ***Tendrils*** axillary, 4-12 cm long, the basal 2-4 cm straight and the rest spiral. ***Leaves*** thin, light green to green, ovate-cordate, nearly triangular in outline, lobed and sub-lobed to various degrees or unlobed, cordate and cuneate at base, acute or acuminate at apex, the margins entire, undulate, irregularly or coarsely crenulate or regularly dentate; venation ending up in spathulate hydathodes which is sometimes like broad short bristles at margins and dent tips, lateral veins 4-5 pairs on each side of the midrib, the lower most pair running parallely close to the margin of the cordate sinus, but soon branching out in to 3-4 veinlets; the upper surface and margins with scattered short hairs (10x), the lower surface densely short hairy; petiole slender to medium thick, 3-7 cm long, 1-1.5 mm in diameter, longitudinally grooved. ***Staminate flowers*** solitary in axils or often a loose fascicle with a separate lower one; peduncles 3-7.5 cm long (usually 5-6 cm), light green, thin; pedicels sub sessile, 2-3 mm long, whitish-yellow, subtended by and protected inside a reniform clasping swollen bract, 4-5 × 8-10 mm, light green, cucullate, with 8-12 longitudinal veins attached to the pedicel by base at one side; calyx (cup) funnel-shaped, lobes 5, light green, narrow acute, up to 6 × 1 mm; petals 5, free, pale yellow, glandular, oblong-lanceolate, 12-22 × 5-8 mm; acute at apex with 3-5 sub parallel veins branching sideways. Stamens 5, two of them with a pair of anthers and the other with a single anther, filaments 2-3 mm long, anthers subtriangular, 2-3 mm long, extrose, yellowish-brown on inner side, each anther with a single 'S' shaped pollen locule,

filaments at base extended to petal base covering the nectary; disc inconspicuous. ***Pistillate flowers*** solitary in leaf axils; peduncles thin, very short 0.5-2.0 cm long; pedicels thin, 2-4 cm long, subtended by a small bract of 3-4 × 2-6 mm; bracts reniform with acute tip just like in male but of small size; sepals 5, semi persistent, green, narrow, 3-6 x 0.8 mm, acute at apex; petals 5, same as in male flower; ovary oblong-ovoid to urn-shaped, 6-9 x 2-3 mm, rounded at base, clothed with short soft glandular spines all over the surface except receptacle base; nectary 5, small, white, butt- like cylindrical structures between petals at stylar base on the disc; styles short, up to 4 mm long, glandular hairy, stigmatic lobes 3, each lobe 'V' shaped, up to 3 x 5 mm, lemon-yellow, cushiony, glandular. ***Fruits*** broadly ovoid-oblong, rounded at base, abruptly conical with rostrate tip at apex, 3-4 x 2-3 cm, the entire surface covered with soft short spines (except the beak), light green or dark green, turning uniformly orange on ripening, splitting from base into three irregular pieces and rolling back exposing scarlet red arils (seeds). ***Seeds*** 2-3 mm across, black lustrous and golden-lined (when fresh), sculptured on surfaces, small round to slightly oval or shortly stellate (round-ovate and smooth in Central Indian specimens), seed coat brittle, shell hard, membrane thin, whitish, endosperm oily with characteristic aromatic odour when crushed.

Type: Peninsular India Orientalis, Nandaradah, *Rottler s.n.* (K).

Specimens examined: India, Kerala, Iddukki: Kattappana, 23 October 1997, M. Dan 14135 (TBGT); West Bengal, South 24-parganas: Sundarbans, Ghata pak, August 1902, D Prain s.n. (CAL); Bihar, Champaran: Motihari, 18 August 1964, SP Banerjee 1145 (CAL); Haryana, Hissar: Hissar bir, 10 August 1885, JF Duthie s.n. (CAL); Jammu & Kashmir, Naovshera, 30 June 1876, CB Clarke s.n. (CAL); Karnataka, Mysore: Biligirirangan hills, 8 September 1978, SR Ramesh kfp 2667 (CAL); Tamil Nadu, Courtalam (Kuttalam), 27 June 1901, CA Barber s.n. (MH); Kanyakumari: Vallathithodu, 500 m, 6 September 1976, AN Henry 48241 (MH); Salem: Rasipuram, 1,150 m, 14 July 1978, KM Mathew and Rajendran 14833 (RHT); Bombay: Trombay, September 1907, A Meebold 8906 (CAL); Raigarh: Neral, Thaburuwadi, 2 July 1959, NA Irani NI 4174 (BLAT); Andhra Pradesh, Vishakhapatnam: Kotturu (Koduru), 250 m, 28 November 1961, NP Balakrishnan 864 (CAL); Gujarat, Junagadh: Sasan, Gir Forests, 22 July 1957, GS Puri 30028 (BSI); Rajasthan, Pali: Sarandana, 396 m, 18 August 1975, BV Shetty 1792 (CAL, BSIJO)

Distribution: Highest distribution in the Deccan Plateau and to a small extent in coastal Kerala (South of Palakkad gap), Gujarat, Orissa, West Bengal, Rajasthan, Madhya Pradesh, Uttar Pradesh, plains of Punjab and rarely in Jammu and Kashmir.

Vernacular names: kakrol (Hindi), kartoli (Mar.), karonda (Raj.), erumapaval, venpaval (Mal.), thulapava, kuruvithalaipavai, palupakkai (Tam.), Akakara (Telugu)**.**

Ecology: The taxon prefers low elevation forests and openings in Western Ghats up to 350 m. Soil types vary from sandy loam in coastal Kerala to clay loam to alluvial soil in riverbeds (major habitat) to laterite soils and hard laterite rock crevices and black cotton soil in Deccan plateau or clay loam in Bundelkhand.

Taxonomic notes: Following Chakravarty's revision of Cucurbitaceae (1982), three distinct entities have been identified as *M. dioica* in all the Indian herbaria, without even designating them sub-specific or varietal status. *M. dioica sensu stricto* should be restricted to small forms adapted to plains, low elevations and coastal areas with anthesis in the evening and having small, pale yellow, and intensely musky scented flowers. Stout forms with day anthesis and large showy flowers occurring in mid and high elevation Western Ghats are separated out as a new species and are discussed in detail under *M. sahyadrica*. Material from North Eastern India is treated as *M. subangulata* ssp. *renigera*. Even though, there is a general resemblance overlying the three different taxa, they show clear-cut morphological distinction in floral guides, flower colour, size, calyx structure and colour and petal colour, besides pollinator specificity and distinction in anthesis time (Joseph *et al*., 2006).

4. *M. sahyadrica* Joseph and Antony 2007, *Nord. J. Bot*. 24(5): 539-542.

A dioecious robust tendrillar climber, vines up to 5-6 m high, the tap root perennial (up to 5 years), tuberous, fusiform when young, subglobose or bulged irregularly when matures, 10-18 cm long, 5-10 cm. across, outer skin brownish and inner flesh whitish yellow. ***Stems*** stout, cylindric turning quadrangular as it matures, the internodes 5-10 cm long, nodes quadrangular, blackish green, distinctly long hairy. ***Tendrils*** medium thick, unbranched, 8-15 cm long, 4-5 cm of base uncoiled, remaining coiled. ***Leaves*** heterophyllous; petiole 3-8 cm

long, 1-1.5 mm in dia, medium thick, longitudinally grooved above; blades medium thick, ovate, broadly triangular in outline, 3-5 lobed or entire, 10-16 × 8-18 cm, deeply cordate at base with a subangulate juncture with petiole, sometimes hastate, acute or acuminate at apex, margins highly variable, entire, undulate or coarsely crenulate, lateral veins 5-7 pairs, the lower pair running close to the margin of the subangulate petiole juncture, hairs short, scattered without, snowy white within. ***Male flowers*** axillary, solitary or a loose fascicile of 5-7 (up to 15) flowers and in such case the lowermost flower produced separately and early; peduncles 2-5 cm long; dark green, pedicels short, 0.8-1 cm long, whitish green subtended and covered by an inflated bract, up to 1 × 1.5 cm, reniform, margins cucullate; calyx base funnel shaped, up to 8 mm long and 1cm. across, purplish black, lobes free, up to 1 × 0.6 cm, yellowish white at centre and blackish purple at base and margins, elliptic-oblong, recurved at apex, margins and apex scarious, densely hairy within and sparsely hairy without; petals 5, free, fleshy, obovate, up to 4 × 1.5 cm, bright yellow with a greenish yellow narrow base, veins prominent (embossed), each petal bearing a small tongue like ciliate appendage near the base; stamens 3, 2 of them with a pair of anthers, the other with a single anther, filaments up to 3 mm long, anther 2-3 x 1-2 mm, extrose, thecae dull black, 'S' shaped with abundant orange pollen, pollen grains tricolpate. ***Pistillate flowers*** solitary in leaf axils; peduncles 0.5- 2.0 cm, often less than 1 cm; pedicel short, up to 0.5 cm long, subtended by a small rudimentary bract,1-3 × 0.5-5 mm; sepals 5, green, persistent, 0.8-1.3 x 1-3 mm, equal, lanceolate, acuminate at apex densely glandular hairy within and without; petals 5, free, fleshy, up to 4 × 2 cm, narrow, greenish yellow and ciliate at base, widening towards middle, bright yellow; veins 5-7, sub parallel; nectary 5, white, short cylindrical, alternating with petals, protected by a spur at the base of petals; ovary inferior, oblong-ovoid, 1-1.5 × 0.2-0.4 cm, more or less densely clothed with soft papillae of 1 mm length; style up to 6 mm long, whitish yellow, stigma up to 4.0 × 9.0 mm, cushiony, trifid, each lobe again sub lobed dichotomously. ***Fruits*** broadly ellipsoid, ovoid to fusiform or top shaped with round blossom end and rostrate distal end, 5-7.5 × 3-4.2 cm in size, 9-12 cm in circumference, 35-50 g in weight, dark green turning bright orange on ripening, densely clothed with soft short spines; spines 2-4 mm long; arils sweet to taste, ripe fruits aromatic and slightly bitter. ***Seeds*** black, shining, loosing its luster on drying, round stellate to slightly cog wheel shaped, warty-dentate on margins sculptured on faces with irregular furrows and ridges, 0.2-0.3 × 0.2-0.3 cm, seed coat brittle, hard shell like, the membrane very thin, smooth, blackish green, conspicuously veined, endosperm oily, distinctly aromatic when crushed.

Type: INDIA, Kerala, Thrissur District: NH-47, Thrissur-Palakkad road at Erumbupalam, outskirts of Peechi-vazhani wildlife sanctuary, 23 October 2003, Joseph John 133 (Holotype, CAL; Isotype, MH).

Specimens examined: INDIA, Maharashtra, Rajgarh: Kanakeswar, 30 October 1982, HD Sane 2147 (AHMA); Rajgarh: Amba ghat, 17 September 1961, C Saldhana CS 7205, CS 7206 (BSI); Tamil Nadu, Coimbatore: Siruvani, 21 August 1960, AN Henry ANH 371(BLAT); Coimbatore: Karian shola, Anaimalai, 1,012 ft, 1 October 1912, CEC Fisher s.n. (CAL); Nilgiris: Kodaikanal Ghat, 17 November 1897, CA Barber s.n. (MH); Guddallur: Rockwood R.F, 1,000 m, 5 August 1975, E Vajravelu 90447 (MH); Goa, South Goa: Perideterm, Cumbari, 500 ft, 5 October 1970, NP Singh s.n. (BSI); Karnataka, Chickmagalur: Mudigere-Bantwal rd, 850 m, 7 October 1979, CJ Saldhana s.n. (CAL); Dakshin Kannada: Sampaje, 8 November 1900, CA Barber s.n. (MH); Uttar Kannada: Hulekal Ghat, 9 September 1962, RS Raghavan 83073 (BSI); Kerala, Palakkad: Sholayar, Malakkarappa, 800 m, 29 October 1999, K Joseph John 3111(IARI); Idukki: Kulamavu, 700 m, 3 October 1983, CN Mohanan 152254 (MH).

Distribution: Endemic to Western Ghats of Kerala, Tamil Nadu, Karnataka, Goa and Maharashtra.

Ecology: The taxon is highly niche specific. Restricted to acidic forest soil in moist forests, it grows on well-drained slopes. Altitudinal preference was noticed for mid and high ranges of Western Ghats from 250-800 m with higher frequency at 600-800 m coffee and cardomom estates are the ideal habitats.

Vernacular names: Madahagalikkai (in Dakshin Kannada, Uttar Kannada, Coorg and Shimoga), Katteli and Kadu hagali (in Uttar Kannada District), Kadu peerakai (in parts of Dakshin Kannada), Pothupaval, Vaikka, Kakkachi, Karayachakka, Kattupaval and Mullen paval (in Kerala).

Taxonomic notes: This taxon is a new species described from Western Ghats (Joseph and Antony, 2007). It was treated as *M. dioica* in Chakravarty's revision of

Cucrbitaceae and hence all the specimens were labelled as *M. dioica*. However, collections from Mahabaleswar-Kanakeswar (Maharashtra) were labelled as *M. subangulata* Blume (AHMA). *M. subangulata* was reported as rare in semi-evergreen and evergreen forests in Belgaum, Western Karnataka by Saldhana (1985), probably based on this taxon. It differs from Wight's icon of *M. dioica* in its flower being large (5 times bigger than *M. dioica*), showy, opening in the day, not being musky scented and robust plant growth manifested in all organs. However, the fruits resemble *M. dioica*, besides being a tuberous perennial. The material has a general resemblance to *M. subangulata* Blume ssp. *subangulata* (Scortechini 549, CAL) in the leaves, male bract, petals with incurved scales (= spurs/appendages). However, the male flower sepals are not typically broad ovate; male flower calyx is cupular (not saucer shaped) and fruits are not ridged or longitudinally alate but softly densely echinate.

5. *M. subangulata* Blume 1826, Bijdr. Fl. Ned. Ind. 15: 928; CB Clarke 1879, in Hook.f., Fl. Brit. India 2: 617, p.p; Cooke 1903, Fl. Pres. Bomb. 1: 530; Gamble 1919, Fl. Pres. Madr. 3: 532; Chakrav. 1959, Rec. Bot. Surv. India 1: 97, p.p.; id.1982, in SK Jain *et al.*, Fasc. Fl. India 11: 95, p.p.; Backer 1963, in Backer et Bakh. f., Fl. Java I: 299; Keraudren 1975, in Aubrev. et. J.-F. Leroy, Fl. Camb., Laos, Vietnam, 15:41; C Jeffrey 1980, Kew Bull. 34: 790; de Wilde and Duyfjes 2002, Bot. zhuarn. 87(3): 145-148.

Taxonomic notes: CB Clarke, Gamble and Chakravarty have enumerated this species in their treatments, without assigning any subspecific status. De Willde and Duyfjes (2002) has bifurcated this species to two subspecific entities, of which only one (ssp. *renigera*) occurs in India.

Key to Subspecies

1a. Plants stout, fruits 5-8 cm long, densely soft spiny with remnant ridges **ssp. *renigera***

1b. Plants delicate, fruits 3-5 cm long, irregularly ridged or longitudinally alate on surface **ssp. *subangulata***

Momordica subangulata* ssp. *renigera (G. Don) WJ de Wilde 2002, *Bot. zhuarn.* 87(3): 147-148.

A dioecious vine, climbing up to 8-10 m high, the roots (tap root, secondary and tertiary roots) tuberous, tubers both sessile and non sessile, fusiform to globoid or subgloboid to irregularly bulged, often branched, 3-7 × 2-5 cm. ***Stems*** stout, the internodes 7-11 cm, quadrangular, grooved, nodes slightly bulged, often twisted. ***Tendrils*** simple, axillary, 15-17 cm long, the basal 5-7 cm erect, the rest when uncoiled measuring up to 10-12 cm long. ***Leaf*** (blade) medium thick, light green, ovate cordate, unlobed, 8-12 × 7-11 cm, acuminate at apex, cuneate at base, the basal flaps almost touching the petiole or overlapping giving rise to two sinus or cavities, the margins undulate and coarsely denticulate with fine bristles projecting as continuation of veinlets; veins 3-5, ascending and many pinnate from midrib ending up in fine network of areoles, 4-5 mm across, glabrous above, glandular hairy below; petioles 7-10 cm long, thick, channeled longitudinally, margins finely ridged. ***Flowers*** large, solitary (male occasionally a loose fascicle of 3-7 flowers), axillary, showy, creamish-yellow, up to 9 cm across, opening early in the morning, withering by afternoon and falling (petals) by evening. ***Staminate flowers*** with peduncles 4-6 cm long, pedicel 0.5-1 cm long, subtended and covered inside a reniform bract, 2 × 2.5 cm, light green, plicate with about 15 ribs, shining, glabrescent inside, pubescent outside; calyx cup saucer shaped, sepals 5, greenish crimson, united at the base, 10 × 7mm, ovate, acuminate at apex; petals 5, 5-6 × 3-4 cm, free, fleshy, prominently networked with 5-7 sub parallel veins and intricate cross veins, creamish-yellow with intense colouration towards base, obovate, acuminate at apex, narrow at base, highly imbricate, 3 inner petals with blackish purple blotch of 7 × 6 mm size and long glandular hairs; nectary, orange yellow, enclosed in calyx cup, scales 3, very prominent, flap like; stamens 3, two of them with a pair of anthers, the other with a single anther, filaments up to 4 mm long, black on sides, thecae yellowish white and dull brown bearing abundant orange yellow pollen. ***Pistillate flowers*** with peduncles short, 1-1.3 cm long, pedicels 10-17 cm long (Mizoram, Gangtok, Kahikuchi specimens); bracts minute, rudimentary, near axil, often a scar of 2 × 1 mm size; sepals 5, 5-9 × 1-1.5 mm persistent, acute at apex; corolla and scales as in male; ovary oblong ovoid, dark green, 1.5-2 × 0.6 cm, rounded at base, finely echinulate on surface; nectary 5, white butt like cylindrical structures protected inside the petal base, touching the style; style 5 to 7 mm long, pale yellow, stigma cushiony, up to 4 × 6 mm, trilobed. ***Fruits*** broadly ovoid-ellipsoid, with doom shaped ends and a prominent rostration (3-5 mm) at base, 7-8 × 13-14 cm, each weighing 50-80 g; densely softly echinate, rarely with remnant ridges at base, spines 2-3 mm long, light green turning yellow and finally bright orange on

ripening, exposing the seeds (35-50 per fruit) by basal splitting of the fruit and rolling back of the split lobes; flesh thick, (5-6 mm), aril deep red; ***Seeds*** black, flat, sub-orbicular to sub-tridentate, rectangularly stellate-cog wheel shaped, 6 × 3 mm and up to 4 mm thick, sculptured on faces with grooves and dented edges, margins with a double row of wart like small protruberances.

Type: Wall. Cat. No: 6743, Prome hills, Myanmar (CAL)

Specimens examined: India, Arunachal Pradesh, Lohit: Deopani riverbank, 2 October 1969, AS Rao 48182 (CAL); Tripura, West Tripura: Kumargarh, 25 July 1957, DB Deb 900 (CAL); Nagaland, Kohima: Naga Hills, September 1886, D Prain s.n. (CAL); Meghalaya, Jaintia Hills: Garampani, east of Jowar, 30 October1956, G Panigrahi 4216 (CAL); Sikkim, above goreedora, 30 September 1868, LS Kurz s.n. (CAL); Gangtok, 21 October 2003, K Joseph John 3927 (RHK); Assam, North Cachar: Halflong, 10 August 1908, WG Craib s.n. (CAL); North Lakhimpur: Lakhimpur, 2 June 1919, U. Kanjilal 7563 (BSISH); Nagaon, Doboka RF, 3.5 miles, 450 m, NP Balakrishnan 39519A (BSISH); Andaman & Nicobar Islands, Havlock Island, 30 August 2002, K Joseph John 3825 (RHK).

Distribution: Observed both wild and in cultivation in the North Eastern states with a preponderance in Khasi, Garo and Jaintia hills of Meghalaya, hill jungles of Kokrajhar and Kamrup district in Assam.

Ecology: Clay loam, forest soils; have wider adaptability to varying altitudes from sea levels in Andaman Islands to 1,800 m in Sikkim.

Common names and vernacular names: Teasle gourd, bhat karela (stuffed fruits cooked along with rice in Assam, hence the name bhat karela), Lamkarote (Manipur), Meeta chottele (Nepal-Sikkim), Kaksa (Bihar), Kakrol (Bengal), Karkul (Mizoram).

Taxonomic notes: Chakravarty treated these specimens under *M. dioica* even when recognizing the extra long fruit stalks. It is clearly distinct for many characters like cordate unlobed leaf lamina, very distinct petal blotches, large creamish-white petals, very large and kidney shaped male flower bracts, broad ovate and blackish purple male calyx and saucer shaped receptacle cup. It does not match with Wight's icon of *M. cochinchinensis* or Philippine-Andaman-Assamese *M. cochinchinensis* specimens lodged at CAL and PBL either. Petiole and lamina bases are not gland-dotted and seeds are smaller than that of *M. cochinchinensis*. Further, seed shape is rectangular unlike the broad octagonal-stellate shape in *M. cochinchinensis*. Following Chakravaty, this taxa has been treated as *M. dioica* by Indian botanists whereas, the agricultural scientists refers to it as *M. cochinchinensis*. Some workers made a distinction by treating it as a tetraploid form of *M. dioica* (Mishra *et al*., 1983).

6. *M. cochinchinensis* (Lour.) Spreng. 1826, Syst. Veg. 3: 14; CB Clarke 1879, in Hook. f., Fl. Brit. India 2: 618; Cooke 1903, Fl. Pres. Bomb. 1: 530; Duthie 1903, Fl. Upper Gang. Pl. 1: 370; Prain 1903, Beng. Pl. 1: 522; Gamble 1919, Fl. Pres. Madras 3: 532; Kanjilal et al. Fl. Assam 2: 330. 1938; Chakrav. 1959, Rec. Bot. Surv. India 17,1: 95, p.p.; id.1982, in SK Jain *et al*., Fasc. Fl. India 11: 92; Keraudren 1975, in Aubrev. et. J.-F.Leroy, Fl. Camb., Laos, Vietnam: 38,f.8; C. Jeffrey 1980, Kew Bull. 34: 790, p.p, id. 2001, in Hanelt, Mansf. Encyl. Agric. Hort. 3: 1521-22; de Wilde & Duyfjes 2002, Bot. zhuarn. 87(3): 137-138; *Muricia cochinchinensis* Lour. 1790, Fl. Cochinch. 2: 596; Ser. 1828, in A. DC., Prodr. 3: 318; *M. mixta* Roxb. 1832, Fl. Ind. 3:709; Wight et Arn. 1834, Prodr. Fl. Ind. Orient.1: 349; *M. macrophylla* Gage 1908, Rec. Bot. Surv. India 3: 6; Chakrav. 1959, Rec. Bot. Surv. India 17,1: 94, id.1982, in SK Jain *et al*., Fasc. Fl. India 11: 94.

Type: Cochin China (Vietnam), *Loureiro s.n.* (BM)

Dioecious, stout perennial climber up to 20 m high, roots tuberous, woody, all parts glabrous. ***Leaves*** entire or 3-5, palmately lobed, or 3 foliolate (leaflets ± elliptic with minute petiole), broadly ovate or sub-orbicular in outline, up to 10 x 16 cm, base cordate (sometimes with 2-4 glandular bead like projections towards cordate margin), acute or acuminate at apex or acuminate, margins entire, undulate or remotely dentate; petiole 5-12 cm long, usually with 2-6 conspicuous bead like crateriform glands (Assam and Andaman specimens). ***Flowers*** solitary, axillary, male sometimes in a loose fascicle of 5-7, with a separate basal one. ***Male flowers*** with subapical bract; peduncles 8-12 cm long, bract cucullate, suborbicular or reniform, 20-40 mm wide, ± scabrous, rounded at base, acute at apex, margins undulate, veins subparallel, very prominent outside; pedicels 5-8 mm long, receptacle tube saucer shaped, 4-5 × 8-12 mm, blackish outside; sepals coriaceous, 10-12 × 4-8 mm, ovate-oblong or triangular, acute at apex, blackish, finely scabrid; petals subelliptic, 2.5-4 × 6-7 cm, conspicuously sub parallel

veined, scales 3, at the base of the blotched petals, protecting the nectary; inner 3 petals with purple bull's eye mark at base, filaments short, fleshy, 5-6 mm long, inserted at the base of the receptacle tube, anthers variable in size, 'S' shaped, connective swollen. ***Female flower*** with small or rudimentary bract; sepals linear oblong, 4-10 mm long; petals as in male; ovary ellipsoid oblong, 12-15 mm long, densely soft muricate; style 8-9 mm long. ***Fruit*** ovoid or oblongoid, bulged at middle, 10-15 × 6-10 cm, rostrate at base and stalk 5-12 cm long; pericarp densely tuberculate with uniformly short round conical structures or interspersed with larger tubercles; single fruit weighing between 350-500 g or more, green turning orange on ripening and bursting irregularly; ***Seeds*** many, variable in size, 1-1.5 x 0.8-1.2 cm, broadly ovate hexa-octagonal with flat sculptured surfaces, subtridentate at ends and margins, testa black.

Specimens examined: Philippines, Lucban: Luzon Island, May 1906, Elmer 7526 (CAL); Bangla Desh, Chittagong hill tract, April 1911, G King 49 (CAL); Burma (Myanmar), Mergui, April 1911, A Meebold s.n. (CAL); India, Andaman Islands: South Andamans, Haldayapur hill jungle, 1892, King s.n. (CAL); South Andamans, Humfreygunj, 27 May 1973, NP Balakrishnan 165 (PBL); South Andaman, Adasig, 11 July 2002, K Joseph John 4526 (RHK); Assam, Sibsagar, May 1886, AT Gage s.n. (CAL); Cachar: Badarpur, 12 August 1903, AT Gage s.n. (CAL)

Distribution: Widespread in South and South East Asia from North East India, Myanmar and Chittagong hill tracts of Bangladesh, China, Taiwan, Malaysia, Vietnam to Philippines. In India, it occurs rarely in the wild in Assam, Manipur and occasional in South Andamans and to a small extent cultivated in Assam, Jharkhand and Andaman Islands as a homestead vegetable. Even though, reported from Deccan and Western Ghats (South Canara and Mysore) by Gamble (1919) and Chakravarty (1982), there are no specimens in Indian Herbaria from peninsular South India, but only from Andamans and North Eastern states.

Habitat and ecology: Open forests and coastal scrub jungles (Andamans) and tropical evergreen openings in Assam up to 1000 m.

Common and vernacular names: Crow cucumber, Golkakra (Beng.), Hathikarela (Assam), Cochinchina gourd, Spike fruited crow cucumber, Sweet gourd.

Taxonomic notes: *M. cochinchinensis* and *M. macrophylla* Gage have been treated as two distinct entities by Chakravarty (1982) citing the lobed (former) and unlobed (latter) nature of leaves. Leaf lobing is more of an environmental character in dioecious taxa as evidenced by both lobed and unlobed leaves in the same plant at different stages of plant growth. *M. cochinchinensis* shows various leaf lobing patterns even nearly 3-foleolate with minute petiolule, giving the superficial appearance of a palmately compound leaf. Hence, our study leads us to agree with Jeffrey (1980; 2001) and de Wilde and Duyfjes (2002) in treating *M. macrophylla* as synonymous with *M. cochinchinensis*.

Doubtful Taxa

1. *M. denudata* (Thwaites) CB Clarke 1879, in Hook. F., Fl. Brit. India 2: 618; Trimen 1894, Handb. Fl. Ceylon 2:249; Chakrav.1946, Ind. J. Agric. Sci. 16, 1: 50; id.1959, Rec. Bot. Surv. India 17, 1: 98; id. 1982, in SK Jain *et al.*, Fasc. Fl. India 11: 93; *M. dioica* Willd. var. *denudata* Thwaites 1859, Enum. Pl. Zeyl.: 126.

Type: Sri Lanka, C.P. 1615 s. coll. (Holotype, PDA; Isotype, CAL)

Notes: The Travencore specimens (Meebold 12241, 'Kavala Cochi' and Meebold 12769, 'near Kottayam and Kavalay'), originally labelled as *M. dioica*, have been determined by Chakravarty as *M. denudata*, which in fact are typical specimens of *M. dioica*. It is not clear how he arrived at this identification. Interpretation of male inflorescence needs clarification. It might probably be a case of the male flowers in 'loose fascicles' and many flowers emerging from the same axil, giving the false appearance of a 'branched inflorescence' (as reported to be in *M. denudata*). This feature is common in all the taxa from the high rainfall areas.

de Wilde explicitly states that he has listed the species exclusively based on bibliographic compilation and that he has not seen the Type specimen. It is true in all other cases as well and probably a case of perpetuation of 'the original error' in judgement. Even after conducting extensive field surveys throughout reported areas of occurrence in Kerala, *i.e.*, low elevation coastal areas especially Quilon (Gamble, 1919) and Thrissur (Chakravarty, 1946), we failed to locate a live specimen matching with Type specimen CP 1615 (CAL). Based on descriptions of the species by Trimen (1894), Cooke (1903), de Wilde and Duyfjes (2002) and our own observations of the type specimen (CP 1615), presence of *M. denudata* in Kerala (India) is fairly doubtful. This

taxon requires a great deal of further research with living material and until complete specimen with seeds and tubers has been studied in detail, no conclusions could be arrived at the validity of *M. denudata*.

Taxonomic Summary

Of the seven species placed by Chakravarty (1982) in the genus *Momordica*, four are accepted at species level in this treatment. They are *M. balsamina* L., *M. charantia* L., *M. cochinchinensis* (Lour.) Spreng. and *M. dioica* Roxb. (in a strict sense). As treated here, the *M. dioica* sensu stricto consists of the delicate forms distributed in the Deccan plateau and Central India; North Eastern elements of *M. dioica* is placed under *M. subangulata* Blume ssp. *renigera* (G Don) WJ de Wilde and stout forms from Western Ghats separated as new species (*M. sahyadrica* Joseph and Antony). *M. subangulata* Blume (as described by him) do not occur in South and Western India and the specimens ascribed therein are *M. sahyadrica*. Its reported occurrence in North East India must be true and those specimens must be placed under ssp. *renigera*. Of the remaining three species, *M. macrophylla* Gage is placed in synonymy with *M. cochinchinensis*. Presence *M. denudata* (Thwaites) CB Clarke in India is doubtful in the absence of valid herbarium specimens or field collections. *M. cymbalaria*, rightly placed under *Luffa* by Chakravarty, is more allied to *Luffa* than *Momordica* and therefore should be placed under the former genus, though some workers continue to treat it under *Momordica*.

Acknowledgements

We are grateful to the authorities of BSI, CAL, BSISH, BSIJO, MH, AHMA, BLAT, KFRI, TBGT, RHT, IARI, PBL and CALI for permission to study the herbarium specimens and access to the type section. Dr WJJ O de Wilde and Dr PL Narasimhan, IBLO at Kew, UK were kind enough to examine a few doubtful specimens and to forward some useful literature. Financial assistance provided by Kerala State Council for Science, Technology and Environment (STEC), Thiruvananthapuram to the second author is gratefully acknowledged.

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Genetic Variability and Correlation Studies among Advanced Lines of Groundnut under Agro-Climatic Conditions of North East Hill (NEH) Region

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The introduction of groundnut germplasm in North East Hill (NEH) region of India is essential to enrich genetic resources for crop improvement. The soil under NEH region is characterized by with pH less than 5.5 (acidic) and Ca, P, Mg and K deficiencies. In view of this, a field experiment was conducted during *Kharif*, 2007 at foothills of Experimental and Extension Centre, Andro, Imphal East, Manipur to assess the genetic parameter, character association and path analysis for nine different morphological traits among eighteen advanced genotypes in groundnut. The genotypes demonstrated highly significant difference (P<0.01) for all the traits studied. High estimates of GCV and heritability coupled with genetic advance as per cent of mean were registered for number of mature pods, number of primary branches and pod yield. The correlation and path coefficients analysis also showed that number of mature pods and number of primary branches had significant and positive correlation with pod yield as well as maximum positive direct effect on pod yield. Hence, results clearly showed that genetic improvement of pod yield can be initiated by putting positive selection pressure on number of mature pods and number of primary branches in groundnut. The hierarchical analysis by complete linkage method using Euclidean distance classified the eighteen advanced genotypes in two genetically diverse clusters with 5 (I) and 13 (II) genotypes. The second cluster further divided in to two clusters (II A and II B) with 7 and 6 genotypes, respectively. The genotypes from diverse clusters may be utilized in crossing programme to produce desirable segregants for developing high yielding acidic tolerant genetic stock/varieties.

Key Words: ***Arachis hypogaea*, Correlation coefficients, Genetic variability, Hierarchical clustering Path analysis,**

Introduction

Groundnut (*Arachis hypogaea* L.) is the World's fourth most important source of edible oil and third most important source of vegetable protein. Groundnut seeds contain high quantity of edible oil (50%), easily digestible protein (20%) and carbohydrates (25%). In India, about 80% (6 million ha) of total groundnut area is confined to Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka, and Maharashtra with 84% (6 million tonnes) of total production (Anonymous, 2008). With the demand of ever increasing population as well as malnutrition problem, the expansion of groundnut cultivation in the non-traditional area of north east is the only alternative where the yield potential of 3 to 4 t/ha of pods are easily achieved in 100-120 days (Singh *et al*., 2006). In order to exploit north eastern areas of the country, the evaluation of superior genotypes is important for utilization in breeding programme or for using them as such as varieties after conducting preliminary yield trials. Identification of superior genotypes, therefore, becomes imperative for promoting its introduction, productivity and quality of produce. However, for their efficient use in breeding programme the introduced genotypes need to be classified into different groups based on variability available for the best exploitation of heterosis as well as for ease in selection. The selection of superior genotypes based on yield per se is very complicated in groundnut compared to other crops due to the fact that economic part (pods) is formed under the soil which necessitates to establish the magnitude and direction of association of pod yield with its direct and indirect components. Hence, basic information on genetic parameters and nature of association is required in formulating appropriate breeding programme for targeted environments. In view of the above perspectives, the present study was taken up to assess genetic parameters and nature of association among yield and its contributing characters in advance breeding lines of groundnut for rainfed situation under foot hills of Manipur.

Materials and Methods

The eighteen semi spreading advanced lines including 10 from International Crop Research Institute for Semi Arid Tropics (ICRISAT), Hyderabad; 6 from Bhabha Atomic Research Centre (BARC), Mumbai and 2 released varieties were evaluated at Experiment and Extension Centre, Andro, Imphal East District, Manipur (latitude 24º45'N, longitude 94º03'N, altitude 810 m above msl and average annual rainfall 1,400 mm) during *Kharif*,

2007. The soil of experimental field is sandy clayey loam having pH 5 to 5.3, EC 0.25 to 0.29 dsm^{-1} and 0.06 to 0.72% organic carbon. The availability of N, P and K in the soil is 283, 18.6 and 124 kg/ha, respectively. The experiment was laid out in Randomized Complete Block Design with three replications. Each genotype was sown in raised bed of 5×1.5 m^2 size accommodating 5 rows each of 5 m length with spacing of 30×10 cm. The recommended package of practices was followed to raise the good crop. The lime application at recommended dose of 300 kg/ha was also applied as side placement at the time of pegging (35-40 days after sowing) due to acidic nature of soil. At flowering and maturity stages, the observations were recorded on days to 50% flowering, days to maturity, plant height (cm), primary branches/plant, mature pods/plant, 100-kernel weight (g), shelling out turn (%), oil content (%) and pod yield/plant (g) from ten randomly selected plants in each plot in each replication. The plot mean values were subjected to analysis of variance. The genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated according to the method outlined by Burton (1952). Heritability (broad sense) and expected genetic advance (as per cent of mean) was estimated as per Johnson *et al*. (1955). Correlation coefficients and path analysis were calculated as explained by Singh and Chaudhary (1985). The advance lines were also clustered by complete linkage method using Euclidean distances. In complete linkage method, the distance between clusters are determined by the greatest distance between any two genotypes in the different clusters. Estimation of Euclidean distance and cluster analysis was performed by Statistica (1996).

Results and Discussion

Variability Analysis

The analysis of variance revealed highly significant differences for all the traits under study indicating adequate scope for selection of superior and diverse genotypes (Table 1). The extent of variability measured in terms of range, grand mean, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability (broad sense) and genetic advance of nine characters are presented in Table 2. The narrow differences between phenotypic and genotypic coefficients of variation were observed for all the characters indicating the less influence of environment on expression of characters studied. The high estimates of PCV and GCV were obtained for pod yield, number of mature pods and number of primary branches and revealed that genotypes have a broad genetic background as well as good potential that will respond positively to selection for improving these characters. The higher magnitude of GCV and PCV was also reported by Kadam *et al*. (2007) for pod yield, number of mature pods and primary branches; and by John *et al*. (2005) for number of mature pods and pod yield. The moderate PCV and GCV values were also observed for 100-kernel weight, plant height

Table 1. Analysis of variance showing mean of squares for nine characters in advanced groundnut genotypes

Source of variation	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Mature pods/ plant	100-kernel weight (g)	Shelling (%)	Oil content (%)	Pod yield/ plant (g)
Replications	0.68	4.09	14.45	0.68	4.80	15.07	13.51	2.98	1.06
Genotypes	52.88**	241.84**	46.55**	14.79**	50.33**	261.66**	20.81**	35.07**	30.03**
Error	1.39	2.43	3.27	0.86	1.02	3.26	2.64	2.40	0.34

** Significant at P<0.01

Table 2. Estimates of genetic parameters for nine characters in advanced groundnut genotypes

Characters	Mean±SE	Range	Coefficient of variation (%)		Heritability (%) (broad sense)	Genetic advance	Genetic advance as % of mean
			GCV	PCV			
Days to 50% flowering	32.9±0.68	26.3-44.3	12.58	13.08	92.5	8.20	24.92
Days to maturity	110.96±0.90	98.3-125.6	8.05	8.17	97.04	18.12	16.33
Plant height (cm)	26.38±1.04	20.9-32.9	14.39	15.95	81.49	7.07	26.80
Primary branches/plant	8.33±0.53	5.4-13.4	25.85	28.4	84.42	4.08	48.94
Mature pods/plant	12.15±0.58	7.2-22.4	33.36	34.39	94.12	8.10	66.69
100-kernel weight (g)	52.47±1.04	39.9-68.8	17.68	18.02	96.35	18.77	35.76
Shelling (%)	64.39±0.93	59.4-68.8	3.82	4.58	69.52	4.23	6.57
Oil content (%)	42.87±0.89	37.0-49.7	7.69	8.50	81.91	6.15	14.35
Pod yield/plant (g)	8.06±0.33	4.4-14.6	39.10	39.65	96.71	6.37	79.06

and days to 50% flowering indicating substantial amount of genetic variability. The characters, *viz.*, shelling per cent and oil content had the lower estimates of GCV and PCV indicating a limited opportunity to further improve these characters.

The coefficient of variation indicated only the extent of variability present in different characters and did not indicate its heritable portion. Heritable portion can be ascertained with greater degree of accuracy when it is associated with genetic advance. In present study, high heritability was accompanied with high genetic advance as per cent of mean for pod yield, number of mature pods, 100-kernel weight and primary branches indicating the presence of additive genetic effects. Similar observations were also reported by John *et al*. (2005) for both number of mature pods and pod yield; and by Kadam *et al*. (2007) for pod yield. The high heritability along with moderate to low genetic advance as per cent of mean were observed for days to 50% flowering, plant height, days to maturity, oil content and shelling per cent. This suggested that these characters might be controlled by both additive and non-additive gene action and selection based on such characters may be effective to some extent.

High estimate of genotypic coefficients of variation and heritability coupled with genetic advance as per cent of mean was registered for number of primary branches, number of mature pods and pod yield indicating predominance of additive gene effects and simple directional selection may be effective to improve these characters.

Correlation and Path Coefficients Analysis

The genotypic and phenotypic correlation studies are essential in evaluating the possibility of simultaneous improvement for many characters and also the impact of selection for one trait on the other related ones under particular environment. The genotypic correlations were generally higher than their corresponding phenotypic correlations (Table 3). The lower values of phenotypic correlations may be attributed to lower modifying effect of environment on the association of characters at the gene level (Mamun-Hossain and Joarder, 1987). The results pertaining to correlation revealed that number of primary branches and number of mature pods were highly significant and positively correlated with one another as well as pod yield at both genotypic and phenotypic levels which indicated that these two characters are important components for improvement of pod yield in groundnut and also the possibility of simultaneous improvement of these trait by selection. Such positive association of pod yield with number of primary branches and mature pods was also reported by Lakshmaiah *et al*. (1983). The pod yield exhibited non-significant but positive association with days to 50% flowering (r_g=0.374, r_p=0.370), days to maturity (r_g=0.427, r_p=0.414) and plant height (r_g=0.454, r_p=0.393), whereas, it showed non-significant and negative association with 100-kernel weight (r_g=0.249, r_p=-0.242) and shelling per cent (r_g=-0.324, r_p=-0.265). The oil per cent had relatively weak positive association with pod yield (r_g= 0.085, r_p= 0.102). Similar results were in agreement with findings of Uddin *et al*. (1995) for 100-kernel weight and of Mane

Table 3. Genotypic (G) and phenotypic (P) correlation coefficients among nine characters in advanced groundnut genotypes

Characters		Days to maturity (cm)	Plant height plant	Primary branches/ plant	Mature pods/ (g)	100-kernel weight (g)	Shelling (%)	Oil content (g)	Pod yield/ plant
Days to 50% flowering	G	0.816 **	0.301	0.491*	0.171	-0.063	-0.477*	0.301	0.374
	P	0.783 **	0.255	0.469*	0.173	-0.047	-0.350	0.285	0.370
Days to maturity	G		0.404	0.561*	0.356	-0.194	-0.503*	0.442	0.427
	P		0.362	0.509*	0.343	-0.190	-0.435	0.385	0.414
Plant height (cm)	G			0.218	0.460	-0.186	-0.263	0.269	0.454
	P			0.184	0.435	-0.185	-0.218	0.274	0.393
Primary branches/plant	G				0.729**	-0.425	-0.349	0.414	0.744**
	P				0.638**	-0.404	-0.318	0.338	0.670**
Mature pods/plant	G					-0.248	-0.345	0.332	0.790**
	P					-0.234	-0.274	0.286	0.752**
100-kernel weight (g)	G						0.483*	0.098	-0.249
	P						0.429	0.087	-0.242
Shelling (%)	G							-0.063	-0.324
	P							0.019	-0.265
Oil content (%)	G								0.085
	P								0.102

*,**= Significant at P<0.05 and P<0.01 levels, respectively

et al. (2008) for days to maturity and oil per cent. In the present study, the 100-kernel weight displayed positive and significantly genotypic correlation with shelling per cent. Days to 50% flowering and days to maturity exhibited positive and significant genotypic and phenotypic correlations with each other and with primary branches which indicated that higher number of primary branches might be expected with prolonged days to maturity.

Path coefficient analysis (Table 4) based on pod yield revealed that all the traits except shelling per cent and oil content exhibited positive direct effects on pod yield. Number of primary branches made maximum and positive direct contribution (0.691) and also exerted appreciable magnitude of indirect influence (0.504) towards pod yield via number of mature pods. Pod yield was highly influenced by number of primary branches and mature pods both directly and indirectly. The direct effect of number of mature pods on pod yield was also observed by Uddin *et al*. (1995) and Mane *et al*. (2008). The genotypic correlation coefficients of these two characters were also positive and highly significant. Hence, emphasis on these two traits for groundnut improvement may be rewarding. The plant height showed moderate direct effect on pod yield in spite of non-significant but considerable estimate of correlation coefficients with pod yield. This indicated that plant height could be included in selection criteria list. On the other hand, oil per cent exerted the highest negative direct effect (-0.428) on pod yield following by shelling per cent (-0.016). Similar observations were also recorded by Francies and Ramalingam (1997) in F_2 population of groundnut. It was observed that correlation of 100-kernel weight with pod yield was negative but its direct effect was moderate and positive, so that a restricted simultaneous model is to be followed, *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effects (Singh and Kakar, 1977). Further, the residual factor was low which suggests that the variables chosen in the present study were sufficient to explain pod yield**.** These findings are in agreement with Azad and Hamid (2000).

The results of correlation and path coefficients analysis revealed that number of primary branches and mature pods had highly significant and positive correlation as well as maximum direct effect on pod yield. Thus, selection for these two traits could be of greater importance for selecting better genotypes for pod yield in groundnut.

Hierarchical Cluster Analysis

Hierarchical cluster analysis has been carried out to choose the parents for hybridization. This approach helps in reducing the large amount of data about the parents to manageable proportions (Peter and Martinalli, 1989). Multivariate hierarchical clustering was performed for nine different morphological characters (Fig.1). The eighteen advanced lines were mainly grouped into two genetically diverse clusters with 5 (I) and 13 (II) genotypes at 36.5 linkage distance units. The cluster II was again divided into two sub clusters, *i.e.*, II A and II B at 31.8 linkage distance units with 7 and 6 genotypes, respectively. Based on inter cluster distance and *per se* performance, the genotypes, namely, ICGV 4122 and ICGV 4148 (cluster I), and ICGV 3157 and ICGV 3063 (cluster IIA) for pod yield along with primary branches and mature pods; ICGV 3206 (cluster IIA) for earliness and TDG 56 (cluster IIB) for large seed size (as confectionary purpose) due to high 100-kernel weight (>60 g) may be utilized in groundnut breeding programme. Further, the clustering pattern from dendrogram clearly depicted that the lines from same location were grouped in to single cluster. Thus, again choice of parents for hybridization should be decided on the basis of genetic diversity rather than geographical diversity.

Table 4. Genotypic path analysis of different quantitative characters on pod yield in advanced groundnut genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Mature pods/ plant	100-kernel weight (g)	Shelling (%)	Oil content (%)	r_g with pod yield/ plant (g)
Days to 50% flowering	**0.006**	0.018	0.088	0.340	0.057	–0.015	0.008	–0.129	0.374
Days to maturity	0.005	**0.022**	0.118	0.388	0.120	–0.046	0.008	–0.189	0.427
Plant height (cm)	0.002	0.009	**0.291**	0.150	0.155	–0.044	0.004	–0.115	0.454
Primary branches/plant	0.003	0.012	0.063	**0.691**	0.246	–0.101	0.005	–0.177	0.744**
Mature pods/plant	0.001	0.007	0.135	0.504	**0.338**	–0.059	0.005	–0.142	0.790**
100–kernel weight (g)	–0.000	–0.004	–0.054	–0.294	–0.084	**0.238**	–0.008	–0.042	–0.248
Shelling (%)	–0.003	–0.011	–0.076	–0.241	–0.116	0.115	**–0.016**	0.027	–0.323
Oil content (%)	0.002	0.009	0.078	0.286	0.112	0.023	0.001	**–0.428**	0.084

Residual = 0.404; Direct effects = diagonal; Indirect effects = above and below diagonal

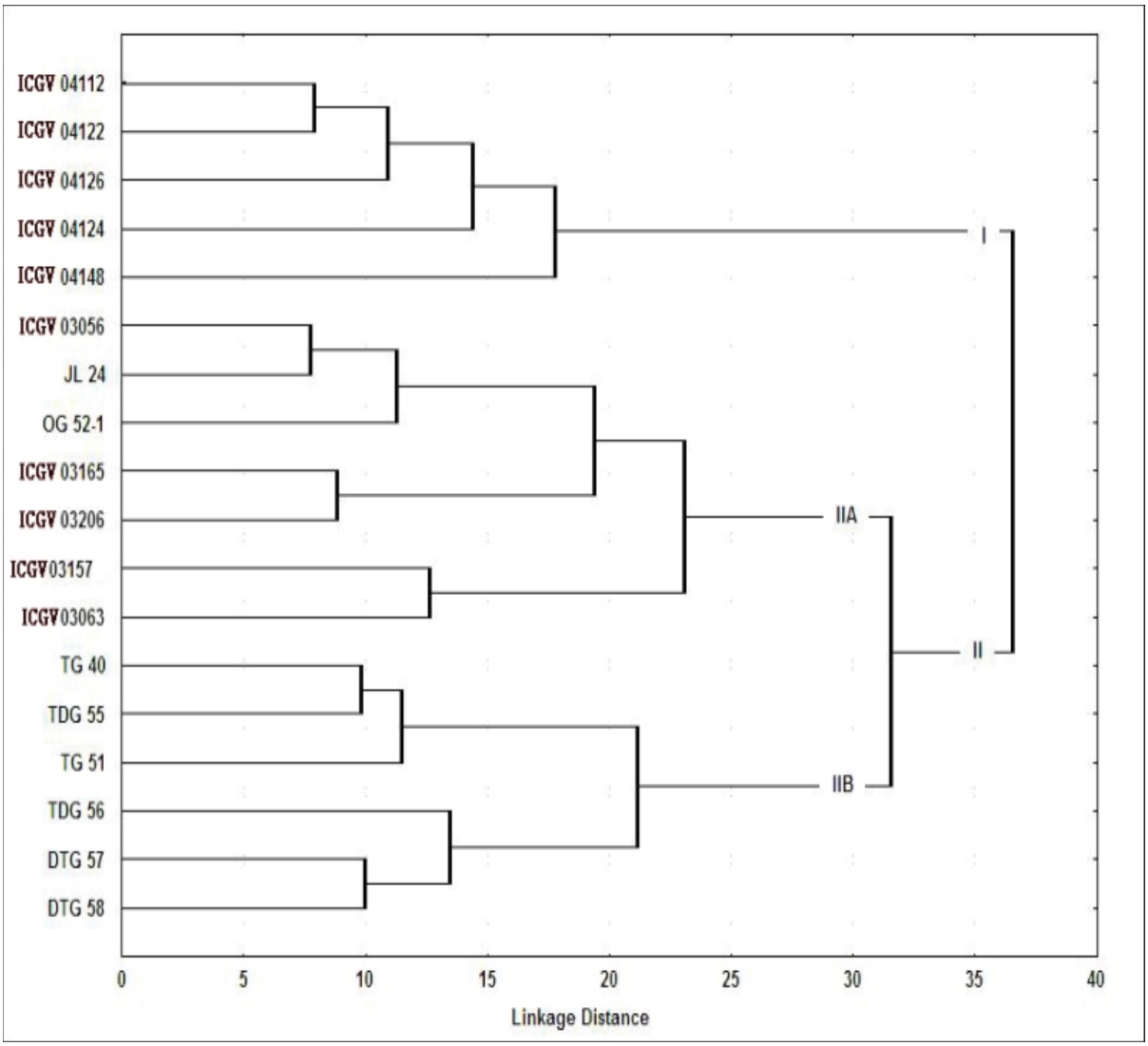

Fig. 1: Dendrogram depicting the genetic diversity among groundnut breeding lines

Acknowledgements

The authors express grateful thanks to Dr SN Nigam, Principal Scientist (Groundnut Breeding), ICRISAT, Patancheru and Dr AM Badigannavar, Nuclear Agril. and Biotechnology Division, BARC, Mumbai for supplying the seed materials.

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Variability in Nutmeg (*Myristica fragrans* Houtt.) under High Rainfall and High Altitude Kodagu Region of Karnataka

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The vegetative, fruit, seed and mace characters of 23 accessions of nutmeg (*Myristica fragrans* Houtt.) were studied for variability at Indian Institute of Spices Research, Cardamom Research Centre, Appangala, Karnataka. Accessions exhibited wide range of variability for different characters studied. Maximum variability was recorded for fresh seed yield per tree and minimum variability was recorded for the leaf and seed characters. Medium to high variability was recorded for mace characters. Among the 23 accessions studied, the maximum fresh seed weight (16.5 g) was recorded in IC548880, the other promising accessions for different economic characters were IC548896 for dry seed weight (10 g/fruit), IC548921 for dry seed yield (9.2 kg/tree), IC548892 for dry mace weight of a fruit (2.1 g/fruit) and IC548928 for dry mace weight of a tree (1,045g/tree).

Key Words: Fruit, Mace, *Myristica fragrans*, Nutmeg, Variability

Introduction

Nutmeg (*Myristica fragrans* Houtt.) (Family: Myristicaceae) is believed to be native of Bonda Islands of Eastern Indonesia, formerly called the 'Spice Islands'. In India, it is mainly cultivated in South India particularly in certain pockets of Kerala, Tamil Nadu and Karnataka, which was originally introduced by the British during the 18th century (Krishnamoorthy *et al*., 2001). The name '*Myristica*' is derived from the Greek word 'Myron', a sweet liquid distilled from the plant (Everett, 1981). It is a dioecious or monoecious tree. Being an obligatory cross pollinated crop, wide natural variability is observed in nutmeg with respect to vegetative and reproductive characters (NRCS, 1989). The present investigation was therefore undertaken to study the existing variability under high rainfall, high altitude, region of Kodagu, (Karnataka) with an aim to estimate the variability for various morphological, fruit and mace characters.

Materials and Methods

The study was conducted in 2006-07 crop season on 25 year old seedling progenies of nutmeg trees planted as mixed crop in cardamom plantation at the Cardamom Research Centre, Appangala, which is located 12º26'N latitude and 75º45'E longitude at an altitude of 1000 MSL. It falls under cool humid and high rainfall zone with 2500-3500mm rainfall per annum. Twenty-three nutmeg accessions, *viz*., (IC548880, IC548881, IC548892, IC548896, IC548909, IC548913, IC548917, IC548919, IC548920, IC548921, IC548922, IC548926, IC548928, IC548929, IC548930, IC548936, IC548937, IC548940, IC548941, IC548944, IC548945, IC548947 and IC548948) constituted the experimental material. Observations were recorded on various characters, *viz*., tree girth (cm), leaf length (cm), leaf breadth (cm), petiole length (cm), fruit length (cm), fruit width (cm), single fruit weight (g); fresh fruit yield (kg/tree), number of fruits/tree, pericarp thickness (cm), pericarp fresh weight (g), pericarp dry weight (g), seed length (cm), seed width (cm), fresh seed weight (g), dry seed weight (g), fresh seed yield (kg/tree), dry seed yield (kg/tree), mace thickness (cm), fresh mace weight (g), dry mace weight (g), fresh mace yield (g/tree) and dry mace yield (g/tree) were recorded in the season. The data was statistically analyzed for range, mean and co-efficient of variation between genotypes (Panse and Sukhatme, 1995).

Results and Discussion

The data on range, mean, standard deviation and coefficient of variations and three best genotypes for each character are presented in Table 1. Wide range of variation was observed between genotypes for fresh seed yield (kg/tree), dry seed yield (kg/tree), fresh mace yield (g/tree) and dry mace yield (g/tree). The fresh fruit yield (kg/tree) ranged from 0.79 to 88.24 kg/tree with mean of 25.79 kg/tree and coefficient of variation was 107.11 per cent. Accession IC548920 recorded maximum fresh weight (88.24 kg/tree). Fresh seed yield (kg/tree) ranged from 0.09 to 20.07 kg per tree with a mean of 4.33 kg per tree and coefficient of variation was 117.16 per

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Table 1.

Characters	Range	Mean	SD	CV (%)	Promising accessions
Tree girth (cm)	29-72	54.58	10.93	20.03	IC548928, IC548937, IC548917
Leaf length (cm)	11.70-15.68	13.27	1.08	8.10	IC548892, IC548913, IC548926
Leaf breadth (cm)	4.62-6.72	5.59	0.60	10.76	IC548913, IC548892, IC548909
Petiole length (cm)	0.98-1.36	1.11	0.09	7.85	IC548892, IC548981, IC548896
Fruit length (cm)	4.28-7.70	5.95	0.63	10.65	IC548896, IC548909, IC548944
Fruit width (cm)	3.72-6.94	5.07	0.57	11.31	IC548896, IC548920, IC548922
Single fruit weight (g)	34.10-144.80	64.26	20.66	32.15	IC548896, IC548922, IC548945
Fresh fruit yield/tree (kg)	0.79-88.24	25.79	27.63	107.11	IC548920, IC548921, IC548928
No. of fruits/tree	12-1759	488.52	507.76	103.94	IC548921, IC548928, IC548920
Pericarp thickness (cm)	1.10-2.20	1.39	0.27	19.29	IC548896, IC548929, IC548919
Pericarp fresh weight (g)	28.40-146.40	52.34	22.01	42.05	IC548896, IC548945, IC548921
Pericarp dry weight (g)	3.18-12.80	6.65	2.42	36.38	IC548880, IC548945, IC548892
Seed length (cm)	2.28-3.60	2.92	0.29	10.08	IC548896, IC548880, IC548920
Seed width (cm)	1.96-3.70	2.47	0.46	18.60	IC548880, IC548921, IC548896
Fresh seed weight (g)	5.40-16.50	8.72	2.68	30.78	IC548880, IC548896, IC548921
Dry seed weight (g)	2.50-10.00	4.50	2.05	45.49	IC548896, IC548880, IC548945
Seed fresh weight/tree (kg)	0.09-20.07	4.33	5.07	117.16	IC548921, IC548920, IC548928
Seed dry weight/tree (kg)	0.06-9.23	2.06	2.39	115.90	IC548921, IC548920, IC548928
Mace thickness (cm)	0.10-0.20	0.14	0.03	22.89	IC548892, IC548940, IC548881
Fresh mace weight (g)	0.50-5.40	2.04	1.00	49.15	IC548892, IC548922, IC548909
Dry mace weight (g)	0.20-2.10	0.71	0.43	61.03	IC548892, IC548940, IC548909
Mace fresh weight/tree (g)	30-4239	1049.8	1226.36	116.82	IC548921, IC548922, IC548928
Mace dry weight/tree (g)	5.60-1045.00	260.18	296.56	113.98	IC548928, IC548920, IC548921

cent. Accession IC5448921 recorded maximum fresh seed yield per tree. Dry seed yield ranged from 0.06 to 9.23 kg per tree with a mean of 2.06 kg per tree with coefficient of variation of 115.9 per cent. Accession IC548921 recorded maximum seed dry weight. Fresh mace yield ranged from 30 to 4,239 g per tree with a mean of 126.36 g per tree with 116.8 per cent coefficient of variation. Dry mace yield ranged from 5.6 to 1,045 g per tree with coefficient variation 113.98. Accession IC548928 recorded maximum mace dry weight.

Medium variability was recorded for single fruit weight (g), fresh pericarp weight (g/fruit), dry pericarp weight (g/fruit), fresh seed weight (g/seed), dry seed weight (g/seed), fresh mace weight (g/fruit), dry mace weight (g/fruit).

Single fruit weight ranged from 34.1 to 144.8 g with a mean of 64.26 g per fruit and coefficient of variation 32.15 per cent (Fig. 1). Accession IC548896 recorded maximum single fruit weight (144.8 g per fruit). Number of fruits per tree ranged from 12 to 1,759 with 103.94 per cent coefficient of variation. Pericarp fresh weight ranged from 28.4 to 146.4 with a mean of 52.34 g per fruit and coefficient of variation was 42.05 per cent. Accession IC548896 recorded maximum pulp fresh weight of 146.4 g per fruit. Pericarp dry weight ranged from 3.18 to 12.8 g with a mean of 6.65 g per fruit with coefficient of variation 36.38 per cent. Accession IC548880 recorded maximum dry pericarp weight. Fresh seed weight ranged from 5.4 to 16.5 g with a mean of 8.72 g and coefficient of variation was 30.78 per cent (Fig. 2). Accession IC548880 recorded maximum fresh seed weight (Fig. 3). Dry weight of seed ranged from 2.5 to 10 g per seed with a mean of 4.5 g per seed and coefficient of variation was 45.49 per cent.

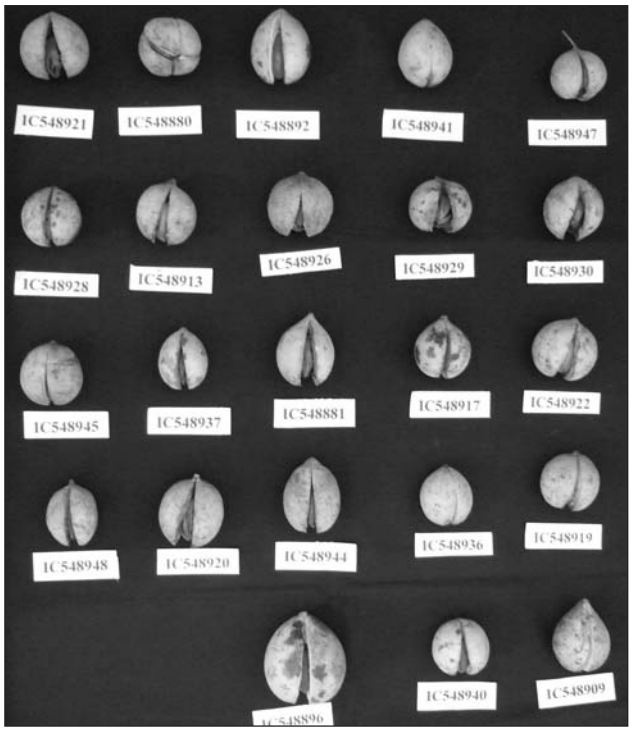

Fig. 1: Variability in nutmeg fruits

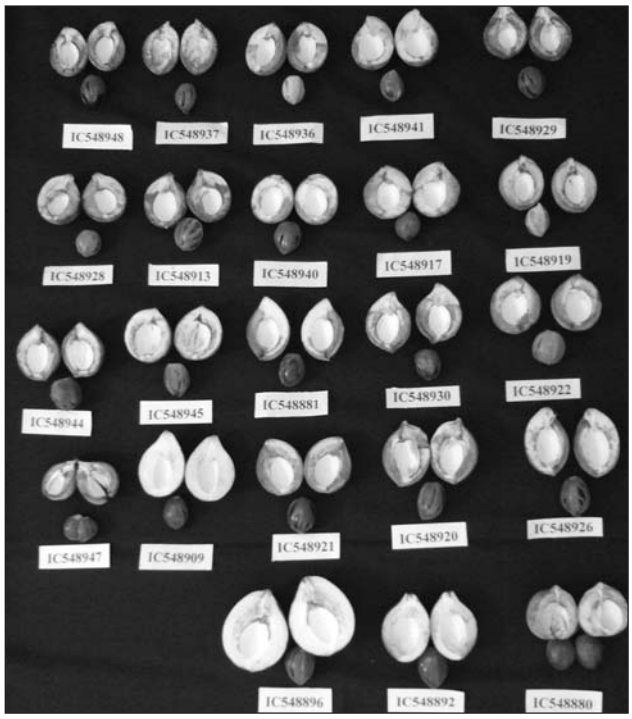

Fig. 2: Variability in nutmeg seeds

Accession IC548896 recorded maximum seed dry weight. Fresh mace weight ranged from 0.5 to 5.4 with a mean of 2.04 g per fruit and coefficient of variation was 49.15 percent. Accession IC548892 recorded maximum fresh mace weight of 5.4 g per fruit. Dry mace weight ranged from 0.2 to 2.1 with a mean of 0.71 g of mace per fruit and coefficient of variation was 61.03 per cent. Accession IC548892 recorded maximum dry mace weight of 2.1 g of mace per fruit.

Low level of coefficient of variation was recorded for tree girth, leaf length, leaf breadth, fruit length, fruit width, pulp thickness, seed length, seed width and mace thickness. Tree girth ranged from 29 to 72 cm with a mean of 54.58 cm and coefficient of variation was 20.03 per cent. Accession IC548928 recorded maximum tree girth of 72 cm. Leaf length, leaf width, petiole length and fruit width recorded low variability. Seed width ranged from 1.96 to 3.7 cm with a mean of 2.47

Fig. 4: Twin seeds

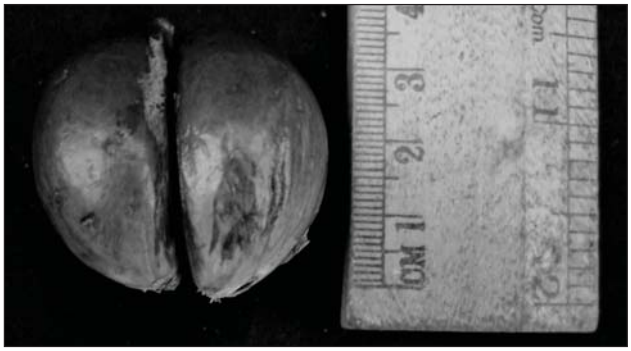

Fig. 3: IC548880–Maximum dry pericarp and fresh seed weight

cm and coefficient of variation was 18.6 per cent. Accession IC548880 recorded maximum seed width of 3.7 cm. Mace thickness ranged from 0.1 to 0.2 with a mean of 0.14 cm and coefficient of variation was 22.89 per cent. Accession IC548892 recorded maximum mace thickness.

Accession IC548896 recorded higher dry seed weight, seed length, single fruit weight, fruit width, seed length, single fruit weight, fruit width, fruit length, and IC548921 recorded higher fresh seed yield, dry seed yield (kg/tree) and fresh mace yield of 4,239 g per tree. The dry seed weight (kg/tree) is comparable to released verities (Nirmal Babu *et al.*, 2001).

Few accessions recorded special characters like twin seeds (Fig. 4), low pulp to seed ratio, triangular seed shape, deep red colour aril, rose colour aril, high pulp seed ratio are presented in Table 2.

All these accessions were conserved in cardamom cropping system under the regulated shade of higher forest tree canopy. Shade regulation of bigger shade trees will further enhance yield per tree and quality and weight of seed and mace. The superior genotypes, which are suitable, can be used for developing genotypes for cultivation as mono or mixed crop in cardamom, coffee or tea estates or under homestead cultivation.

Table 2. Qualitative characters recorded in different genotypes

Characters	Genotypes
Deep red aril	IC548892, IC548896, IC548929, IC548936
Rose colour aril	IC548920
Dark black seed	IC548936
Bold seed	IC548896
Elongated (triangular) seed	IC548936
Twin seeds	IC548880, IC548921, IC548924, IC548947, IC548948

Acknowledgment

The authors are thankful to the Director, Indian Institute of Spices Research, Calicut for providing facilities.

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Classification of Rapeseed-mustard Varieties Based on Seed Quality to Select Parental Types for Breeding Programme

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Forty-four varieties of different *Brassica* group of crop among released and notified varieties having best quality traits were selected to classify into different clusters to select parental types for breeding programme. All the varieties were classified into six clusters considering 10 quality traits (Table 1) using SPAR-2 and INDOSTAT software programme. Though the varieties in 3 clusters (Cluster #1, #5 and #6) are having a mixture of different *Brassica* species, but having best quality traits which can be selected for breeding programme, available within the species in different clusters to enhance the quality of oil in different *Brassica* crops. It was also revealed from the study that statistically all the species of *Brassica* are same in quality as they fell in the same cluster.

Key Words: Breeding, Classification, Rapeseed-mustard

Introduction

Varieties are the key factors of modern technologies to enhance production and contribute 25 to 35 per cent in it. Viewing the present scenario of different oil quality in international market, it is urgently required to improve the quality of rapeseed-mustard oil to lower the cholesterol level in blood to sustain in the international market. Saturated fatty acids (SFA) in high percentage are undesirable as they are of hypercholesteremic nature. However, monounsaturated fatty acids (MUFA) and long chain polyunsaturated fatty acids (PUFA) are nutritionally desired quality of oil. These two unsaturated fatty acids are known to lower the cholesterol level in blood, as they are hypocholesteremic nature (Mathur and Sharma, 1991). Further, polyunsaturated fatty acids, namely, linoleic acid (w-6) and linolenic acid (w-3) are essential fatty acids as our body can not synthesize them and they are involved in many important metabolic functions. Rapeseed-mustard oil is the second most important source of vegetable oil in the world. The total consumption of the rapeseed-mustard oil in India is estimated about 1.91 million MT (Kochu Babu, 2007). Mustard oil has a high proportion of unsaturated fatty acids and mix of both monounsaturated and polyunsaturated fatty acids. It has also lower saturated fatty acid content than other edible oil. Mustard oil due to its odour and pungency is the preferred oil from many parts of India. Till date classification of rapeseed-mustard has been done based on the morphological characters of yield attributes (Mishra *et al*., 2007).

The present study was undertaken with an aim to classify rapeseed-mustard varieties into different groups/ clusters based on the quality aspects of released and notified rapeseed-mustard varieties with a view to improve the quality of *Brasicca* crops after hybridization.

Materials and Methods

Based on passport data available (Chauhan *et al.*, 2001; Chauhan and Singh, 2004) on maturity of rapeseed-mustard crop (early, medium and late), stratified random sampling procedure was adopted to select 44 released and notified most popular different *Brassica* species for this study. The varieties of different *Brassica* species were selected such as, 2 from brown sarson, 4 from gobhi sarson, 7 from toria, 2 from yellow sarson, 27 from Indian mustard and 2 from Karan rai for this study. NIR (Dickey-Johan, USA) based method from intact seed which is faster, cost effective, environmentally safe, cheaper and nondestructive is used to record 10 different quality characters, namely, oil content; protein; fibre; glucosinolate (GSN); saturated fatty acid (16:0 + 18:0); oleic acid (18:1); linoleic acid (18:2); linolenic acid (18:3); eicosanoic acid (20:1) and erucic acid (22:1) for classification of 44 notified varieties into different groups/ clusters to select parental types for further breeding programme to enhance the oil quality of *Brassica* seed (Carpenter *et al*., 1976).

Results and Discussion

The 10 quality characters along with mean and CV were considered to be the base for classification into different

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clusters. Viewing the CV of different quality characters it revealed that the most variable quality character is fibre (cv=36.01) followed by oleic acid (cv=31.59); ecosonoic acid (cv=24.19); linolenic acid (cv=20.31); glucosinolate (cv=19.81) and saturated fatty acid (cv=19.13) (Table 1). SPAR-2 software developed by IASRI, New Delhi, was used to analyze the data for group classification. All the 44 varieties were classified into six groups/ clusters as F-Statistics (Rao, 1952) in the process of statistical analysis, is found maximum in the case of cluster # 6. Viewing within mean sum of square calculated using INDOSTAT software, it revealed that most variable cluster was cluster # 5 (wmss=40.8), followed by cluster # 2 (wmss=32.3), cluster # 4 (wmss=26.1), cluster # 3 (wmss=21.3), cluster # 1 (wmss=17.9) and cluster 6 (wmss=17.4) (Table 2) (Mishra *et al*., 2007). Though the varieties in 3 clusters (cluster # 1, # 5 and # 6) are having a mixture of different *Brassica* species, but having best quality traits which can be selected for breeding programme, available within the species in different clusters to enhance the quality of oil in *Brassica* crops. It was also revealed from the study that quality wise and statistically all the species of *Brassica* were same as they fell in the same cluster. Viewing correlations of different characters it revealed that only saturated fatty acid (16:0 + 18:0) is having positive significant correlation at 1% level of significance with that of oleic acid (18:1) and ecosanoic acid (20:1), but having negative significance correlation at 1% level of significance that with erucic acid (22:1). Protein is also having negative significant correlation (at. 01 levels) with fibre. Oleic acid (18:1) is having negative significant correlation (at. 01 levels) that with linolenic acid (18:3) and erucic acid (22:1). Similarly, it revealed from the correlation table that linoleic acid (18:2) is having negative significant correlation with erucic acid (22:1). Ecosanoic acid (20:1) is also having negative significant correlation (at 0.01 levels) with erucic acid (22:1) (Table 3). Mean and coefficient of variance (CV) of all the characters of different clusters have been calculated (Table 4 and 5). As far as saturated fatty acid (16: 0 + 18:0) is concerned between clusters, it is in desirable level. The maximum fatty acid was observed in cluster # 2 (3.00), followed by cluster # 3 (2.95); cluster # 6 (2.35); cluster # 4 (2.32) and cluster # 1 (2.22) etc. Oleic acid (18:1), a constituent of MUFA, the most vital component of oil, good for health was observed maximum in cluster # 3 (16.17); followed by cluster # 1 (12.45); cluster # 4 (12.26); cluster # 2 (12.1) etc. So, the varieties in these clusters may be selected for breeding purposes to have good quality of oil (Table 4). A comparative study of variability in oleic acid (18:1) between the clusters have been observed and found maximum variability in cluster # 3 (CV=49.44) followed by cluster # 6 (CV=27.40); cluster # 4 (CV=25.78) and cluster # 1 (CV=15.95) etc. (Table 5). It was further observed that maximum variability as well as mean between the clusters for linoleic acid (18:2), a constituent of PUFA was found in cluster # 4 (CV=21.86; mean=17.23, respectively) (Table 4 and 5), so varieties from cluster # 4 may be selected for breeding purposes to take care of linoleic acid (18:2) in the oil. Erucic acid (22:1) between the clusters was observed maximum in cluster # 5 (53.48) (Table 4), but variability in the same cluster was observed 4.33 (Table 5), so the varieties of cluster # 5 may be selected for breeding programme within species to reduce erucic acid (22:1) in the oil.

Table 1. Characters, their mean and coefficient of variance (CV)

S.No.	Character Name	Mean	CV
1	Oil content	40.13	4.13
2	Protein	20.58	4.85
3	Fibre	10.68	36.01
4	Glucosinolate (GSN)	84.71	19.81
5	Saturated fatty acid 16:0+18:0	2.40	19.13
6	Oleic acid (18:1)	12.51	31.59
7	Linoleic acid (18:2)	16.13	12.74
8	Linolenic acid (18:3)	12.30	20.31
9	Eicosanoic acid (20:1)	8.41	24.19
10	Erucic acid (22:1)	48.16	10.78

Table 2. Classified # 6 clusters based on 10 qualities traits mentioned in Table 1

Cluster	No. of varieties	Mean	Within MSS	Name of the varieties
1	8	24.87	17.9	Kranti, Pusa Bold, RH-30, RH 781, RL-1359, Rohini, JT 1, PT 507
2	2	27.52	32.3	Kiran, PC-5
3	6	22.41	21.3	RCC 4, Sanjucta A, TH 68, KBS 3,Neelam, Sheetal
4	8	27.65	26.1	Basanti, Krishna, PBR-91, PCR-7, Pusa Bahar, Pusa Jag, Bhawani, PBT 37
5	7	25.99	40.8	CS-52, RH 8812, RH 8113, Varuna, PT 303, Jhumka, Pusa Gold
6	13	25.75	17.4	Bio-902, GM-1, GM-2, JM-1, PBR-97, RH 819, RN 393, Sej-2, Vardan, TL 15, KS 101, GSL 1, GSL 2

Table 3. Correlations of different characters

Characters	Oil	Protein	Fibre	GSN	16:0+18:0	18:1	18:2	18:3	20:1	22:1
Oil	–	–0.193	0.121	–0.114	–0.034	–0.032	–0.225	–0.287	0.194	0.217
Protein		–	–0.400**	–0.100	0.134	0.204	0.192	0.076	–0.041	–0.260
Fibre			–	–0.21	–0.155	–0.012	–0.148	–0.248	0.004	0.227
GSN				–	–0.255	–0.270	–0.033	0.138	–0.173	0.235
16:0+18:0					–	0.642**	0.154	–0.265	0.588**	–0.755**
18:1						–	0.088	–0.533**	0.289	–0.708**
18:2							–	–0.001	–0.054	–0.455**
18:3								–	–0.208	0.046
20:1									–	–0.529**
22:1										–

** Correlation is significant at the 0.01 level.

Table 4. Cluster wise mean of different characters along with over all mean of all the characters

Cluster	Oil	Protein	Fibre	GSN	16:0+18:0	18:1	18:2	18:3	20:1	22:1
1	39.63	20.73	10.94	77.45	2.22	12.45	16.11	13.21	8.50	47.49
2	38.44	20.55	10.67	105.59	3	12.1	16.55	12.45	10.8	45.1
3	40.15	20.93	9.14	53.89	2.95	16.17	16.88	11.30	9.49	43.23
4	40.10	20.68	8.73	106.99	2.32	12.26	17.23	12.5	7.98	47.66
5	40.99	20.02	16.21	82.32	2.13	11.14	15.23	10.71	7.67	53.48
6	40.23	20.58	9.46	87.77	2.35	11.80	15.53	12.91	8.13	48.77
Over all mean	40.13	20.58	10.68	84.71	2.40	12.51	16.13	12.30	8.41	48.16

Table 5. Cluster wise CV of different characters along with over all CV of all the characters

Cluster	Oil	Protein	Fibre	GSN	16:0+18:0	18:1	18:2	18:3	20:1	22:1
1	5.74	5.25	35.98	3.74	15.02	15.95	8.91	15.80	21.96	5.43
2	7.05	4.27	5.77	10.74	4.71	5.84	7.26	24.42	5.24	4.08
3	1.58	4.64	7.29	9.65	20.28	49.44	10.06	13.12	33.91	16.90
4	3.35	3.07	13.85	6.82	14.31	25.78	21.86	19.37	20.84	12.76
5	4.04	5.26	34.20	6.25	10.75	19.18	5.83	21.96	12.19	4.33
6	3.96	5.67	21.85	3.73	17.40	27.40	9.04	23.20	25.56	7.89
Over all CV	4.13	4.85	36.01	19.81	19.13	31.59	12.74	20.31	24.19	10.78

Conclusion

Considering inter and intra distance matrix of the different clusters (Table 6), breeding can be performed between the varieties of cluster # 5 and cluster # 1 (d=2.11) followed by cluster # 6 and cluster # 1 (d=2.11); cluster # 5 and cluster #6 (d=2.26) cluster # 6 and cluster # 4 (d=5.41) etc. to improve the quality of rapeseed-mustard oil for good health (Chauhan *et al.*, 2004).

Acknowledgement

The authors wish to acknowledge the referee's valuable comments, leading to improve the manuscript in this form.

Table 6. Inter- and Intra-distance matrix of six clusters

Cluster	1	2	3	4	5	6
1	1.02	99.49	7.76	10.35	2.11	2.11
2		5.60	122.76	96.53	88.29	97.78
3			3.24	31.06	11.99	13.94
4				2.54	8.87	5.41
5					1.57	2.26
6						1.19

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Floristic Diversity of Potential Horticultural Plants in Bay Islands

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Andaman and Nicobar Islands have 2,574 known species of plant and out of which, 162 genera and 381 species belonging to 13 families are wild relatives of horticultural crops. Among these, 39 species which are most important are discussed here for their possible horticultural exploitation including 12 species which are indigenous to these islands. Conservation methodology, research to be carried out, potential domestication, pest and disease resistant sources for breeding programs have been discussed. Studies on the intraspecific and interspecific variability should be carried out for their exploitation in crop improvement programmes. Screening for biotic reaction should be studied and potential uses of these in breeding programs with biotechnological tools can be planned.

Key Words: Wild species, Horticultural importance, Diversity, Conservation, Utilization

Introduction

Andaman and Nicobar Islands consist of a fragile ecosystem and need special attention to conserve the biodiversity. These islands are included in the list of worldwide biodiversity hot spots. The geographical area of this Union Territory is 8,293 km^2 and 86 per cent of it is under reserve and protected forests. Geographically, these islands form one of the most interesting region of India.

In India, there are four known hotspots of biodiversity which are Western ghats, North-east, Trans-Himalayas and Andaman and Nicobar Islands. These hot spots have their presence not only in India but also in the neighbouring countries, for example, Western Ghats are extended to Sri Lanka, North-east to Myanmar, Trans-Himalaya to Bhutan, Tibet, Sikkim and China, and Andaman and Nicobar Islands are extended to Malaysia and Thailand. Therefore, the spectrum of biodiversity present in our country is also present in the contiguous areas of the other countries as well within hot spots. Hot spots are declared for their richness in biodiversity but this diversity is being lost at an alarming rate. Therefore, conservation, digitalization and utilization of this gene pool is very important.

Extensive damage was caused in Andaman and Nicobar Islands due to a severe earthquake measuring about 9.3 in Richter scale followed by Tsunami (high tidal waves) in the morning of 26th December, 2004. Almost entire population and habitat of this territory have been directly or indirectly affected. Out of 54,000 ha of cultivable land in Andaman and Nicobar Islands, about 11,000 ha was damaged and due to ingress of seawater about 4,500 ha of land is still under submergence and needs reclamation for cultivation. Coastal lands are badly affected due to tsunami, which lead to the destruction of flora of this area.

Apart from this sudden catastrophe, the other main causes for genetic erosion are improper conservation practices, encroachment in the forest areas and imbalance of population density of species in the habitat with special reference to heterozygous flora and fauna.

As per the latest record, botanists have identified 2,574 species with 1,752 Dicots, 672 Monocots, 8 Gymnosperms, and 142 Pteridophytes (Thothatri, 1962; Pandey and Diwakar, 2008). However, there might be lot of other useful flora, which might have been recorded by botanists from time to time and published. An example is the latest addition of an economically important species of *Vanilla* named as *Vanilla sanjappae* from Little Andaman.

Materials and Methods

The literature that is available in different journals has been thoroughly screened for horticulturally important families, genera and species. All the literature has been pooled and digitalized for further utilization. During this course of work many important wild relatives of horticultural plants have been noticed. Even though all horticulturally relevant literature has been collected, in this paper discussion has been restricted to few important species. Some of them can be readily domesticated and many of them can be used in breeding program, upon locating useful genes which are given in the Table 1 with their possible horticultural uses.

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Table 1. Some of the wild species with horticultural importance in A & N Islands

(*Abbreviations: A = Andaman; N = Nicobar; M = Mainland; O = Outside India; E = Endemic species; R = Rare)

S.No.	Scientific name	Family	Habit	Uses	Horticultural uses	Distribution			
						A	N	M	O
1	*Mangifera andamanica* (Andaman-Jungli am)	Anacardiaceae	Tree	Wood may be used for fuel and agricultural implements. Fruit is small and eaten sometimes by local people and tribals.	Worth investigating as a rootstock for mango.	✓(E)	-	-	-
2	*Mangifera camptosperuma*	Anacardiaceae	Large tree	Wood may be used for agricultural implements. Fruits are consumed by the Shompens.	Can be used as a good rootstock.	✓	✓	-	✓
3	*Mangifera griffithi*	Anacardiaceae	Tree	Fruits edible. Wood is used for agricultural implements.	Can be used as a good rootstock and have to be domesticated.	✓	-	-	✓
4	*Mangifera nicobarica*	Anacardiaceae	Tree	Fruits are edible. Wood is used for agricultural implements.	Can be used as a good rootstock.	-	✓(E)	-	-
5	*Mangifera sylvatica*	Anacardiaceae	Large tree	Poultice of young leaves is used in swelling of joints. Leaf decoction is ingested to treat dysentery, leucorrhoea, and blennorrhoea. A decoction of the root with *Tectaria crenata* Cav. is a cure for gonorrhoea. Sap from the leaves, mixed with grated coconut is smeared on the head to make the hair long and pliant.	The trees should be conserved and multiplied for further use.	✓	✓	-	✓
7	*Spondias pinnata* (Andamans-Gue, Wild mango)	Anacardiaceae	Large tree	Fruits are eaten as a vegetable when raw and as a fruit when ripe. Young leaves are cooked and eaten as a vegetable by the settlers. Flowers are eaten as such, made into curry or used as for flavoring. Wood is soft and perishable employed for packing cases, canoes or boats.	Can be domesticated.	✓	✓	✓	✓
8	*Annona glabra* (Alligator's apple; Jangli sitaphall)	Annonaceae	Small tree	The fruit is edible. Wood and roots are used for making floats and corks. Pulp can be made into jelly.	Can be used as a rootstock for custard apple for adapting to saline conditions.	✓	-	✓	✓
9	*Colocasia esculenta* (Taro, Dasheen, Eddo, Nicobarese–Tahangen, Kamum)	Araceae	Herb	Rhizomes are consumed as a vegetable. Rhizome is boiled and eaten by the Shompens of the Great Nicobar Islands. Rhizomes may be used for production of industrial alcohol and taro mucilage may be used as a size for impermeable paper. Seeds, although considered somewhat poisonous, are recommended as a remedy for indigestion, flatulence and disorders of parturient women.	Can be domesticated after proper selection from available variability.	✓	✓	✓	✓
10	*Areca triandra* (Nicobarese–Kahkoh; Onge–Tikane)	Arecaceae	Tall tree	Ruminate endosperm is chewed by the tribals with wild betel leaf. It is used as a substitute for *A. catechu.* An Ayurvedic drug Puga extracted from *A. catechu* is used in distaste, diorrhoea and rheumatism, which can be tried from this species also.	Can be domesticated.	✓	✓	✓	-
11	*Garcinia andamanica*	Clusiaceae	Tree	Poles and pillars are made from the trunks for construction of huts by the tribals. Fruits are primarily consumed fresh but are also canned and used to make juices and jellies.	Can be domesticated after selection from available variability.	✓(E)	-	-	-

Contd.

Table 1 Contd.

S.No.	Scientific name	Family	Habit	Uses	Horticultural uses	Distribution A	N	M	O
12	*Garcinia cowa* (Cowa fruit; *Cowa mangosteen)*	Clusiaceae	Tree	Fruits are edible and consumed by the Jarawas and the Great Andamanese. Fruits are acidic and can be made into jam or preserve. Dried slice of the fruit are used in dysentery. Young leaves are cooked and eaten as vegetable by the Burmese.	Can be domesticated as a fruit cum spice.	✓	✓	✓	✓
13	*Momordica cochinchinensis*	Cucurbitaceae	Perennial climber	Tender fruits are valued as a vegetable. Young leafy shoots are cooked and eaten. Root is expectorant and used in treatment of edema of the legs.	Can be readily domesticated to be used as a vegetable. Variability should be studied.	✓	✓	✓	✓
14	*Dioscorea alata* (Greater yam)	Dioscoreaceae	Vine	A widely cultivated yam bearing tubers and can be ground into a meal and area also used as a vegetable. These are considered anthelmintic and used in leprosy, piles and gonorrhoea. These are eaten during convalescence from phthisis, kidney and spleen disorders and used by some tribals when a person is spitting blood and also as a maturative poultice on boils.	Should be checked for its dosage content and can be domesticated.	✓	✓	✓	✓
15	*Dioscorea pentaphylla* (Onge – Titorev; Great Andamanese – Tole; Jarawas – Amina)	Dioscoreaceae	Vine Forb/ herb	Tubers are edible. These are consumed only after repeated boiling and washing. Leaves are eaten in times of scarcity. Flowers are consumed as a vegetable. Tubers and roots are consumed by all the tribals of the Bay Islands. Tubers are considered tonic and also used for swellings.	Should be checked for its dosage content.	✓	–	✓	✓
16	*Atylosia scarabaeoides*	Fabaceae	Trailing or climbing herb	A decoction of the roots is given to treat inflammation of the mouth, nose and throat. Root or the entire plant is made into a paste and mixed with coconut oil and then applied on the head for fifteen days to check falling hair or to cure baldness by some tribals. A decoction of the leaves is given in dysentery and is given to women after childbirth.	Can be tested for treatment of hair fall and products can be developed.	–	✓	✓	✓
17	*Canavalia ensiformis* (Jack bean, Horse bean)	Fabaceae	Annual legume	Vine is cultivated for forage and greens. Very young pods are eaten as snap–beans but these are said to create abdominal complaints, hernia and colic.	–	✓	✓	✓	✓
18	*Tephrosia purpurea* (Wild indigo)	Fabaceae	Herb	Used as a green manure. It is used in bronchitis and bilious febrile attacks and also for boils, pimples and bleeding piles. The roots and seeds are reported to be insecticidal and pesticidal. Pulverized roots are smoked for relief from asthama and cough.	–	–	✓	✓	✓

Contd.

Table 1 Contd.

S.No.	Scientific name	Family	Habit	Uses	Horticultural uses	Distribution A	N	M	O
19	*Artocarpus altilis* (Bread-fruit; Onge-Baluonge; Nicobarese-Pomp)	Moraceae	Tall tree	Wood is used for beams, posts, rafters etc. Nicobarese make small canoes from the trunk. Bark yields a fibre which is used for painting canoes and caulking boats. Leaves are relished by cattle. Onges consume the fruit after roasting. Seeds are supposed to aid parturition and are also used to treat typhoid or other fevers.	Selection can be made for better yielding promising types.	✓	✓	✓	✓
20	*Musa acuminata*	Musaceae	Perennial herb	Wild banana plant bearing edible fruits. Both seeded and seedless varieties occur.	Can possess resistant genes for diseases.	✓	✓	-	-
21	*Musa balbisiana* var. *andamanica*	Musaceae	Perennial herb	Ancestral wild banana are considered inedible because of the seeds they contain. Can be used in breeding programmes.	Can possess discrete resistant genes.	✓(E)	-	-	-
22	*Myristica andamanica* (Wild nutmeg; Nicobarese–Kinhanmo)	Myristicaceae	Slender handsome tree	Fruits are reported to be used like cultivated nutmeg. The aqueous extract of the nuts is used by the Nicobarese for stomach trouble. The powder of roasted fruit is taken by them in malarial fever.	Checked as a root stock. The quality should be checked for fragrance. Variability found should be exploited.	✓(E)	✓(E)	-	-
23	*Horsfieldia glabra* (Onge– Jugane)	Myristicaceae	Moderate sized tree	It is a source of an Ayurvedic drug *Jatiphalam* which is used in indigestion and diarrhoea. Bark and leaves are aromatic and used to treat intestinal infections. Bark is also a remedy for sores and pimples. Onges eat the raw fruit during abdominal pains.	Checked as a rootstock for nutmeg.	✓	✓	✓	✓
24	*Knema andamanica*	Myristicaceae	Moderate sized tree	It yields a wood which may be used for house building purposes. A decoction of the scarping of the bark is utilized to treat abdominal illness and diarrhoea.	Checked as a rootstock.	✓(E)	-	-	-
25	*Syzygium claviflora* (Wild jamun)	Myrtaceae	Moderate sized tree	Fruits are edible. Seeds are used as astringent in bilious diarrhoea and in diabetes. Fermented fruit juice acts as stomachic, carminative and diuretic. Nicobarese women consume its fruits during pregnancy to improve their haemoglobin percentage.	–	✓	-	✓	✓
26	*Syzygium samarangense* (Wild rose apple)	Myrtaceae	Tree	Fruit is edible and also used in liver complaints.	–	✓	✓	-	✓
27	*Vanilla andamanica*	Orchidaceae	Climber	Said to be used for extraction of *Vanilla* drug	Can be used in breeding programmes.	✓	✓(E)	-	-
28	*Vanilla sanjappae*	Orchidaceae	Climber	Fruits may be used as a flavouring agent.	Can be used in breeding programmes.	✓(E)	-	-	-

Contd.

Table 1 Contd.

S.No.	Scientific name	Family	Habit	Uses	Horticultural uses	Distribution A	N	M	O
29	*Piper betle* (Betel; Nicobarese–Humo, Hiyo, Takoocho)	Piperaceae	A shade loving vine	Leaves are widely used as masticatory with areca nuts. Leaf paste mixed in coconut oil and sea water is tied on fractured bones as a plaster by the Nicobarese. Leaf decoction is used for healing wounds. In other preparation these are used on ulcers, boils, bruises, ulcerated nose and to cleanse wounds.	Can be domesticated and flowering types can be used in breeding programmes.	✓	✓	✓	✓
30	*Piper clypeatum*	Piperaceae	Vine	Leaf decoction used for healing wounds.	–	-	✓(E)	-	-
31	*Piper ribesioides* (Choi jal)	Piperaceae	Woody climber	Powdered stem is used as a spice in curries, especially non-vegetarian cookery. Sold in market and are having high market value.	Can be cultivated for commercial exploitation.	✓	-	-	✓
32	*Rubus moluccanus* (Nicobarese–Voknutto)	Rosaceae	Large shrub or small tree	Fruits are edible and eaten by the Shompens. The Juice of roots is used for fistula. Leaf paste is boiled in coconut oil and applied by the Nicobarese to cure the pain in joints. Fruits are given to children to prevent night-micturition.	Nutritional potential has to be studied.	✓	-	✓	✓
33	*Atalantia spinosa* (Wild lime)	Rutaceae	Small tree	Fruits are edible. Oil from berries is used externally in chronic rheumatism and paralysis.	Domestication potential for nutritive value.	✓	✓	✓	✓
34	*Citrus medica* (Citron, Acid lime, Nicobarese- Limong)	Rutaceae	Small tree	Wood is used for agricultural implements and walking sticks. Fruits are used mainly for pickle. Roots are, useful in vomiting, constipation and urinary calculus. An infusion of the fresh shoots is used as a appetitive and vermifuge and is a remedy for stomachache. The preserved rind is used as a remedy for dysentery.	Can be a resistant root stock and may possess genes against citrus diseases.	✓	✓	✓	✓
35	*Nephelium longana* (Longan; Nicobarese–Cham-rev.)	Sapindaceae	Tree	Fruits resembles litchi, but with less succulent aril. These are eaten fresh, dried and canned. Wood is used for furniture and agricultural implements. The fleshy part of the fruit is considered to be nutritive, roborant and benefiting spleen, heart, kidney, lungs and mental faculties. Seed oil is applied to snake bite to absorb venom.	Should be checked for variability and selection may improve the edible portion.	✓	✓	-	✓
36	*Camellia drupifera* (Let-pet Tea of Burma)	Theaceae	Evergreen shrub	Leaves are used as a substitute for the tea and the seed oil may be used as a lubricant for soap making and after refining for edible purposes.	Can be domesticated and produce can be sold to curious tourists.	✓	-	✓	✓
37	*Corchorus capsularis* (White jute)	Tiliaceae	Annual/ perennial	Plant is a source of jute fibre, used for gunny bags, coarse cloth, twine and carpets. Leaves are considered medicinal and consumed along with food as a tonic.	Can be used for making eco-friendly substitute for polythene bags.	✓	-	✓	✓

Contd.

Table 1 Contd.

S.No.	Scientific name	Family	Habit	Uses	Horticultural uses	Distribution A	N	M	O
38	*Alpinia manii* (Great Andamanese– Jini, Jilli)	Zingiberaceae	Herb	Plant is considered to be used by aborigines of Andaman as a bee repellent.	Good for gardening purposes.	✓	✓(E)	-	-
39	*Amomum aculeatum*	Zingiberaceae	Shrub	Ripe fruits are sore in taste and consumed by Nicobarese.	Good for gardening purposes.	✓(R)	-	-	-
40	*Amomum fenzlii*	Zingiberaceae	Shrub	Ripe fruits are sore in taste and consumed by Nicobarese. Juice of the plant parts is used by the shompens of Great Nicobar as a bee repellent.	Good for gardening purposes.	-	✓(E)	-	-
41	*Zingiber odoriferum*	Zingiberaceae	Herb	Stem juice is being used as a tranquiliser for honeybee.	Good for gardening purposes.	✓	-	✓	✓
42	*Zingiber spectabile*	Zingiberaceae	Robust aromatic herb	It could be grown as an ornamental.	Good for gardening purposes.	✓	✓	✓	-
43	*Zingiber squarrosum*	Zingiberaceae	Robust herb	Petioles are chewed when thirsty by the 'Onges'.	Good for gardening purposes.	✓(E)	-	-	-
44	*Zingiber zerumbet*	Zingiberaceae	Perennial herb	Rhizome is used as a hot remedy for cough, asthma, worms, leprosy and other skin diseases. Boiled rhizome is given in pulmonary infection.	Good for gardening purposes.	✓	✓	✓	✓

Results and Discussion

The floristic diversity of horticulturally important families in Bay Islands is given below. In Malvaceae, there are 9 genera with 20 species. Malvaceae is one of the important families which represent okra and many vegetables and ornamental plants. In Rutaceae, there are 13 genera with 29 species. The family is of great economic importance under tropical climates for its numerous edible fruits of the *Citrus* genus. The non-citrus fruits include the white sapote (*Casimiroa edulis*) and the bael (*Aegle marmelos*). In Vitaceae, there are 4 genera with 16 species. The wild relatives can be screened for resistance for powdery mildew and anthracnose. In Myristicaceae, there are 4 genera with 11 species. The family has been recognised by most taxonomists best known for fragrant and spicy seeds of nutmeg (*Myristica fragrans*). Wild nutmeg (*Myristica andamanica*) may be useful as a rootstock for *Myristica fragrans* to overcome the dioecious nature. Female plants of nutmeg can be grafted on rootstocks thus increasing the percentage of bearing trees in an orchard. In Anacardiaceae, there are 13 genera with 26 species. This family includes several economically important species. Notable plants include cashew (type genus *Anacardium*), mango, poison ivy and smoke tree. Wild mango and wild cashew may become good rootstock with competitive root as they are adapted to forest competition. In Cucurbitaceae, there are 12 genera with 22 species. This family commonly known for melons and gourds includes crops like cucumbers, squashes (including pumpkins), luffas, melons and watermelons. The family is predominantly distributed around the tropics, whose edible fruits were amongst the earliest cultivated plants in both the Old and New Worlds. In Poaceae, there are 79 genera with 207 species. It includes casual crops grown around the world, lawn and forage grasses and bamboo widely used for construction. In Orchidaceae, there are 60 genera with 142 species. Orchidaceae is the largest family of the flowering plants (Singh and Medhi, 2006). Wild species of *Vanilla* like *V. andamanica & V. sanjappae* can be crossed with cultivated species to get good segregation. In Arecaceae, there are 18 genera with 45 species. Palms are one of the most well-known and extensively cultivated plant families. Arecaceae family has great economic importance which include coconut, dates and rattan cane. In Zingiberaceae, there are 8 genera with 22 species. The wild relatives are having ornamental value as well as

possess genes for disease resistance with special reference to root rots. The bee tranquilizer *Amomum aculeatum* used by Onge tribes is a giant ginger which can be a green bush in planted gardens. In Amaranthaceae, there are 7 genera with 11 species. Some of the genes include *Alternanthera*, *Amaranthus* and *Celosia.* Wild species may posses more nutrients than the cultivated once and have to be worked out for their utilization in breeding programmes. In Solanaceae, there are 7 genera with 18 species. It is an important source of food, spice and medicine. Wild brinjal is resistant to bacterial wilt which can be used in breeding programmes. In Musaceae, there is 1 genus with 5 species. The largest and most economically important is *Musa*, which is reported to contain AA, 1 ABB, 4 AAB and 21 BB genome, useful in breeding programmes (Uma *et al*., 2005). Such research finding about other wild varieties of horticulturally important species are of great help to the researchers, breeders and conservationists. The research and conservation should be more focused on indigenous species with special reference to the rare and endangered species. Biotechnological techniques have broken the barriers of genetic incompatibility facilitating transfer of useful genes found in wild relatives in to cultivated crops. Potential species which are used as fruits, vegetables and for medicinal purposes have to be checked for their nutritional values. Some of the fruits like cowa mangosteen (*Garcinia cowa*), Burmese grape (*Vitis* sp.) can be brought under domestication for niche marketing. Geographical isolation, environmental and genotypic interactions may show some phenotypic characters which may be useful to breeders. Even though, some of these genotypes are present elsewhere in the world, geographical isolation, micro- and macro-mutations might have brought in some heritable differences which may be selected carefully and studied. More research work is necessary in these crops to consolidate the information and these should be conserved before they become rare and endangered. There is a need for concerted action to make better use of these species to improve the biotic stress and nutritional availability in cultivated crops by screening and gene transfer for more stability. The urgent need to properly characterize, evaluate and documentation of these species is equality very important. Field gene banks can be developed which may be of interest to tourist, botanist and breeders.

Acknowledgements

The authors are grateful to the Department of Biotechnology for financial help through the project 'Digital Database on Plant Resources of Andaman and Nicobar Islands'. They are also grateful to the Director, CARI and Director, BSI Kolkata for providing logistical support.

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Genetic Diversity for Yield and its Component Traits in Pearl Millet Germplasm

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One hundred and five genotypes of pearl millet representing different countries were studied for genetic divergence analysis utilizing Mahalanobis D^2 technique. The analysis of data revealed that significant difference was observed among the genotypes for all the traits. Based on the genetic distance (D^2 value), the 105 accessions were grouped into 22 clusters. Of the 22 clusters formed, cluster II was the largest with 63 genotypes followed by cluster III with 10 accessions. Among the twelve characters studied, the most important character contributing to the divergence was days to maturity and the traits like productive tillers/plant, grain yield/ear, peduncle length, grain yield/plant and 1000-seed weight were next in the order. Cluster I and XVII had maximum inter cluster distance suggesting wide diversity and by utilizing these accessions from these clusters desirable segregants may be evolved through hybridization. Maximum diversity was observed between IP-9416 vs. ICTP-8203, IP-5275 vs. IP-14644, IP-8276 vs. IP-18742.

Key Words: Genetic diversity, Cluster, Pearl millet, D^2 technique, Peduncle length

Introduction

Pearl millet (*Pennisetum glaucum* L.) is the fifth most important cereal food crop in India. Information on genetic diversity analysis helps to identify the genetically diverse genotypes for their use in breeding programmes. Choosing genetically diverse parents will enable the expansion of genetic base and development of superior types and greater success can be achieved through judicious choice of parents for hybridization based on genetic divergence. Crosses between divergent parent usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971). Of the several methods available Mahalanobis's generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating population considering a set of parameters together rather than inferring from indices based on morphological similarities and polygenic relationship.

Mahalanobis's D^2 statistics has been followed by several workers on a wide range of crop species, including pearl millet, to measure the genetic distance among the breeding lines and to identify characters responsible for such divergence. The present investigation aims to determine the genetic diversity among 105 accessions of pearl millet of indigenous and exotic origin using cluster analysis based on morphological traits.

Materials and Methods

The material for the present investigation comprised 105 accessions of pearl millet including 26 lines from India and 79 from African countries, *viz.*, Togo, Sudan, Tanzania, Mali, Camerron, Zimbabwe, Namibia, Nigeria, Burkino Faso, Ghana, and nine from ICRISAT, Hyderabad. Thus, the material represented a wide range of geographic diversity. The experiment was carried out in a Randomized Block Design with three replications at Regional Agricultural Research Station, Bijapur (University of Agricultural Sciences, Dharwad) during *Kharif,* 2004 and 2005. Each accession was grown in two lines of 4 m length. The spacing adopted between rows and between plants with in a row was 50 cm and 15 cm, respectively. The data on days to 50% flowering, days to maturity, plant height, ear length, ear girth, flag leaf area, peduncle length, ear weight, grain yield/ear, grain yield/plant and 1000-seed weight were recorded on five randomenly selected labeled plants for all the entries in each replication All the observations except days to 50% flowering were taken at maturity. The mean data of two seasons was subjected to statistical analysis using Mahalanobis D^2 statistic to assess genetic divergence. The accessions were grouped on the basis of minimum generalized distances using the Tocher's method (Rao, 1952).

Results and Discussion

Analysis of variance revealed significant difference among the accessions for all the characters studied, indicating the existence of wide genetic divergence among them. Based on D^2 values, 105 genotypes were grouped in 22 clusters, indicating the presence of large amount of

diversity among the genotypes (Table 1). Maximum number of genotypes (63) were in cluster II, ten were grouped in cluster III, four each in cluster I, XV and XVII (Table 1) The dendrogram of 105 pearl millet genotypes depicting the spatial position of each cluster in relation to others is presented in Fig.1.

The intra- and inter-cluster D^2 values among the 22 clusters are presented in Table 2. Cluster XV had the maximum intracluster distance of 24.6 followed by cluster II (23.6) and cluster III (22.0). The inter cluster distance ranged between 12.9 minimum (X and XI) and 249.0 maximum (I and XVII). The inter cluster proximity

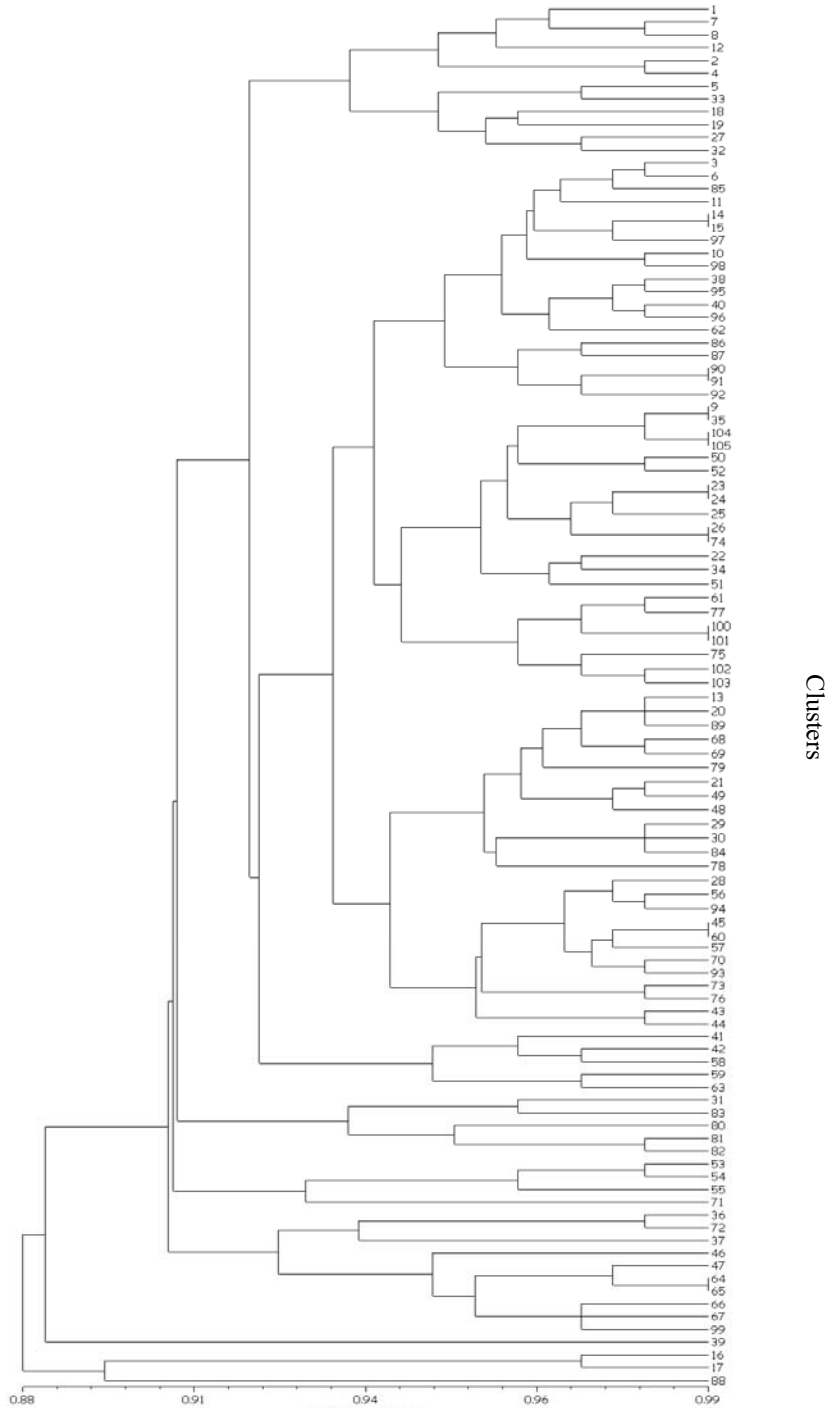

Fig. 5: Dendrogram of 105 pearl millet germplasm lines

Table 1. Distribution of 105 pearl millet genotypes into different clusters

Cluster number	Total number of genotypes in each cluster	Genotypes included in the clusters	Origin
I	4	IP-9140, IP-9286, IP-15857, IP-15899	India=1 Togo=1 Tanzania=2
II	63	IP-11211, ICTP-8203, WC-075, IP-8540, ICMV-221, IP-15355, IP-15256, IP-4759, IP-15257, IP-14942, IP-10394, IP-3150, IP-4169, IP-15220, IP-15273 IP-12779, IP-7838, IP-17978, IP-12682, IP-8276, IP-8069, IP-12768 IP-17566, IP-17753, IP-9301, IP-17493, IP-17690 IP-10761, IP-10914, IP-10839, IP-10945 IP-15817, IP-15710, IP-15681, IP-15829 IP-10085, IP-6451, IP-6417, IP-10186, IP-6460, IP-6545 IP-12901, IP-14497, IP-6125 IP-14028, IP-16911, IP-16449, IP-8818, IP-16402, IP-14026 IP-19246, IP-17144, IP-18657, IP-18742, IP-19388 IP-5275, IP-19067, IP-13137 IP-11503, IP-13840, IP-10339, IP-13875 IP-8416	India=15 ICRISAT=7 Togo=5 Sudan=4 Tanzania=4 Mali=6 Camerron=3 Zimbabwe=6 Namibia=5 Nigeria=3 Burkino Faso=4 Ghana=1
III	10	IP-14038 IP-16196, IP-4695, IP-4779 IP-17979 IP-14644, IP-14778 IP-19321 IP-7488 IP-8429	Zimbabwe=1 India=3 ICRISAT-1 Camerron=2 Namibia=1 Tanzania=1 Nigeria=1
IV	1	IP-11680	Sudan=1
V	1	IP-10811	Sudan=1
VI	1	IP-15364	India=1
VII	1	IP-19243	Namibia=1
VIII	1	IP-19361	Namibia=1
IX	1	IP-18800	Namibia=1
X	1	IP-12474	India=1
XI	4	IP-11577, IP-13833 IP-18625 IP-16690	Burkino Faso=2 Namibia=1 Zimbabwe=1
XII	1	IP-16197	India=1
XIII	1	IP-13154	Nigeria=1
XIV	1	IP-18389	Namibia=1
XV	4	IP,13645, IP-4331 IP-17144, IP-16638	India=2 Zimbabwe=2
XVI	1	IP-10826	Sudan=1
XVII	4	IP-17028, IP-10488, IP-18621 IP-7440	Zimbabwe=2 Namibia=1 Tanzania=1
XVIII	1	IP-10085	Mali=1
XIX	1	IP-6510	Mali=1
XX	1	IP-8229	ICRISAT=1
XXI	1	IP-3799	India=1
XXII	1	IP-9149	India=1

seems to be minimum between cluster X and XI as indicated by lowest inter cluster distance of 12.9. Hence, the genotypes included in cluster I and XVII may be selected for more effective crossing programme and should result in wide spectrum of variability to operate selection in segregating population. Presence of diversity among pearl millet genotypes of the present study is in accordance with earlier reports (Yadav, 1994; Hepziba *et al*., 1995).

Based on D^2 values, per cent contribution of different characters towards divergence was obtained. Among the twelve quantitative characters studied the most important

Table 2. Average intra-cluster inter-cluster distances for 22 clusters in 105 pearl millet genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX	XXI	XXII
I	6.0	231.8	253.0	218.6	239.9	227.8	232.4	221.9	218.6	218.8	229.2	225.4	221.8	225.0	242.1	236.9	249.0	242.7	231.6	198.3	220.0	141.8
II		23.6	33.5	31.6	31.9	34.4	29.7	30.7	28.3	33.0	28.5	30.5	39.2	31.7	36.7	29.4	33.3	42.4	34.6	57.8	73.5	218.0
II			22.0	51.4	35.0	48.4	32.9	41.3	47.9	51.8	44.1	41.6	50.1	49.7	35.0	35.2	32.5	41.2	42.1	74.0	89.9	235.3
IV				0.00	43.8	30.0	46.6	40.3	14.0	14.7	14.8	41.1	47.4	14.6	52.0	35.4	39.7	57.1	45.0	59.1	67.8	210.2
V					0.00	23.1	42.3	48.6	37.3	36.3	33.4	45.5	57.5	40.4	48.5	44.3	31.6	18.3	22.0	61.2	71.1	226.9
VI						0.00	51.8	51.3	24.0	20.4	21.9	48.3	59.6	28.9	55.9	47.7	36.8	34.7	26.9	56.9	62.8	219.3
VII							0.00	20.3	43.8	49.2	45.3	23.4	27.9	46.3	32.0	29.6	44.0	49.2	43.8	58.5	80.2	215.5
VIII								0.00	38.0	45.9	44.0	14.4	17.6	45.1	28.9	35.7	51.0	54.9	43.6	48.5	78.1	206.8
IX									0.00	15.0	18.0	38.6	46.4	16.8	48.9	35.3	38.1	49.6	37.7	55.0	66.3	211.8
X										0.00	12.9	46.5	55.2	16.9	57.3	40.0	37.7	49.8	40.3	58.6	64.3	213.4
XI											0.00	43.7	52.8	14.8	51.5	34.0	29.2	47.7	39.3	63.4	69.2	220.7
XII												0.00	13.8	45.3	26.7	40.1	51.5	50.4	37.1	42.8	71.1	205.7
XIII													0.00	51.7	31.9	43.2	60.3	63.2	50.0	48.1	76.2	200.4
XIV														0.00	55.2	30.2	33.9	56.1	46.9	66.3	66.1	218.0
XV															24.6	43.3	50.5	51.9	43.3	60.9	87.3	219.9
XVI																0.00	30.5	58.4	53.6	75.1	82.6	224.8
XVII																	21.9	45.3	45.8	79.5	84.0	237.2
XVIII																		0.00	19.6	59.3	78.4	227.4
XIX																			0.00	43.8	66.9	215.1
XX																				0.00	63.2	181.9
XXI																					0.00	200.8
XXII																						0.00

Underlined figures indicates intra-cluster distance

Percent contribution of each character towards genetic divergence in pearl millet

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Productive tillers/ ear	Plant length (cm)	Ear girth (cm)	Flag leaf area (cm^2)	Peduncle length (cm)	Ear weight (g)	Grain yield per ear (g)	Grain yield per plant (g)	1000-grain weight (g)
% Contribution	0.13	32.58	0.09	36.23	0.42	0.35	0.00	0.48	0.04	0.31	20.26	9.12

Table 3. Cluster means values for twelve traits of 22 clusters in 105 pearl millet genotypes

Characters	Percent contribution of each character towards genetic divergence in pearl millet											
	Days to 50 % flowering	Days to maturity	Plant height (cm)	Productive tillers/ ear	Plant length (cm)	Ear girth (cm)	Flag leaf area (cm^2)	Peduncle length (cm)	Ear weight (g)	Grain yield per ear (g)	Grain yield per plant (g)	1000-grain weight (g)
I	51.33	86.83	182.24	2.58	20.98	7.51	85.36	21.10	35.02	22.18	61.72	11.28
II	50.22	86.66	172.97	2.13	23.52	7.68	81.21	21.97	49.80	26.72	62.16	9.63
III	51.17	87.80	176.89	2.07	25.18	7.63	79.03	21.54	48.26	26.00	60.90	8.73
IV	51.67	90.33	168.00	1.93	19.10	7.50	93.00	19.83	47.87	20.20	32.67	7.70
V	50.33	85.00	185.63	2.63	24.23	6.00	87.60	22.43	53.40	30.70	73.67	10.20
VI	51.33	87.67	190.67	2.07	29.80	5.73	99.40	23.37	43.33	20.23	47.97	8.83
VII	50.00	83.33	171.57	2.47	23.23	8.23	92.13	23.27	48.67	23.30	69.10	10.77
VIII	50.00	85.00	170.10	1.97	21.63	8.10	81.03	21.33	42.33	21.73	50.13	9.00
IX	48.67	86.67	160.47	2.00	28.73	8.37	71.50	20.70	43.00	19.83	37.50	7.17
X	46.67	84.67	171.83	2.13	23.83	6.93	73.33	22.37	44.17	21.57	70.30	12.63
XI	48.25	86.00	174.00	2.60	25.20	6.10	78.00	22.20	46.50	24.80	65.90	10.80
XII	51.33	89.00	171.23	2.23	29.17	8.23	67.93	19.03	53.07	21.43	37.53	6.80
XIII	45.00	83.67	190.83	1.57	19.27	6.97	88.17	24.00	60.97	34.67	86.00	13.70
XIV	47.67	86.67	171.00	2.67	23.37	8.07	75.00	20.17	42.03	21.50	50.83	7.70
XV	48.83	84.75	171.47	2.00	24.13	7.00	84.15	19.43	48.69	22.05	45.96	8.02
XVI	46.33	85.00	170.60	2.47	20.87	8.83	69.50	25.33	51.23	25.33	57.93	10.13
XVII	50.33	86.83	176.21	2.08	26.79	9.20	83.13	23.65	49.73	26.73	62.31	8.88
XVIII	52.67	89.00	188.67	2.90	24.83	6.73	99.83	26.63	53.57	27.77	67.00	11.20
XIX	54.00	92.00	203.03	1.93	20.67	9.17	71.13	27.93	42.67	20.20	43.20	6.70
XX	50.67	86.33	189.83	2.30	20.60	8.63	79.50	21.47	51.77	28.67	60.87	11.07
XXI	49.00	85.67	187.13	2.10	22.20	8.63	54.97	26.60	38.47	27.60	70.67	9.03
XXII	47.00	87.33	189.50	2.20	15.67	9.03	91.27	20.10	40.50	27.30	63.37	10.27

character contributing to the divergence was days to maturity. The traits like productive tillers/ plant, grain yield per ear, peduncle length, grain yield per plant, 1000-seed weight were next in the order. These characters can be given greater importance in selection of potential parents for hybridization. These observations are in line with the observations of earlier workers (Hepziba *et al*., 1995; Quendeba *et al*., 1995).

The existence of diversity among the genotypes was also assessed by the considerable amount of variation in cluster means for different characters (Table 3). Genotypes in cluster VII, XIII, X, XV and VIII were the early maturing. The genotypes in clusters XIX, XIII and VI were tallest, and cluster IX had the dwarf genotype. The cluster mean for ear length ranged from 15.67 cm to 29.80 cm, which were attained by group XXII and VI, respectively. The maximum ear girth was noticed in cluster XVII (9.20) while minimum was observed in cluster V (6.0). Less number of productive tillers per plant was recorded by the individuals in the cluster XIII (1.57), while more number was seen in cluster XVIII (2.90). Regarding peduncle length, cluster XIX had the highest mean value (27.93 cm), while cluster means for flag leaf area was in the range of 54.97 (cluster XXI) to 99.40 cm^2 (cluster VI). The mean values for ear head weight per ear was in the range of 35.02 (cluster I) to 60.97 g (cluster XIII). The maximum grain yield per ear head was produced by genotypes in cluster XIII (34.67 g). The minimum grain yield per ear head was recorded by genotypes in cluster IX (19.83 g). The higher mean grain yield per plant was recorded by the genotypes in cluster XIII (86.00 g), while lower grain yield was noticed in cluster IV (32.67 g). With respect to 1000-grain weight, cluster XIII had highest mean value (13.70 g) followed by cluster X (12.63 g) and cluster I (11.28 g). Cluster XIX had very low mean values for grain weight (6.70 g).

Maximum diversity was observed between IP-9416 vs. ICTP-8203 followed by IP-5275 vs. IP-14644 and IP-8276 vs. IP-18742. These divergent pairs will make 'B' and 'R' line combinations at least on any one of the CMS sources. If such hybrids are good, the corresponding cytoplasmic sources can be used for developing male sterile version and utilized in hybridization programme for developing hybrids or can be involved in crossing programme (B x R) for creating variability to isolate superior 'B' and 'R' lines on one or two cytoplasm.

Acknowledgement

The authors are grateful to ICRISAT, Hyderabad for providing necessary seed materials for the study.

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Reproductive Biology of Tamarind (*Tamarindus indica* L.) under Semi-Arid Tropics of Western India

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Reproductive biology of fifteen elite genotypes of tamarind was studied during the year 2004 and 2005. Peak period of panicle emergence and flowering was recorded in the month of July and August, respectively in majority of genotypes. It was found to be earliest in CPT 1 closely followed by CPT 2, CPT 3, CPT 11 and CPT 13. Variable percentage of anthesis/ dehiscence was registered in different genotypes. Peak period of anthesis was recorded between 7-9 AM in all the genotypes during both the years. None of the genotypes showed anthesis before 5 A M and after 11AM. Anther dehiscence commenced after opening of flowers, *i.e*., at 8AM and continued till 12 noon. Peak period of dehiscence was recorded between 9-11 AM in all genotypes. None of the genotypes showed anther dehiscence before 8 AM and after12 noon. Time taken for complete development of flower ranged from 18-26 days, pollen viability ranged from 80.10-94.13 per cent being highest in CPT 3. Pollen germination ranged from 10.11–18.13 per cent being at the top in CPT 3 (18.13 per cent). Pollen diameter ranged from 34.12- 42.14 micron. Pollen grain was spherical in shape having light yellow colour in all genotypes. CPT 13 recorded maximum panicle length (15.20 cm) and fruit set per panicle (16.80). The peak period of fruit set was recorded in the month of September in majority of genotypes. These genotypes are being further evaluated.

Key Words: Anthesis, Dehiscence, Pollen germination, Pollen viability, Tamarind

Introduction

Tamarind (*Tamarindus indica* L.), a member of sub-family Caesalpiniaceae of family Fabaceae, is highly drought hardy and can be grown in dry land areas and on degraded wasteland. It is considered to be one of the most exquisite and valuable fruits of the tropics and sub tropics. It is the source of timber, fruits, seeds, fodder, medicinal extracts and has potential of industrial use (Karale *et al.*, 1999; Awasthi and Sharma, 1998; Pareek and Awasthi, 2002). It is highly heterozygous, cross-pollinated fruit crop and as such seedlings exhibit a wide range of variations, which aids in the selection of the superior desirable genotypes. Due to cross pollination and predomination of seed propagation over a large period of time, it gives immense opportunity to locate elite trees having horticultural traits. Tamarind flowers are always borne on newly emerging vegetative shoots irrespective of the time of year. In tamarind, anthesis starts in the morning as early as 4.30 AM and continues up to 8.30 AM with peak period at 6.30 AM (Karale, 2002). Thimaraju *et al*. (1977), Usha and Singh (1994), Sharma *et al.* (1994), Kumar *et al.* (2004) Singh and Singh (2004) and Singh *et al.* (2004) have also studied floral biology of tamarind, Jalphai (*Elaeocarpus floribundus* Bl), guava, peach and pear genotypes under various climatic conditions. Peak period of anthesis and dehiscence from 6.30-8.30 AM was observed in different guava genotypes (Dhaliwal and Singla, 2002; Singh, 2004). Fruit set was only 36 per cent with open pollination and increased to 56 per cent with cross-pollination in tamarind (Usha and Singh, 1996). In spite of the fact that tamarind can withstand adverse climate and grow in various types of soil, only a few attempts to improve its varietal wealth have been made under semi-arid regions. To begin with development of new elite genotypes, the information on detailed reproductive biology of the crop is essential. Therefore, studies were undertaken to gather this type of information under semi-arid conditions of western India.

Materials and Methods

The tamarind trees are found scattered through out Gujarat from cultivable land to waste lands. An extensive survey was carried out in district Panchamahals and fifteen promising genotypes were selected during the year 2004 and 2005 that had fairly wide spectrum of variability of various characters and they were considered as experimental materials. Thirty healthy panicles in each genotype were randomly selected to record panicle length and fruit set per panicle. To observe the time for anthesis and dehiscence, 50 flower buds expected to open the next days were tagged on the previous evening. The number of fully opened flowers was noted at one-

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hour interval (starting from 5.00 AM in the next morning). Fully opened flowers were marked with delible ink to avoid recounting. Like wise for dehiscence, fully dehisced anthers were removed to avoid confusion. These observations continued till all the 50 flower buds in each genotype anthesised/dehisced completely during the years of experimentation. The pollen viability in different genotypes was tested with two per cent acetocarmene solution. The pollen from freshly dehisced anthers was put on the slides. About 2 drops of freshly prepared 2 per cent acetocarmine solution was added to the slides and was covered gently with a cover slip. The mounted pollens were examined under the microscope after about 15 minutes, when they had attained proper staining. Pollen which stained deeply, looked normal and symmetrical were considered to be viable and the remaining ones as non-viable. Observations on pollen germinability was recorded by using hanging drop method in 15 per cent sucrose solution after 24 h.

Results and Discussion

The observations on flowering studies, presented in Table 1, showed that peak period of panicle emergence was recorded in the month of July in majority of genotypes. It was noted in the month of August in CPT 9, CPT 10, CPT 14 and CPT 15. There was only one genotype, *i.e.*, CPT 1 which recorded peak period of panicle emergence in the month of June. The peak period of flowering was found to be earliest in CPT 1 (1st July) closely followed by CPT 2, CPT 3, CPT 4 and CPT 8 (Table 1). Similar trend with respect of panicle emergence and flowering was found in another successive year (2005) in different genotypes. Wide variability in respect of panicle emergence and period of flowering was recorded in mango and litchi under humid sub tropics of eastern India (Singh, 2002; Hoda *et al.*, 2003; Ray *et al.*, 2002; Das *et al.*, 2004).

The data indicated that anthesis started at 5 AM and continued up to 11 AM. The optimum time for anthesis was found from 6 to 9 AM, with the peak period of anthesis from 7 to 9 AM in all the genotypes (Table 2). However, least anthesis was recorded between 10 and 11AM, which was accounted to the tune of 1-3% in all the genotypes. It may be considered as negligible. None of the genotypes showed anthesis before 5 AM and after 11 AM. The anthesis was recorded 43, 42 and 41% in CPT 6, CPT 3 and CPT 5, respectively between 7 to 8 AM while CPT 1 recorded 35 per cent anthesis between 7 to 8 AM (Table 2). CPT 1 was the first to show higher rate of anthesis (6 per cent) followed by CPT 4, CPT 7 and CPT 9 between 5 to 6 AM. However, delayed anthesis was registered in CPT 3, CPT 13 and CPT 6, *i.e.*, 3 per cent between 5-6 AM. Anthesis between 10-11 AM ranged from 1 to 3 per cent in all the genotypes.

Data pertaining to anther dehiscence (Table 2) indicated that anther dehiscence commenced after opening of the flower, *i.e.*, at 8 AM and continued up to 12 AM. The peak period for anther dehiscence was registered from 9 to 11 AM in all the genotypes and it was considered as the most effective period for anther dehiscence, possibly due to the fact that temperature during these hours are usually higher than that in the morning and evening hours and fall in humidity during this period may also have accelerated the dehiscing process. None

Table 1. Time of panicle emergence and flowering in tamarind genotypes

Genotypes	Time of panicle emergence						Time of flowering					
	2004			2005			2004			2005		
	Start	Peak	Completion	Start	Peak	Completion	Start	Peak	Completion	Start	Peak	Completion
CPT1	22 May	6 June	27 June	18 May	8 June	28 June	15 June	1 July	20 July	17 June	2 July	22 July
CPT2	17 June	2 July	23 July	14 June	4 July	25 July	12 July	29 July	12 Aug.	13 July	28 July	14 Aug.
CPT3	18 June	3 July	24 July	17 June	6 July	25 July	13 July	30 July	18 Aug.	10 July	27 July	20 Aug.
CPT4	20 June	12 July	3 Aug.	21 June	14 July	4 Aug.	28 July	14 Aug.	28 Aug.	29 July	17 Aug.	29 Aug.
CPT5	23 June	15 July	5 Aug.	18 June	18 July	7 Aug.	1 July	15 Aug.	29 Aug.	3 July	18 Aug.	28 Aug.
CPT6	1 July	14 July	3 Aug.	2 July	13 July	2 Aug.	2 Aug.	17 Aug.	28 Aug.	1 Aug.	15 Aug.	27 Aug.
CPT7	2 July	20 July	7 Aug.	5 July	22 July	9 Aug.	11 Aug.	28 Aug.	12 Sept.	13 Aug.	29 Aug.	15 Sept.
CPT8	25 June	12 July	28 July	28 June	10 July	27 July	28 July	15 Aug.	26 Aug.	26 July	14 Aug.	28 Aug.
CPT9	13 July	1 Aug.	24 Aug.	12 July	3 Aug.	22 Aug.	6 Aug.	28 Aug.	10 Sept.	8 Aug.	25 Aug.	13 Sept.
CPTI0	12 July	2 Aug.	26 Aug.	15 July	4 Aug.	24 Aug.	12 Aug.	29 Aug.	13 Sept.	10 Aug.	28 Aug.	15 Sept.
CPT11	16 July	3 July	25 July	17 June	5 July	27 July	14 July	30 July	19 Aug.	12 July	28 July	20 Aug.
CPTI2	22 June	10 July	28 July	18 June	12 July	25 July	1 Aug.	14 Aug.	28 Aug.	2 Aug.	12 Aug.	25 Aug.
CPTI3	28 June	10 July	2 Aug.	24 June	13 July	4 Aug.	2 Aug.	16 Aug.	28 Aug.	3 Aug.	18 Aug.	27 Aug.
CPTI4	14 July	2 Aug.	22 Aug.	17 July	3 Aug.	20 Aug.	13 Aug.	27 Aug.	13 Sept.	10 Aug.	25 Aug.	15 Sept.
CPTI5	16 July	8 Aug.	24 Aug.	15 July	6 Aug.	22 Aug.	16 Aug.	28 Aug.	14 Sept.	17 Aug.	27 Aug.	17 Sept.

Table 2. Time of anthesis and dehiscence in different genotypes of tamarind

Genotypes		Flowers opened and anthers dehisced at hourly interval (%)							Flowers opened and anthers dehisced at hourly interval (%)						
		2004							2005						
		5-6	6-7	7-8	8-9	9-10	10-11	11-12	5-6	6-7	7-8	8-9	9-10	10-11	11-12
CPT1	A	6	20	35	32	4	3	0	5	21	36	31	5	2	0
	0	0	0	0	9	40	45	6	0	0	0	7	42	47	4
CPT2	A	4	22	40	31	2	1	0	3	21	42	30	3	1	0
	0	0	0	0	8	38	47	7	0	0	0	9	38	47	6
CPT3	A	3	22	42	30	2	1	0	1	24	40	32	2	1	0
	0	0	0	0	8	41	48	3	0	0	0	7	41	48	4
CPT4	A	5	19	38	32	4	2	0	4	20	37	32	5	2	0
	0	0	0	0	8	40	46	6	0	0	0	8	42	44	6
CPT5	A	3	21	41	32	2	1	0	2	19	42	34	2	1	0
	0	0	0	0	9	39	45	7	0	0	0	8	40	44	8
CPT6	A	4	20	43	30	2	1	0	3	18	45	31	2	1	0
	0	0	0	0	8	40	44	8	0	0	0	9	40	45	6
CPT7	A	5	19	38	**33**	3	2	0	4	20	40	32	2	2	0
	0	0	0	0	9	40	43	8	0	0	0	8	40	44	8
CPT 8	A	4	21	37	34	3	1	0	5	20	38	**33**	3	1	0
	0	0	0	0	9	40	45	6	0	0	0	10	39	46	5
CPT9	A	4	19	37	33	4	2	0	5	21	38	32	3	1	0
	0	0	0	0	10	39	44	7	0	0	0	9	38	45	8
CPT10	A	5	20	40	30	4	1	0	5	21	42	28	2	2	0
	0	0	0	0	8	40	45	7	0	0	0	10	38	45	7
CPT11	A	4	22	39	31	2	2	0	5	23	40	30	1	1	0
	0	0	0	0	1I	36	43	10	0	0	0	12	35	42	11
CPT12	A	4	23	40	29	3	1	0	3	22	43	28	2	2	0
	0	0	0	0	7	40	45	8	0	0	0	8	39	45	8
CPT13	A	3	24	39	30	3	1	0	5	19	40	32	3	1	0
	0	0	0	0	10	42	44	8	0	0	0	10	40	45	5
CPT14	A	4	20	39	30	5	2	0	3	21	40	28	4	4	0
	0	0	0	0	8	40	45	8	0	0	0	8	40	43	9
CPT15	A	5	22	36	30	5	:2	0	4	21	36	30	6	3	0
	D	0	0	0	9	38	43	10	0	0	0	10	37	41	12

A= Anthesis, D= Dehiscence

of the genotypes showed anther dehiscence before 8 AM and after 12 AM. It was recorded that CPT 3, CPT 2 and CPT 4 showed maximum anther dehiscence (48, 47 and 46 %, respectively) between 10 to 11 AM. Dehiscence of anthers ranged from 3-12 per cent in different genotypes between 11-12 AM. The similar pattern was followed during the successive year 2005. These observations are found in conformity with the findings of Singh *et al.* (2004a). In tamarind, anthesis starts in the morning as early as 4.30 AM and continues up to 8.30 AM with peak of anthesis at 6.30 AM and after 8.30 AM there was no anthesis (Karale, 2002). Thimmaraju *et al*. (1977) reported that peak anthesis and dehiscence took place at 6.00 AM and 10.30 AM, respectively in tamarind. Peak period of anthesis and dehiscence was recorded between 6-8 AM in guava during both the seasons (winter and rainy), none of the genotypes showed anthesis before 4 AM and after 11 AM, anther dehiscence commenced just after opening of flowers, *i.e.*, at 5 AM and continued till 11 AM (Singh and Singh, 2004). Sandhu *et al.* (1987) reported that dehiscence in guava varieties took place15-30 minutes prior to the opening of flowers and the peak period of dehiscence was found between 6-9 AM. The variability in flower biology of tamarind genotypes under various climatic conditions might be due to location and varietal characteristics.

In tamarind, flower bud initiation began with resumption of the vegetative growth, just after leaf fall. The flower buds were borne on the current season's growth in different genotypes. The observations on flowering studies presented in Table 3 showed that tamarind genotypes differed in their time requirement to complete the bud development and it ranged from 18-26 days being highest in CPT 7, closely followed by CPT 5, CPT 6, CPT 8 and CPT 14, however it was noted to be least in CPT 1 and CPT 4. Thimmaraju *et al.* (1977) reported that flower bud development took about 20 days from first visible initiation in tamarind. The Varietal variability in respect of flowering period has also been reported by Sharma *et al.* (1994) Singh *et al*. (2004) and Kumar *et al*. (2004) in Jalphai (*Elaeocarpus floribundus* Bl), pear and peach genotypes,

Table 3. Pollen characteristics of tamarind genotypes

Genotypes	Time taken for flower development (Days)		Pollen viability (%)		Pollen germination (%)		Pollen diameter (Micron)	
	2004	2005	2004	2005	2004	2005	2004	2005
CPTI	18	19	83.69	84.63	14.19	14.54	34.12	35.17
CPT2	20	21	84.50	85.39	15.08	15.12	36.50	37.19
CPT3	22	23	93.50	94.13	18.13	18.34	35.63	35.93
CPT4	18	19	92.13	93.10	17.15	17.60	40.12	41.12
CPT5	23	22	90.50	91.12	16.70	16.80	39.13	40.14
CPT6	24	24	91.20	92.14	16.14	16.90	41.12	42.14
CPT7	25	26	88.34	89.13	15.03	15.17	37.13	38.39
CPT8	23	24	86.39	87.16	14.10	14.14	38.20	39.40
CPT9	20	22	84.12	85.39	12.60	13.00	36.13	37.89
CPTI0	23	22	86.39	88.10	15.10	15.30	37.12	38.14
CPT11	18	21	80.10	81.23	10.11	10.23	36.14	37.10
CPTl2	20	23	84.40	83.10	15.50	15.80	39.34	39.20
CPT13	19	24	83.60	85.60	13.60	13.90	40.40	41.10
CPTl4	19	26	88.30	86.20	16.80	16.95	41.00	41.45
CPTI5	18	23	84.20	86.12	14.00	13.50	38.00	37.21
CD (P=0.05)	—	—	1.12	0.68	1.14	1.02	1.36	1.12

respectively under various climatic conditions.

Stainability test was employed as an index of pollen viability. In acetocarmine solution (2.0%), maximum pollen viability (93.50%) was observed in CPT 3, which was closely followed by CPT 4, CPT 6 and CPT 5, however minimum pollen viability was observed in CPT 11 (80.10%). Similar trends were observed in the year 2005. Kumar *et al.* (2004) reported that pollen viability ranged from 74.90-94.22 per cent in different peach cultivars under Uttaranchal conditions. Singh *et al.* (2004b), obtained 75.60-88.00 per cent pollen viability in different pear cultivars.

Pollen germination was very poor irrespective of the genotypes (Table 3). The maximum pollen grain germination was recorded in CPT 3 (18.13 per cent) closely followed by CPT 4, CPT 5 and CPT 6, while it was found to be least in CPT 11 (10.11 per cent). Differences in pollen germination may be due to varying percentage of pollen viability in different genotypes. Pollen diameter varied from 34.12- 41.38 microns. Pollen grain was spherical in shape having light yellow colour in all genotypes. Almost similar trend was recorded during the year 2005. There was marked variation in average panicle length in most of the genotypes and CPT 13 recorded the maximum panicle length (15.00 cm), closely followed by CPT 8 (14.60 cm), CPT 15 (14.00 cm) and CPT 10 (13.40 cm). Least panicle length was found in CPT 1 (9.20 cm). CPT 4, CPT 5, CPT 9, and CPT 11 were statistically at par with each other in respect of average panicle length. Similar pattern was followed by different genotypes pertaining to panicle length during the year 2005.

Table 4. Panicle length, fruit set per panicle and time of fruit set in tamarind genotypes

Genotypes	Average panicle length (cm)		Fruit set per panicle		Date of fruit set					
					2004			2005		
	2004	2005	2004	2005	Start	Peak	Completion	Start	Peak	Completion
CPT1	9.20	9.30	8.60	8.80	18 July	2 Aug.	18 Aug.	17 July	] Aug.	20 Aug.
CPT2	9.40	9.70	8.00	9.80	10 Aug.	28 Aug.	10 Sept.	9 Aug.	27 Aug.	] I Sept.
CPT3	12.50	13.70	13.40	3.80	12 Aug.	29 Aug.	15 Sept.	10 Aug.	27 Aug.	16 Sept.
CPT4	11.60	12.80	1.10	9.20	27 Aug.	12 Sept.	22 Sept.	26 Aug.	10 Sept.	20 Sept.
CPT5	11.00	9.20	8.20	8.10	2 Aug.	10 Sept.	25 Sept.	I Aug.	12 Sept.	26 Sept.
CPT6	12.20	12.00	15.00	13.10	1 Sept.	13 Sept.	22 Sept.	3 Sept.	12 Sept.	23 Sept.
CPT7	13.96	13.82	9.10	9.50	10 Sept.	22 Sept.	28 Sept.	8 Sept.	20 Sept.	26 Sept.
CPT8	14.60	15.40	13.50	12.40	26 Aug.	12 Sept.	22 Sept.	25 Aug.	II Sept.	20 Sept.
CPT9	11.50	12.70	8.20	8.40	5 Sept.	24 Sept.	29 Sept.	4 Sept.	22 Sept.	28 Sept.
CPT10	13.40	12.80	9.50	9.10	10 Sept.	22 Sept.	30 Sept.	II Sept.	20 Sept.	28 Sept.
CPT11	11.20	11.00	6.80	8.10	14 Aug.	25 Aug.	12 Sept.	13 Aug.	26 Aug.	13 Sept.
CPT12	13.00	13.80	7.20	8.50	2 Sept.	10 Sept.	22 Sept.	I Sept.	I I Sept.	23 Sept.
CPT13	15.00	15.20	16.80	15.20	I Sept.	10 Sept.	23 Sept.	3 Sept.	9 Sept.	24 Sept.
CPT14	]3.04	]3.00	7.10	7.60	10 Sept.	20 Sept.	27 Sept.	12 Sept.	18 Sept.	28 Sept.
CPT15	14.00	14.20	5.80	6.60	15 Sept.	19 Sept.	30 Sept.	13 Sept.	17 Sept.	29 Sept.
CD (P=0.05)	0.80	0.78	1.13	1.19						

Variation in number of fruit set per panicle was recorded and it was found to be highest in CPT 13 (16.80), closely followed by CPT 6 (15.00), CPT 3(13.40) and CPT 8 (13.50) (Table 4). Date of fruit set varied from middle of July to middle of September in different genotypes. In majority of genotypes, peak period of fruit set was observed in the middle of September. Though, flowering is profuse in tamarind, the fruit set under natural conditions is low, ranging from 3-5 %, which can be increased to about 50-55 % under artificial cross pollination. Fruit set was only 36 per cent with open pollination and increased to 56 per cent with cross pollination (Usha and Singh, 1996). Kumar *et al.* (2004) reported that pollen germination ranged from 62.12-78.23 per cent in different peach cultivars under Uttaranchal conditions. Pollen grain viability ranged from 91.05-97.91 per cent among different genotypes of pomegranate (Sharma and Bist, 2003). Dhaliwal and Singla (2003), Hoda *et al.* (2003), Singh *et al.* (2004), Singh and Singh (2005b) and Singh and Singh (2005a) recorded wide variation in reproductive attributes of guava, mango, tamarind, *Jamun* and *Mahua* respectively under various climatic conditions. These promising genotypes are being further evaluated.

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Genetic Variability, Correlation Coefficient and Path Analysis of Seed and its Component Traits in Forage Maize (*Zea mays* L.)

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Genetic variability, character association and path analysis for seed yield and its contributing traits were worked out in 100 forage maize accessions along with a control variety, namely, African Tall. These materials were collected from Madhya Pradesh, Rajasthan and Uttar Pradesh. The results indicated that phenotypic coefficients of variation, in general, were relatively higher than the corresponding genotypic coefficient of variation for seed yield and contributing traits. The number of kernels per row, shank diameter, seed yield per plant and cob length showed more variation than the other characters. Heritability in conjunction with genetic advance showed days to maturity, seed yield per plant and plant height to be the most important character for improvement through selection. Seed yield per plant, was found to be significantly and positively associated with test weight, number of kernels per row, kernel width, kernel length, shank diameter and cob length. The path coefficient analysis revealed that characters like test weight, number of kernels per row and shank diameter had positive direct effect on seed yield. From the above findings it may be concluded that an ideal plant type in forage maize for seed yield could be described as one which is characterized by more number of kernels per row, test weight and shank diameter. The selection based on these characters might help in improving seed yield in forage maize both directly and indirectly.

Key Words: Correlation, Forage maize, Germplasm, Path analysis

Introduction

In any crop, germplasm serves as valuable source of base population and provides scope for wide variability. Information on the nature and degree of genetic diversity would help the plant breeder in selecting the right type of parents for breeding programme.

The genetic improvement in forage maize, however could not make head way and the gap still remain to be filled up through development of improved dual purpose variety in this crop. Systematic information on the extent of genetic diversity in existing forage maize germplasm, behaviour of seed yield components and their association with direct and indirect effect is scanty or hardly available. Keeping the above point in view, the present investigation was therefore undertaken with a view to find out the various genetic parameters of variability and to understand the association of various quantitative traits in forage maize.

Materials and Methods

A core collection comprising of one hundred accessions of forage maize (*Zea mays* L.) was made from Madhya Pradesh, Rajasthan and Uttar Pradesh. These accessions were evaluated with control variety of forage maize (African Tall) in a Randomized Block Design with three replications at Central Research Farm, Indian Grassland and Fodder Research Institute, Jhansi. Each accession was evaluated in a plot of two rows of 4 m length at 0.40 m apart. The observations were recorded on 12 metric traits at maturity of the crop. Phenotypic and genotypic coefficient of variation, heritability and genetic advance were computed as per method of Johnson *et al.* (1955). Phenotypic correlation coefficient was calculated (Searle, 1961) and path analysis was done by the procedure given by Dewey and Lu (1959).

Results and Discussion

The analysis of variance revealed significant differences among the accessions. The data on seed yield and its contributing traits, range, mean, phenotypic (PCV) and genotypic (GCV), coefficient of variation, heritability and expected genetic advance are presented in Table 1. Considerable range in variation was observed for all the characters. Phenotypic coefficients of variation values showed relatively high values than corresponding genotypic coefficients of variation for all the traits under study. It indicated the effects of environment in the expression of traits. The PCV, which gives a picture of the extent of phenotypic variability in the population, ranged from 7.31 to 21.79 per cent for various traits. The PCV was moderate for characters like number of kernels per row (21.79%) followed by shank diameter

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Table 1. Variability parameters for seed yield and component traits

Character	Range	Mean	PCV (%)	GCV (%)	h^2 (%) (Broad sense)	GA (% of mean)
Days to 50% silking	43.00 – 59.22	47.95	7.31	5.41	54.80	8.26
Plant height (cm)	148.44 – 268.93	190.17	11.78	7.22	37.60	9.12
Number of leaves/plant	9.81 – 17.44	11.95	10.85	7.38	46.30	10.38
Dry fodder yield/plant	41.57 – 170.29	93.46	14.78	11.07	56.10	17.09
Days to maturity	70.00 – 119.33	81.62	8.66	7.75	80.10	14.29
Cob length (cm)	11.87 – 21.34	15.73	14.46	7.81	29.10	8.71
Cob width (cm)	3.06 – 3.90	3.48	8.28	0.98	1.40	0.29
No. of kernel/ row	10.00 – 14.74	12.36	12.51	5.12	16.70	4.29
No. of kernels/ row	19.59 – 40.42	30.62	21.79	12.60	33.40	15.02
Shank diameter (cm)	0.98 – 1.62	1.25	19.15	5.87	9.40	4.00
Kernel length (cm)	0.75 – 1.02	0.86	9.94	4.02	16.40	3.49
Kernel width (cm)	0.74 – 0.99	0.83	10.51	3.43	10.70	2.41
Test weight (g)	14.53 – 25.73	19.93	10.54	6.05	33.00	7.18
Seed yield/plant (g)	126.21 –261.61	184.51	15.19	9.97	43.10	13.48

Residual = 0.2981; r = Phenotypic correlation with seed yield

(19.15 %), seed yield per plant (15.19 %) and cob length (14.46 %). Rest of the characters showed low values of PCV.

Genotypic coefficient of variation, which gives a picture of the extent of genetic variability in the population, ranged from 0.98 to 12.60 per cent. Maximum GCV was found for number of kernels per row and seed yield per plant. Thus, these traits further offered scope for genetic improvement. The remaining traits, however, showed low values of GCV. From the study of PCV and GCV, the number of kernels per row, seed yield per plant and cob length were found to be the most important characters. These results were largely in accordance with those reported by Satyanarayna and Sai Kumar (1995). With the help of genotypic coefficient of variation alone, it is not possible to determine the amount of heritable variation. Heritable variation can be found out with greater degree of accuracy when heritability in conjunction with genetic advance is studied. Hence, both heritability and genetic advance will determine to get a clear picture of the scope of improvement in various characters through selection. Highest values for heritability was found for days to maturity and days to 50% silking while it was moderate to seed yield per plant, plant height, number of kernels per row, test weight and cob length. Rest of the traits were showing low values of heritability. Similarly, highest values for genetic advance were observed for seed yield per plant and plant height while, it was moderate for days to maturity. Remaining characters showed low values of genetic advance. These findings are in conformity with the previous findings of Sviridov (1979), Claudio and Patricio (1988), El-Harary (1989), Arha *et al*. (1990), Pischedd and Magoja (1990), Mani and Bisht (1996) and Tusuz and Balabanli (1997)**.** From the study of heritability and genetic advance, days to maturity, seed yield per plant and plant height to be the most important characters for improvement through selection. Mani and Bisht (1996) reported high heritability along with high genetic advance for days to 50% silking, seed yield and cob length while it was moderate for plant height.

The phenotypic correlation coefficients for 11 metric traits in maize (Table 2) revealed that test weight, number of kernels per row, kernel width, kernel length, shank diameter and cob length, exhibited positive and significant association with the seed yield per plant. Similar results with regard to correlation coefficient of seed yield with test weight, number of kernels per row and cob length have been reported by Singh and Singh (1993), Rahman *et al*. (1995), Wang *et al*. (1997) and Rana *et al*. (2000). Therefore, these characters should be kept in mind while making selection for improvement in seed yield of maize. Among other component traits, test weight had positive and significant correlation with kernel length, days to 50% silking, kernel width, days to maturation, plant height and seed yield per plant. Number of kernels per row showed positive and significant correlation with seed yield and its contributing traits like cob length while kernel width exhibited positive and significant correlation with kernel length, seed yield per plant and cob width. Kernel length had significant positive association with seed yield, test weight, kernel width, cob width, days to maturity, plant height and days to 50% silking. Shank diameter showed positive and

Table 2. Estimates of phenotypic correlation coefficients among various seed yield characters

Characters	Days to maturity	Plant height (cm)	Cob length (cm)	Cob width (cm)	No. of kernel row	No. of kernels/ row	Shank diameter (cm)	Kernel length (cm)	Kernel width (cm)	Test weight (g)	Seed yield/ plant
Days to 50% silking	0.815	0.445**	-0.102	0.050	-0.124	-0.241*	-0.086	0.238*	0.156	0.531**	-0.032
Days to maturity		0.524	-0.062	0.037	-0.089	-0.282**	-0.074	0.302**	0.142	0.503**	-0.022
Plant height			0.054	0.068	-0.124	-0.093	-0.001	0.268**	0.118	0.472**	0.118
Cob length				0.127	-0.003	0.534**	0.336**	0.006	0.090	-0.010	0.222*
Cob width					0.368**	0.055	0.157	0.359**	0.211*	0.145	0.168
No. of kernel rows						0.039	0.090	0.025	-0.370**	-0.201*	-0.052
No. of kernels/ row							0.141	-0.073	-0.096	-0.229*	0.319**
Shank diameter								0.027	0.071	0.052	0.264**
Kernel length									0.509**	0.539**	0.276**
Kernel width										0.513**	0.295**
Test weight											0.410**

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

significant association with seed yield and its contribution traits like cob length whereas cob length exhibited positive and significant correlation with yield and its related traits such as number of kernels per row and shank diameter.

The path coefficient analysis carried out at phenotypic level (Table 3) including along with important fodder yielding traits like number of leaves per plant and dry fodder yield per plant and some seed yield contributing traits with positive direct effect was shown by test weight (0.5451) and number of kernels per row (0.4553) followed by shank diameter (0.1930). Therefore, these traits can be found rewarding for increasing seed yield. Direct positive contribution of kernels per row has been reported by Singh and Major (1993) and Rana *et al.* (2000) whereas for number of kernels per row and 1000-seed weight by Debnath and Khan (1991). Characters like number of leaves per plant, cob length and dry fodder yield per plant had negative direct effect on seed yield, on the contrary, Rahman *et al.* (1995) revealed that cob length was the main contributor to seed yield.

Further, results indicated that test weight had negative direct effect on yield *via* number of kernels per row and number of leaves per plant, shank diameter showed substantial indirect contribution to yields through number of kernels per row, kernel width showed positive contribution to yield directly and indirectly *via* test weight. Cob length had indirect significant positive effect on yield through test weight. Kernel length had significant direct effect on yield. It also showed considerable positive effects on yield indirectly through test weight.

In the light of above findings, it may be concluded that an ideal plant type in forage maize for seed yield could be described as one having more number of kernels per row, test weight, cob length and shank diameter. The improvement and selection based on these characters might result in increase in seed yield in forage maize.

Acknowledgement

Financial and scientific assistance received from NATP (Plant Biodiversity) provided by NBPGR, New Delhi, is gratefully acknowledged.

Table 3. Path coefficient analysis of various characters contributing to seed yield

Characters	Days to 50% silking	No. of leaves/ plant	Dry fodder yield/ plant	Days to maturity	Cob length	Cob width	No. of kernels/ row	Shank diameter	Kernel length	Kernel width	Test weight	r
Days to 50% silking	-0.0637	-0.0462	-0.0382	0.0526	-0.0132	0.0112	0.0276	0.0092	0.0078	0.0058	0.2672	0.216*
No. of leaves/ plant	-0.0326	–0.1011	-0.0237	-0.0216	-0.0047	0.0044	-0.0346	0.0073	0.0002	0.0094	0.3167	0.174
Dry fodder yield/ plant	-0.0422	-0.0635	-0.0377	-0.0118	-0.0155	0.0045	0.0027	0.0135	0.0002	0.0121	0.3336	0.250*
Days to maturity	-0.0168	-0.0562	-0.0127	-0.0264	-0.0118	0.0067	0.0073	0.0162	0.0012	0.0138	0.0682	0.267*
Cob length	-0.0230	-0.0060	-0.0074	0.0016	**-0.0791**	0.0056	0.2431	0.0649	0.0000	0.0064	-0.0055	0.222*
Cob width	-0.0078	-0.0102	-0.0039	-0.0226	-0.0100	**0.0438**	0.0250	0.0303	0.0003	0.0137	0.0790	0.168
No. of kernels/ row	-0.0248	0.0077	-0.0002	0.0178	-0.0422	0.0024	**0.4553**	0.0272	-0.0001	-0.0062	-0.1248	0.319**
Shank diameter	-.0.0094	-0.0038	-0.0026	0.0286	-0.0266	0.0069	0.0642	**0.1930**	0.0000	0.0046	0.0283	0.264**
Kernel length	-0.0198	-0.0270	-0.0119	-0.0073	-0.0005	0.0157	-0.0332	0.0052	**0.0008**	0.0331	0.2938	0.276**
Kernel width	-0.0056	-0.0146	-0.0070	-0.0112	-0.0078	0.0092	-0.0437	0.0137	0.0004	**0.0651**	0.2796	0.295**
Test weight	-0.0168	-0.0587	-0.0231	-0.0084	0.0008	0.0063	-0.1043	0.0100	0.0004	0.0334	**0.5451**	0.410**

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Near Infrared Spectroscopy (NIRS): A tool for Quality Evaluation of Intact Safflower Germplasm

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A key element of successful development of new cultivars is availability of inexpensive and rapid methods for measurement of fatty acids in seeds. Oilseeds are important sources of vegetable oils. Genetic variation for fatty acid composition is essential for genetic improvement of the oil quality and developing new cultivars. Screening of the large number of germplasm collections requires use of non-destructive analytical technique. About 400 accessions of the safflower were scanned by NIRS as intact seed, and their reference values regressed against different spectral transformations by modiûed partial least squares regression. A calibration set of thirty two accessions (n=32) was analysed by both NIRS and gas-liquid chromatography (GLC) and calibration equations for the major fatty acids were developed. Equation was checked with external validation set of 30 samples. Calibration was focused on the possibility of screening seed samples of different composition of oleic acid (C18:1) and linoleic acid (C18:2) using NIRS analysis.Calibration equation demonstrated a close relationship between NIRS and GLC data for oil (r^2=0.891), palmitic (r^2=0.940), stearic (r^2=0.921), oleic (r^2=0.780) and linoleic acid (r^2=0.939). The results indicated that NIRS could be used to rapidly determine the fatty acid composition in rapeseed seeds in the breeding programmes for high quality rapeseed oil. The results demonstrated that NIRS is a non-destructive, reliable and rapid selection tool for oil quality evaluation. We concluded that a reliable estimation of oil content, palmitic acid, stearic acid, oleic acid and linoleic acid content in intact seeds of safflower is possible by using NIRS technique.

Key Words: Fatty acids, Near Infrared Spectroscopy, Oil content, Safflower

Introduction

Safflower (*Carthamus tinctorius* L.), a member of the family of the Asteraceae, is one of the oldest cultivated crops. Apart from the use as edible oil, safflower is a crop for multiple purposes. Dyes extracted from florets can be used as natural food colour or to tint natural cosmetics. Safflower has very valuable oil for human nutrition, because of high contents of polyunsaturated fatty acids, especially linoleic acid (Honermeier, 2006). Safflower seed oil content varied from 20% to 45% (Belgin *et al.*, 2007). Safflower oil contains about 71% to 75 % linoleic acid and 16% to 20% oleic acid followed by palmitic and stearic acids. Improvement of nutritional and/or functional properties of Safflower oil by modiûcation of safflower fatty acid (FA) composition is a current objective of plant breeders. Regardless of the target, identification and tracking of traits is a major element of plant breeding. Therefore, availability of inexpensive and rapid methods for determination of fatty acid composition of seed samples is a key element of success for development of new grain cultivars.

Research papers published over the last decade demonstrated applicability of NIR spectroscopy for FA profiling in oilseeds. Calibration models for single rapeseed developed by Velasco *et al.* demonstrated comparatively close relationships between GLC measurements and those of NIR spectroscopy for oleic (r^2= 0.85, calibration set size n = 530) and erucic (r^2= 0.88, n = 219) FA. However, no reliable correlation existed for linoleic (r^2= 0.56, n = 530) and linolenic (r^2= 0.53,n = 530) acids. An earlier experiment with bulk rapeseeds conducted by Velasco and Becker resulted in excellent cross validation results for oleic, linoleic, linolenic, and erucic acids (r^2 = 0.95–0.98, n = 220). In contrast, determination coefficients for palmitic, stearic, and eicosenoic acids in bulk rapeseeds were not as high: 0.76, 0.62, and 0.69, respectively (all n= 220).

In safflower, the predictive ability of NIR spectroscopy for FA analysis is not well documented. The objectives of this study were to investigate the applicability of NIR for analysis of FA composition in whole safflower

Materials and Methods

Plant Materials

Four hundred accessions of safflower received from Germplasm Evaluation Division, NBPGR, New Delhi were used to develop a NIRS prediction model for the determination of oil quality parameters.

Total Oil Content of Seed

The safflower seeds were dried to 4-5% moisture level in oven at 108°C for 16 to 18 h. The oil content of the seed samples were determined by a non-destructive

method using a Newport NMR analyser (Model-4000) from Oxford Analytical Instruments Ltd. U.K. after calibrating with pure safflower oil.

Fatty Acid Analysis by Gas Liquid Chromatograph (GLC)

Samples of safflower seeds were freshly grounded (Remi homogenizer) and weighed so that 40 mg oil are obtained when extracted with 10 ml solvent mixture consisting of chloroform: hexane:methanol (8:5:2 v/v/v). The extracts obtained were dried at 60°C in nitrogen gas for 30 min. Methyl esters of oil samples were prepared according to the method of Neff *et al*. (1994) with slight modifications. 1µl of the hexane extract was injected into a highly polar HP Innowax capillary column of 30m length (inner diameter: 0.32m, film thickness: 0.5 µm, split: 1:80). A Hewlett Packard gas chromatograph, model 6890 equipped with flame ionization detector (FID) was used. The injector and detector temperatures were 260°C and 275°C respectively. Oven temperature was programmed from 150°C holding at 1 min. to 210°C at the rate of 15°C/min., followed by 210°C to 250°C at the rate of 5°C/min. for 12 min. Peaks of fatty acid methyl esters were identified by comparing their retention time with that of the known standards, run under similar separation conditions, peak integration was performed applying HP3398A software.

NIR Reflectance Analysis

Collection of Spectra

About 2 g intact seed of safflower were scanned on a Monochromator NIR Systems Model TR-3712-6 (Foss Tecator Near Infrared Analyzer Systems: Silver Springs MD 20904, USA) in reflectance mode. The reflectance spectra (Log 1/R) from 400 to 2500 nm were recorded at 2 nm interval.

Calibration and Validation

Calibration models were developed on the entire dataset (n=400) using cross validation. Further, from the overall set, samples were selected using the algorithms available in the WinISI (version 3.10) (Infrasoft International, Port Matilda PA, USA) software package (Shenkand Westerhaus,1993) where 32 samples were used as the training or calibration set, while the remaining 30 as the external validation set for testing the calibration models.

Calibration was performed by using modified partial least square (MPLS) on the range from 400 to 2500 nm. The log 1/R spectra were transformed into their first and second derivative and Detrend scatter correction (Barnes *et al*, 1989) was computed at the gaps of 4 nm and smoothing over segments of length of 4 nm.

Calibration statistics calculated included standard error of calibration (SEC) and coefûcient of determination (R^2). The equations were then validated using the external set of 30 accessions to assess standard error of performance (corrected for bias) (SEP(C)) and coefûcient of determinations (r^2). The prediction accuracy of the models was tested on the validation set using the root mean square of the standard error of prediction (RMSEP), bias and the coefûcient of correlation (R) (Fearn, 2002, Williams, 2001).The residual predictive deviation (RPD=SD/SECV), deûned as the ratio between the standard deviation of the population (SD) and the SECV for the NIR predictions, is a useful statistic that is often applied to evaluate how well a calibration model can predict chemical data (Fearn, 2002; Williams, 2001).

Results and Discussion

Spectral Analysis

The raw NIR reflectance and second derivative spectra of intact seed samples are shown in Fig. 1. The main absorption bands are observed at 1214 nm related to C-H stretching 2nd overtone (-CH_2), 1496 nm related to C-H stretching 1st overtone, 1724 nm related to CO (oil) and C-H stretching 1st overtone (-CH_2), 1936 nm related to OH bending 2nd overtone (water), and 2308 nm related to C-H bending 2nd overtone (oil). The information of functional group in spectrum was searched from WinISI software. Lipid has absorption band around 1360 nm, 1725 nm, 1760 nm, 2140 nm, 2190 nm, 2310 nm, 2323 nm and 2347 nm. Some of these absorption bands can be seen 1356 nm, 1388 nm, 1508 nm, 1720 nm, 2225 nm and 2290 nm due to lipid reflected in chemical structure of the constituent. The overall spectrum shows strong absorption bands related with oil and water, and is similar to those of other oil crops such as perilla, peanut, soybean, and sesame, especially, in near-infrared region (Choung *et al*., 2005; Kim *et al*., 2006). The second derivative spectra had a trough corresponding to each peak in the original spectra, removing the overlapping peaks and baseline effects (Osborne *et al.,* 1993). The average spectrum of the second derivative (Fig. 1) showed absorption bands at 1212, 1726, 1760, and 2306 nm related to hydrocarbon (-CH) in the NIR region.

Calibration Models for Fatty Acid Composition

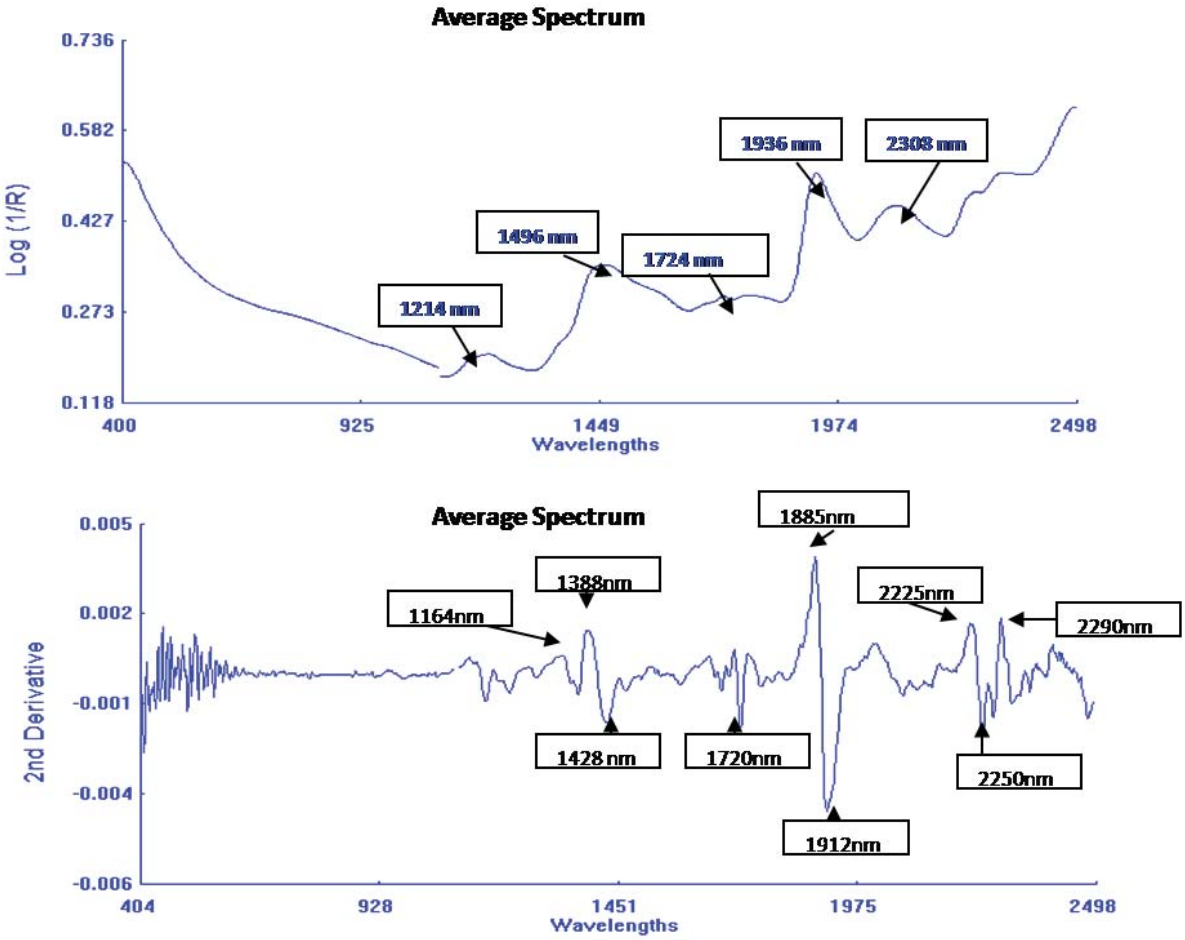

Fig. 1: Raw spectrum (log 1/R; A) and second derivative (B) of NIRS average spectrum of intact seeds of safflower

Since oil quality is a significant concern, particularly for the content of oleic and linoleic acids, which are considered to be good sources for human body. Several workers have reported the oil content and FA profile of safflower oil. The oil content in safflower seed ranged from 20% to 45% (Raie *et al.*, 2006, Belgin *et al.*, 2007). FA composition of oil can be an indicator of its stability, physical properties, and nutritional value. The calibration equations for all the constituents using mathematical treatment 2,4,4,1 were developed. The MPLS regression model in the whole NIR spectra range (400-2500 nm) using the second derivative transformation with scatter correction (SNVD) of raw reflectance spectra yielded the equations of each FA composition showing higher values of R^2 (0.960-0.971) indicating and the equations could be used for screening the FA composition in intact seeds of rapeseed. R^2 means the contribution ratio of the calibration equation to the whole vibrations, and if R is higher than 0.7, the calibration equation explains more than 50% of the component vibrations. Table 1 shows the calibration and validation statistic of the best model.

The equation exhibited the r^2 values of 0.891 for oil, 0.940 for palmitic, 0.921 for stearic, 0.780 for oleic, and 0.939 for linoleic acid. The established mean value for oil content is 33.23% with RPD value 3.0. Similarly the established mean value for palmitic, stearic, oleic and linoleic are shown in Table 1. The higher the value of the RPD the greater the probability of the model to accurately predict the chemical composition of samples outside the calibration set. It was reported that an RPD value greater than three (range 3.1–4.9) is considered fair and recommended for screening purposes, an RPD value greater than ûve (range 5–6.4) is considered good for quality control (Fearn, 2002; Williams, 2001). The RPD values were 4.06, 3.58 and 4.02 respectively for stearic acid, palmitic acid and linoleic acid, indicating the good reliability of the calibration equation. Figure

Table 1. Calibration and external validation statistics for intact safflower germplasm for oil and different fatty acid

	Calibration				External-validation			
	Min	Max.	Mean	SEC	R^2	SEP(C)	r^2	RPD
Oil	30.25	36.78	33.52	0.29	0.92	0.45	0.891	3.00
Palmitic acid	3.44	9.04	6.24	1.18	0.96	0.27	0.940	4.06
Stearic acid	0	7.03	3.44	0.23	0.96	0.313	0.921	3.58
Oleic acid	5.37	31.05	18.21	0.72	0.97	1.50	0.780	2.06
Linoleic acid	59.39	80.03	72.21	0.73	0.97	0.75	0.939	4.02

2 represented laboratory reference values against NIRS predicted values in the validation set for individual FA composition (oil, palmitic, stearic, oleic and linoleic), showing also the relationship between NIRS and reference.

The correlation of co-efficient showed highly significant negative correlation between oleic and linoleic acids (Table 2). Correlation coefficient greater than 0.71 or smaller than -0.71 have been suggested to be biologically meaningful (Skinner *et al.*, 1999). In the literature it is reported that oleic acid concentration is controlled by its conversion to linoleic acid, probably as a result of the enzymatic activity of oleic desaturase. A significant negative correlation was observed between oleic with linoleic and oil content, linoleic with stearic acid. Palmitic acid had a significant correlation with oil content and stearic acid.

Most oil and fatty acid equations developed for safflower seed showed sufûcient accuracy for using this technique as a valuable tool for the analysis of these components. The R^2 shown by the equations for oil and fatty acid determination in safflower seeds, indicated from good to excellent quantitative information (Shenk and Westerhaus, 1996). On the other hand, it was observed that the prediction statistics for all the individual

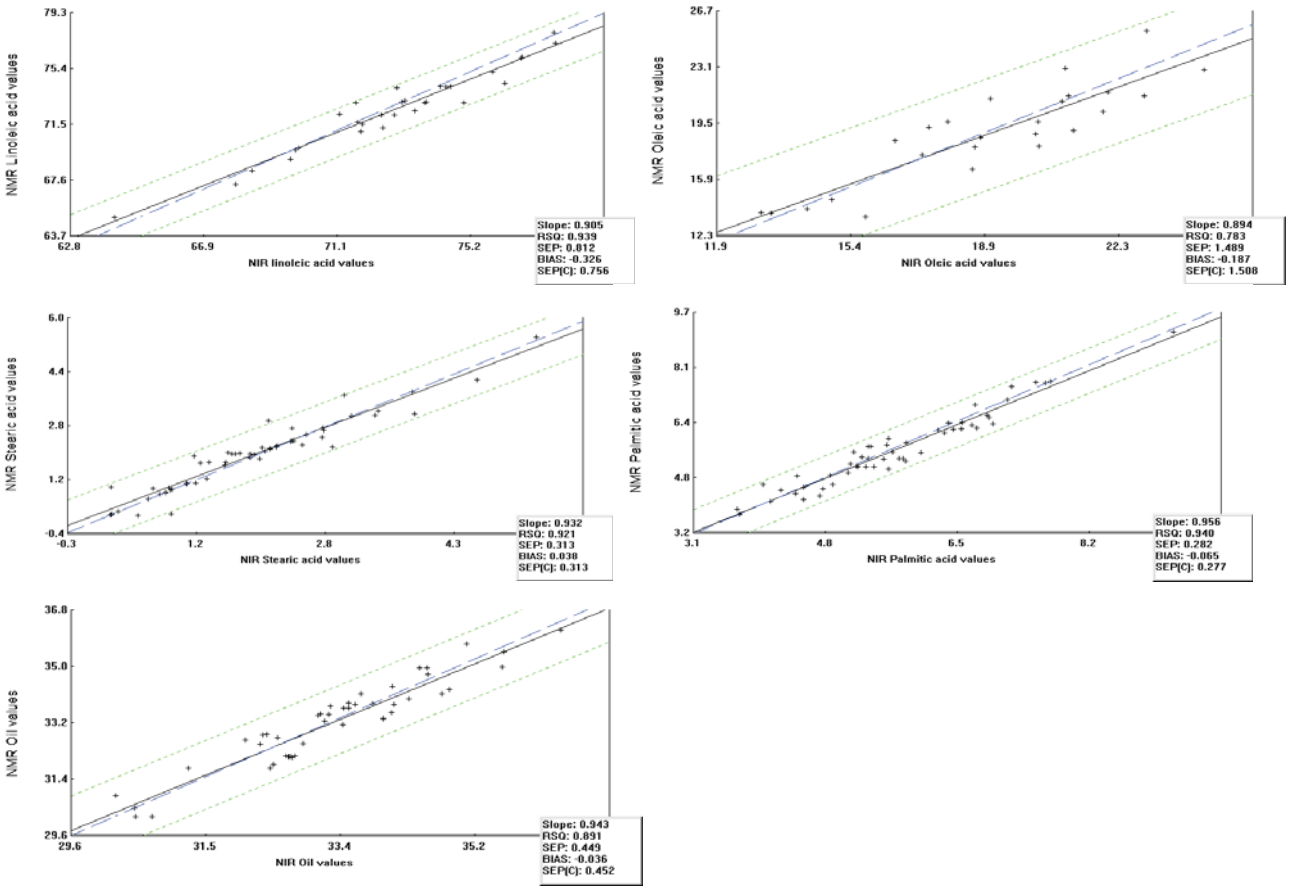

Fig. 2: Scatter plots of NIRS vs. reference values for oil and fatty acids in the cross validation set (n=32) of intact seed samples of safflower

Table 2. Correlation co-efficient between oil content and the fatty acid concentrations in safflower[a]

	oil	palmitic	stearic	oleic	linoleic
oil	1	0.27*	0.082	–0.12**	–0.015
palmitic		1	0.22*	–0.36*	0.025
stearic			1	–0.034	–0.26*
oleic				1	–0.91*
linoleic					1

[a]Correlation shown in bold face type are significant at 1%(*) and at 5%(**) level of significance

constituents are having high values of coefficient of determination (r^2) and the model developed in this study had higher RPD value (>3.0) for most of the constituents, which actually used to evaluate the reliability of calibration models and thus being useful for screening (Williams and Sobering, 1996).

Thus, we can conclude that the NIRS equations developed over safflower germplasm have allowed accurate predictions of multiple quality components in a simultaneous way.

Thousands of seed samples are generated by plant selection and breeding programmes which commonly look to develop progress in several traits simultaneously. Low cost, rapid methods are required to support such programs. Reflectance spectroscopy makes NIRS an ideal tool for screening for quality traits in safflower plant breeding programmes.

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Genetic Variation in Nut and Kernel Quality Characteristics of Walnut Selected from District Budgam of Kashmir Valley

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An intensive survey of walnut tree was conducted in Budgam district of Kashmir valley during 2006. Forty three bearing trees of walnut were selected across the district and nuts from selected seedling trees have been characterized for different in-shelled and shelled characters in laboratory. Most of the accession were round in shape, medium smooth in shell texture and light medium in shell colour whereas, rest of in-shelled characters had varied response. Regarding kernel characters only fourteen genotypes had well filled kernels and most of the accession had light to dark kernel colour. Kernel percentage was recorded highest in accession QCL6W-39 (58.00%) and lowest of 25.00% in the accession QCL6W-5 and recorded highest (21.8%) contribution towards diversity as compared to other metric traits. Highest coefficient of variation was observed for Kernel Weight (133.37%) followed by Nut Weight (54.59%) and Kernel percentage (35.54%). The variation for Nut Length, Diameter at Cheek and Suture were 16.65, 15.15 and 11.86 respectively. From this survey, it is concluded that the accession no. QCL6W-7, QCL6W-8, QCL6W-16, QCL6W-18, QCL6W-23, QCL6W-35, QCL6W-36, QCL6W-38, QCL6W-39 and QCL6W-44 can be earmarked for utilization in future breeding programme for development of walnut varieties having better qualitative and quantatives characters.

Key Words: Characterization, Evaluation, Kernel, Nut, Walnut

Walnut is principal nut crop of Jammu and Kashmir as it accounts for 80 per cent of total walnut production of country with an average productivity of 1.4 t/ha (Bhat and Ahmad, 2001), which is very low as compared to Iran (3.2 t/ha) and USA (2.64 t/ha). Indian walnut occupied a special position which have 5 per cent share in the international market and rank among five top producing countries in the world (Ahmad and Simnani, 2001). Almost all existing plantation of walnut in North-West Himalaya are of seedling origin which posing problem of late bearing, giant size of tree and variation in the shape, size, colour and quality characters of nut and kernel that ultimately hampers the grading of nut and kernel for export (Ahmad *et al.* 2007). The North-West Himalayan region of India is endowed with very rich genetic diversity in walnut. Nevertheless, the propagation techniques have not been standardized yet. As a result farmers prefer to raise walnut sapling through seed which does not give true-to-type planting material (Iqbal *et al.*, 2004) and leads to the variability in nut and kernel characters. Bhat *et al*. (2000) reported that all walnut plantations in Jammu and Kashmir owe their origin from non-descriptive type of seedling and therefore, are extremely heterogeneous in important quality attributes like nut size and colour of kernel. Under All India Co-ordinated Improvement Programme on Nut Crops, various walnut accession were collected which ultimately resulted in release of two varieties of walnut, namely, Sulaiman and Hamdan from SKUAST-K, Shalimar (Bhat and Ahmad, 2001). In order to further increase the varietal spectrum of walnut for different objectives, an intensive survey was conducted in district 'Budgam' where almost all plantation of walnut are existed on *karawa* land (upland plateau) and is totally rainfed. Keeping in view the above fact, an attempt was made to exploit the existing genetic diversity of walnut for having desirable yield and superior kernel quality attributes for use in future breeding programme.

Materials and Methods

Survey of walnut tree was conducted in Budgam district of Kashmir valley during August to September 2006, situated at altitude ranges from 1700 to 2300 msl. Forty-three bearing trees of walnut were selected across the district and individual tree was assigned separate accession number as QCL6-W-1 to QCL6-W-44. Nut samples from every accession have been evaluated for different in-shelled and shelled characters in laboratory. The collected samples were dehulled properly, washed and dried in shade for 20 days. Random sample of 10 nuts were selected from each accession for study of unshelled and shelled traits, namely, nut shape, shell texture, shell

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colour, shell strength, shell seal, shell integrity, kernel filling, kernel colour and ease of kernel removal as described in the descriptor of walnut provided by IPGRI (Anonymous, 1994). The dried sample from each accession was randomly taken for study of various metric nut traits, namely, shell thickness (mm), diameter at cheek (mm), diameter at suture (mm), nut length (mm) and kernel length (mm) by the use of Vernier Caliper and nut weight (g) and kernel weight (g) work out by highly sophisticated digital balance. The kernel colour was recognized as per the classification chart (Anonymous, 1999) and kernel percentage was calculated as per the method given by Hendricks *et al.* (1985). The data was analyzed in R-software as suggested by Gomez and Gomez (1984).

Results and Discussion

The data pertaining to various unshelled and shelled traits of seedling walnut trees showed wide variation for all the studied traits (Table 1). The nut shape of walnut accession of district Budgam ranged from round to broad elliptical. Most of the accession were round in shape, whereas accession QCL6W-1, 2, 14, 20, 21, 22, 37, 39 and 44 were broad elliptical. Seven accessions QCL6W-6, 8, 13, 33, 34, 38 and 42 were ovate shaped, three accessions QCL6W-18, 25 and 36 having long

Table 1. Qualitative characters of walnut genotypes from district Budgam

Accession Number	Nut shape	Shell Texture	Shell Colour	Shell Strength	Shell Seal	Shell Integrity	Kernel Filling	Kernel Colour	Ease of Removal
QCL6-W-1	Broad Elliptic	Rough	Light	Weak	Weak	Incomplete	Moderate	Light	Moderate
QCL6-W-2	Broad Elliptic	Medium	Medium	Intermediate	Intermediate	Intermediate	Moderate	Medium	Difficult
QCL6-W-3	Round	Medium	Medium	Intermediate	Intermediate	Intermediate	Moderate	Light	Difficult
QCL6-W-4	Round	Rough	Dark	Intermediate	Intermediate	Incomplete	Well	Medium	Difficult
QCL6-W-5	Round	Smooth	Light	Intermediate	Strong	Intermediate	Moderate	Light	Moderate
QCL6-W-6	Ovate	Medium	Medium	Intermediate	Strong	Intermediate	Well	Medium	Difficult
QCL6-W-7	Round	Medium	Medium	Weak	Weak	Complete	Well	Medium	Easy
QCL6-W-8	Ovate	Smooth	Medium	Weak	Weak	Intermediate	Well	Light	Easy
QCL6-W-9	Round	V. Rough	Medium	Intermediate	Very Strong	Incomplete	Poor	Medium	Difficult
QCL6-W-10	Round	Smooth	Medium	Intermediate	Intermediate	Complete	Well	Dark	Moderate
QCL6-W-11	Round	Rough	Light	Intermediate	Intermediate	Complete	Moderate	Dark	Difficult
QCL6-W-12	Round	V. Rough	Dark	Strong	Very Strong	Incomplete	Moderate	Medium	Difficult
QCL6-W-13	Ovate	Rough	Medium	Strong	Strong	Intermediate	Moderate	Light	Difficult
QCL6-W-14	Broad Elliptic	Medium	Light	Intermediate	Strong	Intermediate	Moderate	Light	Moderate
QCL6-W-15	Cordate	Rough	Medium	Intermediate	Strong	Intermediate	Poor	Medium	Difficult
QCL6-W-16	Elliptic	V. Smooth	Medium	Intermediate	Weak	Complete	Moderate	Light	Moderate
QCL6-W-17	Round	Medium	Medium	Intermediate	Strong	Intermediate	Well	Medium	Moderate
QCL6-W-18	Long Trapezoid	Medium	Medium	Intermediate	Weak	Intermediate	Well	V. Light	Easy
QCL6-W-19	Round	Medium	Light	Strong	Very Strong	Intermediate	Moderate	Light	V. Difficult
QCL6-W-20	Broad Elliptic	Rough	Dark	Intermediate	Intermediate	Incomplete	Moderate	Medium	Moderate
QCL6-W-21	Broad Elliptic	Medium	Medium	Strong	Strong	Intermediate	Moderate	V. Light	V. Difficult
QCL6-W-22	Broad Elliptic	Medium	Dark	Strong	Strong	Intermediate	Moderate	V. Light	Difficult
QCL6-W-23	Short trapezoid	Smooth	Medium	Intermediate	Intermediate	Intermediate	Well	Light	Moderate
QCL6-W-24	Round	Medium	Light	Intermediate	Intermediate	Intermediate	Moderate	V. Light	Difficult
QCL6-W-25	Long Trapezoid	Medium	Medium	Intermediate	Weak	Intermediate	Moderate	Medium	Difficult
QCL6-W-26	Round	V. Rough	Medium	Weak	Very Strong	Intermediate	Moderate	Dark	Easy
QCL6-W-27	Round	Medium	Dark	Strong	Very Strong	Incomplete	Moderate	Amber	Moderate
QCL6-W-28	Round	Smooth	Medium	Intermediate	Very Strong	Intermediate	Moderate	Medium	Easy
QCL6-W-29	Round	V. Rough	Dark	Strong	Strong	Intermediate	Moderate	Medium	Difficult
QCL6-W-31	Round	Smooth	Light	Weak	Very Weak	Complete	Moderate	Dark	Easy
QCL6-W-32	Round	Medium	Medium	Papery	Intermediate	Complete	Moderate	Light	Moderate
QCL6-W-33	Ovate	Smooth	Light	Intermediate	Strong	Intermediate	Moderate	Dark	Difficult
QCL6-W-34	Ovate	Rough	Medium	Strong	Very Strong	Incomplete	Well	Light	Moderate
QCL6-W-35	Round	Medium	Medium	Weak	Strong	Intermediate	Well	Light	Moderate
QCL6-W-36	Long Trapezoid	Medium	Light	Weak	Weak	Intermediate	Well	V.Light	Moderate
QCL6-W-37	Broad Elliptic	Medium	Light	Intermediate	Strong	Intermediate	Moderate	V.Light	Difficult
QCL6-W-38	Ovate	Rough	Light	Weak	Weak	Intermediate	Well	V.Light	Easy
QCL6-W-39	Broad Elliptic	Smooth	Dark	Intermediate	Intermediate	Complete	Well	Light	Moderate
QCL6-W-40	Round	Rough	Medium	Strong	Intermediate	Incomplete	Moderate	Medium	Difficult
QCL6-W-41	Short Trapezoid	Smooth	Light	Strong	Strong	Intermediate	Moderate	Light	Difficult
QCL6-W-42	Ovate	Medium	Dark	Intermediate	Very Strong	Intermediate	Moderate	Medium	Moderate
QCL6-W-43	Round	Medium	Light	Intermediate	Intermediate	Complete	Moderate	Light	Moderate
QCL6-W-44	Broad Elliptic	Smooth	Medium	Weak	Weak	Intermediate	Well	Medium	Moderate

trapezoid shape and, two accessions QCL6W-23 and 41 were having short trapezoid shape. One accession QCL6W-15 had cordate shape. The variation in the nut shape of walnut is due to its seedling origin, which is highly heterozygous in nature and such type of variation in nut shape has also been reported by various workers namely Panday and Sinha (1984), Bhat *et al.* (1999) and Sharma and Sharma (2001). About 40-60 % of walnut are sold as inshell in India, hence, the smoothness of the shell and its light colour is most important characteristic which attract consumer and farmers get good return from medium smooth to very smooth nuts. In the present finding, the shell texture observed were medium to smooth shell in almost all accession except one accession *i.e.*, QCL6W-16 which had very smooth shell. Further, light shell colour was recorded in accessions QCL6W-1, 5, 11, 14, 19, 24, 31, 33, 36, 37, 38, 41 and 43, whereas accessions QCL6W-4, 12, 20, 22, 27, 29, 39 and 42 had dark shell colour and rest of the accessions had medium shell colour. Shell strength rangeds from weak (QCL6W-1, 7, 8, 26, 31, 35, 36, 38 and 42) to strong (QCL6W-12, 13, 19, 21, 22, 27, 29, 34, 40 and 41) whereas rest of the accessions were found to be intermediate. Weak shell seal was observed in accessions QCL6W-1, 7, 8, 16, 18, 25, 36, 38 and 44, whereas strong and very strong seal was observed in QCL6W-5, 6, 13, 14, 17, 21, 22, 29, 33, 35, 37, 41 and QCL6W-9, 12, 19, 26, 27, 28, 34 and 42 respectively. Complete shell integrity was found in accession QCL6W-7, 10, 11, 16, 31, 32, 39 and 43, whereas incomplete shell integrity in accessions QCL6W-1, 4, 9, 12, 27, 34 and 40 and rest of the accessions had intermediate shell integrity. These shell characters of nut crops are of utmost important as they determine crack out quality of nuts, bleaching, insect and pest damage, overall consumers acceptability and their market prize. The consumer acceptability is governed by shell texture and shell colour. Sen and Tekintas (1992) used shell colour as one of the parameters to characterize the superior types while as Bhat *et al.* (1999) suggested that the shell strength constitute an important component of nut character and it determines the cracking out quality of walnut and its market prize. As far as kernel filling is concerned, more than half of the selected genotype of walnut is moderately filled (QCL6W-4, 6, 7, 8, 10, 17, 18, 23, 34, 35, 36, 38, 39 and 44) to poorly filled (QCL6W-9 and 15). The kernel colour "very light to light" is considered desirable for consumer acceptability. In the present study, the kernel colour varied from very light to dark in colour. The accessions QCL6W-18, 21, 22, 24, 36, 37 and 38 had very light kernel colour and accessions QCL6W-10, 11and 27 had amber kernel colour, while rest of the accessions have light to dark kernel colour.

The data presented in the Table 2 revealed that wide variation in the metric nut traits of all 43 walnut accessions has been observed. The Shell Thickness varies from 1.28 mm in accession QCL6W-36 to 2.56 mm in accession QCL6W-3 with the average of 1.81 mm and least coefficient of variation of 11.09% was observed. Hence, the shell thickness contribution towards genetic diversity is only 0.87%. The present finding is in contrary to the result of Sharma and Sharma (2001) who have reported 3.54% contribution toward diversity indicating that the little bit more variation in shell thickness in walnut genotype of Himachal Pradesh as compared to Budgam district of Kashmir valley. Diameter at Cheek was recorded to be the highest in QCL6W-40 (45.20 mm) followed by QCL6W-11 (40.53 mm) and lowest was recorded in QCL6W-24 (26.51 mm) with mean of 33.74 mm and this character contributes 16.33% toward diversity. Similarly, the minimum diameter at suture was in accession QCL6W-24 (25.98 mm) and maximum of 41.00 mm in accession QCL6W-12 with the mean of 33.58 mm. The maximum nut length (46.75 mm) was observed in accession QCL6W-42, whereas minimum length in accession QCL6W-43 (29.78 mm) with mean of 38.64 mm. These components of nut are important as they determine the overall nut volume. Similar results were also reported by Bhat *et al.* (1999) and Sharma and Das (2003).

The nut weight is the most important character as it determines the yield and kernel percentage. In this survey, the maximum nut weight was recorded in accession QCL6W-40 (22.11gm) and minimum of 7.76gm in the accession QCL6W-32 having a mean weight of 15.54 gm. The highest kernel weight (10.70gm) was recovered from accession QCL6W-39 and lowest weight (3.41 gm) from the accession QCL6W-24. The maximum coefficient of variation was found in kernel weight which constitutes about 133.37% but the percent contribution towards diversity was only 4.18%. Kernel percentage was recorded highest in accession QCL6W-39 (58.00 %) and lowest of 25.00% in the accession QCL6W-5, with the mean of 45.04% and recorded highest (21.81%) contribution towards diversity as compared to other metric traits. The minimum kernel length was observed in accession

Table 2. Analysis of quantative characters of walnut genotypes from district Budgam

Accession Number	Nut length (mm)	Dia. at cheek (mm)	Dia. at suture (mm)	Shell thickness (mm)	Nut weight (gm)	Kernel weight (gm)	Kernel length (mm)	Kernel percentage (%)
QCL6-W-1	36.53	31.97	31.49	1.36	11.61	5.23	29.22	45.00
QCL6-W-2	35.59	31.71	33.38	1.52	12.15	5.63	25.15	46.00
QCL6-W-3	32.35	29.34	29.67	2.56	10.1	4.44	25.48	44.00
QCL6-W-4	36.77	31.66	30.40	1.49	11.48	5.55	27.46	49.00
QCL6-W-5	34.99	32.56	32.39	1.91	17.35	4.53	28.69	25.00
QCL6-W-6	36.53	35.79	33.41	2.09	13.63	6.55	29.17	49.00
QCL6-W-7	43.32	38.56	37.19	1.62	18.21	9.85	35.14	54.00
QCL6-W-8	42.02	30.93	32.49	2.14	13.29	6.50	34.33	49.00
QCL6-W-9	38.61	35.92	37.91	1.71	13.96	6.43	31.69	47.00
QCL6-W-10	34.24	27.98	28.42	1.72	9.83	4.67	25.33	49.00
QCL6-W-11	40.70	39.40	38.04	1.56	19.54	9.29	32.89	48.00
QCL6-W-12	44.95	38.47	41.00	1.96	18.56	7.49	29.86	41.00
QCL6-W-13	43.96	39.34	36.78	1.85	18.18	8.30	31.93	46.00
QCL6-W-14	32.45	30.88	30.41	1.86	10.64	4.80	23.61	45.00
QCL6-W-15	37.33	39.49	35.90	2.14	16.56	5.48	26.57	34.00
QCL6-W-16	45.11	30.10	31.12	1.46	13.72	6.57	34.40	49.00
QCL6-W-17	37.49	37.56	34.91	1.6	15.28	6.92	28.40	46.00
QCL6-W-18	44.80	36.94	35.97	1.69	17.75	8.52	34.13	49.00
QCL6-W-19	40.12	34.47	34.83	2.34	17.89	7.46	29.66	42.00
QCL6-W-20	38.71	29.35	30.29	1.53	11.32	5.71	29.50	51.00
QCL6-W-21	42.45	37.54	36.40	2.15	19.32	7.65	32.89	40.00
QCL6-W-22	37.95	32.08	34.58	2.04	13.62	5.29	29.06	40.00
QCL6-W-23	37.30	33.09	33.77	1.67	13.08	6.54	29.62	50.00
QCL6-W-24	31.15	26.51	25.98	1.78	7.92	3.41	23.77	44.00
QCL6-W-25	40.64	31.91	32.78	1.61	13.62	5.87	29.85	44.00
QCL6-W-26	39.23	40.53	35.51	2.27	16.58	7.88	29.58	47.00
QCL6-W-27	41.34	40.35	39.47	2.13	21.79	9.30	31.88	43.00
QCL6-W-28	33.24	29.95	30.12	1.71	11.07	5.14	25.58	47.00
QCL6-W-29	36.69	35.54	33.65	1.65	13.69	6.18	29.30	46.00
QCL6-W-31	39.97	37.52	34.66	1.80	15.38	7.03	31.52	46.00
QCL6-W-32	31.68	29.73	28.10	1.35	7.76	3.43	23.75	45.00
QCL6-W-33	46.49	35.89	33.38	1.53	15.99	7.25	34.88	45.00
QCL6-W-34	38.10	33.15	34.54	1.72	13.19	6.75	28.95	52.00
QCL6-W-35	37.45	35.33	35.45	1.82	16.68	9.01	29.04	54.00
QCL6-W-36	44.77	37.26	35.46	1.28	17.59	9.04	34.81	52.00
QCL6-W-37	34.73	29.95	30.97	1.83	11.28	4.83	30.01	43.00
QCL6-W-38	40.79	31.69	31.62	1.29	11.47	5.73	30.52	51.00
QCL6-W-39	40.69	34.78	33.19	1.58	18.66	10.70	34.43	58.00
QCL6-W-40	45.00	45.20	39.41	1.80	22.11	10.41	35.62	47.00
QCL6-W-41	33.00	37.64	34.75	1.83	16.26	7.47	27.49	45.00
QCL6-W-42	46.75	35.79	33.32	1.59	15.36	6.20	33.53	40.00
QCL6-W-43	29.78	27.75	26.28	1.41	7.96	3.76	22.69	47.00
QCL6-W-44	37.59	33.43	34.00	0.83	11.69	6.65	31.83	55.00
Range	29.78-46.75	26.51-45.20	25.98-41.00	0.83-2.56	7.76-22.11	3.41-10.41	22.69-35.14	25.00-58.00
Mean	38.64	33.74	33.58	1.81	15.54	8.63	29.51	45.04
SE Mean	0.81	0.77	0.68	0.60	1.48	2.31	.067	1.19
C.V.	16.65	15.15	11.86	11.09	54.59	133.37	11.23	35.54
S.D	4.08	3.89	3.44	0.30	7.39	11.55	3.35	5.96
Percent contribution	18.71	16.33	16.26	0.87	7.52	4.18	14.30	21.81

QCL6W-43 (22.69 mm) and maximum (35.62 mm) was observed in accession QCL6W-40. These results are in conformity with finding of various workers while working with different cultivars and seedling trees of walnut in different region of India (Panday and Sinha, 1984; Sharma and Sharma, 2001; Bhat *et al*., 1999 and Sharma and Das, 2003).

The genotypic variation of metric traits of studied accessions of walnut are concerned, highest coefficient of variation was observed for kernel weight (133.37 %) followed by nut weight (54.59 %) and kernel percentage (35.54 %). The variation for physical nut length, diameter at cheek and suture were 16.65, 15.15 and 11.86 respectively. Sundouri and Sharma (2005) noted that this variation is due to the seedling origin of bearing trees which exhibits lot of heterozygosity among the seedling tree and may also be due to pleotropic gene effect and environment. From the foregoing

discussion, it is concluded that the accession no. QCL6W-7, 8, 16, 23, 35, 36, 38, 39 and 44 have been earmarked for utilization in future breeding programme for development of walnut varieties having better qualitative and quantative shelled and inshelled characters in terms of shell strength, shell seal, ease of removal, nut weight, kernel weight and kernel percentage. Tree of these five accession may also be used for clonal propagation and to replace existing seedling origin trees by means of top working that help in further improving the quality of shelled and inshelled characters of walnut and their overall contribution in strengthening the varietal spectrum of walnut germplasm.

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SHORT COMMUNICATION

Screening for Resistance Against Northern Corn Leaf Blight (*Exserohilum turcicum)* in Temperate Maize Lines

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Ten early duration maize lines, namely, CM 128, V 327, V 335, V 13, V 128, V 17, V 336, CM 129, V 53 and V 27, were screened against northern corn leaf blight (*Helminthosporium turcicum* or *Exserohilum turcicum*) under field as well as under artificial epiphytotic conditions. Five inbreds, namely, V 335, V 13, V 336, V 53 and V 27 were identified as resistant while rest five, *viz.*, CM 128, V 128, V 327, V 17 and CM 129 were found susceptible. In the pooled disease scores across the three seasons, the highest mean score of 4.0 was recorded for V 128, indicating high level of susceptibility, whereas, lowest mean score of 1.5 recorded for V 335, showed high level of resistance across the locations. The promising inbreds can be utilized as a resistant donor in breeding programme. These inbreds possessing resistance to northern corn leaf blight can be used successfully in developing high yielding early maturing varieties for the hill region.

Key Words: *Exserohilum turcicum*, Maize, Resistance, *Turcicum* leaf blight

The production of the maize in hilly areas (Kumaoun hills) of India is low as compared to the other areas of the nation. The major cause of low yield is Northern corn leaf blight which causes a wide range (28-91%) of yield losses in maize (Sharma and Aujla, 1968; Pant *et al.,* 2000; Singh *et al.,* 2003).

Success of any crop improvement programme depends on the nature and magnitude of genetic variability present in the crop. The effectiveness of selection largely depends on the amount of heritability for traits under study. Therefore, present study was undertaken to reduce the loss from *Turcicum* leaf blight (*Helminthosporium turcicum* pass or *Exserohilum turcicum*) through selecting early maturing resistant maize materials. An attempt has been made to evaluate the variability in present materials of maize.

Turcicum leaf blight is the most common as well as chronic problem of maize in the hills. Passerini, from Italy was first to describe the turcicum leaf blight in 1876. In India, Butler *et al*. (1920), first observed this disease in maize. It is the most prevalent form in all the major maize growing regions of India during rainy (*kharif*) as well as winter (*rabi*) season (Lal, 1991). The disease can substantially reduce the grain yield of maize over a wide range from 28 to 91% (Ullstrup, 1951; Chenulu and Hora, 1962; Sharma and Aujla, 1968; Pant *et al*., 2000). Severe disease conditions prevailing at the time of ear formation may cause total grain loss.

This disease has also been observed to be the most important in the hills, mainly in Jammu and Kashmir, Himachal Pradesh, Sikkim, West Bengal, Meghalaya, Tripura, Assam and Uttarakhand. The symptoms first develop on lower leaves and successively progress to upper leaves of the plant under favourable conditions. In severe disease condition, the entire foliage generally gets killed, giving the appearance of frosted leaves. The ears and kernels are seldom infected, but some lesions do develop in the outer husk. The typical symptoms seen on a susceptible host are long elliptical (4 to 20 cm long and 1 to 5 cm wide), greyish-green to brown (tan) in colour. Spores are produced in the lesions, which are olive-green to black, and usually produce concentric rings, giving the entire spot a target like appearance. Spores from the primary lesions re-infect the host producing secondary cycle of the disease (Partridge, 1997). The presence and absence of this type of lesions are governed by host-pathogen interaction (Carlos, 1987).

Ten maize inbred lines with different genetic background and origin were evaluated against *Turcicum* leaf blight under artificial epiphytotic condition during *Kharif* 1998 and 1999 at Hawalbagh, Almora and *Rabi* 1998-99 at Amberpet, Hyderabad. Heavily infected leaves with *Turcicum* leaf blight were collected during last season and ground to powder and stored at room temperature. The powdered inoculum was inoculated as per procedure. A pinch of the leaf powder was dropped

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into the whorl of each plant, commencing from 20 days after planting. The inoculation was preferably done late in the afternoon till the pre-tasseling stage 4 times at weekly intervals. Spray of spore suspension with spore concentration of $2.5x10^4$/ ml was done on plants, commencing from 20 days after planting till pre-tasseling stage at 5-7 days interval. The disease severity was recorded at flowering stage and dry silk stage in the terms of intensity following the rating scale of 1.0 to 5.0 with 0.5 intermediate rating (Payak and Sharma, 1982). Intermediate ratings between two numbers (1.25, 1.5, 1.75, 2.25, 2.75, 3.25, 3.5, 3.75, 4.25, 4.5 and 4.75) was also recorded. Row-to-row spacing of 60 cm and plant-to-plant of 25 cm was maintained at both the locations. Fertilizer doses @ of 160 kg N, 60 kg P_2O_5 and 40 kg K_2O were applied to the crop at both the locations.

Mean score for *Turcicum* leaf blight recorded during *Kharif* 1998 and 1999 are presented in the Table 1. Mean score of *Turcicum* leaf blight during *Kharif* 1998 ranged from 1.8 (V 53) to 4.0 (V 17) while, during *Kharif* 1999 it varied from 1.9 (V 13) to 4.5 (V 17). The five inbreds, namely, CM 128, V 327, V 128, CM 129 and V 17 exhibited above 3.0 score and were identified as susceptible while rest of five inbreds, V 335, V 13, V 336, V 53 and V 27 with disease of score of less than 2.5, were found to posses resistance. V 17 recorded the maximum disease score of 4.5 during *Kharif* 1999, was highly susceptible, whereas the minimum disease score of 1.8 was recorded for V 53 during *Kharif* 1998, which indicated high level of resistance for *Turcicum* leaf blight.

The disease mean scores for *Turcicum* leaf blight recorded during *Rabi* 1998-1999 are presented in the Table 2. The highest mean score (3.9) was recorded for V 17, while the lowest (1.5) for V 335. Out of ten inbreds tested during the season, five, namely, V 335, V13, V 336, V 53 and V 27 indicated resistance for *Turcicum* leaf blight, while remaining five (CM 128, V 327, V 128, V 17 and CM 129) showed susceptibility.

The disease reaction for *Turcicum* leaf blight was pooled across three seasons in two environments and is presented in the Table 3. The highest mean score of 4.0 was recorded for V 128, indicating highest level of susceptibility and lowest mean score (1.8) was recorded for V 335 indicating highest level of resistance across the environment. The other susceptible inbred lines on the basis of pooled score were, CM 128 (4.0), V 327 (3.7), V 128 (4.0), V 17 (4.1) and CM 129 (3.3), while inbreds having score of 1.8 (V 335), 2.0 (V 13), 2.1 (V 336), 2.0 (V 53) and 2.3 (V 27) were resistant to turcicum leaf blight.

In a similar study, Singh *et al.* (2003), identified 17, 27, 111 and 10 inbred lines developed at Almora as resistant, moderately resistant, susceptible and highly susceptible to *maydis* leaf blight caused by *Bipolaris maydis* (*Cochliobolus heterostrophus*). Their study, which involved about 65 genotypes, also indicated susceptibility of CM 128, V 327, V 128, V 17 and

Table 1. Mean disease reaction of maize inbreds *Turcicum* leaf blight, *Kharif* 1998 and 1999 at Hawalbagh, Almora

No.	Inbred lines	1998	1999	Mean	Type of reaction
1	CM 128	3.5	3.8	3.7	S
2	V 327	3.8	4.1	3.9	S
3	V 335	2.0	2.0	2.0	R
4	V 13	2.3	1.9	2.1	R
5	V 128	3.8	4.1	3.9	S
6	V 17	4.0	4.5	4.3	S
7	V 336	2.0	2.3	2.1	R
8	CM 129	3.0	3.5	3.3	S
9	V 53	1.8	2.0	1.9	R
10	V 27	2.3	2.5	2.4	R

S-susceptible (2.6 to 5.0), R-resistant (1.0 to 2.5)

Table 2. Mean disease reaction of maize inbreds for *Turcicum* leaf blight, *Rabi* 1998-99 at Amberpet, Hyderabad

No.	Inbred lines	1998-99	Type of Reaction
1	CM 128	3.0	S
2	V 327	3.3	S
3	V 335	1.5	R
4	V 13	1.7	R
5	V 128	4.0	S
6	V 17	3.9	S
7	V 336	2.0	R
8	CM 129	3.5	S
9	V 53	2.2	R
10	V 27	2.0	R

S-susceptible (2.6 to 5.0), R-resistant (1.0 to 2.5)

Table 3. Pooled mean disease reaction of maize inbreds *Turcicum* leaf blight (Hawalbagh and Hyderabad)

No.	Inbred lines	1998 (*Kharif*)	1998-99 (*Rabi*)	1999 (*Kharif*)	Pooled	Type of Reaction
1	CM 128	3.5	3.0	3.8	3.4	S
2	V 327	3.8	3.3	4.1	3.7	S
3	V 335	2.0	1.5	2.0	1.8	R
4	V 13	2.3	1.7	2.0	2.0	R
5	V 128	3.8	4.0	4.1	4.0	S
6	V 17	4.0	3.9	4.5	4.1	S
7	V 336	2.0	2.0	2.3	2.1	R
8	CM 129	3.0	3.5	3.5	3.3	S
9	V 53	1.8	2.1	2.0	2.0	R
10	V 27	2.3	2.0	2.5	2.3	R

S-susceptible (2.6 to 5.0), R-resistant (1.0 to 2.5)

V 27, while V 335, V 13, V 336 and V 53 showed resistance reaction.

Elliott and Jenkins (1946) screened 200 inbred lines, 126 crosses and 184 double crosses against the *Turcicum* leaf blight and found that NC34 was the most resistant while CI123, K715, KY114, MO21A, T49B, T105, BK115, CI15 and TX116 showed traces of infection and the resistant to *Turcicum* leaf blight was transmitted to hybrid progeny. In a similar study, conducted by Gowda and Kaisar (1990) tested 37 maize lines for resistance to *Exserohilum turcicum*. Of these 10 were resistant and 12 were moderately resistant. Rathee *et al.* (1999) reported 8 genotypes having high level of disease resistance.

The inbred lines identified to possess resistance to *Turcicum* leaf blight in the present study, can be used successfully in developing high yielding early maturing varieties for the hill region having high level of resistance to *Turcicum* leaf blight.

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SHORT COMMUNICATION

Development of New Flash Flood Tolerant Genotype of Rice for Coastal Saline Lowlands of Tamil Nadu

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Key Words: Flood tolerance, Rice, Salt tolerance, Submergence

Development of improved cultivars for the vast rainfed lowlands of Asia has lagged far behind that for irrigated areas. This lacuna is not surprising considering the number of traits required for modern rainfed lowland cultivars. In addition to the acceptable grain quality and resistance to insects and diseases that irrigated cultivars require, rainfed lowland cultivars must have sufficient tolerance to abiotic stresses that predominate in their respective environments. From a survey in eastern India, submergence is identified as the third most important of 42 biotic and abiotic stresses that limit rice production in rainfed lowlands (Widawsky and O'Toole, 1990).

Flash flooding and submergence are wide spread in South East Asia, Bangladesh and North-eastern India, and affect at least 22 million hectares (16 per cent of world rice area) including 15 million hectares of potential short duration flash floods in rainfed lowlands and 5 million hectares of deep water rice (Khush, 1984). Submergence for more that 2-3 days kills most rice cultivars (Mishra *et al*., 1996). When rice plants are subjected to flash flood, they should adapt themselves to two drastic environmental changes: the change from aerobic condition to anaerobic condition during complete submergence and the subsequent change from anaerobic to aerobic condition when the flash flood water recedes. Flash flood submergence may occur at any growth stage of rice crop and yield loss in severe cases may be 100 per cent (Mohanty *et al*., 1982). MacKill *et al*. (1996) and Lafitte *et al.* (2006) emphasized on breeding varieties that have intermediate height, stiff and non-lodging culms and moderate submergence tolerance for such growing situations.

Therefore, an attempt was made at the Department of Agricultural Botany, Faculty of Agriculture, Annamalai University, Tamil Nadu to develop saline tolerant high yielding rice variety suitable for *tsunami* affected coastal lowlands of Cuddalore district of Tamil Nadu (Sabesan, 2005). Initially, 26 rice genotypes comprising of 17 mutant cultures, eight high yielding varieties and a traditional variety were evaluated at the Plant Breeding Farm (11º24´N latitude, 79º44´E longitude and + 5.79 msl) for 12 different quantitative and qualitative characters, *viz*., days to first flower, productive tillers per plant, panicle length, number of grains per panicle, thousand grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant (Table 1) and were grouped into thirteen clusters using Mahalanobis D^2 statistics (Sabesan, 2008).

Ten lines and three testers representing the thirteen clusters were selected as parents for hybridization programme. They are IR 42, AUR 7, AUR 1, AUR 12, AUR 8, CO 43, AUR 10, ASD 16, AUR 9, Jeeraga samba, ADT 49, PY 5 and Annamalai Mutant Ponmani. The selected 13 genotypes were crossed in Line x Tester mating design to produce 30 hybrids during *Navarai*, 2003 (January–April). All the 30 F_1 hybrids were

Table 1. Composition of D^2 clusters in rice

Cluster	Number of genotypes	Genotypes identity
I	7	CO 43, AUR 5, AUR 13, IR 36, BPT 5204, AUR 6, ADT 43
II	2	AUR 4, Annamalai Mutuant Ponmani (AMP)
III	2	Karnool sona, *Jeeraga samba*
IV	1	AUR 7
V	4	AUR 9, AUR 14, AUR 11, AUR 2
VI	2	IR 42, AUR 3
VII	1	AUR 1
VIII	1	AUR 8
IX	2	ADT 39, AUR 15
X	1	AUR 12
XI	1	AUR 10
XII	1	PY 5
XIII	1	ASD 16

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advanced to F_2 generation during *Samba*, 2003 (August–December).

Out of the 30 F_2 generations evaluated during *Samba*, (August–December) 2004 the F_2 progenies of the cross ASD 16/PY 5 showed appreciable tolerance to salinity under field conditions. The soil pH of the field was 8.01 and the pH of the irrigation water was 8.20. The soil type was clay with clayey loam texture. The parents ASD 16 and PY 5 belong to clusters of intermediate intercluster distance. Single plant selections made in F_2 generation were forwarded to F_3 and F_4 generations during *Samba*, 2004 and *Navarai*, 2005 (January–April), respectively. F_5 generation raised in *Samba*, 2005 remained completely submerged for eight days by flash flooding(DFO, 2005). The short statured lines which tolerated flood were forwarded to succeeding generations (Table 2).

The F_8 generation grown is *Samba*, 2007 remained completely submerged for 12 days because of flash flooding (Table 3) from 7 DAT to 19 DAT (DFO, 2007). It remained partially submerged for another three days (Fig. 1). No lodging was observed after desubmergence. The leaves were erect and dark green before submergence and after desubmergence. The plant height at maturity was 80 cm (Fig. 1).

Submergence tolerance can be defined as 'the ability of rice plant to survive 10-14 days of complete submergence and renew its growth when the water subsides' (Catling, 1992). The importance of low shoot elongation during submergence and lodging resistance was reported by Kawano *et al*. (2008). Most of the existing rice cultivars are seriously damaged by flash flooding. Extensive shoot elongation is detrimental under flash flood conditions as it exhausts energy storage and when water recedes, the plants tend to lodge. This reduces both productivity, grain quality, and renders the crop susceptible to pest and disease. Positive association between survival and limited stem elongation was reported by Setter and Laureles (1996), Singh *et al*. (2001) and Lafitte *et al.* (2006).

The progress made so far in developing improved cultivars for the rainfed lowland that combine ample submergence tolerance with good agronomic traits is still far from excellent. Although FR 13A has long been known as lowland rice most tolerant to flash flooding, its direct utilization as a tolerant donor is limited by its poor agronomic traits such as the presence of long awn, short and thick grains, photoperiod sensitivity and low productivity (Setter and Laureles, 1996).

The newly developed short statured rice culture AURC 02-05-2 exhibited excellent tolerance to flash flooding besides tolerance to salinity. Association of submergence stress with salinity, cold, nutrient and drought stresses is also reported by Ito *et al.* (1999). This might be because one of the parents ASD 16 is a saline resistant variety.

Table 2. Rainfall and weather data for the year 2005

Week no.	Period	Temperature (ºC)		RH (%)	HBSS (hrs)	Rainfall (mm)	WV (km/hr)
		Max.	Min.				
42	Oct. 15-21	32.2	23.6	93	6.5	109.4	1.4
43	Oct. 22-28	29.9	22.5	95	3.7	103.4	0.8
44	Oct. 29-Nov. 4	32.5	24.2	90	5.8	022.2	2.1
45	Nov. 5-11	26.6	22.0	97	0.0	**591.0**	2.4
46	Nov. 12-18	29.0	20.3	91	5.7	002.8	2.2
47	Nov. 19-25	27.5	21.1	95	2.7	**331.1**	3.3

RH- Relative humidity, HBSS-Hours of bright sunshine, WV-Wind velocity
Source: Meteorology Data, Faculty of Agriculture, Annamalai University

Table 3. Rainfall and weather data for the year 2007

Week no.	Period	Temperature (ºC)		R.H (%)	HBSS (hrs)	Rainfall (mm)	WV (km/hr)
		Max.	Min.				
39	Sept. 24-30	34.6	24.7	79	8.0	0.8	5.9
40	Oct. 01-7	34.6	24.4	82	6.6	14.6	5.6
41	Oct. 8-14	34.6	24.7	84	8.4	22.4	2.4
42	Oct. 15-21	30.7	24.1	88	5.4	40.3	0.4
43	Oct. 22-28	28.1	23.3	97	2.8	**599.4**	0.6
44	Oct. 29-Nov. 4	30.1	23.7	91	6.2	63.2	1.3

RH-Relative humidity, HBSS-Hours of bright sunshine, WV-Wind velocity
Source: Meteorology Data, Faculty of Agriculture, Annamalai University

Fig. 1: Flash flood tolerant rice genotype AURC 02-05-2

The culture AURC 02-05-2 produced 12 tillers, all of them productive. The panicle length was 21.9 cm with 245 grains per panicle. One thousand grains weight was 21 g. Days to 50% flowering was 110-115 and days to maturity was 135-150 days. Grain length was 8 mm and breadth was 2.7 mm. Kernel color was white. Kernel length was 6.1 mm and breadth was 2.4 mm with kernel L/B ratio of 2.54. Kernel length after cooking was 10.2 mm and breadth after cooking was 3.4 mm. Boot leaf length was 32 cm and boot leaf width was 1.8 cm. The yield performance of this line was 5.52 t/hectare. While, rice yields in the rainfed lowlands of eastern India are generally low, averaging 2.4 t/hectare (IRRI, 2002). One peculiar character of this newly identified rice ideotype was the persistence of dark green colour of leaves even during submergence. Erect stature with non-lodging character was another peculiarity of this culture. This culture showed field tolerance to pests and diseases. This culture is in the pipe line of variety release.

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SHORT COMMUNICATION

Development of Introgressed Lines with Unique Characteristics in *Brassica carinata*

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Three lines of *Brassica carinata* 08-304, 08-312, 08-316 derived from inter specific hybridization were evaluated for morphological traits during 2007-08 and 2008-09. These lines showed significant increase in shoot length, 1000-seed weight and significant decrease in maturity duration as compared to check Kiran. Development of these lines is important for Karan rai improvement programme in India.

Key Words: *Ethiopian mustard*, Interspecific hybridization, Introgressed lines

Karan rai or Ethiopian mustard (*Brassica carinata* A. Braun) is a mustard crop suitable for rainfed and low moisture condition. It is a natural amphidiploid between *B. nigra* and *B. oleracea* and believed to be originated in Ethiopian highlands. Besides its tolerance to moisture stress, Karan rai is a reservoir of number of disease resistant genes prevalent in India like white rust, *Alternaria* blight and stem rot (Malik, 1990; Getinet *et al*., 1996). Despite such advantages, this crop could not find favour with farmers largely being a long duration crop along with other inherent short commings like low test weight, short shoot length etc. Most of its agronomic features suit rainfed conditions. However, in India, rapeseed-mustard is now largely grown on conserved moisture with one life saving irrigation. Therefore, the variety should posses the characteristics which suit this kind of agronomy. Looking into these considerations, the present investigation was planned to transfer some desirable agronomic traits from *B. juncea* in the genetic background of *B. carinata.*

The present investigation was initiated during the year 1999-2000 at NRCRM, Bharatpur, where an interspecific hybridization programme was planned. One of the released varieties of Indian mustard, namely, Varuna was crossed with a germplasm line of *B. carinata*. Pedigree bulk method was carried out and evaluation of plant to row progenies was followed during subsequent years. Segregating progenies of interspecific crosses were carried to F_6 stage through selfing. During *Rabi* 2006-07, rigorous selection was done at F6 stage on the basis of plant type. The selection criterion was mainly on the basis of plant type. The plant showing *juncea* type features were retained in one group and those showing *carinata* types having introgression features (on the basis of plant type) from *juncea* background were kept in another group. The third group was of pure *carinata* type where no visible symptoms of introgression from *juncea* background were noticed. The plants showing introgression features were selfed and grown in 4 rows of 4 m length during *Rabi* 2007-08 along with check variety Kiran (check of *carinata*). Three lines showing desirable features like early maturity, long shoot and bold seeds were isolated from group of introgressed lines and characterized for morphological features and harvested separately. These lines were found true to the type. These introgressed lines were again sown during *Rabi* 2008-09 along with Kiran in 5 rows of 5 m length with two replications. The observations were recorded on sample of 5 plants and then averaged over the two years 2007-08 and 2008-09. Student t-test (Sharma, 1998) was applied to test the significance of difference between means of check variety and introgressed lines. Rating of entries for reaction to *Alternaria* blight and white rust was done as per scale given by Conn *et al*. (1990).

The average mean and range of introgressed lines 08-304, 08-312 and 08-316 for different morphological traits along with check Kiran has been presented in Table 1. Perusal of data indicated that all the three lines flowered and matured earlier than the control. The maturity of these lines is significantly different from the control. Line 08-314 matured earlier followed by 08-316 and 08-312. Further, days to maturity showed a positive correlation with days to flowering initiation. Main shoot length of Karan rai is short but introgressed lines reported here showed main shoot length up to 78.1 cm (08-304) in comparison to control (38.5 cm) followed by 08-316 (65.2 cm) and 08-312 (62.3 cm). Main shoot length of these lines was also significantly different from the control. Another yield component in

Table 1. Characterization (average mean of 2007-08 and 2008-09) of introgressed lines with unique characteristics in *Brassica carinata*

Line	PH	DFI	DM	FZL	MSL	PB	S/P
08-304	158-164(161.4)	42.5-43(42.7)*	141.5-143(141.7)*	84.5-94.5(87.5)	67.5-83.5(78.1)*	6.5-8(7.1)	284-384.5(338.9)
08-312	173-194(183.4)	58.5-61(59.8)*	145.5-146.5(146)*	72-100(84.4)	53.5-69(62.3)*	6.5-11.5(8.9)	291.5-406.5(343.8)
08-316	166-184(174)	57-59(58)*	142.5-144 (143.2)*	83.5-90(85.6)	56.5-76(65.2)*	9-11.5(9.7)	344.5-437.5(385.5)
KIRAN	180-198(186.6)	75-76.5(76)	152-154.5(153.3)	58.5-74.5(65.9)	35-43(38.5)	8.5-13.5(11.5)	317.5-407.5(351.1)

Line	S/S	1000-SW	OC	Disease reaction	
				AB	WR
08-304	14-16.5(15.7)	4.4-5.6(4.9)*	38.5-40.7(39.5)	2	0
08-312	12-15(13.7)	3.7-4.0(3.91)*	40.0-41.6(40.6)	1	0
08-316	12.5-16(14.5)	2.7-2.8(2.79)	39.8-41.7(40.7)	1	0
KIRAN	14.5-17(15.1)	2.9-3.2(3.02)	38.6-40.5(39.3)	1	0

***** = Significantly different from control plant, Figures in parenthesis indicates mean of the character
(PH=Plant height, DFI=Days to flowering initiation, DM=Days to maturity FZL=Fruiting zone length, MSL=Main shoot length, PB=Primary branch, S/P=Silique/plant, S/S=Seed/siliqua, SW=Seed weight, OC=Oil content, AB=*Alternaria* blight, WR= White rust)

this crop is 1000-seed weight, the line 08-304 recorded maximum 1000-seed weight of 4.90 g in comparison to control (3.02 g) followed by line 08-312 which is also significantly different from the control. However, line 08-316 has low 1000 seed weight which is lower than the control. The reduction in days to flowering initiation and days to maturity, increase in main shoot length and 1000-seed weight in these introgressed lines are desirable features from agronomic point of view of *B. carinata* cultivation in India and may be attributed to transfer of desirable gene complexes from *B. juncea* background through interspecific hybridization. Further, reaction of these lines to diseases, *i.e.*, *Alternaria* blight and white rust is comparable to check Kiran except line 08-304 for AB reaction (Table 1). On the basis of this study, it can be concluded that line 08-304 and 08-312 can be used as a genetic stock for early maturity, long main shoot and 1000-seed weight while line 08-316 can be used as a donor for early maturity and long main shoot in Karan rai improvement programme.

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SHORT COMMUNICATION

Correlation and Path Analysis of Yield and its Components in Strawberry (*Fragaria* × *ananassa* Duch.)

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Eighteen varietal germplasm was selected for correlation and path analysis of yield and their plant and berry characters. The fruit yield per plant exhibited significant positive correlation with flower truss per plant, number of flower per plant, number of crown per plant, number of leaves per plant and fruit weight suggesting that yield can be effectively improved through selection of these components whereas, it showed non-significant negative correlation with days to 50% flowering, fruit set, fruit weight, fruit breadth, fruit volume and total sugars indicating that these characters have least significance for improving fruit yield in strawberry. The path coefficient analysis revealed that fruit length, acidity and fruit breadth showed maximum direct effect whereas fruit volume, total sugars, fruit weight and days to 50% flower had negative direct effect on strawberry yield. From present study, it can be concluded that characters like days to 50% flowering, number of flowers per plant, fruit weight, fruit volume and fruit set which exhibited appreciable direct effect on yield proved as important component of yield and the selection based on these characters may result in development of high yielding genotypes

Key Words: Genetic diversity, Strawberry, Varietal screening

Strawberry (*Fragaria×ananassa* Duch.) being temperate region crop, is cultivated in the states of J&K, HP and Uttarakhand. Presently, its cultivation is also getting momentum in sub tropical and tropical states like Haryana, Punjab, Uttar Pradesh, Maharashtra, Karnataka and West Bengal. Strawberry is known for its attractive, luscious appearance, taste and nutritive value with pleasant aroma. Now, it enjoys a very lucrative market avenue owing to its heavy demand in the food beverage and processing industries. Strawberries genotypes under cultivation have much variability in quality and yield related parameters. Yield is complex and polygenic character which depends on various components and is highly affected by internal and external factors. The state of J&K is known to give maximum avenue to a degree of clonal variation in this crop and high degree of variability as has been seen and reported in strawberry in India (Das *et al.,* 2006). This crop is being propagated by runners which provide unique advantage in bringing improvement through clonal selection. Very little efforts have been made in the state to make it a remunerative enterprise. Therefore, sustained efforts are needed for genetic amelioration of this crop. Hence, the present investigation was carried out to assess the association between yield and its components and their direct and indirect contribution to the yield.

The present investigation was carried out at strawberry block of Division of Pomology, Sher-e-Kashmir University of Agricultural Sciences and Technology (Kashmir), Shalimar, situated at latitude 35º5´-34º7´N and 74º5´-74º9´E with an elevation of 1,588 msl. In the study, there were 18 varietal germplasm which included collection from different strawberry growing states of India, including some exotic cultivars. The cultivars were grown in Randomized Block Design with three replications at spacing of 30 cm × 30 cm in plot size of one square meter during the years 2006 to 2008. All recommended cultural practices were followed as per the packages and practices. Observations were recorded for three consecutive years and accordingly five random plants were taken per cultivar in each replication. Berry characters, *viz*., berry length, berry breadth, berry weight, berry volume, acidity, total soluble solids and total sugars were analyzed. TSS was determined by Atago pocket refractrometer (0-93-º Brix), and acidity was determined by the method suggested by AOAC (1970). Whereas, plant characters, *viz*., days to 50% flowering, flower truss per plant, number of flowers per plant, number of crowns per plant, number of leaves per plant, number of berries per plant, fruit set and yield per plant were recorded in field and data generated was pooled. The correlation study was computed as per

the method suggested by Johnson *et al.* (1955) and path coefficient as per Dewey and Lu (1959).

The analysis of variance revealed highly significant difference among the genotypes for all the characters. The fruit yield per plant exhibited significant positive correlation association with flower truss per plant, number of flowers per plant, number of crowns per plant, number of leaves per plant and fruit weight suggesting that yield can effectively be improved through selection of these component characters (Table 1) whereas, it showed non-significant negative correlation with days to 50% flowering, fruit set, fruit breadth, fruit volume and total sugars indicating that these characters have least significance for improving fruit yield in strawberry. Significant positive correlations with fruit yield for number of flower per plant, number fruit per plant and fruit weight were also reported by Mohanty (2003), and Devi and Arumugam (1999).

Significant positive correlation also existed between number of flowers per plant with fruit set, number of flowers per plant with TSS, number of flowers per plant with yield per plant, days to 50% flowering with fruit. There were a positive correlations with number of trusses per plant, number of crowns per plant, number of leaves per plant, fruit set (%), fruit weight with the yield per plant. However, negative correlations existed between TSS with fruit volume, acidity with total sugars and total sugars with fruit volume and fruit breadth. Since, there is a positive association among these component characters, the selection aimed for improvement of any character shall itself influence other character in desirable direction. Significant negative correlation existed between days to 50% flowering with flower truss per plant, fruit set with flower trusses per plant, number of leaves per plant with number of flower per plant and number of crowns per plant suggesting that such type of negative correlation among these components will not be helpful as selection for particular character shall have adverse affect on the other traits.

Among the quality parameters, TSS and acidity revealed significant positive association with fruit yield, fruit volume and total sugars with fruit weight which otherwise is less important as low acidity and high fruit volume and total sugars are desirable in strawberry. It is therefore, suggested that the undesirable linkage between fruit yield and acidity needs to be broken through a suitable hybridization programme followed by selection of transgressive segregation (Dalia and Wilson, 2002). On the other hand, fruit set had significant positive association with days to 50% flowering indicating that there is possibility to select genotypes with high percentage of fruit set. However, fruit set had negative significant correlation with flower truss per plant and number of flower per plant suggesting that selection for genotype with high percentage of fruit set have adverse effect on flower truss per plant and number of flower per plant. From this study, it is quite obvious that fruit set, fruit weight, fruit length, fruit breadth and fruit volume are the major characters affecting the yield and hence simultaneous selection for all these traits would lead to overall improvement in yield.

Although correlation studies are helpful in determining the components of yield but they do not provide a clear picture of nature and extent of contributions made by number of independent traits. Path coefficient analysis technique devised by Wright (1921), which provides an effective means of finding out specific forces producing a given correlation. Such information provides a realistic basis for allocation of appropriate weightage of various attributes, while designing a pragmatic breeding programme for improvement of yield. On the basis of correlation analysis, fruit set, fruit weight, fruit length, fruit breadth and fruit volume were observed to be significantly and positively correlated with yield. However, direct and indirect effects of all the characters worked out in present study gave somewhat different picture. The path coefficient analysis (Table 2) revealed that fruit length, acidity and fruit breadth showed maximum direct effect followed by flower truss per plant, number of crown per plant, TSS whereas fruit volume, total sugars, fruit weight and days to 50% flower had negative direct effect. Yadav and Singh (1996) suggested that the characters which showed maximum direct effects should be considered in selection programme for improving yield.

Regarding indirect effect, it was observed that days to 50% flower exhibited positive indirect effect towards yield through fruit length and flower truss per plant, through fruit length and days to 50% flowering, fruit set through number of crowns per plant and number of flower per plant, fruit weight through number of flower per plant and fruit volume, fruit volume through fruit weight, TSS through fruit weight. Indirect effect towards yield through various characters was also reported by Das *et al*. (2006) and Nazir *et al.* (2006) suggested that for selecting genotype with higher yield the indirect

Table 1. Correlation association between various pairs of characters in strawberry

Parameters	Days to 50% flowering	Flower trusses per plant	No. of flowers per plant	No. of crowns per plant	No. of leaves per plant	Fruit set (%)	Fruit weight (g)	Fruit length (mm)	Fruit breadth (mm)	Fruit volume (cc)	TSS (%)	Acidity (%)	Total sugars (%)	Yield per plant (g)
Days to 50% flowering	**1.000**	-0.3607	-0.4998	-0.0435	-0.3380	0.1978	-0.3161	-0.4292	0.1506	-0.1494	0.0788	0.1574	0.1055	-0.3770
Flower trusses/plant	-0.3607	**1.000**	0.5303**	0.2699*	0.1744*	-0.0506	0.2512	0.3118	-0.1507	-0.0080	-0.0415	0.1804	-0.4123	0.6827
No. of flowers/plant	-0.4998	0.5303	**1.000**	0.5600**	-0.2477	-0.3058	-0.2563	-0.2008	-0.5465	-0.3056	0.0041	0.5213	-0.3425	0.5245
No. of crowns/plant	-0.0435	0.2699	0.5600	**1.000**	-0.1032	0.1290	0.0637	-0.0738	-0.2416	0.0244	-0.0136	0.4720	-0.2320	0.2949
No. of leaves/plant	-0.3380	0.1744	-0.2477	-0.1032	**1.000**	0.2797**	0.0919**	0.4012	0.3986	0.5283	-0.0329	-0.5594	0.2492	0.1044
Fruit set (%)	0.1978	-0.0506	-0.3058	0.1290	0.2797	**1.000**	0.6584	-0.5085	0.5034	0.2797	-0.6802	0.1309	0.4286	-0.3850
Fruit weight (g)	-0.3161	0.2512	0.2563	0.0637	0.0919	0.6584	**1.000**	0.0202*	0.2947	0.0827	-0.1865	-0.0311	-0.3405	-0.0082
Fruit length (mm)	-0.4292	0.3118	0.2008	-0.0738	0.4012	-0.5085	0.0202	**1.000**	-0.0393	0.1163*	0.3067	-0.2141	-0.1130	0.6759
Fruit breadth (mm)	0.1506	-0.1507	-0.5465	-0.2416	0.3986	0.5034	0.2947	-0.0393	**1.000**	0.5991	-0.2221	-0.2865	-0.5392	0.1215
Fruit volume(cc)	-0.1494	-0.0080	-0.3056	0.0244	0.5283	0.2797	0.0827	0.1163	0.5991	**1.000**	-0.1119	-0.1814	0.0323	0.0086
TSS (%)	0.0788	-0.0415	0.0041	-0.0136	-0.0329	-0.6802	-0.1865	0.3067	-0.2221	-0.1119	**1.000**	-0.1310	0.4477	0.1025
Acidity (%)	0.1574	0.1804	0.5213	0.4720	-0.5594	0.1309	0.0311	-0.2141	-0.2865	-0.1814	-0.1310	**1.000**	-0.1880	0.3773
Total sugars (%)	0.1055	-0.4123	-0.3425	-0.2320	0.2492	0.4286	0.3405	0.1130	0.5392	0.0323	-0.4477	-0.1880	**1.000**	-0.2192
Yield per plant (g)	-0.3770	0.6827	0.5245	0.2949	0.1044	-0.3850	0.0082	0.6759	-0.1215	-0.0086	0.1025	0.3773	-0.2192	**1.000**

* Significant at 0.05 % and ** at 0.01%

Table 2. Path coefficient analysis showing direct (bold) and in direct effect of different characters on yield of strawberry

Parameters	Days to 50% flowering	Flower trusses per plant	No. of flowers per plant	No. of crowns per plant	No. of leaves per plant	Fruit set (%)	Fruit weight (g)	Fruit length (mm)	Fruit breadth (mm)	Fruit volume (cc)	TSS (%)	Acidity (%)	Total sugars (%)	Yield per plant (g)
Days to 50% flowering	**-0.3830**	0.1381	0.1951	0.0167	0.1294	-0.0758	0.1211	0.1644	-0.0577	0.0572	-0.0302	-0.0603	-0.0404	0.1444
Flower trusses/plant	-0.1278	**0.3543**	0.1879	0.0956	0.0618	-0.0179	0.0890	0.1105	-0.0534	-0.0028	-0.0147	0.0639	-0.1461	0.2418
No. of flowers/plant	0.1138	-0.1207	**-0.2277**	-0.1275	0.0564	0.0696	-0.0583	-0.0457	0.1244	0.0696	-0.0009	-0.1187	0.0780	-0.1194
No. of crown/plant	-0.0078	0.0483	0.1003	**0.1760**	-0.0185	0.0231	0.0114	-0.0132	-0.0432	0.0044	-0.0024	0.0845	-0.0415	0.0528
No. of leaves/plant	-0.0112	0.0058	-0.0082	-0.0034	**0.0332**	0.0093	0.0031	0.0133	0.0133	0.0176	-0.0011	-0.0186	0.0083	0.0035
Fruit set (%)	0.0093	-0.0024	-0.0143	0.0060	0.0131	**0.0469**	0.0309	-0.0238	0.0236	0.0131	-0.0319	0.0061	0.0201	-0.0180
Fruit weight (g)	0.0882	-0.0701	-0.0715	-0.0178	-0.0256	-0.1837	**-0.2790**	-0.0056	-0.0822	-0.0231	0.0520	-0.0087	-0.0950	0.0023
Fruit length (mm)	-0.2933	0.2130	0.1372	-0.0504	0.2741	-0.3474	0.0138	**0.6832**	-0.0269	0.0795	0.2096	-0.1463	0.0772	0.4618
Fruit breadth (mm)	0.0850	-0.0850	-0.3083	-0.1363	0.2249	0.2840	0.1662	-0.0222	**0.5642**	0.3380	-0.1253	-0.1616	0.3042	-0.0686
Fruit volume (cc)	0.0674	0.0036	0.1378	-0.0110	-0.2382	-0.1261	-0.0373	-0.0524	-0.2701	**-0.4509**	-0.0506	0-0818	-0.0145	0.0039
TSS (%)	0.0066	-0.0035	0.0003	-0.0011	-0.0028	-0.0571	-0.0156	0.0257	-0.0186	0.0094	**0.0839**	-0.0110	-0.0376	0.0086
Acidity (%)	0.0985	0.1129	0.3263	0.2954	-0.3501	0.0819	0.0195	-0.1340	-0.1793	-0.1135	-0.0820	**0.6259**	-0.1176	0.2361
Total sugars (%)	-0.0226	0.0883	0.0734	0.0497	-0.0534	-0.0918	-0.0729	-0.0242	-0.1155	0.0069	0.0959	0.0403	**-0.2142**	0.0469

Residual effect = 0.06

influence of different traits should be given due weightage along with characters which exerted direct effect.

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SHORT COMMUNICATION

Bandsize-Binary: A Program to Convert Size Data to Binary Data

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Bandsize-Binary is windows based computer program, developed in Visual Basic 6 environment for converting electrophoresis gel size data to binary data. It is a user friendly program provided with several features to perform accurate analysis and display of inputed molecular biology data. On the click of *submit* button programs runs to convert microsatellite data to binary data. In the end, it flashes the message of successful data conversion on the right hand side of the form. In addition, the program also provides facility to calculate heterozygosity of markers in the data sheet. Heterozygosity (*H*) is a widely used measure of the allelic diversity or informativeness of a genetic marker. The informativeness of a genetic marker increases as *H* increases. This program provides graphical user interface that makes it more accessible for casual computer users and more convenient for the experienced computer user. Bandsize-Binary program is a very useful tool for researchers and persons involved in DNA fingerprinting.

Key Words: Binary data, DNA fingerprinting, Electrophoresis gel size data, Molecular marker

Molecular markers have become essential tools for population genetics, conservation biology and evolutionary studies as well as for molecular mapping and gene tagging (Jarne and Lagoda, 1996). They have proven to be powerful tools in the assessment of genetic variation and in the elucidation of genetic relationships within and among species. Several molecular markers, *viz*., RFLP (Becker *et al.*, 1995), RAPD (Tingey and Deltufo, 1993), SSRs (Levinson and Gutman, 1987), ISSRs (Albani and Wilkinson, 1998), AFLP (Mackill *et al*., 1996) and SNPs (Vieux *et al*., 2002) are presently available to assess the variability and diversity at molecular level (Joshi *et al.*, 2000). Information regarding genetic variability at molecular level could be used to help, identify and develop genetically unique germplasm that compliments existing cultivars.

There are several bioinformatics applications for analysis of molecular biology data in public domain on World Wide Web (www). The sequence analysis software tools such as FASTA, BLAST, CLUSTALW and other sequences analysis tools became very popular. However, there are not many other easy to use tools available for conversion of molecular biology lab data (such as DNA Polymorphic band data) to binary format. These data analyses softwares are common in the science, as the scientists in need of new analyses develop algorithms, and then crystallize the algorithms as software. Most of the basic biosequence analyses are developed by scientist such as FASTA, BLAST etc. In this paper an effort has been made to describe a program entitled 'Bandsize-Binary'. This program has been developed to provide a facility of data conversion from band size to binary format and also to know informativeness of markers by heterozygosity analysis.

Bandsize-Binary is a windows based computer program. It is developed in Visual Basic 6 environment. Visual Basic is an event driven programming language. It enables Rapid Application Development (RAD) of Graphical User Interface (GUI) applications. It helps to access databases using Data Access Objects (DAO), Remote Data Objects (RDO), or Activex Data Objects (ADO). The language not only allows programmers to easily create simple GUI applications, but also provides flexibility to develop fairly complex applications. On hardware site it requires an IBM PC or compatible with an Intel Pentium IV processor or heigher CPU and 64 or more MB of Random Access Memory (RAM). A mathematical coprocessor is required to achieve a reasonable computing speed. Window XP or later version of Windows are suitable platforms for running the program.

In case of co-dominant markers (such as SSRs-microsatellites/ minisatellites or RFLPs), alleles are coded simply as their integer size in base pair. In addition to that, Genscan a gene prediction tool (Reference no. 12) inputs automatically genome sequence data and outputs allelic band size data. Researchers try to put the data into data analyses softwares and perform desired

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analysis to interpret data. In general, most of the softwares for molecular data analysis require data into binary format such as NTSYS PC. Band size-Binary program has been developed to convert huge bandsize data to binary format. The genotype data is recorded in terms of a two-way matrix. The program reads all the band sizes with their locus and markers from an excel worksheet as input file. The input file of Bandsize–Binary program is identical to the Fig. 1, showing sample of genotype data in Excel worksheet. Varieties or cultivars are entered in the first row of Excel worksheet and primers are entered into the rows. The input form, as shown in Fig. 2, prompts to get name of crop and Excel file. On click of *submit* button programs converts size data to binary data. In the end, it flashes the message of successful data conversion on the right hand side of the form. In addition to this, it also informs about number of primers, varieties and records of data sheet. The output file in Excel is saved into the C:\ directory of the computer system. In binary data, presence of band is represented by 1 and absence of band is represented by 0. The format of binary data includes columns as *Sno*, *Bandsize*, *Primer* and *names of varieties*. The values of varieties corresponding to their primer in microsatellite genotype data is represented into *Bandsize* column. Fig. 3a shows binary format of sample data in Excel worksheet.

cultivar	Var1	Var2	Var3	Var4	Var5
Primer1	152	155	160	162	168
Primer1	152	155	152	152	152
Primer2	238	238	243	240	237
Primer2	241	238	243	243	243
Primer3	101	106	106	111	103
Primer3	101	106	110	111	111

Fig. 1: Sample of genotype data in Excel worksheet

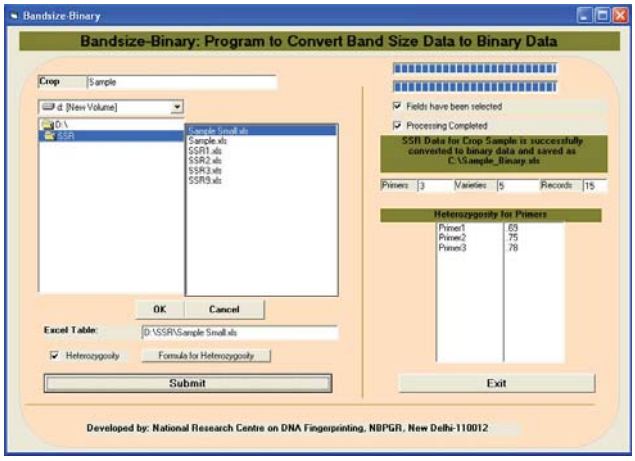

Fig. 2: Form to convert band size data to binary data

In addition, the program also provides facility to calculate heterozygosity of markers in the data sheet. Heterozygosity is one of the analyses to measure informativeness. The Informativeness of genetic marker is measured by the number of alleles and their frequencies. Heterozygosity (*H*) is a widely used measure of the allelic diversity or informativeness of a genetic marker. The informativeness of a genetic marker increases as

Formula for Heterozygosity

$$P_i = \frac{1}{N}\sum_{i=1}^{n} f_i \qquad h = 1 - \sum_{i=1}^{n} P_i^2$$

f_i = Presence of specific band
n = Number of plants in the population
N = Total number of locus i bands in a population
P_i = Allele frequencies
h = Heterozygosity (Nei 1987)

H increases.

Fig. 3b shows calculated heterozygosity report of all the primers in Excel worksheet. At the end of processing, the user gets two output files in Excel format stored in C: drive of computer. Of the two output files, the first file is binary format of size data and second file is the heterozygosity report file. This program can be downloaded from following address: http://www.nbpgr.ernet.in/NRCWEB08/BandsizeBinary.htm. Click on the hyperlink will allow the user to download the setup file for Bandsize-Binary program. This setup

Bandsize	Primer	Var1	Var2	Var3	Var4	Var5
152	Primer1	1	0	1	1	1
155	Primer1	0	1	0	0	0
160	Primer1	0	0	1	0	0
162	Primer1	0	0	0	1	0
168	Primer1	0	0	0	0	1
237	Primer2	0	0	0	0	1
238	Primer2	1	1	0	0	0
240	Primer2	0	0	0	1	0
241	Primer2	1	0	0	0	0
243	Primer2	0	0	1	1	1
101	Primer3	1	0	0	0	0
103	Primer3	0	0	0	0	1
106	Primer3	0	1	1	0	0
110	Primer3	0	0	1	0	0
111	Primer3	0	0	0	1	1

Fig. 3a: Binary format of sample data in Excel worksheet

Fig. 3b: Heterozygosity results generated in Excel worksheet

file has to be installed on computer to run. This is a free of cost program and author can also be contacted for email version.

Band size-Binary Program has been registered at The Registrar of Copyrights, Copyright Office, New Delhi-110001.

This program provides graphical user interface that makes it more accessible for casual computer users and more convenient for the experienced computer user. A wider look of similar type of program in internet took to the conclusion that although there are number of statistical software available in internet on public domain, unfortunately, they are either difficult to use or very expensive. Henceforth, Band size-Binary program will be very useful tool for researchers, and persons involved in DNA fingerprinting.

The author declares that she has no competing interests.

Acknowledgement

I take the opportunity to express my sincere thanks to Dr KV Ravishankar, Division of Biotechnology, Indian Institute of Horticultural Research, Bangalore-560 089 India.

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SHORT COMMUNICATION

Introduction and Establishment of *Gossypium darwinii* (AD5) in India – A Tetraploid Wild Species

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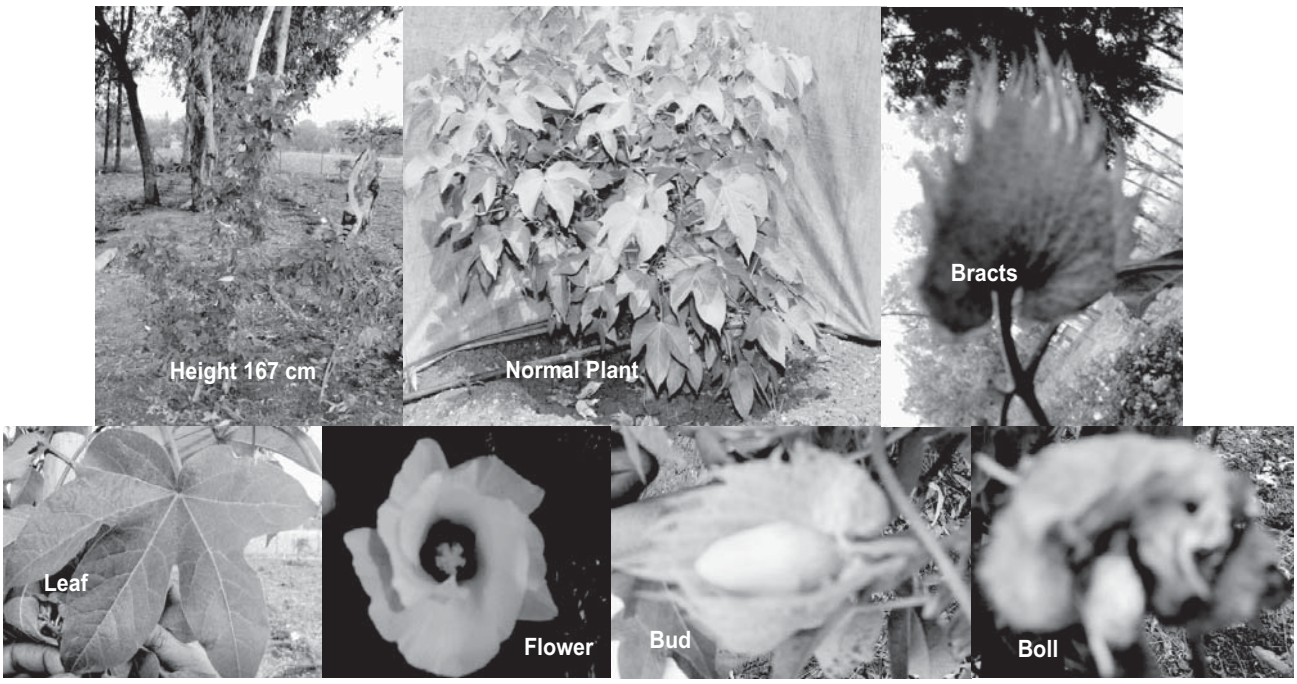

Fig. 1: *G. darwinii* (AD)5 – a tetraploid wild species

G. darwinii (AD5) is a wild allotetraploid species, one of the sources of primary germplasm and has originated from the Galapagos island. It is a relative of cultivated tetraploid species *G.barbadense* (AD2). The seeds of *G. darwinii* were procured form Dr. RJ Kohel, USDA, USA under the enrichment of germplasm programme through NBPGR, New Delhi. *G. darwinii* plants have been introduced and established for the first time in India.

G. darwinii is a perennial shrub, densely branched and moderately hairy. The plant grows to a normal height of 68 cm while one of the three plants established in existing wild species garden of CICR, Nagpur has grown exceptionally tall to a height of 167 cm with spreading of branches upto 94 cm, leaves 8.5–9×5 cm cm, softly tomentose when young, central lobe much longer, linear–oblong acuminate, with deep sinuses on both side drawn and turned in folds, veins prominently coved by trichomes, petioles 3.8–4 cm long. Inflorescence axillary, flower solitary, on short rigid pedicels, bracteoles quite free with no extra floral glands (nectarines), ovate cordate, cut into many very narrow awl-shaped teeth that become almost forked and hooked, membraneous, prominently reticulated completely enclosing the capsule. Flowers very large, wide spreading, yellow, with a dark red plant blotch, calyx undulated or cut square across and pollen grains distinctive. Capsule elongated, long, with acute apex and four loculed, with 8-10 seeds per capsule and light brown lint and fizz.

The introduction and establishment of *G. darwinii* known as a donor for drought and nematode resistance has opened up, avenues for its utilization in introgressive hybridization for the improvement of cultivated cotton. Further *G. darwinii* has been utilized in crossing program to transfer these traits into the cultivated species of cotton.

SHORT COMMUNICATION

Thespesia lampas (L.) – A Close Wild Relative of *Gossypium*

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Fig. 1 (a&b) : Portion of flowering shoot; (c) Seed: Small, dark brown & lint less; (d) Capsule: Dry, loculicidally dehiscent, locules opening longitudinally at 45⁰- 65⁰ angle.

Thespesia lampas Linn. was collected in vegetative form from village: Kolappully; Taluqa: Ottapalam; District: Palakad; State: Kerala and planted in wild species garden of CICR Research Farm, Nagpur (MS).

Taxonomic description

Thespesia lampas is a small shrub, chromosome number n=13 belongs to family Malvaceae; Leaves: broadly palmately lobed, middle lobe larger, rudimentary lobe absent; Venation: reticulate and palmate divergent; Bracts; three, large, persistent; Inflorescence: terminal shoots bearing axillary flowers; Flower; yellow petals with long claw, Petal blotch: present; Ovary: Superior with axile placentation; Fruit: Capsule, dry, brittle, loculicidally dehiscent, 4-6 locules, Locule opening pattern: longitudinal at 45º-65º angle; Seed: Small, dark brown, lintless.

The plants supported abundant vegetative growth but failed to enter into reproductive phase for six consecutive seasons. Nascent unopened flower buds aborted persistently. Plants were however forced to enter into reproductive phase by subjecting it to moisture stress, pruning and lopping. Blooming period of *Thespesia lampas* did not match with *Gossypium anomalum* (B-genome – *Gossypium* wild species). The size of pollen grains of *T. lampas* measured up to 400 µ with pollen tube width measuring up to 123 µ, making it amenable to enter and penetrate into stigma/style of *G. anomalum*. Early efforts are under way to cross it effectively with *G. anomalum*.