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Conservation of Agro-biodiversity : Looking Back and Looking Ahead

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Looking Back

I began my research in the field of agro-biodiversity in 1947 at the Indian Agricultural Research Institute (IARI), New Delhi. The experimental material consisted of species and varieties of non-tuber bearing *Solanum* (Family Solanaceae). *Solanum melongena*, the eggplant (brinjal) belongs to this group. I was amazed at the variety of eggplants, from different parts of India, in the collections made by my supervisor Dr Harbhajan Singh. The goal of my study was to understand the genetic relationships among non-tuber bearing *Solanums*. In 1949, Professor JBS Haldane visited my experimental field and observed: 'I have never seen such variability in quantitative characters as in eggplant; this plant is ideal for studies in the field of quantitative genetics.' He further observed that 'while Indian farmers are nurturing genetic heterogeneity in their fields as part of their preference for risk-distribution agronomy, scientists seem to be worshipping genetic homogeneity.' Genetic homogeneity enhances genetic vulnerability to biotic (pests and diseases) and abiotic (drought, salinity and flood) stresses and this is why in the earlier systems of cultivation, mixed cropping and crop variety mixtures were preferred.

In 1949, I went to the Agricultural University, Wageningen, the Netherlands, to continue my work on Solanaceae, but this time on tuber-bearing *Solanum* species, particularly on potato (*Solanum tuberosum*). The Dutch farmers cultivating potato in the polder lands were facing serious damage to the crop from the golden nematode (*Heterodera rostachiensis*). Professors Dorst and Toxopaeus, with whom I was working, suggested that I should work on breeding potato varieties resistant to the golden nematode. I found from literature that the species *S. polyadenium* from Peru possessed resistance to the golden nematode. This species was in the Commonwealth Potato Collection maintained at Cambridge, UK, by Professor JG Hawkes. I obtained seeds of this and several other species from Professor Hawkes and started crossing them with a popular Dutch potato variety, *Beintije*. Since *S. polyadenium* was a diploid ($2n = 24$), and *S. tuberosum* was a tetraploid ($2n = 48$), I had to double the chromosome

number of *S. polyadenium* in order to cross it with the cultivated potato.

The genetic diversity in *Solanum* species fascinated me and I decided in 1950 to go to Cambridge to work on the Commonwealth Potato Collection. From 1950-52, I did extensive research on tuber-bearing *Solanum* species collected from South America and started to unravel the genetic interrelationships among them. I also traced the origin of the cultivated potato, *S. tuberosum*. This work earned for me the Ph.D. degree of the University of Cambridge in 1952.

In November 1952, I was invited by the University of Wisconsin, USA, to join the Department of Genetics in order to assist in the establishment of an Inter-regional Potato Introduction Station at Sturgeon Bay in Lake Michigan, to house the collection made by Dr Donovan Correll of the US Department of Agriculture. From 1952-54, I undertook extensive gene transfer research from the wild species of tuber-bearing *Solanum*, using several novel cytogenetic techniques. One of the crosses involving the front-resistant species, *S. acaule* from the Lake Titicaca region of Peru-Bolivia border, resulted in the variety Alaska Frostless released for cultivation in Alaska (Swaminathan, 2010).

The work during 1947-54 on both tuber-bearing and non-tuber bearing *Solanum* species led to my conviction that we should do everything possible to conserve agro-biodiversity for future generations. On my return to India from Wisconsin in 1954, I joined the Central Rice Research Institute, Cuttack, to work on the breeding of high-yielding varieties of rice based on crosses between *japonica* and *indica* strains. The aim was to transfer genes for fertilizer response from *japonica* varieties to *indica*. This programme gave rise to varieties like ADT-27 in Tamil Nadu and Mashuri in Malaysia. There were however several problems like semi-sterility and the breeding of rice varieties with high yield potential had to wait until 1964, when the Taiwan variety, Taichung Native-1 (TN 1), containing the *Dee-gee-woo-gen* dwarfing gene became available. I was also fascinated by the genetic variability maintained by tribal families of the Koraput

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district in Orissa. In 1954, the Koraput farm families were sustaining nearly 3,000 strains of rice but now it has come down to about 300, as a result of gradual genetic erosion. This emphasises the need for *ex situ* preservation, while not relaxing on *in situ*, on-farm conservation.

I joined the Indian Agricultural Research Institute, New Delhi late in 1954 and initiated work on the breeding of high-yielding varieties of wheat. Dr BP Pal and his associates were then engaged in breeding wheat varieties for resistance to stem, leaf and stripe rusts (*Puccinia* sp.). I tried different methods like crossing the bread wheat (*Triticum aestivum*) with subspecies *compactum* and *sphaerococum* but these crosses yielded dwarf plants with dwarf panicles and consequently had a low yield potential. In 1959, I came to know of the work of Dr Orville Vogel of the Washington State University, Pullman, USA, in breeding the semi-dwarf winter wheat variety Gaines by incorporating the dwarfing gene from Norin-10 (*daruma*), a variety bred by Dr Gonziro Inazuka of Japan. Dr Vogel had given seeds of this material to Dr Norman Borlaug who was working in Mexico in the breeding of high-yielding and rust-resistant varieties of spring wheat. The history of the introduction of Borlaug's material into India and the subsequent development of outstanding wheat varieties like Sonalika and Kalyan Sona are described in the book *Science and Sustainable Food Security*.

The essential point I wish to make is that biodiversity is the feedstock for successful plant breeding. Most of the successful varieties of rice, wheat and other crops may have 50 or more landraces in their pedigree. Because of the availability of genetic variability, a strategy could be developed in the 1960s to checkmate the spread of leaf, stem and stripe rusts in wheat in North India. On becoming the Director of IARI in 1966, one of the first steps I took was to create a Division of Plant Introduction, to strengthen the ongoing work under the leadership of Dr. Harbhajan Singh in the areas of plant exploration, collection and conservation. Both in rice and wheat extensive collections were made to preserve for posterity a sample of the genetic variability now existing in these crops. During this period, I initiated a programme for the collection and conservation of rice varieties from the northeastern region of India. This collection, known as the Assam Rice Collection, had over 7000 varieties and proved to be a veritable mine of valuable genes.

On becoming the Director General of the Indian Council of Agricultural Research (ICAR) early in 1972, I initiated steps to set up a National Bureau of Plant

Genetic Resources (NBPGR) at the national level and an International Board for Plant Genetic Resources (IBPGR) at the global level through the Consultative Group on International Agricultural Research (CGIAR). I was then Vice-Chair of the Technical Advisory Committee (TAC) to CGIAR. Sir John Crawford of Australia was the Chair of the first TAC set up in 1971. Both NBPGR and IBPGR (now named Bioversity International) have rendered very valuable service in genetic resources collection and conservation. Also, I took steps to establish National Bureaus of Animal and Fish Genetic Resources and later the National Bureau of Forest Genetic Resources.

I was the Principal Secretary of the Ministry of Agriculture during 1979-80. During that period, the Forestry Division was an integral part of the Ministry of Agriculture and, therefore, I had the overall responsibility for shaping the programmes of the forestry sector. One of the earliest steps I took was to review the permission granted for an electricity project in the Silent Valley area of Kerala. This is a unique tropical rainforest and is the home of rich biodiversity. After a careful study of the benefits which the project could confer in the fields of electricity generation and irrigation, I submitted a report to the Cabinet of the Government of India in 1979 advising that the electricity generation project should be given up. I was aware that the acceptance of this suggestion by the then Government of Kerala would be difficult unless I provide alternative pathways of achieving the goals for which the State Government was willing to sacrifice this unique biodiversity paradise. Therefore, I would like to quote the principal recommendations which I made in 1979, which led to this project being abandoned and the whole area set aside as a National Park.

The entire area of 39,000 hectares consisting of (a) Silent Valley forest, (b) New Amarambalam Reserve forests, (c) Kundas forests, and (d) Attapadi reserve forests, should be developed into a **National Rain Forest Biosphere Preserve**. The cost of developing a National Rain Forest Biosphere Preserve may be borne by the Government of India, since the preservation of this unique forest area will be to the benefit of both Kerala and the entire nation. The Silent Valley Environmental Monitoring Committee already constituted by the State Government could become the National Rain Forest Biosphere Preserve Planning and Implementation Committee and start the work immediately under the overall guidance of NCEPC. If developed along proper lines, the Silent Valley Rain Forest Biosphere Preserve can become a sanctuary for valuable

genes in several medicinal and plantation crops, such as pepper and cardamom. This whole region has also been found to be a reservoir of useful genes in rice conferring resistance to some major pests. Therefore, urgent steps should be taken to prevent the erosion of valuable genes from this area.

The Kerala Forest Research Institute at Peechi may be developed into an international research and training centre for the study of tropical rain forest eco-systems. This will be appropriate in view of the widespread interest, particularly in countries in South-East Asia in tropical evergreen rainforest flora and fauna.

A detailed ground water survey of the Palghat and Mallapuram districts should be completed soon and steps should be taken to provide irrigation through the available ground and surface water resources in as much area as possible. I have discussed this with the officers of the Central Ground Water Board and a note on the available knowledge is given in Appendix-VI. The potential for irrigation through mobilizing the available ground water sources seems to be very good. For implementing the irrigation project, **a Palghat and Mallapuram Irrigation Project Committee** may be constituted immediately, jointly by the Central and State Governments. The Central Ground Water Board of the Department of Agriculture and Cooperation can undertake the task of organizing the ground water survey and preparing a blueprint for irrigation in cooperation with the concerned Departments of the State Government. Since the present utilization of draft is only 12 to 15% of annual recharge, arrangements for providing irrigation to 10,000 hectares can be made speedily.

If steps are not taken to satisfy the legitimate socio-economic aspirations of the people of the area. Mere talk about ecology and environment will be met with cynicism and with the question, "Who is more important – man or monkey?" On the other hand, if we proceed with the implementation of SVHEP without taking advantage of alternative methods of providing energy, employment and irrigation, will future generations forgive us for destroying a 50-million year old genetic heritage, particularly at a time when the solar energy option is not an illusion? **The alternative pathways available immediately for providing power, irrigation and jobs at no ecological risk will, in my view, help to achieve the desired social goals more speedily and economically.** It should not be beyond our political, intellectual or financial capability to find solutions which can enable the present day

human population of Palghat and Mallapuram districts to experience a better quality of life without destroying a priceless biological endowment.

Development without destruction will then not be an idle dream, as it will be if the present project is rushed through. If on the other hand, the project is rushed through leading to the destruction of the forests and to the loss of valuable genetic material, SVHEP will become one more testimony to the statement, "Every new source from which man has increased his power on earth has been used to diminish the prospects of his successors. All his progress has been made at the expense of damage to the environment which he cannot repair and could not foresee".

During my tenure as Director General of the International Rice Research Institute, Los Baños, the Philippines (1982-88), I initiated steps to enlarge and streamline the International Rice Germplasm Centre. IRRI now preserves over 100,000 strains of rice. My strategy for conservation was to map the biodiversity hot spots and initiate steps to save the genetic diversity occurring in such endangered habitats. An example is the rice collection made in the interior parts of Myanmar with the help of army personnel since civilians were not allowed to go to some of these areas. The army personnel were trained in genetic resources collection at Yezin. The outstanding rice varieties developed at IRRI under the leadership of Dr GS Khush were the products of an effective use of genetic diversity.

In 1983, I served as a President of the XV International Congress of Genetics held in New Delhi. I chose "Genetic Conservation : Microbes to Man" as the focal theme for the Congress. In my Presidential Address, I suggested that we should establish a global Cryogenic Gene Bank under perma-frost conditions to serve as a "Noah's Ark" in the field of conservation. This proposal fructified when the Government of Norway set up a Global Gene Vault at Svalbard, near the North Pole in 2008. A similar Gene Vault has been set up at Chang La in Ladakh by the Defence Research and Development Organisation of India (DRDO) in 2009. These facilities involve low operational cost and serve as repositories of valuable genetic material. In spite of the growing awareness of the need for conserving biodiversity, its loss is continuing unabated due to habitat destruction, alien invasive species and industrial agriculture. A Biodiversity Literacy Movement is, therefore, an urgent need.

Cryogenic preservation does not allow evolution. *In situ* conservation involves both preservation and evolution.

Therefore, *in situ* conservation and *ex situ* preservation are both important. I assisted the Commonwealth Secretariat and the Government of Guyana in establishing the Iwokrama Rainforest Conservation programme in 1 million hectares of prime rainforest made available by the Government of Guyana. In this programme, as well as in many others with which I have been associated, I introduced the “4C principle”, i.e., conservation, cultivation, consumption and commerce. The “4C principle” generates an economic and social stake in conservation. In my report on the Silent Valley Rainforest in Kerala, submitted in 1979, I proposed the development of this unique rainforest and adjoining forests as a Biosphere Reserve.

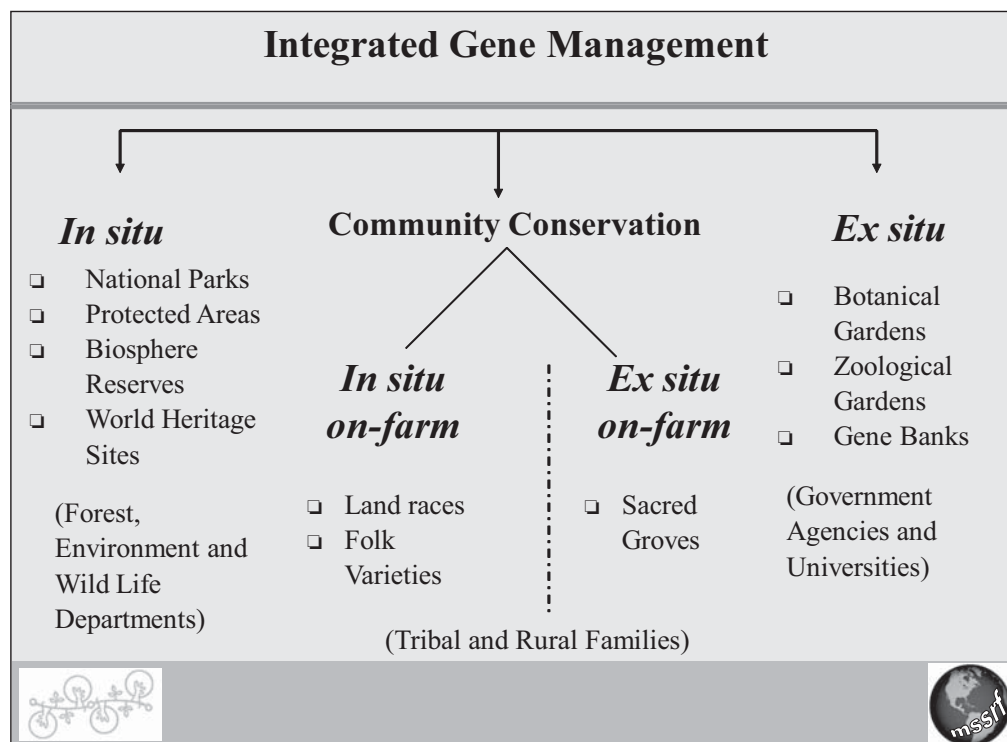
All over the world there is increasing realization of the need to have an integrated conservation strategy involving *in situ* and *ex situ* methods as well as community conservation on the lines I had indicated in my Volvo Prize Lecture (see figure below).

The role of local communities in the conservation and enhancement of biodiversity received inadequate attention and appreciation in the past. Therefore, in the general conference of FAO held in Rome in 1979, I stressed the need for ending the enigma of the poverty of the primary conservers coexisting with the prosperity of those who use their knowledge and material. This led ultimately to the establishment of the FAO Commission on Plant Genetic

Resources at a meeting of the FAO Council chaired by me in November 1983. Also, the concept of Farmers’ Rights was developed and this was given a legal status under the FAO-sponsored International Treaty on Genetic Resources for Food and Agriculture which came into operation in November 2001.

In the early nineties, MSSRF started the preparation of draft legislation for the integrated protection of farmers’ and breeders’ rights. My first draft of such a Bill was supported in an international dialogue held at MSSRF, Chennai in 1994 (Swaminathan, 1995). In 1996, I revised this draft by including farmers’ rights in the title of the Act. Thus, was born the Plant Variety Protection and Farmers’ Rights Act adopted by the Parliament of India in 2002 (Swaminathan, 1996). Following this, the Plant Variety Protection and Farmers’ Rights Authority was set up and the Authority adopted and implemented my suggestion for honouring primary conservers with the Genome Saviour Award.

The community conservation methodology involved promotion of a gene bank (*in situ* on-farm conservation of landraces), a seed bank, a grain bank and a water bank in areas rich in agro-biodiversity. This initiative won for the tribal communities of Koraput in Orissa the Equator Initiative Award at the UN Summit on Sustainable Development held at Johannesburg in 2002. Although,



the UPOV convention has not yet accepted the concept of farmers' rights, it is my hope that my plea that UPOV should become a Union for the Protection of Breeders and Farmers' Rights will become a reality in the near future. Breeders and farmers are allies in the struggle for feeding the ever-growing global population and, hence, their rights should not only be not antagonistic, but should be mutually reinforcing.

During my presidency of the World Conservation Union (IUCN), we took steps to prepare a Draft Global Biodiversity Convention. The Draft was discussed and approved at the IUCN Conference which I chaired and which was held at San Jose in Costa Rica in February 1988. Also, the Keystone Dialogues on Plant Genetic Resources held under my chairmanship during 1989-91, articulated the concept of recognition and reward for primary conservers. The Biodiversity Convention recognises the principles of prior informed consent and benefit sharing. The challenge now lies in getting all nations to accept the concept of farmers' rights and introduce appropriate legislation for the concurrent recognition of breeders' and farmers' rights on the pattern of the Indian legislation.

When I was in the Philippines during 1982-88, I observed that valuable mangrove forests were being removed for establishing aquaculture ponds. Mangroves serve as bio-shields during coastal storms and tsunamis and promote sustainable fisheries. I, therefore, helped to establish an International Society for Mangrove Ecosystem (ISME) in 1989 with the help of UNESCO and the Government of Japan. During my period as Founder-Chairman of ISME (1989-92), a Charter for Mangroves was prepared. In association with the International Tropical Timber Organization (ITTO), MSSRF organised an international training programme on Mangrove Genetic Resources Conservation. Also, research was started in 1992 on the identification and transfer of genes for seawater tolerance from *Avicennia marina* to rice and other crops by a team of molecular geneticists led by Dr Ajay Parida. This work has now yielded several salinity-tolerant rice varieties. Recombinant DNA technology helps in transferring genes across sexual barriers and hence no plant or living organism is useless. For example, *Prosopis juliflora*, considered a noxious weed, has provided genes for drought tolerance. The new genetics has brought to an end the era of reproductive isolation of species.

Looking Ahead

My association with biodiversity conservation and utilisation over 63 years has reinforced my conviction

that we must do our best to halt genetic erosion, promote biodiversity literacy and make biodiversity conservation everybody's business. Biodiversity is a public good resource and should not be privatised. The Global Convention on Biodiversity and FAO's International Treaty for Genetic Resources both emphasise the need for recognising and rewarding the invaluable contributions of tribal and rural families to biodiversity conservation and enhancement. This is why delivering the Sir John Crawford Memorial Lecture in Washington DC in 1990, I pleaded for converting the Union for the Protection of Plant Varieties (UPOV) into a Union for the Protection of Breeders' and Farmers' Rights. The farmer is often a breeder and conserver, in addition to being a cultivator. If today, there are nearly 150,000 strains of rice in the world, it is only because of community conservation.

Agro-biodiversity is the result of interaction between cultural and culinary diversity and hence the conservation of cultural diversity and traditional knowledge are equally important. The traditional methods of conservation like sacred groves and temple trees should be revived, since they integrate the spiritual and practical dimensions of biodiversity conservation.

Climate change has reinforced the urgency of conserving traditional crops and wisdom. In October 2010, some 18000 participants, representing the 193 Parties to the Convention on Biological Diversity, who attended the Nagoya Biodiversity Summit in Japan reiterated the urgency of meeting the unprecedented challenges of the continued loss of biodiversity in an era of climate change. The Strategic Plan of CBD and the "Aichi Target" adopted by the meeting includes 20 major targets organised under five strategic goals that address the underlying cause of biodiversity loss, reduce the pressures on biodiversity, safeguard biodiversity at the ecosystem level, enhance the benefits provided by biodiversity and provide for capacity building.

The Nagoya Protocol included a plan to protect biodiversity by setting targets for 2020. Nations agreed to make 17% of the globe's land area and 10% of coastal and marine areas into protected regions, as opposed to the current levels of 13% and 1%, respectively.

When I was President of IUCN, I used to remark that "conservation without resources becomes just conversation". Fortunately at Nagoya, Japan led the resource mobilisation drive by committing a \$2 billion fund for achieving the "Aichi Target" of halving the rate of biodiversity loss by 2020. I hope other countries will

follow not only with money but also with emotional, spiritual and political commitment.

When I chaired a Committee of the Union Planning Commission in 1980, which recommended the establishment of a separate Ministry of Environment and Forests under strong professional leadership, I had wanted 10% of our land area to be set aside as protected areas. This, however, was not found feasible by other members of the committee. We should adopt this minimum target and try to achieve it by 2020.

Experience has shown that without education and social mobilisation, regulation alone will not work. I have participated in numerous national and international conferences and workshops during the past 60 years where well-intentioned resolutions and targets have been adopted. Even with reference to the UN Millennium Development Goal No 1, *i.e.*, reducing poverty and hunger by half by 2015, progress has been poor in many countries. Unless community understanding and action is combined with national and global resolutions, preventing biodiversity loss will remain a receding goal. For giving local communities space in the management of Biosphere Reserves and National Parks, we should adopt a trusteeship mode, with people and government becoming trustees of these invaluable assets. I got this done in the case of the Gulf of Mannar Biosphere Reserve in Tamil Nadu, by getting its management placed under a Gulf of Mannar Biosphere Trust, with both government and community leaders serving as trustees.

In 2020, there will be a review of the progress made in achieving the “Aichi Target”. Considering past accomplishments, there will be disappointment once again unless there is serious effort for making biodiversity conservation a community-led movement. In most of these conferences, administrators, experts and members of civil society organisations participate. They prepare excellent declarations, but these are not followed up by taking the message to those who are the key actors in the conservation movement at the local level. Reaching the unreached and voicing the voiceless will have to become a mandatory public policy in the area of biodiversity conservation.

The tribal women of Koraput are showing how we can convert **biodiversity hotspots** into **biodiversity happy spots** by launching a biohappiness movement involving concurrent attention to conservation, sustainable use and equitable sharing of benefits. I hope their voices of sanity and hope will be heard in the 2020 Conference, since otherwise targets and resolutions adopted at conferences like Nagoya will continue to remain as desirable but unaccomplished objectives.

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Diversity Analysis of Onion Germplasm Collections from Northern Telangana Region of Andhra Pradesh

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Onion germplasm diversity was collected from three northern Telangana districts of Adilabad, Karimnagar and Nizamabad in April 2009. Seventy-four samples (bulbs-66; seeds-8) were sampled from 33 villages and 23 mandals. Wide range of variation was observed for the two qualitative and six quantitative traits recorded in the field. Majority of the accessions possessed flat globe (34.8%) and globe (36.4%) shapes. White (54.5%), dark red (22.7%) and light red (13.6%) were the more commonly occurring colours. Bulb weight showed maximum diversity, followed by number of centres, neck thickness, equatorial diameter, TSS and polar diameter. Highest TSS (>14%) was observed in IC572010 and IC571965 (Adilabad). Promising accessions for equatorial diameter (>60mm) were identified including ICIC571912, (Karimnagar), IC571972 (Adilabad) and ICIC571973 (Adilabad). These cultivars hold potential for possible utilization in breeding programmes. Specific diversity rich areas identified through DIVA GIS can be developed into onion villages for on-farm *in-situ* conservation.

Key Words: DIVA GIS, *Allium cepa*, Andhra Pradesh, Bulb trait diversity, Onion, TSS

Introduction

Onions are one of the most ancient vegetables known to mankind. They have been cultivated for food, medicinal and religious purposes since Vedic times. Depending on the variety, an onion can be spicy, tangy and pungent or mild and sweet. Cultivated onions, with a primary centre of origin in central Asia and a secondary centre in the Near East (McCullum, 1976), are believed to have been domesticated at several places and occupy a vast area in southern and western Asia. Although, onions are cultivated almost all over the country, the major growing areas are in the states of Andhra Pradesh, Bihar, Gujarat, Karnataka, Madhya Pradesh, Maharashtra, Orissa, Tamil Nadu and Uttar Pradesh. Maharashtra ranks first in onion production with a national share of 24%.

Since its adaptation and acclimatization, onion has been subjected to continuous selection by farmers to suit diverse climatic conditions and market demands. Being cross-pollinated, it always provides scope for selection as variability is continuously created. Since the production of onion needs to be increased and sustained to meet the fast expanding domestic and export markets, exploitation of new and diverse genetic resources, having genes for higher productivity and adaptation to different agro-climatic regions, assumes great importance. Onion is extensively cultivated in the northern Telangana region of Andhra Pradesh, but the area has not been adequately

explored. Hence a survey was undertaken in this region in April 2009 to sample and study the diversity in onion landraces with a view to their possible utilization in onion improvement.

Material and Methods

Based on advice from local officials of the Department of Agriculture, we sampled onion germplasm diversity from 33 onion growing villages in three northern Telangana districts of Adilabad, Karimnagar and Nizamabad. Farmer's fields, farm stores, threshing yards and local markets were chosen as a unit for selective sampling as suggested by Huaman *et al.* (1995). That is, all 'morphotypes' in field, market or threshing yard were identified and 15–25 bulbs of each were collected, this process being repeated at each sampling site. Seed samples were also collected wherever available. Improved varieties grown in this region included "Milky white" and "Bellary Red". Care was taken to sample only landraces based on farmer's information.

Being a highly cross pollinated crop, farmers ensured the purity of their different genotypes by planting for seed with a minimum isolation distance of 500 m between populations to avoid cross contamination through accidental gene flow. Even so, upto 15% admixture was observed in some fields/threshing yards, necessitating the selection of morphotypes.

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Passport data for each sampled accession and the geographical coordinates of its sampling location were recorded, the latter using the Garmin GPS-12 system. Data were also recorded on two qualitative traits – bulb shape and colour and six quantitative traits – polar diameter (mm), equatorial diameter (mm), neck thickness (mm), bulb weight (gm), number of hearts/centers and total soluble solids (TSS). The data on quantitative traits were analyzed using descriptive statistics that included the mean, median, minimum, maximum, standard deviation (SD) and the coefficient of variation (CV). Inter-relationships among traits were assessed using bi-variate scatter plots, Pearson coefficient of correlation and regression. The multivariate techniques of ordination (using non-metric multidimensional scaling, MDS) and hierarchical clustering (using average linkage) were used to detect the presence of any possible grouping of the sampled accessions into distinct genetic classes. Ordination and hierarchical clustering were based on a proximity matrix estimated from four quantitative traits (polar diameter, equatorial diameter, neck thickness, bulb weight) and two qualitative traits (bulb shape and bulb colour) using Gower's measure of similarity (Gower, 1971). In deriving the Gower's measure of similarity, Euclidean distance was used for the four quantitative traits and simple matching coefficient was used for the two qualitative traits. Statistical analyses were carried out using GenStat 12 software. DIVA-GIS version 5.2 (www.DIVA-GIS.org) was used to assess the spatial distribution and variability. Maps on the distribution, diversity and coefficient of variation were generated from a point-to-grid analysis using the *simple* method. All analyses were based on the geo-referenced points and additional attributes of point data recorded on bulb shape, colour, weight, polar diameter, equatorial diameter and neck thickness.

Results and Discussion

A total of 74 samples (bulbs–66, seed–8) were collected from 17 villages and 9 mandals in Adilabad (33 samples), 6 villages in 5 mandals in Karimnagar (11 samples) and 10 villages of 9 mandals in Nizamabad (22 samples). The surveyed region is characterized by an average annual rainfall varying from 750–1150 mm, and temperature from 13°C to 38°C. Red soils are predominant in this region, with *chalkas*, sandy loams and deep black cotton soils in some areas. Onions are vernacularly called as *vulligadda*, *erravulligadda*, *tellavulligadda*, *itchuruvulligadda*, *mutchuvulligadda* in this region. Onion is generally grown in small holdings of 1 to 2 *guntas* (100 m²–200 m²) during

October–November and harvested in March–April. While 81% of the samples were collected directly from the farmer's fields or from the adjacent threshing yards, 19% was sampled from the local markets which were important sources of information on the varieties grown in the area. Majority of the farmers in the region grow improved varieties for commercial purposes but side by side raise land races for home consumption due to preference in taste and flavour. These varieties could be accessed in the local markets usually in the early hours of the morning when the small farmers brought their ware for sale.

A wide range of variability was observed for both qualitative and quantitative traits. Table 1 shows the distribution of the 66 accessions according to their bulb shape and colour. The sampled accessions were characterized by seven shapes and seven colours. Majority of the accessions possessed flat globe (34.8%) and globe (36.4%) shapes. White (54.5%), dark red (22.7%) and light red (13.6%) were the more commonly occurring colours. Among the quantitative traits, bulb weight, with a CV of 43% showed maximum diversity, followed by number of centres (CV = 36%), neck thickness (CV = 24%), equatorial diameter (CV = 17%), TSS (CV = 15%) and polar diameter (CV = 14%) (Table 2). The range of bulb weight, starting with a minimum of 18.0 g, extended to a maximum of 127.0 g.

Considerable diversity was observed among accessions within different bulb colour and bulb shape classes for various quantitative traits. Accessions with dark red and white colours were more diverse for all quantitative traits (Table 3). For example, among the dark red onions, average bulb weight ranged from 21.6 g to 127 g, equatorial diameter from 31.8 mm to 53.4 mm and neck thickness from 2.8 mm to 11.2 mm. Likewise, among the white types, average bulb weight ranged from 18 g to 123 g, equatorial diameter from 36.0 mm to 67.3 mm and neck thickness from 3.1 mm to 10.4 mm. However, for TSS, the white genotypes showed a wider range (8.8% to 15.6%) as compared to the dark red ones (8.8% to 10.8%). Similarly, for bulb shape, accessions with flat, flat globe and globe shapes exhibited larger diversity for all quantitative traits (Table 4). These traits, detailed in the minimal descriptors developed by NBPGR (Mahajan *et al.*, 2000), are important in establishing taxon/accession identity as well as in describing the accessions that may be recorded during the characterization and evaluation. These traits are also the basis for assigning economic value to a genotype. Total soluble solids are a measure

Table 1. Distribution of sampled accessions in different bulb shape and colour classes

Bulb shape (#Acc; %)	Accessions
Circular (3; 4.5%)	IC571932, 571938, 571944
Elliptic (1; 1.5%)	IC571906
Flat (11; 16.7%)	IC571915, 571921, 571930, 571934, 571945, 571953, 571960, 571963, 571991, 572008, 572010
Flat globe (23; 34.8%)	IC 571909, 571910, 571911, 571912, 571926, 571931, 571939, 571941, 571946, 571947, 571950, 571952, 571955, 571958, 571962, 571973, 571974, 571980, 571981, 571984, 571989, 571994, 571998
Globe (24; 36.4%))	IC 571905, 571916, 571927, 571930-1, 571937, 571943, 571948, 571954, 571956, 571959, 571964, 571965, 571968, 571969, 571970, 571972, 571978, 571982, 571986, 571993, 571997, 572001, 572004, 572012
Ovate (3; 4.5%)	IC571908, 571967, 571987
Spindle (1; 1.5%)	IC571976
Bulb colour (#Acc, %)	Accessions
Dark red (15; 22.7%)	IC571908, 571911, 571912, 571930, 571947, 571953, 571964, 571967, 571972, 571976, 571978, 571987, 571993, 572001, 572004
Light red (9; 13.6%)	IC 571932, 571938, 571944, 571948, 571952, 571956, 571960, 571963, 571981
Pink (2; 3.0%)	IC571910, 571931
Red (2; 3.0%)	IC571945, 571969
White (36; 54.5%)	IC571905, 571908, 571909, 571915, 571916, 571921, 571926, 571927, 571930-1, 571934, 571937, 571939, 571941, 571943, 571946, 571950, 571954, 571955, 571958, 571959, 571962, 571965, 571968, 571970, 571973, 571980, 571982, 571984, 571986, 571989, 571994, 571997, 571998, 572008, 572010, 572012
Whitish pink (1; 1.5%)	IC571974
Yellowish white (1; 1.5%)	IC571991

Table 2. Descriptive statistics for quantitative traits

Statistic	Average bulb weight (n = 66)	Number of centres (n = 53)	Equatorial diameter (n = 66)	Neck thickness (n = 66)	Polar diameter (n = 66)	Total soluble solids (n = 53)
Mean	59.5	1.9	50.0	6.6	40.1	11.1
Median	53.6	2.0	49.7	6.4	40.0	10.7
Min.	18.0	1.0	31.8	2.8	27.9	8.2
Max.	127.0	4.0	67.3	11.2	53.4	15.6
SD	25.62	0.70	8.59	1.56	5.48	1.71
CV (%)	43	36	17	24	14	15

SD: standard deviation; CV: coefficient of variation

of the sweetness of the genotype. Red onions are more pungent (but lower TSS) and are generally preferred at the national level (Singh, 1997), while white onions with lower pungency and high TSS are preferred by the dehydration industry (Lawande, 2001). High TSS might also enhance keeping quality (El-Aweel *et al.*, 2000). In the present survey, the highest TSS (>14%) was observed in IC572010 (15.6%, white, flat, Adilabad), IC571965 (14.9%, white, globe, Adilabad) and IC571941 (14.4%, white flat globe, Nizamabad). Among the red onions (24 accessions), the range of TSS was from 8.8% to 10.8% in keeping with the local preferences for higher pungency and less sweetness. Red onions with a high nutritional value are reported to have high anthocyanides and flavonoids and consequently a higher antioxidant and anti cancerous activity. Neck thickness is important in the bulb curing process and preventing disease entry into the bulb during storage (Singh, 1997). High estimates of heritability have

been reported for neck thickness (Mohanty, 2001). The thinnest neck (2.8 mm) was found in IC571910 (pink, flat globe) and IC571911 (dark red, flat globe) both from Karimnagar. Single centeredness is a trait that is associated with bulb firmness (Larsen *et al.*, 2009) and better storability. It is also important for the hotel industry where visual impact, presentation and appearance are essential. Accessions observed with single centres include IC 572001 (dark red, globe, Adilabad), IC571932 (light red, circular, Nizamabad), IC 572008 (white, flat, Adilabad), IC571905 (white, globe, Karimnagar) and IC572012 (white, globe, Adilabad). These cultivars hold promise for possible utilization in breeding programmes.

The relationships among the six quantitative traits are depicted in the scatter plots (Fig. 2). The plots suggest a strong positive association of bulb weight with equatorial diameter ($r = 0.91$, $n = 66$, $P < 0.001$) and polar diameter

Table 3. Variation in quantitative traits for different bulb colours

Bulb Color	Accessions	Average bulb weight (g)			Equatorial diameter (mm)			Number of centres			Polar diameter (mm)			Neck thickness (mm)			Total soluble solids								
		(#)	Mean	Mini	Max	Median	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max							
1= dark red	15	64.0	21.6	127.0	56.6	2	1	4	2	50.1	31.8	67.3	51.8	41.8	32.4	53.4	40.0	6.6	2.8	11.2	6.4	9.8	8.2	10.8	9.8
2 = light red	9	55.9	40.8	73.2	53.6	2	1	3	2	50.2	43.8	55.4	48.6	39.9	34.6	44.9	40.4	6.6	5.2	7.4	6.6	11.9	9.4	13.9	12.2
3 = pink	2	49.9	48.6	51.2	49.9	2	2	2	2	39.5	35.3	43.7	39.5	48.3	48.2	48.3	48.3	4.1	2.8	5.4	4.1	10.6	10.1	11.1	10.6
4 = red	2	54.9	47.8	62.0	54.9	2	2	2	2	49.3	47.0	51.5	49.3	41.0	40.4	41.5	41.0	8.5	7.2	9.8	8.5	10.3	10.3	10.3	10.3
5 = white	36	59.2	18.0	123.0	52.5	2	1	3	2	50.6	36.0	67.3	50.0	38.8	27.9	50.5	38.6	6.6	3.1	10.4	6.3	11.5	8.8	15.6	10.8
6 = whitish pink	1	77.6	77.6	77.6	77.6	3	3	3	3	53.3	53.3	53.3	53.3	44.4	44.4	44.4	44.4	5.4	5.4	5.4	5.4	10.8	10.8	10.8	10.8
7 = yellowish white	1	45.8	45.8	45.8	45.8	2	2	2	2	48.0	48.0	48.0	48.0	37.8	37.8	37.8	37.8	6.0	6.0	6.0	6.0	8.5	8.5	8.5	8.5

Table 4. Variation in quantitative traits for different bulb shapes

Bulb shape	Accessions (#)	Average bulb weight (g)			Number of centres			Equatorial diameter (mm)			Polar diameter (mm)			Neck thickness (mm)			Total soluble solids								
		Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max						
1 = circular	3	44.2	40.8	48.0	43.8	1	1	2	1	47.6	45.6	48.6	48.6	36.8	34.6	37.9	37.9	6.3	5.6	6.6	6.6	12.3	10.7	13.9	12.3
2 = elliptic	1	21.6	21.6	21.6	21.6	2	2	2	2	31.8	31.8	31.8	31.8	32.4	32.4	32.4	32.4	5.8	5.8	5.8	5.8	9.1	9.1	9.1	9.1
3 = flat	11	61.0	38.0	94.4	53.6	2	1	2	2	51.1	40.4	60.1	49.6	40.6	33.1	46.8	41.5	6.1	3.1	9.8	6.1	10.9	8.2	15.6	10.2
4 = flat globe	23	73.8	42.6	123.0	74.8	2	1	4	2	53.6	35.3	67.3	55.2	42.4	33.5	51.2	42.3	6.6	2.8	11.2	6.7	11.1	9.0	14.4	10.8
5 = globe	24	53.4	18.0	127.0	52.4	2	1	4	2	49.1	36.0	67.3	49.5	39.1	27.9	53.4	39.2	6.7	4.9	10.4	6.2	11.1	9.0	14.9	10.6
6 = ovate	3	33.6	20.0	53.6	27.2	2	2	2	2	40.4	36.0	48.7	36.6	35.4	32.0	40.0	34.1	6.6	5.7	7.3	6.8	13.2	13.2	13.2	13.2
7 = spindle	1	22.0	22.0	22.0	22.0	1	1	1	1	33.6	33.6	33.6	33.6	34.5	34.5	34.5	34.5	6.4	6.4	6.4	6.4	10.3	10.3	10.3	10.3

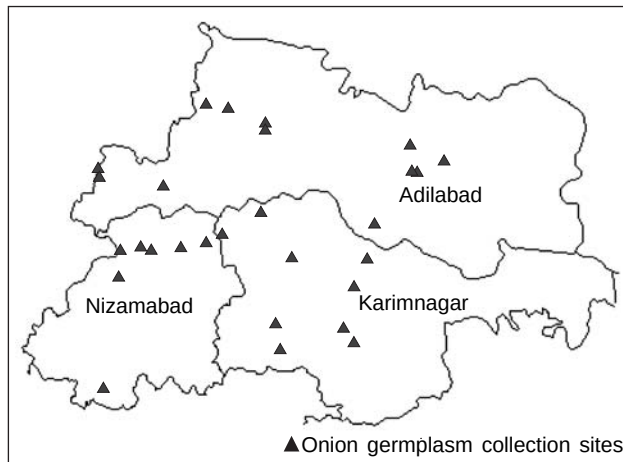


Fig. 1. Onion germplasm collection locations in northern Telangana

($r = 0.78$, $n = 66$, $P < 0.001$). The latter two also exhibit a positive relationship ($r = 0.61$, $n = 66$, $P < 0.001$), as do equatorial diameter and neck thickness ($r = 0.50$, $n = 66$, $P < 0.001$). The strong positive relationship of bulb weight with equatorial diameter and polar diameter suggests that bulb weight (Y) could be reliably predicted from the data of the two explanatory variables equatorial diameter (X_1) and polar diameter (X_2). A regression modeling of this relationship delivers the following prediction equation

$$Y = 31.8 - 3.59 X_1 + 0.057 X_1^2 + 1.48 X_2 \quad (R^2 = 96\%, \text{ root mean square error} = 5.04, P < 0.001, n = 66)$$

High correlation of bulb weight with equatorial and polar diameter was also reported by Trivedi *et al.* (2006), who also reported high estimates of heritability for these traits. As higher yields are associated with large bulbs with a diameter greater than 45 mm (Satyendrakumar *et al.*, 2007), an assessment of equatorial and/or polar diameter in germplasm accessions could give a good estimate of the bulb weight and in turn the yield potential for selection of promising accessions for yield improvement. In the present collection, accessions IC571972 (127 g, dark red, globe) and IC571973 (123 g, white, flat globe) both from Adilabad had the largest bulbs (>120 g). Some promising accessions for equatorial diameter (>60 mm) include IC571912, (Karimnagar), IC571972(Adilabad) and IC571973 (Adilabad).

Ordination plot (Fig. 3) based on non-metric MDS suggests the presence of three distinct groups, mainly

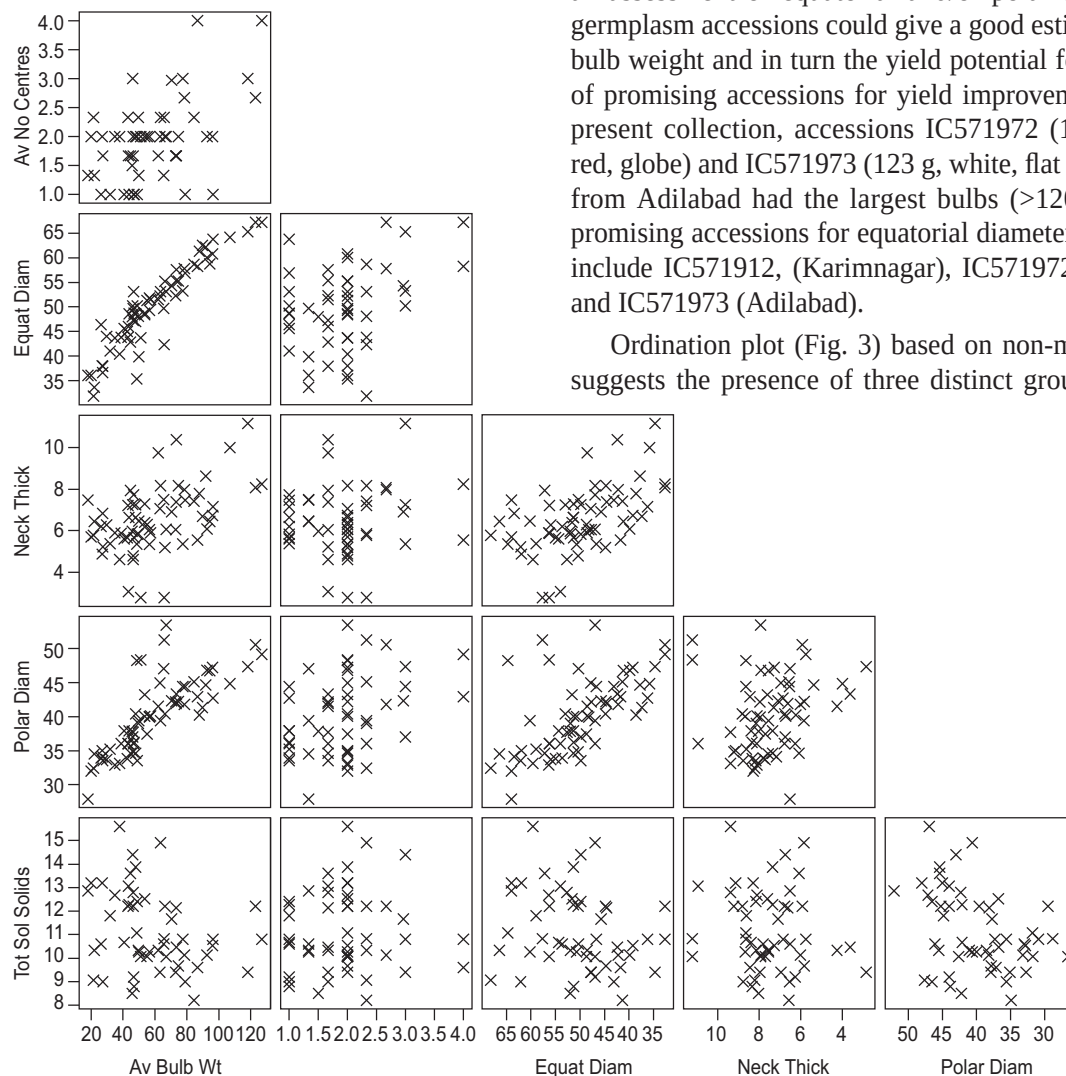


Fig. 2. Scatter plots of relationship among quantitative traits

driven by bulb shape and colour. Thirty five accessions in group 1 were characterized by white coloured onions with flat, flat globe and globe shapes; the 23 accessions in group 2 were a mixed set; while the eight in group 3 were characterized by flat globe onions of dark red, light red, red and whitish pink colours. This grouping, to a large extent, was confirmed by hierarchical clustering (Fig. 4). Accessions from the three districts were distributed in all the three groups suggesting the absence of any boundaries for germplasm exchange. Further, except for bulb weight which was highest in group 3, the mean values for the other quantitative traits did not significantly differ among the groups.

Geographical Information System (GIS) mapping may be effectively used for documentation, diversity analysis, identifying gaps in collection, assessment of loss of diversity, developing new strategies for conservation, and sustainable utilization, particularly in the wake of recent international developments related to food and nutritional security. GIS mapping has been successfully used in assessing biodiversity and in identifying areas of high diversity in horsegram (Sunil *et al.*, 2008), linseed (Sivaraj *et al.*, 2009) and *Jatropha curcas* (Sunil *et al.*,

2009). In the present study, grid maps generated using diversity analysis of DIVA-GIS for bulb colour indicated that eastern and southwestern parts of Adilabad and Nizamabad were highly diverse while the western areas of Adilabad and Karimnagar were less so (Fig. 5); for bulb shape, southwestern Adilabad showed high diversity (Fig. 6); collections from western parts of Adilabad and Nizamabad were more uniform for polar diameter as compared to onion germplasm from eastern Adilabad and Karimnagar (Fig. 7); equatorial diameter of the bulbs showed least variation over all locations (Fig. 8); collections from Karimnagar were highly diverse for neck thickness (Fig. 9); and the most diverse accessions for bulb weight could be collected from northeastern regions of Adilabad (Fig 10).

The analysis of the 66 collections indicates that local populations in specific pockets of Adilabad (Bhaisa, Nirmal, Kagaznagar, Tandur, Bhimni), Karimnagar (Sircilla, Ibrahimpatnam) and Nizamabad (Armur, Yellareddy, Morthad, Kamrapalli) harbor wide variation for bulb colour, bulb shape, bulb weight, neck thickness and %TSS. Rich landrace diversity continues to be grown in this region despite the commercial production of

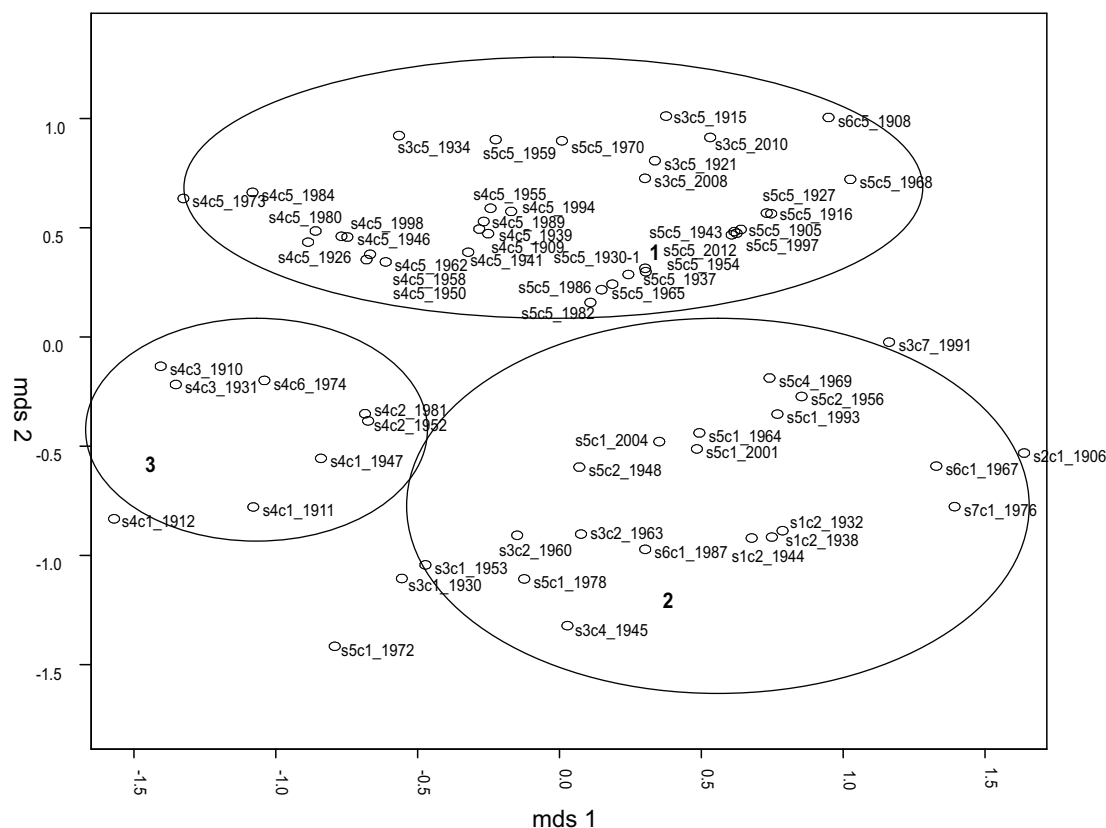


Fig. 3. Ordination plot of 66 onion accessions based on non-metric multi-dimensional scaling

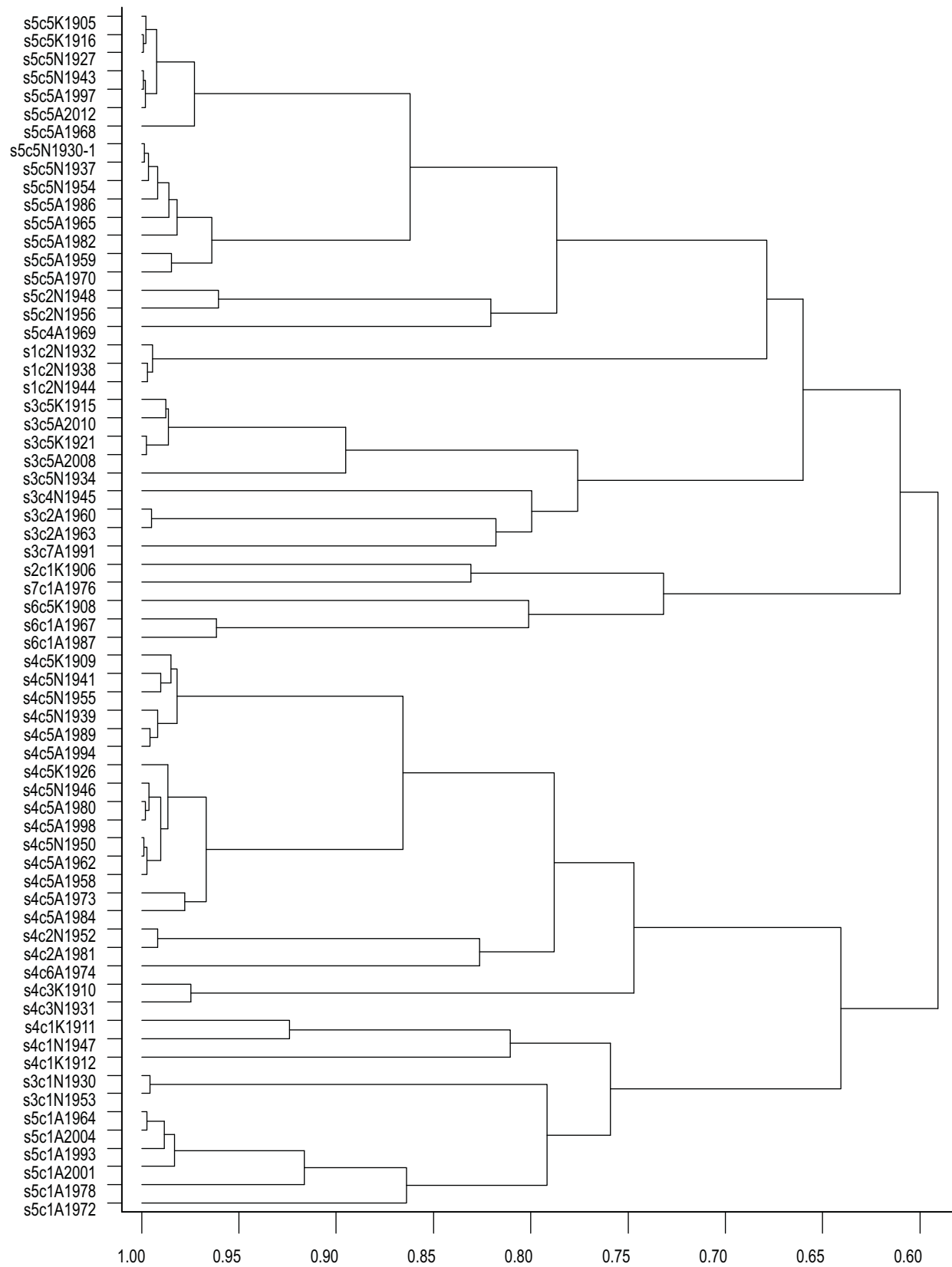


Fig. 4. Hierarchical clustering of 66 onion accessions

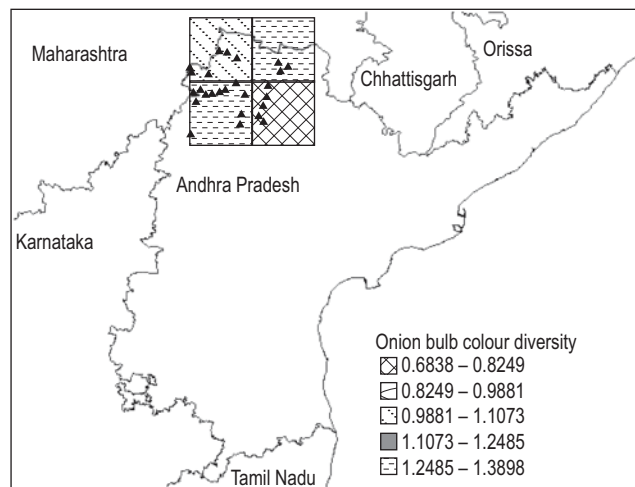


Fig. 5. Grid map showing diversity in bulb colour

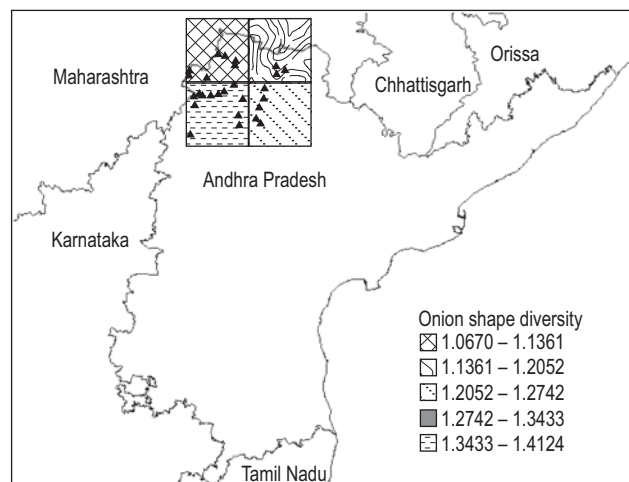


Fig. 6. Grid map showing diversity in bulb shape

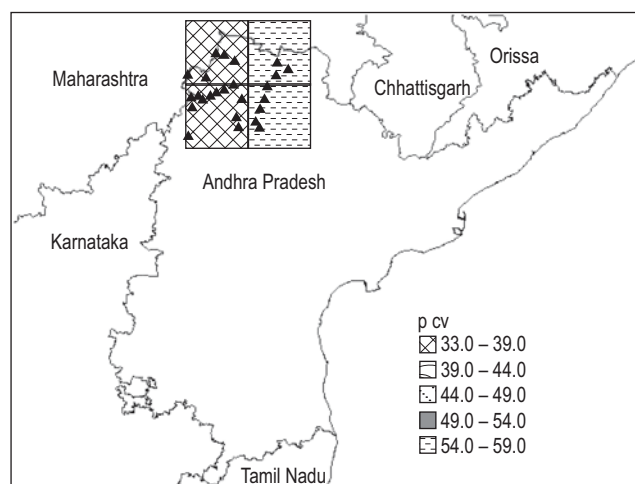


Fig. 7. Grid map showing variation in Polar diameter of bulb

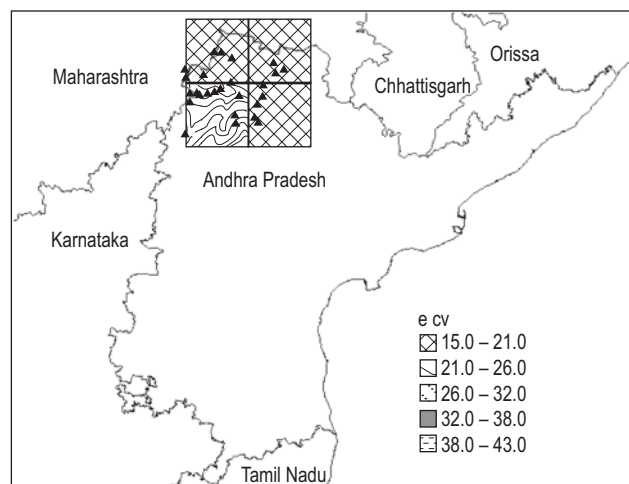


Fig. 8. Grid map showing variation in Equatorial diameter of bulb

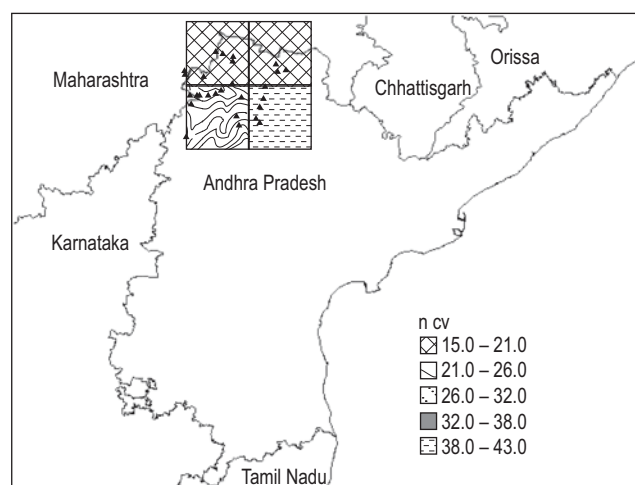


Fig. 9. Grid map showing variation in neck thickness of bulb

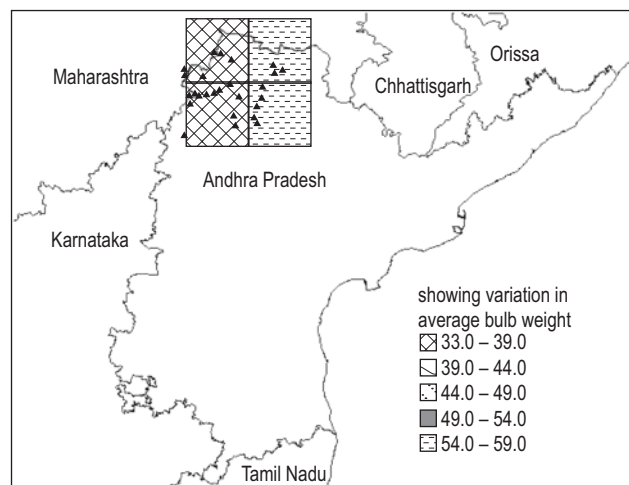


Fig. 10. Grid map showing variation in bulb weight

improved/released varieties. It is suggested that specific diversity rich areas identified can be developed into onion villages for on-farm *in-situ* conservation. The accessions collected are being maintained at the NRC O&G, Pune, and being characterized and evaluated in field for selection and possible utilization in the national onion breeding programmes.

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Genetic Divergence Studies in Drought Promising Rice Genotypes based on Quality Characters

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Grain quality characteristics of 24 drought promising genotypes were evaluated under irrigated and drought conditions for studying variability and genetic divergence. Differences among the genotypes are observed to be highly significant for all the characters; between the environments head rice recovery, alkali spreading value, water uptake, kernel length after cooking and yield are significant, while genotype x environment interaction is only significant for hulling, milling, head rice recovery and water uptake. Water uptake, alkali spreading value and head rice recovery are governed by additive gene action and contributed maximum towards divergence with kernel length after cooking. The D² analysis revealed that genotypes exhibited considerable diversity and were grouped into seven clusters, where cluster I was the largest and contained 18 genotypes while, rest of the clusters contained single genotypes. Based on clustering pattern and *per se* performance five genotypes were identified, which may be used in breeding programme to obtain improved genotypes with desirable attributes for stress environments.

Key Words: Drought tolerance, D² analysis, Variability, Quality characters, Rice

Introduction

India has the largest area under rice production in the world (47 million ha). Rice environments in India are extremely diverse with rainfed lowland being predominant across 15 million ha in eastern India where the water supply is unpredictable and droughts are common (Wade *et al.*, 1999). Drought resistance appears to be the most important single factor in increasing and stabilizing of rice production in rainfed areas (Chaudhary and Rao, 1982). In recent times, there is increasing demand for good grain quality in national as well as in international market. In order to develop genotypes with desirable traits, it is needful to collect, evaluate and utilize the available diversity to suit specific need with regard to specific ecosystem. D² statistics are expected to provide reliable basis for selecting desirable elite and diverse parents for hybridization and exploitation of variability. Keeping this in view, the present investigation was carried out with 24 drought promising rice genotypes to obtain wide array of cross combinations.

Materials and Methods

Field screening experiments for large number of entries (72 from AYT 100-120 days, 38 from AYT > 120 days and 216 from OYT under IRRI-India Drought Breeding

Network) were conducted to identify drought tolerant genotypes during dry season of 2007 and 2008 at Central Rice Research Institute, Cuttack. The experiments were laid out in randomized block design with three replications under both control irrigated (E₁) and drought stress (E₂) conditions. Plants were grown under adequate soil moisture for 30 days after germination under both the conditions. The irrigation was withdrawn for 30 days and beyond, till the susceptible check shows permanent wilting in the stress field, subsequently the plot was re-watered for recovery. Soil moisture content (SMC) during stress period was monitored through periodical soil sampling at 0–15, 15–30 cm soil depth after suspension water. The drought scores and recovery observations were taken as per SES method, 1 to 9 scales (IRRI, 1996). In the control field plants were grown under normal irrigated condition maintaining water level for 5±2 cm till dough stage. Observations were recorded on five competitive plants of the middle row of each plot for yield and 12 quality parameters. The 24 genotypes in the present study were selected on the basis of their drought tolerance and yield potential under severe stress condition, and carried out for quality analysis.

Seed samples were collected after harvest with 14% moisture from both the treatments were analyzed for

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hulling (H), milling (M), head rice recovery (HRR), amylose content (AC), alkali spreading value (ASV) and elongation ratio (ER) as per method given by Govindswamy and Ghosh, 1969. The kernel length (KL) and kernel width (KW) of the grains were measured with dial micrometer. Water uptake (WU) and volume expansion ratio (VER) were determined (Beachell and Stansel, 1963). Pooled analysis of variance (ANOVA) was used to quantify the genetic differences among the genotypes. Multivariate analysis of genetic divergence among varieties was done using Mahalanobis D^2 statistics (1936) and grouping of varieties into clusters by Tochers method (Rao, 1952). The character-wise rank totals were used to calculate the per cent contribution of each character to the total divergence. Averages inter- and intra-cluster distance, ANOVA, coefficient of variation and heritability in broad sense and genetic advance were estimated as per the method given by Singh and Chaudhary (1985).

Results and Discussion

The analysis of variance for the design of experiment indicated the existence of significant variability among the 24 genotypes of rice for all the characters under study (Table 1). The presence of large amount of variability is due to diverse source of the materials as well as environmental influence, which predominantly governed the phenotype. The analysis of variance for pooled data showed that genotype x environment interaction is significant for hulling, milling, head rice recovery and water uptake. This suggested that broad range of diversity existed among genotypes and locations for above said characters

and that the performance of genotypes was differential over location. Overwhelming effect of environment on genetic performance along with G x E interaction suggests that rice varieties bred for one region may not do well in other regions. These findings call for widening the genetic base used in breeding programmes. High genotypic and phenotypic coefficient of variation and high heritability along with genetic advance were found for WU, ASV and HRR while low value of same selection parameters were recorded for rest of the characters (Table 2). These results are in accordance with the findings of Bose *et al.* (2007) and Vanaja and Babu (2006).

Based on D^2 values the genotypes were grouped into 7 distinct non-overlapping clusters (Fig. 1). Cluster I contained approximately 75% of total genotypes under study. Interestingly, only one genotype each constituted the rest of the clusters (Table 3). These monogenotypic clusters included different genotypes from different regions of different countries, indicating that clustering of the genotype did not follow their geographic distributions. Absence of correlation between genetic diversity and geographic diversity suggests that forces other than geographic origin, such as exchange of breeding material, genetic drift, and selection are responsible for diversity, as reported earlier (Murthy and Arunachalam, 1966). A noteworthy observation was that all the check varieties MTU 1010, Swarna and Sambha Mahsuri grouped into different clusters without any genotype indicates their high degree of heterogeneity.

The statistical distances represent the extent of genetic diversity amongst clusters. The average D^2 value within

Table 1. Pooled analysis of variance for quality characters in drought promising lines

Characters	Pooled analysis				
	Environment (1)	Genotype (23)	Replication (1)	Genotype x Environment (G x E) (23)	Error (47)
Hulling (%)	13.50	16.37**	2.34	13.01**	8.67
Milling (%)	3.41	23.48**	15.76**	12.80**	4.25
HRR (%)	58.59**	432.30**	6.51*	52.36**	4.71
KL (mm)	0.01	0.69**	0.02	0.03	0.01
KB (mm)	0.02	0.12**	0.01	0.04	0.01
L/W	0.01	0.33**	0.01	0.05	0.01
ASV	3.96**	13.41**	0.21	0.61	0.19
WU (ml/100/gm)	77748.1**	22399.8**	450.67**	2922.30**	700.14
VER	0.02	0.03**	0.09	0.02	0.01
KLAC (mm)	0.41**	1.96**	0.01	0.13	0.04
ER	0.01	0.05**	0.01	0.01	0.01
AC (%)	1.96	49.81**	1.44	1.59	0.67

*, **, Significant at 5% and 1% levels, respectively.

HRR: Head Rice Recovery, KL: Kernel Length, KW: Kernel Width, L/W: Kernel Length/ Kernel Width, ASV: Alkali Spreading Value, WU: Water uptake, VER: Volume expansion ratio, KLAC: Kernel Length after Cooking (mm), ER: Elongation Ratio & AC: Amylose Content

Table 2. Estimates of mean, range, coefficient of variation, heritability and genetic advance for 12 characters in drought promising rice

Characters	Mean $\pm$ SE m	Range		Coefficient of Variation		Heritability h^2 (b)	Genetic advance	Genetic advance (% of mean)
		Min.	Max.	GCV	PCV			
Hulling (%)	73.57 $\pm$ 1.07	69.33	78.17	2.46	4.33	32.3	2.72	3.69
Milling (%)	62.56 $\pm$ 1.16	58.25	66.00	2.43	5.14	22.4	1.90	3.03
HRR (%)	31.00 $\pm$ 3.28	21.00	51.83	24.30	35.56	46.7	13.59	43.84
KL (mm)	5.62 $\pm$ 0.15	4.87	6.07	3.90	7.45	27.4	0.30	5.39
KB (mm)	2.18 $\pm$ 0.07	1.98	2.41	3.72	8.70	18.3	0.09	4.20
L/W	2.60 $\pm$ 0.12	2.39	2.85	2.36	11.66	4.1	0.03	1.26
ASV	5.17 $\pm$ 0.46	3.00	7.00	29.35	36.79	63.6	3.20	61.82
WU (ml/100/gm)	227.42 $\pm$ 19.29	117.50	360.00	31.77	37.96	70.0	159.65	70.20
VER	4.06 $\pm$ 0.05	3.94	4.25	1.74	3.30	28.0	0.10	2.44
KLAC (mm)	9.67 $\pm$ 0.19	8.63	10.52	5.90	7.57	60.7	1.17	12.14
ER	1.73 $\pm$ 0.04	1.61	1.81	2.53	6.27	16.3	0.05	2.69
AC (%)	24.48 $\pm$ 1.22	18.62	29.57	8.81	15.03	34.4	3.33	13.63

HRR: Head Rice Recovery, KL: Kernel Length, KW: Kernel Width, L/W: Kernel Length/ Kernel Width, ASV: Alkali Spreading Value, WU: Water uptake, VER: Volume expansion ratio, KLAC: Kernel Length After Cooking (mm), ER: Elongation Ratio, AC: Amylose Content

Table 3. Distribution of 24 drought promising rice genotypes in different clusters

Cluster No.	Number of genotypes	Genotypes included	
		Min.	Max.
I	18	ARB 7, ARB 8, ARB 3, IR 78937-B-4-B-B-B, Tipuradhan, IR 70844-10-SRN-43-1-B-B-1-1, IR 55419-04, IR 70215-70-CPA-3-4-1-3, IR 69515-6-KKN-4-UBN-4-2-1-1-1, IR 78875-53-2-2-2, CBO-15-24, DGI 307, IR 74371-46-1-1, IR 83614-503-B, IR 74371-54-1-1, IR 74371-3-1-1, IR 78875-131-B-1-4 and IR 78877-181-B-1-2	
II	1	MTU-1010	
III	1	IR 55423-01	
IV	1	Swarna	
V	1	Sambha Mahsuri	
VI	1	IR 72667-16-1-B-B-3	
VII	1	IR 74371-70-1-1	

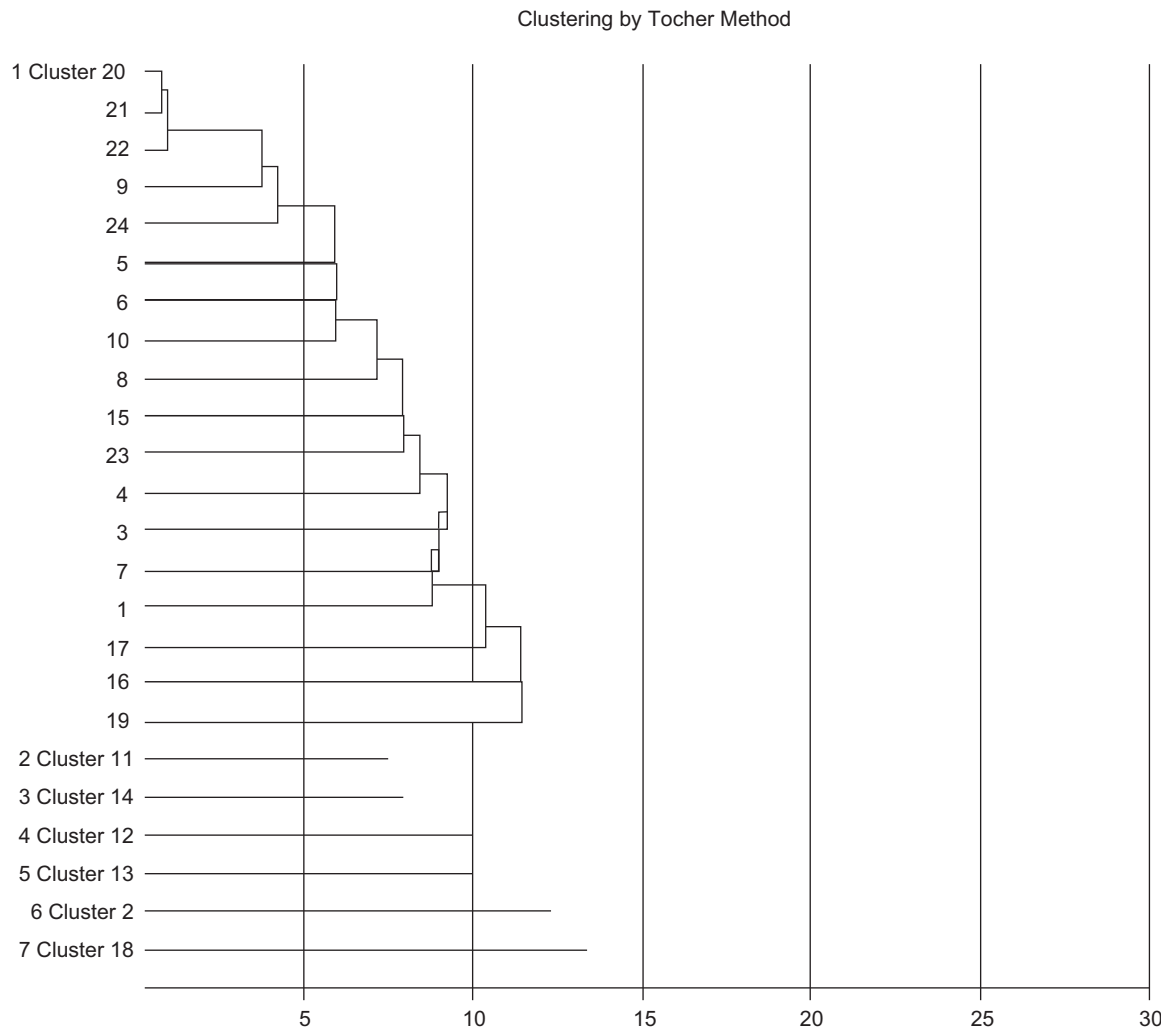


Fig. 1. Different Clusters showing the position of drought promising genotypes (mentioned by serial number)

and between clusters revealed that intra-cluster divergence was possessed by cluster I only ($D^2=3.06$) which included 18 genotypes because rest of the cluster included only one genotype (Table 4). The inter-cluster distance was maximum between cluster IV and VI (6.48). The closest into cluster distance was between cluster III and VI (3.16) which indicated that genotypes of these clusters had maximum number of common gene complexes. High statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates.

The genetic differences between the clusters were reflected in cluster means (Table 5). The highest average cluster mean was reported for milling and AC in cluster IV, for HRR and VER in cluster V and for ER in cluster III while, cluster VII possessed highest mean for KW and

Table 4. Intra- and inter-cluster D^2 among seven clusters

Clusters	I	II	III	IV	V	VI	VII
I	3.06	3.77	4.06	4.21	5.08	4.53	4.36
II		0.00	5.19	3.89	5.59	6.09	4.77
III			0.00	4.77	3.16	4.60	4.60
IV				0.00	5.11	6.48	4.72
V					0.00	4.81	5.79
VI						0.00	5.17
VII							0.00

KL after cooking. All the above-said clusters had single genotype. The cluster I with 18 genotypes exhibited highest mean value for hulling. It is observed that the genotypes desirable for different traits belonged to different clusters. The genotype IR 72667-16-1-B-B-3 in cluster VI registered the highest mean value for KL, L/W, and ASV and WU. The clusters contributing maximum to D^2 values are to

Table 5. Cluster mean for 11 characters

Cluster No.	H (%)	M (%)	HRR (%)	KL (mm)	KW (mm)	L/W	ASV	WU (ml/100/gm)	VER	KLAC (mm)	ER	AC (%)
I	74.58**	62.85	30.72	5.70	2.21	2.59	5.35	276.39	4.08	9.92	1.75	25.09
II	73.33	61.33	14.67	5.61	2.10	2.67	3.00*	275.00	4.00	9.67	1.72	21.18
III	67.67*	63.00	47.33	5.11	2.27	2.25*	3.00*	153.33	4.25**	9.27	1.82**	19.13*
IV	74.33	64.67**	46.00	5.10	2.16	2.36	3.00*	136.67*	3.92*	7.87*	1.54*	28.25**
V	71.00	61.50	56.33**	4.63*	1.69*	2.75	3.00*	140.00	4.25**	8.07	1.74	24.96
VI	72.17	59.33*	33.33	6.17**	1.84	3.35**	7.00**	301.67**	4.00	10.10	1.63	27.58
VII	73.00	63.33	14.50*	6.08	2.68**	2.36	3.33	153.33	4.17	10.43**	1.72	19.91
No. of times ranked 1 st	9	0	28	21	4	27	58	38	1	69	0	21
Contribution (%)	3.26	0.00	10.14	7.61	1.45	9.78	21.01	13.77	0.36	25.00	0.00	7.61

be given greater emphasis for deciding the clusters for the purpose of further selection and hybridization (Table 5). The characters contributing towards genetic divergence showed that maximum genetic divergence was observed for KLAC (25.00%) followed by ASV (21.01%), WU (13.77%) and HRR (10.14%). Hence, above said characters were considered to be important traits and may be used as selection parameters in segregating generations. The least and negligible contribution towards divergence was observed for milling and ER (0.00%). Similar results were earlier reported by Subudhi *et al.* (2009).

Intercrossing of divergent genotypes with desirable traits would lead to greater opportunity for maximum amount of heterosis and utilize them for multiple crossing programmes to accumulate favorable genes in single genotypes. In the view of above discussion, variation in ASV, WU and HRR offers great potential in selecting better genotype for stress environment. There is need to develop rice varieties that will produce acceptable yields in both water-limited and favourable environments with better quality traits, hence, on the basis of inter-cluster distance and *per se* performance, the genotypes *viz.*, Swarna, MTU 1010, Sambha Mahsuri, IR 72667-16-1-B-B-3 and IR 74371-70-1-1 grouped in to different clusters could be used in breeding programme to obtain improved genotypes for water limiting conditions.

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Genetic Divergence under Three Environments in a Minicore Collection of Chickpea (*Cicer arietinum* L.)

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Two hundred and three germplasm lines of minicore collections obtained from ICRISAT, Hyderabad were evaluated for eight quantitative traits under three environments viz. E1 (rainfed 2004–05), E2 (rainfed 2005–06) and E3 (irrigated 2005–06). Mahalanobis' D2 statistic was applied. These genotypes were grouped into 20, 16 and 25 clusters in E1, E2 and E3, respectively. In the present study in all the three environments, the genotypes of different geographic origin were randomly distributed in the clusters. Thus, there is no parallelism between the genetic distance and geographical diversity. The formation of 16, 10 and 18 distinct solitary clusters in E1, E2 and E3, respectively may be due to intensive natural or human selection for diverse adaptive gene complex. The pairs of clusters revealing maximum genetic diversity were identified for all the three environments. It has been suggested that for varietal improvement the hybridization among the genotypes of divergent clusters should be done rather than depending on those genotypes of the cluster having minimum divergence. Genotypes of cluster XIX (ICC13124) had the highest mean value for pod number and earliness in E1. In E2, the genotypes of cluster XV (ICC12654) and XVI (ICC9848) were superior in respect of plant height, pods/plant and 100 seed weight, respectively. In E3, the genotype of cluster XVI (ICC13124) had the highest mean value for seed yield. Cluster XXIII (ICC6279) had the early maturing genotype and cluster XVIII (ICC5879) was superior in respect of pod number and tertiary branches/plant and cluster V (ICC 6816), cluster XI (ICC10341) and cluster XIII (ICC5504) had the tall genotypes. Therefore, these genotypes may be involved in multiple crossing programme to recover transgressive segregates.

Key Words: Chickpea, Genetic divergence, Minicore collection, Quantitative traits

Introduction

The germplasm is the reservoir of genetic diversity, which is base to meet the changing need for developing improved crop varieties. It is also important that considerable variability for economic traits must exist in the germplasm for better exploitation following recombination breeding or selection. The need of parental diversity in optimum magnitude to obtain superior genotypes to recover transgressive segregates has also been repeatedly emphasized (Murthy and Anand, 1966; Arunachalam, 1981). Earlier workers considered genetic distance in the place of origin as index of genetic diversity and used it for selection of parents for hybridization. However the genetic diversity of selected parents is not always based on factors such as geographical diversity/ place of release (Murthy and Arunachalam, 1969; Bhatt, 1970; Gupta *et al.*, 1972). Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as D² statistic and cluster analysis. These procedures characterize genetic

divergence using the criterion of similarly or dissimilarly based on the aggregate effect of a number of agronomically important characters. Genetic diversity is considered to be important for realizing heterotic response in F₁ and a broad spectrum of variability in segregating generations (Arunachalam, 1981). Genetic relationship among genotypes can be measured by similarity or dissimilarity of any number of quantitative characters assuming that the difference between characters of genotypes reflects the divergence of genotypes. In heterosis breeding programme the diversity of parents is always emphasized. More diverse the parent within a reasonable range, better the chances of improving economic characters under consideration in the resulting offspring. Mahalanobis's (1936) D² Statistic is a very sensitive tool for measuring genetic divergence based on quantitative traits and is widely used by many geneticists and breeders for selecting divergent parents for hybridization aiming at yield improvement in chickpea. The present investigation was conducted to identify diverse genotypes for yield and yield component traits

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for their use in chickpea improvement programme. In view of this fact, 203 chickpea minicore collections were evaluated for this study. (i) to determine the magnitude of variability among the germplasm collection for yield and other morpho-physiological traits, (ii) to determine the grouping pattern of genotypes in different clusters and (iii) to identify genetically divers and agronomically desirable genotypes for exploitation in a breeding programme aimed at seed yield potential in chickpea.

Materials and Methods

The experimental material for the present study comprised of 203 chickpea germplasm lines from the minicore collection (Upadhyay and Ortiz, 2001) obtained from ICRISAT, Hyderabad (Andhra Pradesh). These lines were evaluated for assessing genetic diversity under three environments (E_1 , E_2 and E_3) for agronomic traits. The sources of these lines are given in Table 1. Experiments were conducted during *rabi* 2004–05 and 2005–06 under rainfed and irrigated situation at GPB garden, College of Agriculture, Dharwad (Karnataka) in medium black soils in Randomized Complete Block Design with two replications. Each genotype was grown in a single row of 4 m length with 30 cm spacing between rows and 10 cm within the row. Recommended agronomic practices were followed during the period of crop growth in both the situation. The crop was maintained free from weeds, diseases and pests by adopting appropriate plant protection measures. In irrigated situation, two irrigations were provided one at flowering and other at pod formation stage. Observations were recorded for days to 50% flowering (DFF) on line basis. While plant height (PLHT) (cm), number of primary branches per plant (PB), number of secondary branches per plant (SB), number of tertiary branches per plant (TB), number of pods per plant (PPP), seed yield per plant (YPP) and 100-seed weight (SDWT) on five randomly selected plants. Adjusted mean values for all the characters of test genotypes (203) and the estimates of error mean squares were obtained following Federer (1956) and used for subsequent statistical analyses. The Mahalanobis' D^2 statistic analysis was conducted to estimate the intra and inter-cluster distances and to group the genotypes into different clusters. The appropriate number of clusters to group 203 genotypes was determined following the sequential pseudo F-ratio tests.

Results and Discussion

The clustering procedure used in grouping the 203 germplasm lines included in the study comprise the

minicore collections of chickpea which represents the whole range of variation of cultivated species for the assessment of genetic diversity considering eight quantitative characters in three environments. Statistical distance (D^2 value) indicated the index of genetic diversity among the clusters. It would, therefore, be logical to effect crosses between genotypes belonging to clusters separated by the estimates of statistical distances. Based on D^2 values 203 genotypes were grouped into twenty, sixteen and twenty-five clusters in E_1 , E_2 and E_3 , respectively (Table 2) indicating the presence of appreciable amount of diversity among the genotypes under study. This suggested ample scope for selection of superior and diverse genotype for use in programme aimed at enhancing genetic yield potential of chickpea.

The maximum number of genotypes (157) were grouped into cluster II followed by cluster V with 22 genotypes and cluster XI with 5 genotypes. Remaining clusters (III, IV, VI, X and XII to XX) were all solitary, each containing a single genotype. The intra-cluster D^2 values ranged from 140.54 to 212.24 (Table 3–5). The average inter-cluster D^2 value between cluster II, XIII, XI, XV and cluster XX was maximum followed by descending order between these with cluster XIX, XVIII, XIV and XII suggesting that genotypes in cluster XX were relatively more diverse than genotypes in the above selected clusters.

In E_2 , the largest clusters were II, III, IV and IX which comprised of 105, 58, 15 and 10 genotypes, respectively while cluster I and X had 3 and 2 genotypes. The remaining clusters (V, VI, VII, VIII and XI to XVI) were all solitary each containing single genotype. In E_3 , the clusters II, IV and III were the largest comprising 88, 44 and 34 genotypes, respectively. Clusters VI and VIII had 8 and 5 genotypes, respectively while clusters XIX and III had 3 genotypes each. However remaining 18 clusters were solitary clusters. In the present study in all the three environments, the genotypes of different geographic origin were randomly distributed in the clusters. It was observed that clusters having more than one genotype included the genotypes originating from different eco-geographical regions and that the genotypes belonging to the same eco-geographical region were included in different clusters suggesting that geographical diversity does not necessarily represents genetic diversity. This was in agreement with the results obtained earlier in chickpea by various workers (Ramanujam, 1975; Singh and Bains, 1982; Arora, 1992; Jeethava *et al.*, 2000; Jeena and Arora,

Table 1. The sources of chickpea minicore germplasm collections

Sl. No.	ICC No.	Source country	Sl. No.	ICC No.	Source country	Sl. No.	ICC No.	Source country
01	16207	Myanmar	62	7184	Turkey	123	11627	India
02	13523	Iran	63	12654	Ethiopia	124	7819	Iran
03	637	India	64	3325	Cyprus	125	12155	Bangladesh
04	14831	India	65	6802	Iran	126	3631	Iran
5	16903	India	66	8195	Pakistan	127	283	India
06	4639	India	67	11498	India	128	4657	India
07	8261	Turkey	68	3218	Iran	129	4418	Iran
08	6816	Iran	69	11584	India	130	7668	Russia and CISs
09	11764	Chile	70	5845	India	131	3230	Iran
10	9895	Afghanistan	71	11944	Nepal	132	6874	Iran
11	13357	Iran	72	7308	Peru	133	13219	Iran
12	5613	India	73	5878	India	134	15294	Iran
13	8058	Iran	74	14402	ICRISAT	135	13461	Iran
14	1083	Iran	75	10945	India	136	16487	Pakistan
15	10341	Turkey	76	8855	Afghanistan	137	13187	Iran
16	3761	Iran	77	3362	Iran	138	7441	India
17	8607	Ethiopia	78	1915	India	139	9643	Afghanistan
18	15612	Tanzania	79	15610	India	140	2629	Iran
19	9002	Iran	80	9755	Afghanistan	141	15868	India
20	13599	Iran	81	13441	Iran	142	3421	Israel
21	12916	India	82	2277	Iran	143	1180	India
22	16915	India	83	16261	Malawi	144	4182	Iran
23	15406	Morocco	84	4872	India	145	8522	Italy
24	1230	India	85	13764	Iran	146	14077	Ethiopia
25	2969	Iran	86	13863	Ethiopia	147	12537	Ethiopia
26	6279	India	87	13892	Ethiopia	148	2884	Iran
27	5434	India	88	2072	India	149	2720	Iran
28	2242	Algeria	89	15802	Syria	150	12866	Ethiopia
29	5504	Mexico	90	456	India	151	6877	Iran
30	1194	India	91	13283	Iran	152	867	India
31	11664	India	92	8621	Ethiopia	153	12299	Nepal
32	4918	India	93	15333	Iran	154	Annigeri 1	India
33	13124	India	94	11879	Turkey	155	708	India
34	9942	India	95	15888	India	156	2990	Iran
35	95	India	96	14595	India	157	14098	Ethiopia
36	791	India	97	12851	Ethiopia	158	15264	Iran
37	440	India	98	9862	Afghanistan	159	1164	Nigeria
38	506	India	99	16524	Pakistan	160	KAK 2	India
39	12307	Myanmar	100	12726	Ethiopia	161	12328	Cyprus
40	4814	Iran	101	12037	Mexico	162	6537	Iran
41	4841	Morocco	102	14815	India	163	15618	India
42	1923	India	103	2919	Iran	164	3776	Iran
43	6579	Iran	104	16796	Portugal	165	1392	India
44	2210	India	105	12947	India	166	15606	India
45	15518	Morocco	106	10755	Turkey	167	2580	Iran
46	16269	Malawi	107	1422	India	168	2263	India
47	11378	India	108	1098	Iran	169	5879	India
48	2065	India	109	11284	Russia and CISs	170	10393	India
49	11121	India	110	8350	India	171	1161	Pakistan
50	12824	Ethiopia	111	13077	India	172	1356	India
51	14799	India	112	14051	Ethiopia	173	5383	India
52	7315	Iran	113	1398	India	174	5639	India
53	1882	India	114	G 130	India	175	4463	Iran
54	4495	Turkey	115	1397	India	176	1431	India
55	14669	India	116	7571	Israel	177	9848	Afghanistan
56	11198	India	117	1510	India	178	2507	Iran
57	4593	India	118	1205	India	179	1715	India
58	14778	India	119	9402	Iran	180	6571	Iran
59	12028	Mexico	120	13524	Iran	181	12492	ICRISAT
60	15567	India	121	3512	Iran	182	13816	Russia and CISs
61	3946	Iran	122	15435	Morocco	183	67	India

contd

Table 1 contd....

Sl. No.	ICC No.	Source country	Sl. No.	ICC No.	Source country	Sl. No.	ICC No.	Source country
184	7867	Iran	191	1052	Pakistan	198	4533	India
185	L 550	India	192	7272	Algeria	199	6811	Iran
186	8384	India	193	8318	India	200	JGK 1	India
187	1710	India	194	12928	India	201	7255	India
188	5135	India	195	4567	India	202	762	India
189	6293	Italy	196	10399	India	203	7554	Iran
190	16374	Malawi	197	6263	Russia and CISs			

Table 2. Distribution of 203 minicore germplasm collection of chickpea in different clusters under three environments (E1, E2 & E3)

Clusters	No. of genotypes			Serial No. of genotypes		
	E1	E2	E3	E1	E2	E3
I	3	3	3	1, 3, 2	74, 104, 84	16, 38, 57
II	157	105	88	170, 179, 141, 117, 165, 181, 200, 62, 53, 111, 10, 186, 160, 118, 95, 167, 51, 195, 156, 120, 39, 148, 152, 104, 105, 203, 145, 108, 172, 194, 76, 157, 153, 190, 135, 55, 193, 132, 198, 75, 114, 81, 55, 50, 34, 43, 199, 124, 188, 18, 103, 57, 83, 14, 92, 121, 134, 93, 20, 126, 61, 159, 63, 94, 48, 197, 52, 35, 136, 17, 131, 183, 122, 149, 12, 79, 123, 161, 74, 158, 102, 25, 45, 90, 140, 192, 201, 26, 44, 37, 98, 171, 8, 89, 58, 129, 196, 22, 176, 100, 41, 59, 67, 130, 60, 90, 175, 21, 110, 174, 115, 106, 27, 127, 9, 78, 80, 96, 139, 133, 69, 73, 162, 202, 113, 71, 187, 23, 77, 173, 42, 168, 169, 40, 16, 38, 64, 185, 68, 163, 87, 137, 184, 128, 140, 91, 177, 116, 7, 189, 182, 36, 49, 109, 178, 66, 84.	1, 124, 65, 183, 100, 71, 25, 203, 44, 131, 3, 105, 60, 142, 51, 68, 6, 120, 175, 52, 174, 24, 13, 177, 133, 129, 172, 42, 61, 64, 162, 50, 48, 19, 185, 96, 7, 66, 108, 44, 59, 168, 10, 118, 170, 81, 137, 176, 157, 126, 171, 196, 21, 143, 55, 57, 54, 92, 43, 101, 201, 20, 103, 5, 114, 46, 178, 156, 128, 17, 160, 152, 166, 198, 26, 70, 180, 190, 153, 37, 191, 18, 197, 113, 161, 82, 132, 192, 73, 138, 136, 28, 188, 91, 130, 134, 56, 9, 99, 116, 107, 106, 112, 49, 125, 18	1, 85, 105, 71, 146, 189, 114, 106, 127, 83, 25, 183, 61, 12, 200, 111, 182, 80, 178, 47, 58, 44, 41, 135, 75, 53, 48, 26, 59, 129, 163, 79, 101, 77, 116, 143, 65, 88, 176, 64, 132, 100, 181, 39, 22, 96, 174, 168, 120, 73, 6, 131, 145, 84, 104, 63, 126, 91, 144, 72, 175, 78, 122, 28, 98, 62, 156, 36, 110, 35, 23, 103, 137, 166, 67
III	1	58	34	54	97, 146, 2, 167, 80, 147, 148, 47, 67, 110, 135, 145, 75, 95, 195, 14, 35, 23, 63, 127, 140, 121, 199, 189, 194, 202, 38, 115, 62, 111, 149, 102, 173, 98, 30, 88, 39, 94, 155, 85, 186, 181, 179, 182, 90, 72, 45, 34, 22, 8, 119, 83, 32, 77, 109, 123, 19, 36.	3, 43, 21, 117, 192, 30, 196, 94, 107, 14, 24, 60, 20, 19, 17, 69, 118, 37, 32, 34, 119, 161, 43, 113, 140, 92, 142, 151, 46, 87, 133, 86, 74, 149
IV	1	15	44	47	53, 58, 41, 117, 150, 76, 151, 169, 40, 15, 154, 11, 93, 69, 87	102, 97, 188, 2, 115, 177, 136, 54, 90, 95, 147, 169, 159, 141, 130, 18, 13, 134, 50, 164, 10, 81, 158, 193, 157, 198, 5, 7, 194, 108, 66, 180, 42, 139, 152, 185, 187, 199, 170, 150, 49, 153, 171, 203
V	22	1	1	13, 82, 85, 144, 151, 143, 72, 112, 138, 65, 142, 154, 101, 80, 180, 97, 15, 147, 150, 32, 24, 19	184	8
VI	1	1	8	191	139	52, 172, 162, 197, 184, 191, 179, 190
VII	1	1	1	31	31	82
VIII	1	1	5	164	127	124, 155, 202, 121, 123
IX	1	10	1	166	12, 31, 29, 79, 78, 163, 159, 86, 158, 4	9
X	1	2	1	28	164, 165	138
XI	5	1	1	88, 119, 6, 30, 155	33	15
XII	1	1	1	125	141	165
XIII	1	1	1	99	16	29
XIV	1	1	1	46	122	148
XV	1	1	1	56	200	11
XVI	1	1	1	29	104	33
XVII	1	1	33			70
XVIII	1	1	11			125
XIX	1	3	107			186, 195, 173
XX	1	1	4			76
XXI		1				109
XXII		1				163
XXIII		1				27
XXIV		1				4
XXV		1				154

E1 (rainfed 2004–05); E2 (rainfed 2005–06); E3 (irrigated 2005–06)

Table 3. Average intra- (diagonal) and inter-cluster distances in chickpea minicore in E₁ (Rainfed 2004-05)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV	Cluster XVI	Cluster XVII	Cluster XVIII	Cluster XIX	Cluster XX
Cluster I	140.54	232.04	223.09	239.07	237.5	236.78	227.77	222.97	288.26	469.76	255.94	629.77	245.78	700.76	214.61	247.28	283.26	910.02	661.01	1516.19
Cluster II	0	410.6	425.76	594.14	414.48	19.55	473.42	659.53	678.26	115.62	1211.56	108.15	1354.35	405.65	201.37	377.34	377.34	1554.12	1262.23	2401.47
Cluster III	0	0	16.12	271.73	46.52	364.76	141.28	296.43	157.79	299.41	277.41	332.99	360.64	363.96	237.58	324.12	324.12	405.78	343.52	976.35
Cluster IV	0	0	0	329.66	29.96	367.77	96.57	296.71	138.28	325.54	266.05	396.11	348.17	426.12	240.03	292.7	377.48	377.48	390.92	890.5
Cluster V	0	0	0	347.38	607.89	338.81	298.32	168.24	590.98	617.32	373.03	532.46	383.05	210.74	564.58	538.18	648.61	648.61	272.94	1133.11
Cluster VI	0	0	0	0	0	0	109.27	313.68	158.56	293.81	353.2	411.63	385.39	403.41	256.3	306.65	421.6	402.28	936.67	936.67
Cluster VII	0	0	0	0	0	0	404.04	639.24	592.09	76.8	1147.57	130.99	1257.01	443.3	186.69	337.4	1453.93	1200.04	2230.66	2230.66
Cluster VIII	0	0	0	0	0	0	198.17	230.36	368.89	283.5	457.9	341.96	372.84	234.28	137.65	137.65	476.15	490.05	795.94	795.94
Cluster IX	0	0	0	0	0	0	187.86	509.08	632.24	329.78	616.1	354.81	308.19	502.34	393.32	393.32	572.42	392.74	927.69	927.69
Cluster X	0	0	0	0	0	0	212.24	467.3	383.84	575.81	473.59	639.96	349.95	390.99	445.28	445.28	565.38	565.38	912.72	912.72
Cluster XI	0	0	0	0	0	0	0	1036.81	64.46	1156.15	343.45	84.94	232.03	1288.22	1133.62	1133.62	2065.44	2065.44	2065.44	2065.44
Cluster XII	0	0	0	0	0	0	0	1047.94	43	716.77	778.71	659.4	90.79	158.32	298.12	298.12	1388.6	1138.55	2249.81	2249.81
Cluster XIII	0	0	0	0	0	0	0	1226.52	256.89	97.05	273.78	805.15	87.13	94.45	222.35	222.35	948.56	989.28	1389.43	1389.43
Cluster XIV	0	0	0	0	0	0	0	792.36	960.42	805.15	87.13	94.45	222.35	222.35	222.35	222.35	948.56	989.28	1389.43	1389.43
Cluster XV	0	0	0	0	0	0	0	0	298.13	319.16	990.8	717.88	1679.22	1679.22	1679.22	1679.22	990.8	717.88	1679.22	1679.22
Cluster XVI	0	0	0	0	0	0	0	0	0	0	0	77.38	1038.45	1028.43	1710.84	1710.84	1038.45	1028.43	1710.84	1710.84
Cluster XVII	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cluster XVIII	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cluster XIX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cluster XX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 4. Average intra- (diagonal) and inter-cluster distances in chickpea minicore in E₂ (Rainfed 2005-06)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV	Cluster XVI
Cluster I	131.28	473.87	360.6	288.77	232.55	632.86	236.31	211.51	351.12	873.28	266.65	313.78	266.55	207.18	573.55	1203.21
Cluster II	144.44	645.7	645.7	286.02	372.42	467.6	561.68	837.02	581.29	1304.03	809.68	265.78	598.43	723.47	400.2	1003.62
Cluster III	274.13	738.3	738.3	729.97	729.97	600.22	488.24	668.02	518.72	670.63	525.54	691.3	636.67	416.97	559.12	1170.95
Cluster IV	0	0	0	48.57	708.34	787.96	466.76	356.17	650.68	1457.7	553.3	201.56	335.73	587.37	753.2	1293.86
Cluster V	0	0	0	0	0	269.07	314.44	218.14	504.14	1408.71	439.97	149.31	204.3	397.45	702.27	1372.35
Cluster VI	0	0	0	0	0	0	497.17	1179.04	437.58	628.42	593.3	533.95	613.21	814.6	599.72	401.43
Cluster VII	0	0	0	0	0	0	0	384.73	52.59	591.77	119.81	221.69	90.56	142.17	500.86	744.93
Cluster VIII	0	0	0	0	0	0	0	0	608.63	1347.43	378.14	482.36	361.06	233.09	960.77	1864.85
Cluster IX	0	0	0	0	0	0	0	0	0	533.8	194.83	268.83	241.19	226.96	433.19	612.49
Cluster X	0	0	0	0	0	0	0	0	0	237.55	504.94	1155.72	831.02	809.88	1094.19	572.18
Cluster XI	0	0	0	0	0	0	0	0	0	0	0	407.58	154.06	267.76	860.01	814.1
Cluster XII	0	0	0	0	0	0	0	0	0	0	0	0	250.08	444.89	380.84	962.24
Cluster XIII	0	0	0	0	0	0	0	0	0	0	0	0	0	260.43	755.07	942.59
Cluster XIV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	588.1	1328.12
Cluster XV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	183.38	1144
Cluster XVI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 5. Average intra- (diagonal) and inter-cluster distances in chickpea minicore in E₃ (Irrigated 2005–06)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV
Cluster I	95.9	246.4	199.5	468.47	376.57	404.46	523.8	147.86	135.6	150.08	370.34	142.56	146.91	425.58	154.65
Cluster II		143.32	540.47	210.71	173.72	180.65	252.42	180.92	267.41	306.18	178.67	253.48	186.45	208.77	211.02
Cluster III			141.76	886.77	774.95	804.46	892.28	298.97	252.09	259.41	759.86	270.22	313.95	791.92	290.54
Cluster IV				0	169.79	99.71	300.97	387.94	431.3	474.36	118.74	410.9	350.91	44.02	449.9
Cluster V					0	72.41	286.27	246.85	382.17	386.7	27.58	304.14	207.8	202.86	350.25
Cluster VI						0	256.57	262.79	297.34	323.58	46.12	260.02	189.68	107.62	375.32
Cluster VII							157.57	282.51	511.05	569.7	296.88	482.93	331.63	286.88	309.54
Cluster VIII								0	147.22	125.71	259.8	86.56	37.57	301.58	72.15
Cluster IX									0	83.43	306.69	114.31	69.53	405.83	148.43
Cluster X										0	356.46	29.63	98.02	370.69	225.99
Cluster XI											0	300.52	181.37	182.41	318.97
Cluster XII												0	68.73	293.82	218.99
Cluster XIII													0	305.98	92
Cluster XIV														0	442.19
Cluster XV															0

contd

Table 5 contd...

Clusters	Cluster XVI	Cluster XVII	Cluster XVIII	Cluster XIX	Cluster XX	Cluster XXI	Cluster XXII	Cluster XXIII	Cluster XXIV	Cluster XXV
Cluster I	287.94	239.23	292.19	471.14	418.55	548.35	754.7	591.11	453.41	830.25
Cluster II	546.74	253.03	579.73	422.25	192.46	282.83	604.28	788.26	273.05	621.12
Cluster III	260.66	418.44	259.8	618.69	847.96	975.55	934.55	528.72	813.59	1096.8
Cluster IV	693.29	337.56	868.34	738.05	138.49	87.6	821.94	1293.35	117.3	954.43
Cluster V	768.05	334.29	837.14	658.32	233.3	257.65	912.71	1187.92	298.67	912.79
Cluster VI	780.79	275.45	760.42	725.44	166.27	79.23	905.5	1232.59	206.92	953.54
Cluster VII	842.45	400.97	889.32	328.26	307.24	341.9	397.52	805.68	359.31	412.1
Cluster VIII	364.08	166.96	346.38	265.49	422.25	422.82	498.32	469.23	414.33	615.55
Cluster IX	279.88	189.47	374.49	578.65	407.71	388.87	830.93	727.86	350.88	979.2
Cluster X	414.68	215.59	231.85	660.41	458.87	416.85	984.27	777.58	477.81	1105.44
Cluster XI	659.67	296.56	863.03	688.64	213.52	190.97	910.87	1232.21	172.51	984.87
Cluster XII	425.12	176.64	183.09	594.62	443.25	395.19	893.15	728.99	466.29	1009.74
Cluster XIII	343.94	147.24	393.62	414.42	397.27	359.65	666.44	649.18	328.67	802.49
Cluster XIV	704.44	286.71	647.95	688.26	188.89	84.59	780.2	1141.62	230.71	917.58
Cluster XV	256.28	217.66	481.38	577.63	421.64	535.79	373.43	390.42	323.45	488.96
Cluster XVI	0	401.24	569.93	577.63	869.6	899.01	749.4	643.91	522.09	1152.41
Cluster XVII		233.76	428.44	505.21	404.76	370.19	689.11	740	346.84	850.36
Cluster XVIII			0	771.77	820.21	871.7	1062.41	626.47	937.62	1155.17
Cluster XIX				0	688.07	887.21	78.38	225.18	656.04	146.81
Cluster XX					0	148.22	837.67	1185.16	212.1	729.07
Cluster XXI						0	980.65	1407.78	218.78	1068.38
Cluster XXII							0	354.35	740.87	145.82
Cluster XXIII								176.1	1193.85	453.37
Cluster XXIV									0	922.19
Cluster XXV										0

Table 6. Contribution of individual character in the divergence among 203 accessions of chickpea minicore collections under three environments

Characters	Times ranked first			% contribution towards diversity		
	E ₁	E ₂	E ₃	E ₁	E ₂	E ₃
Days to 50% flowering	5775	8733	10528	28.17	42.59	51.35
Plant height (cm)	1606	608	1334	7.83	2.97	6.51
Primary branches/plant	66	133	213	0.32	0.65	1.04
Secondary braches/plant	1083	190	2069	5.28	0.93	10.09
Tertiary branches/plant	566	859	477	2.76	4.19	2.33
Pods/plant	161	100	842	0.79	0.49	4.11
100-seed weight (g)	8254	4852	3921	40.26	23.66	19.12
Yield/plant	2992	5028	1119	14.59	24.52	5.46

2002). This means that geographic diversity, though important, may not be the only factor in determining the genetic divergence. The genetic diversity is the outcome of several factors including geographical diversity. Therefore selection of varieties for hybridization should be based on genetic diversity rather than the geographic diversity. The clustering of genotypes from different eco-geographic locations into one cluster could be attributed to the frequent exchange of breeding material from one place to another and its further selection in different geographic regions which could result in genetic drift or due to unidirectional selection pressure by the breeders of different locations (Murty and Arunachalam, 1969; Singh and Bains, 1982). Hybridization among diverse parents is likely to produce heterotic hybrids and desirable transgressive segregants in advanced generations. Therefore, a hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high mean for almost all component traits. Shinde *et al.* (1997) felt that even the temperature and rainfall pattern, respectively could influence crop characters of the same races. Similar results were also reported in chickpea by Arora (1992), Jeethava *et al.* (2000), Sivakumar and Muthiah (2001) and Jeena and Arora (2002). In the present investigation, 16, 10 and 18 solitary clusters were observed in E₁, E₂ and E₃, respectively. The formation of such a large number of distinct solitary clusters may be due to intensive natural or human selection for diverse adaptive gene complex.

Contribution of Characters to Divergence

The contribution of individual character towards genetic divergence has been worked out in terms of number of times it appeared first (Table 6). Over three environments studied, it is observed that days to 50% flowering (42.59% and 51.35%) contributed maximum to the genetic diversity in E₂ and E₃ environments while 100-seed weight

(40.26%) was contributed maximum towards genetic divergence in E₁ followed by days to 50% flowering (28.17%) and seed yield/plant (14.59%). The remaining characters contributed very low to this parameter. Several researchers have reported different characters contributing for genetic diversity in chickpea. Katiyar (1978) concluded that pod number/plant contributed maximum towards divergence. Study by Anil Kumar *et al.* (1993); Sarvaliya and Goyal (1994); and Kumar (1997) indicated that test weight was the major contributor towards diversity. Days to 50% flowering was the major contributor to diversity in the present study as also reported by Shinde *et al.* (1997). A study on genetic diversity by Jeethava *et al.* (2000) has revealed that seed yield/plant, pods/plant and test weight contributed maximum to genetic diversity. Thus contributing characters differ in respect of their contributions to the genetic diversity. Mostly expression of these characters differs due to environmental influence on the genotypes studied, besides the nature of genetic material under investigation.

The genetic diversity is directly related to the success of hybridization for developing varieties/releasing variability. The choice of parents is of paramount importance in any breeding programme. Selection based on extent of genetic divergence has been successfully adopted in pulses (Ramanujam, 1975) and has been used in planning hybridization programme by Rao and Chopra (1989).

In the present investigation it was observed that the genotypes of cluster XIX (ICC13124) had the highest mean value for pod number and earliness in E₁. In E₂, the genotypes of cluster XV (ICC12654) and XVI (ICC9848) were superior in respect of plant height, pods/plant and 100-seed weight, respectively. In E₃, the genotype of cluster XVI (ICC13124) had the highest mean value for seed yield. Cluster XXIII (ICC6279) had the early maturing genotype and cluster XVIII (ICC5879) was superior in respect of pod number and tertiary branches/

plant and cluster V (ICC6816), cluster XI (ICC10341 and cluster XIII (ICC5504) had the tall genotypes. The clusters differed with respect to their *per se* performance.

A close look at Table 7 indicated that the clusters excelled in respect of different characters in 2004–05 rainfed experiment. The clusters XIX, XII, IX can be used as source of genes for high pod number, clusters XX and XVIII used as source of genes for higher 100 seed weight. The clusters XIX, V, XX, XIV can be used as good source of genes for earliness. The genotypes from these clusters may be accordingly selected as parents in crossing programme to incorporate genes for characters for which they excelled in performance during 2004–05 rainfed condition. During 2005–06 rainfed conditions, the clusters XV, XII, IX and XI can be used as source of genes for high pod number, clusters XVI, cluster X and VI used as source of genes for higher seed weight. The clusters VIII, XI and XIV can be used as good source of genes for earliness. From the irrigated experiment, the clusters XXIII and III appeared to be as good source of genes for earliness, clusters XVIII, XIV and cluster XII as source of genes for higher pods number. The clusters XXV, XXII, XXIII, and XIX can be used as good source of genes for bold seeded types. The genotypes of these clusters may be accordingly selected as parents in crossing programme to incorporate genes for characters for which they excelled in performance during their respective environments. Therefore, these genotypes may be involved in multiple crossing programme to recover transgressive segregates.

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Table 7. Cluster means for eight characters in chickpea minicore in three environments

Clusters	PLHT (cm)			PB			SB			TB			PPP			SDWT (g)			YPP (g)		
	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3	E1	E2	E3
I	60.70	49.31	53.58	35.88	38.60	46.42	2.56	3.54	3.69	14.41	8.35	9.09	19.00	15.80	18.50	14.05	15.88	16.39	16.92	17.82	19.07
II	78.00	68.47	65.37	32.50	42.33	48.19	2.90	3.92	3.56	15.00	9.46	8.69	19.00	16.86	19.09	9.25	14.83	18.85	12.65	14.24	19.47
III	63.50	56.48	43.68	37.50	40.13	47.31	2.50	3.96	3.86	13.00	9.88	10.21	17.00	17.95	21.18	22.80	18.16	17.36	13.30	28.16	21.92
IV	67.00	55.50	75.00	32.00	32.30	49.05	2.25	2.35	3.65	13.50	4.75	10.00	18.50	7.00	20.40	23.20	12.95	14.50	16.10	9.00	32.20
V	39.50	50.50	72.00	35.00	33.85	63.75	3.15	3.00	3.25	12.50	6.25	7.00	16.00	16.20	14.35	16.50	13.00	15.25	12.50	8.00	12.75
VI	66.00	67.03	73.50	38.50	38.00	55.70	3.00	3.93	4.85	18.00	8.71	12.50	24.50	15.68	24.10	22.75	24.53	14.00	16.15	18.23	15.85
VII	79.00	48.50	70.18	34.50	41.90	52.79	2.75	3.90	4.26	18.50	9.75	11.66	20.00	29.95	21.31	11.05	21.60	26.64	13.95	13.30	21.20
VIII	63.00	38.00	57.00	37.50	41.05	59.40	2.50	2.85	3.30	15.25	6.05	12.45	18.50	15.25	18.75	20.35	12.45	22.00	24.65	14.45	17.55
IX	47.58	52.00	55.00	34.60	49.45	48.05	2.51	5.05	5.15	12.82	12.95	15.20	18.14	32.00	27.80	18.18	23.40	13.95	22.85	13.70	21.55
X	69.55	53.38	55.00	44.95	39.77	49.25	2.55	3.22	4.00	14.15	7.63	15.80	18.93	20.29	17.90	25.78	31.19	13.10	17.90	26.78	13.20
XI	76.50	43.00	72.00	58.00	33.15	62.70	2.25	2.85	4.50	17.50	8.05	9.65	20.00	16.35	16.90	32.00	111.50	44.50	13.50	14.15	20.05
XII	46.50	57.00	57.00	31.50	41.75	54.15	2.00	2.95	4.60	8.75	6.70	13.75	13.00	26.30	21.40	45.50	136.00	127.50	22.05	8.35	12.05
XIII	72.00	47.00	58.50	57.00	25.10	60.95	2.50	3.05	5.05	11.00	9.40	13.65	14.50	24.50	23.20	41.50	27.50	67.50	12.80	9.80	17.75
XIV	40.50	44.00	72.50	32.00	48.10	48.75	2.25	3.80	2.90	14.50	15.50	11.50	17.50	29.25	22.35	44.00	67.00	146.00	21.45	18.05	27.00
XV	49.00	66.67	55.00	62.00	54.80	53.85	2.25	4.43	5.00	10.50	8.73	12.20	22.75	40.27	17.80	40.00	145.00	39.50	16.10	21.85	25.70
XVI	76.50	67.00	47.00	57.50	45.50	57.40	2.50	3.60	4.50	10.75	6.20	10.90	17.25	14.80	22.80	40.50	25.00	90.00	20.55	13.55	49.30
XVII	71.00	60.00	58.00	53.08	53.08	53.08	2.25	5.00	4.90	12.00	13.11	17.00	25.07	43.50	100.81	15.35	34.05	18.45	20.55	13.55	49.30
XVIII	47.50	48.00	35.50	38.85	35.50	38.85	2.00	5.35	5.35	11.50	12.65	12.65	21.50	26.30	26.30	33.80	16.85	17.82	29.60	18.70	10.20
XIX	35.00	55.00	32.00	52.60	32.00	52.60	3.50	3.75	3.75	15.35	10.00	10.00	18.50	16.25	16.25	28.55	35.70	35.70	13.00	28.55	17.30
XX	40.50	73.00	31.50	29.85	31.50	29.85	2.25	3.85	3.85	15.50	15.50	15.50	19.00	17.35	17.35	37.90	14.85	14.85	31.25	17.30	17.30
XXI		75.50		42.65		42.65		3.70			15.65			26.75			82.00	12.80		23.35	
XXII		58.00		49.25		49.25		4.15			11.40			24.35			77.50	39.75		40.90	
XXIII		42.38		45.99		45.99		3.64			10.99			92.50			92.50	36.25		25.09	
XXIV		71.00		48.20		48.20		7.25			13.50			56.50			56.50	15.80		39.75	
XXV		61.00		36.10		36.10		4.00			7.80			26.50			26.50	39.90		20.55	

E₁ (Rainfed 2004–05), E₂ (Rainfed 2005–06) and E₃ (Irrigated 2005–06)

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Genetic Diversity Studies in Indigenous Pearl Millet [*Pennisetum glauccum* (L.) R. Br.] Accessions Based on Biometrical and Nutritional Quality Traits

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The aim of this research was to study genetic divergence among the pearl millet [*Pennisetum glauccum* (L.) R. Br.] accessions obtained from Millet Breeding Station, Coimbatore and clustering them into homogenous groups based on yield components and nutritional quality traits for the hybridization programme. Genetic divergence analysis was done based on multivariate analysis using Mahalanobis's D^2 statistics. The experimental material consists of 61 elite germplasm lines grouped into eight different clusters based on yield components, nutritional and anti-nutritional traits. The maximum divergence with high mean performance was observed between clusters II, V and VII. Hence, hybridization between the genotypes of these clusters may exhibit high heterosis as well as high level of production and quality. Zinc content contributed maximum to the genetic divergence followed by phytate phosphorus and crude fat content. The result indicate that, presence of ample variation for grain zinc in pearl millet germplasm can be exploited for further improvement of pearl millet cultivars with respect to grain zinc content. The low contribution to genetic divergence by other characters may be due to precedent domestication and selection towards uniformity for yield characters. The presence of significant genetic variability among the evaluated germplasm accessions suggests that, variability can be exploited for improvement of grain nutritional quality and yield traits through hybridization of genotypes from different clusters and subsequent selection from the segregating generations.

Key Words: Cluster distance, Genetic divergence, Germplasm accessions

Introduction

Pearl millet [*Pennisetum glauccum* (L.) R. Br.] is an important food crop and is vital source of energy for the millions of poor inhabiting the semi-arid tropics. This crop occupies 10 m ha in India which shares one third of world production area. The crop is cultivated for grain and fodder purpose in the semi-arid regions of Africa and Indian subcontinent (Devos *et al.*, 2006). However, in United States (US) and Europe, pearl millet is grown as a fodder and feed crop for livestock. The quest for increasing yield is though, a primary concern for an increasing world population which has achieved self-sufficiency in food production quantitatively (green revolution), but not in quality. Hence, priority of breeders may be to breed for quality with higher amount of micronutrients especially iron (Fe) and zinc (Zn) in edible part (grains), which is most frequent deficient minerals in cereal based human diets and globally estimated that five million people are deficient in both the elements. As pearl millet is highly cross pollinated, genetic variability in the species is well distributed both within and among cultivars. Assessment of genetic variability and identification of superior genotypes are prerequisite for crop-breeding programme. Pearl millet produces nutritious grains that

are a rich source of protein, calcium, phosphorus, iron and zinc compared to other major cereal crops (Devos *et al.*, 2006). Millets typically contain higher quantities of essential amino acids especially methionine, cysteine and fat content than maize, rice, wheat and sorghum (Obilana and Manyasa, 2002). Being drought-tolerant, higher protein concentration and protein quality compared to other cereals, scientists hope to increase its use as feed grain for both humans and animals alike. Recently, a large variation for grain Fe (30.1 to 75.7 mg kg⁻¹) and Zn (24.5 to 64.8 mg kg⁻¹) content in pearl millet germplasm accessions, breeding lines, improved populations, commercial open-pollinated varieties (OPVs) and hybrid parents have been reported by Velu *et al.*, 2007. Similarly, variability for grain Fe (46.9 to 85.6 mg kg⁻¹) and Zn (36.4 to 69.9 mg kg⁻¹) was reported in commercial and pipeline hybrids developed in India (Velu *et al.*, 2008). Till recently, only few genetic studies have been carried out for micronutrients especially for grain Fe and Zn (Jambunathan and Subramanian, 1988). Genetic resources of pearl millet are untapped that need attempt to improve protein content in harvested varieties for significant yield improvements (Rai *et al.*, 1999).

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In spite of, having superior grain quality, millet contains some anti-nutritional factors such as phytic acid, which reduce bioavailability of nutrients. At present anti-nutritional factors are low in pearl millet but in future, their level need to be monitored to keep them at lower levels (Govindaraj, 2006). Large number of the population suffers from chronic malnutrition where pearl millet is used as food crop, (Khush, 2008). Thus, improvement in nutritive quality of grains along with the sustained yield may prove useful for alleviating malnutrition. Aforesaid facts suggest that, pearl millet has all the potential, and present study was conducted to determine diversity and superior lines for use as parent in hybrid development

Materials and Methods

Sixty-one pearl millet genotypes were selected based on earlier studies on yield and its componential traits for the present study at Millet Breeding Station, Tamil Nadu

Agricultural University (TNAU), Coimbatore, to study and evaluate genetic divergence by D^2 statistics. They are currently being used in breeding programs at the same centre/or at the breeding programs at state agricultural universities and national research centre in India. Seeds of these accessions were maintained by the Millet Breeding Station (now Department of Plant Genetic Resources (Table 1). The field experiment was carried out during 2006 under the prevailing environmental conditions at TNAU, Coimbatore. All the entries were sown manually and the plot size of 4 m and row-to-row and plant-to-plant distance was 60 and 15 cm, respectively, in a Randomized Complete Block (RCBD) Design with three replications. The crop was grown under uniform conditions to minimize environmental variability to the maximum possible extent. The data were recorded on five randomly selected plants in each plot at each replication for eight morphological characters (Table 2).

Table 1. List of genotypes used in the study (materials source: millet breeding station, TNAU, Coimbatore)

Sl. No.	Genotypes	Sl. No.	Genotypes
1.	PT1796	31.	PT 4664
2.	PT 2198	32.	PT 4760
3.	PT 2243	33.	PT 4896
4.	PT 2582	34.	PT 4976
5.	PT 2610	35.	PT 5005
6.	PT 2659	36.	PT 5010/2
7.	PT 2835/1	37.	PT 5021
8.	PT 3311	38.	PT 5072
9.	PT 3397	39.	PT 5077
10.	PT 3488	40.	PT 5099
11.	PT 3559	41.	PT 5118
12.	PT 3657	42.	PT 5179
13.	PT 3687	43.	PT 5188 (Y)
14.	PT 3718	44.	PT 5241
15.	PT 3755	45.	PT 5541
16.	PT 3758	46.	PT 5547
17.	PT 3764	47.	PT 5552
18.	PT 3987	48.	PT 5554
19.	PT 4060	49.	PT 5564
20.	PT 4219	50.	PT 5604
21.	PT 4266/2	51.	PT 5605
22.	PT 4377	52.	PT 5625
23.	PT 4440	53.	PT 5722
24.	PT 4464	54.	PT 5744
25.	PT 4470	55.	PT 5765
26.	PT 4508	56.	PT 5843
27.	PT 4551	57.	PT 5856
28.	PT 4572	58.	PT 5864
29.	PT 4591	59.	PT 5913
30.	PT 4619	60.	PT 5914
		61.	PT 5939

PT – *Pennisetum typhoides* (old botanical name)

Table 2. Analysis of variance for biometrical and mineral quality characters in indigenous pearl millet accessions

Source of variation	df	Mean Squares														
		Day to 50% flowering	Plant height (cm)	No. of productive tillers	Panicle length (cm)	Panicle girth (cm)	Days to maturity	100-grain weight (g)	Grain yield/plant (g)	Crude protein (%)	Crude fat (%)	Phytate phosphorus (mg)	Phosphorus (mg)	Calcium (mg)	Iron (mg)	Zinc (µg)
Replication	2	0.051	2.685	0.026	0.292	0.077	0.234	0.000	2.602	0.735	0.025	0.374	264.6	0.265	0.011	0.2461
Genotypes	60	12.994**	486.21**	0.30**	8.95**	0.451**	5.27**	0.003**	73.78**	5.11**	2.43**	1438.21**	1690.62**	40.39**	2.88**	1271.45**
Error	60	0.517	20.340	0.009	0.430	0.037	0.192	0.001	1.460	0.243	0.008	0.855	146.455	0.390	0.007	0.2739

** Significant at $P < 0.01$ level

After thrashing, cleaning and weighing, the grains from each entry were dried in hot air oven at 60⁰ C for 6h. The grains were then ground in Willey mill separately, and the powder was stored in properly labeled butter paper cover for further analysis. The crude protein content was estimated using method by Humphries (1956). The crude fat determined by Soxhlet apparatus with petroleum ether (AOAC, 1960). Phytic acid estimation was done using the method of Wheeler and Fernel (1971), estimation of calcium was based on versenate titration method as suggested by Jackson (1973). Phosphorous from the grain sample was determined as per Vanadomolybdo phosphoric yellow color method (Piper, 1966). The Fe and Zn estimation were done by using Atomic Absorption (Jackson, 1973). Protein and fat estimation carried out at the Department of Forage, Centre for Plant Breeding and Genetics, TNAU. Determination of calcium, phytate phosphorus and phosphorus were carried out at Department of Soil Science and Agricultural Chemistry, TNAU. The iron and zinc content estimated at Department of Environmental Science, TNAU. The statistical analysis was done for ANOVA by using GenStat 12th edition Statistical software (VSN International Ltd, 2009). Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D² statistic (Mahalanobis, 1936) using NTSYS statistical software (Rohlf, 1996).

Results and Discussion

Analysis of variance revealed significant differences between the genotypes for all the characters studied, revealing the existence of substantial amount of variation among the genotypes (Table 2). The Mahalanobis D² statistic has been found to be favourable for estimating genetic divergence between genotypes for selection in the breeding programme. The success in obtaining highly heterotic hybrids and creating greater variability for efficient selection of useful recombinants in breeding programmes depend on the degree of divergence between the parents chosen (Murty and Tiwari, 1967). For exploiting heterosis as a means of increasing production, it is necessary to utilize parents with maximum genetic divergence. The more diverse the parents more are the chances of pronounced heterotic effects and increased spectrum of variability in the segregating generations.

In the present study, Wilks criterion was used for simultaneous test of significance of the differences in the mean value of character. Highly significant difference was observed among genotypes for all the characters,

suggesting the existence of considerable divergence in the given genetic material and justified the need to estimate squared distance values for the genotype combinations using these characters. Diversity based on either quality characters or mineral content is not given much importance in the past breeding track whilst the aim of the breeding programme is mainly focused on yield improvement. Hence, diversity based on quantitative characters is preferable than diversity based on quality characters.

Based on D^2 value estimates of genetic divergence, the 61 pearl millet accessions were grouped into eight distinct clusters (Fig. 1). The cluster analysis suggested the resolution of sixty one genotypes into eight distinct clusters following Tocher's method of clustering, indicating wide diversity in the experimental material for majority of the characters studied including nutritional characters. Cluster I consisted of a maximum of 31 genotypes (51 %), cluster III consisted 15 accessions (25%) and II consisted six accessions (10%) of the genetic materials used in the study (Fig 1). Remaining clusters (V, VI, VII, and VIII) were contributing only one genotype each. The uneven distribution of genotypes to different clusters and most genotypes falling into few clusters suggested that, indigenous germplasm collected from the same geographic area were not necessarily closely related and different regions did not necessarily have different genetic background and being spread in the country. Similar results were reported by various researchers previously (Garg and Gautam, 1988; Walia and Garg, 1996; Singh *et al.*, 2003; Prabhu *et al.*, 2005). Cluster IV comprising of five genotypes had the highest intra cluster distance (94.26) indicating the high divergence among the genotypes of the cluster. While considering the inter cluster distances, it was found that minimum inter cluster distance (81.17) was noticed between cluster I and V which explain that the genotypes in these clusters would have been evolved by similar evolutionary procedure. Thus, crossing of genotypes from these two clusters may not produce a high amount of heterotic expression in the F_1 s and broad-spectrum of variability in segregating (F_2) populations (Gashaw *et al.*, 2007). Maximum inter cluster distance (299.78) was noticed between cluster II and V (Table 3). Lines for hybridization can be selected on the basis of large inter-cluster distance to generate useful recombinants in the segregating populations. Increasing parental distance implies a greater number of constraining alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generations following a

cross of distantly related parents, the greater will be the opportunities for successful selection for any character of yield interest (Ghaderi *et al.*, 1984) for instance, the present study showed considerable variability for panicle length which was depicted in the figure 2. (Data were not shown).

Cluster mean performance of grain yield and other important contributing characters such as, number of productive tillers (4.35), panicle length (27.60 cm), panicle girth (6.85 cm), 100 grain weight (1.07 g), grain yield/plant (77.22 g), crude protein (13.22), and phosphorus (361.80 mg) was highest for cluster VII and moderately high for cluster II with high iron and zinc, indicated that, inbreds from this genetic cluster will serve as potential parents for improvement of grain Fe and Zn content, which is most prevalent deficiency in human beings where, there is inherent soil deficiency. Cluster V had high mean value for calcium, early maturity, low fat content and considerably low phytate phosphorus (Table 4). It is important to note that, early flowering and early maturity makes the cultivars more suitable by enabling them escape from terminal drought (end of the season), in this regard cluster V and VI had the early maturity and early flowering genotypes respectively, suggests crossing between individual from these clusters will produce hybrids suitable for cultivation in drought prone environments of western and northern parts of India. Keeping this in mind, it appeared that crosses between genotypes belonging to clusters II, V, and VII in all possible combination would not only exhibit high heterosis but also increase the level of production and nutritional quality where pearl millet plays an important role in human food and industrial sector, such as poultry feed and pig feed with high nutritious values. Hence, it is essential to improve the quality of pearl millet. The outstanding *per se* performance by the each genotype from the selected clusters may serve as potential genotypes for future breeding programme with respect to traits concerned (Table 5).

In addition to general features of variation and divergence, this study also provides the information on the potent characters that contributes to the divergence between the genotypes. It was found that the maximum contribution to the genetic divergence was accounted by zinc content (65.41%) followed by phytate phosphorus (23.17%) (Table 4). The low contribution to genetic divergence by other characters may be due to the fact that selection towards uniformity in these characters could have caused an eroding effect on genetic diversity (Das and

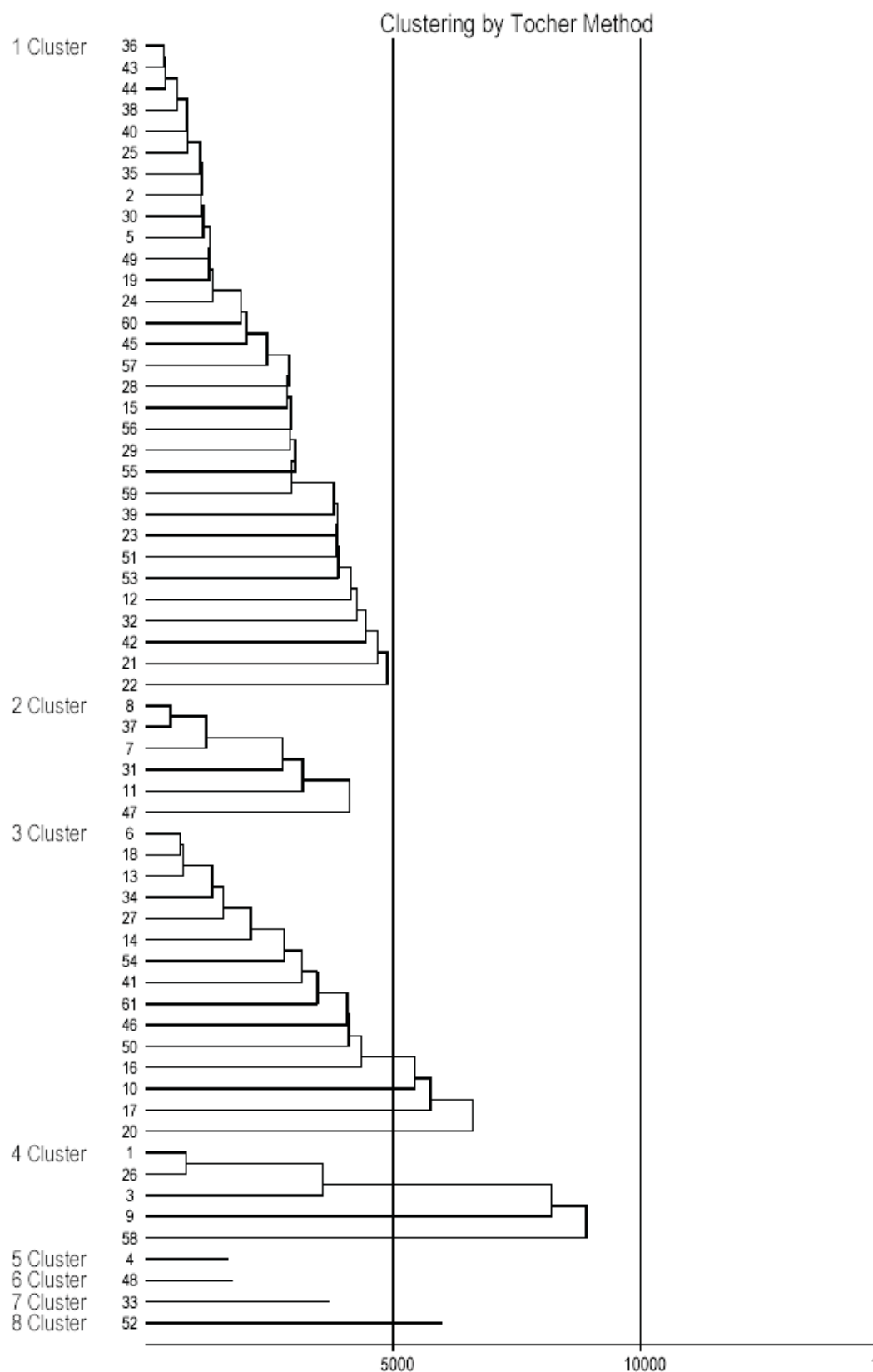


Fig. 1. Clustering for 61 genotypes in pearl millet based on fifteen characters

Table 3. Average intra- (in bold) and inter-cluster D² distances in indigenous pearl millet accessions

Cluster No.	I	II	II	IV	V	VI	VII	VIII
I	58.10	276.17	139.83	238.14	81.17	212.90	87.49	144.52
II		61.03	157.94	171.89	299.78	94.79	240.42	256.16
III			68.57	160.17	165.08	103.90	117.79	151.41
IV				94.26	225.12	118.08	230.41	148.54
V					0.00	225.48	129.56	102.63
VI						0.00	185.12	179.45
VII							0.00	175.43
VIII								0.00

Table 4. Cluster mean values for biometrical and nutritional quality characters in indigenous pearl millet accessions

Cluster No.	Day to 50% flowering	Plant height (cm)	Number of productive tillers	Panicle length (cm)	Panicle girth (cm)	Days to maturity	Crude protein (%)	Crude fat (%)	Phytate phosphorus (mg)	Phosphorus (mg)	Calcium (mg)	Iron (mg)	Zinc (µg)	100 grain weight (g)	Grain yield per plant (g)
I	48.69	192.63	3.73	23.29	6.25	85.39	12.43	3.94	213.73	345.6	36.69	2.43	117.26	1.01	61.61
II	48.67	194.33	3.73	22.54	6.09	84.94	12.31	4.02	225.41	353.6	37.74	5.22	186.17	0.99	62.28
III	49.65	198.67	3.80	23.11	6.07	85.02	11.98	4.04	216.46	343.2	33.29	3.76	149.82	1.01	62.36
IV	49.10	202.00	3.52	20.89	6.42	84.55	12.43	3.77	141.51	289.2	34.06	4.43	167.42	0.99	60.48
V	53.50	211.5	3.80	19.90	6.13	82.91	11.99	3.15	169.95	306.0	42.85	2.46	113.75	0.96	52.87
VI	46.50	174.5	3.35	23.12	6.29	85.00	10.28	3.95	200.37	351.6	41.12	5.46	169.01	1.01	52.29
VII	47.50	198.00	4.35	27.60	6.85	87.78	13.22	6.90	229.53	361.8	41.65	4.65	131.66	1.07	77.22
VIII	53.50	203.50	3.35	22.60	5.98	85.24	10.57	3.37	138.95	269.9	31.56	2.07	131.50	1.01	52.25
% contribution to divergence	0.05	0.05	—	0.11	—	—	0.71	5.96	23.17	—	0.66	3.66	65.41	0.11	0.11

The bold numbers are the highest and lowest mean values for each character

Table 5. Outstanding genotypes based on yield and nutritional characters in the selected genetic clusters

Clusters No. (1)	Characters (2)	Genotypes (3)
II	Iron and Zinc	High: PT 1796, PT 2835/1, PT 4508, PT 4664, PT 5021, PT 5552
	Days to 50% flowering	Late: PT 2582, PT 2835/1, PT 4551, PT 4572, PT 5625, PT 5939
	Panicle length	Low: PT 1796, PT 2243, PT 2582
	Days to maturity	Early: PT 5604, PT 5864
	100-grain weight	Low: PT 4470, PT 5552
V	Crude fat	Low: PT 5099, PT 2659, PT 3718, PT 4440, PT 5765, PT 5864, PT 5188 (Y)
	Calcium	High: PT 2835/1, PT 4664, PT 5843
	Zinc	Low: PT 5241, PT 5179, PT 5188 (Y), PT 4266/2, PT 4464
	Days to 50% flowering	Early: PT 3687, PT 3311, PT 3657, PT 3764, PT 5765
	Plant height	Dwarf: PT 5072, PT 5021, PT 4060, PT 5099, PT 5118
VI	Number of productive tillers	Low: PT 3657, PT 3488, PT 2243
	Crude protein	Low: PT 5604, PT 3488, PT 3764, PT 4377, PT 4591, PT 5021
	Number of productive tillers	High: PT 5939, PT 4760, PT 4896
	Panicle length	High: PT 5547, PT 4896, PT 5913, PT 5939
	Panicle girth	High: PT 5914, PT 5547, PT 2243, PT 5605, PT 5552, PT 5541
VII	Days to maturity	Late: PT 4508, PT 4551, PT 4266/2, PT 4572, PT 4377, PT 4664, PT 4760
	100-grain weight	High: PT 5856, PT 5744, PT 5179, PT 4896, PT 4760, PT 5722
	Grain yield/plant	High: PT 5939, PT 4896, PT 5856, PT 5914, PT 5744, PT 5179, PT 4760, PT 3559
	Crude protein	High: PT 5118, PT 3718, PT 3657, PT 4508, PT 5564, PT 5843, PT 5914
	Crude fat	High: PT 3758, PT 4760, PT 4896, PT 5179, PT 5744, PT 5856
	Phytate phosphorus and Phosphorus	High: PT 4377, PT 4219, PT 4664
	Days to 50% flowering	Late: PT 2582, PT 2835/1, PT 4551, PT 4572, PT 5625, PT 5939
	Plant height	Tall: PT 5939, PT 4760, PT 4664, PT 2582, PT 3559, PT 5010/2, PT 5077
	Number of productive tillers	Low: PT 3657, PT 3488, PT 2243
	Panicle girth	Low: PT 3764, PT 5021, PT 3987, PT 5564
VIII	Grain yield/plant	Low: PT 3755, PT 2582, PT 3488, PT 4060, PT 4619, PT 5554, PT 5625
	Phytate Phosphorus	Low: PT 1796, PT 2243, PT 4508, PT 4591, PT 5625, PT 5864, PT 2582, PT 3397, PT 5010/2, PT 5072, PT 5547, PT 5914, PT 5939
	Phosphorus	Low: PT 5547, PT 5625, PT 2610, PT 3397
	Calcium	Low: PT 5552, PT 5547, PT 1796, PT 3488, PT 5241, PT 5564, PT 5604
	Iron	Low: PT 4464, PT 5010/2 PT 5072, PT 5188 (Y) PT 5241 PT 5541

Borthakur, 1973) which showed that genetic variability was reduced in the course of domestication and selection. There is possibility of operation of a similar phenomenon on genotypes of certain clusters showing less contribution towards the genetic divergence.

From this study, genotypes in clusters II, V and VII possess desirable combinations of traits and thus, the

genotypes of these three clusters hold great promise as parents to obtain promising heterotic expression in F_{1s} and may create considerable variability in the segregating populations. The wealth of information will help to select the superior indigenous accession for productivity with acceptable nutritional qualities, which are not only exploited for the current agricultural advances, but can

also be used to generate the genetic resources, that can be employed in hybridization programme for nutritional improvement in human as well as animals.

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Seed Storage Protein Profiles of Pea (*Pisum sativum* L.) Genotypes using SDS-PAGE

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Using polyacrylamide slab gel electrophoresis, the water soluble seed proteins could be resolved in 42 bands distributed in six zones. One hundred and thirteen cultivars were categorized into 28 groups; each group had distinct and different electrophoretic banding patterns. However, within the group cultivars were also further distinguishable by the intensity of staining of bands. It was possible through electrophoresis to differentiate phenotypically similar cultivars for example UU-12, Multifreezer, Piourette, Starcovert, Bonneville and IP-3. Cultivar Meethi Phali with a specific characteristic of edible pod type formed a separate group with 9 bands. Most of the varieties showed no distinct patterns which would allow their characterization. There were a few specific bands in each variety and most of them; although exclusive, appeared at such a low frequency that varietal characterization was not possible.

Key Words: Electropherogram, Genotypes, Pea, SDS-PAGE, Seed protein

Introduction

The use of the seed protein profile, obtained by electrophoresis, for resolving taxonomic and evolutionary problems has been greatly expanded in the last decade. Stability is one of the main features of the seed protein. For this reason it has been suggested as an additional tool for species identification besides other traditional approaches (Wolf, 1980; Bushuk *et al.*, 1987).

Characterization of germplasm using biochemical fingerprinting has got special attention due to its increased use in crop improvement and the selection of desirable genotypes for breeding crops. Protein profiling, an independent, emerging sub-specialty of proteomics, is poised to provide unprecedented insight into biological events. Unlike DNA sequencing, where capillary electrophoresis changed everything by allowing high-throughput sequencing, no equivalent exists for proteins. The use of genetic markers and protein profiling is also successfully used to resolve the taxonomic and evolutionary problems of several crop plants (Ladizinsky and Hymowitz, 1979). Unfortunately, except for a few genera, extensive screening of germplasms to uncover variability in the seed protein profile is generally lacking. The concept of genetic distance has been widely used as a tool in determining diversity through multivariate analysis to choose genetically diverse parents (Ghosh and Gulati, 2002). Very little information is available on

the geneology of pea varieties, the amount of variability still available to breeding populations and the relationship between the pea varieties used for fodder, food or feed. The present study has been undertaken to get better knowledge on the architecture of genetic diversity within *Pisum sativum* L.. In view of above considerations, the electrophoretic characterization of available germplasms based on SDS-PAGE of seed protein had been done in the present investigation.

Materials and Methods

One-dimensional SDS-polyacrylamide vertical slab gel electrophoresis was carried out to determine the protein profiles per banding patterns of buffer extracted (Tris base, SDS and Mercaptoethanol) seed proteins excluding seed coat in 113 vegetable pea genotypes (Garffin 1990). The extraction procedure of Matta and Gatehouse (1982) was followed. The procedure developed by Laemmli (1970) was followed for gel preparation and running. The electropherogram of each gel was prepared diagrammatically locating the bands in lines on the basis of their relative front mobility values (rf value). Relative front mobility was calculated as per following formula:

$$Rf = \frac{\text{Distance between origin and band}}{\text{Distance between origin and tracking dye}}$$

The electropherograms (banding patterns) are shown in Plate 1.

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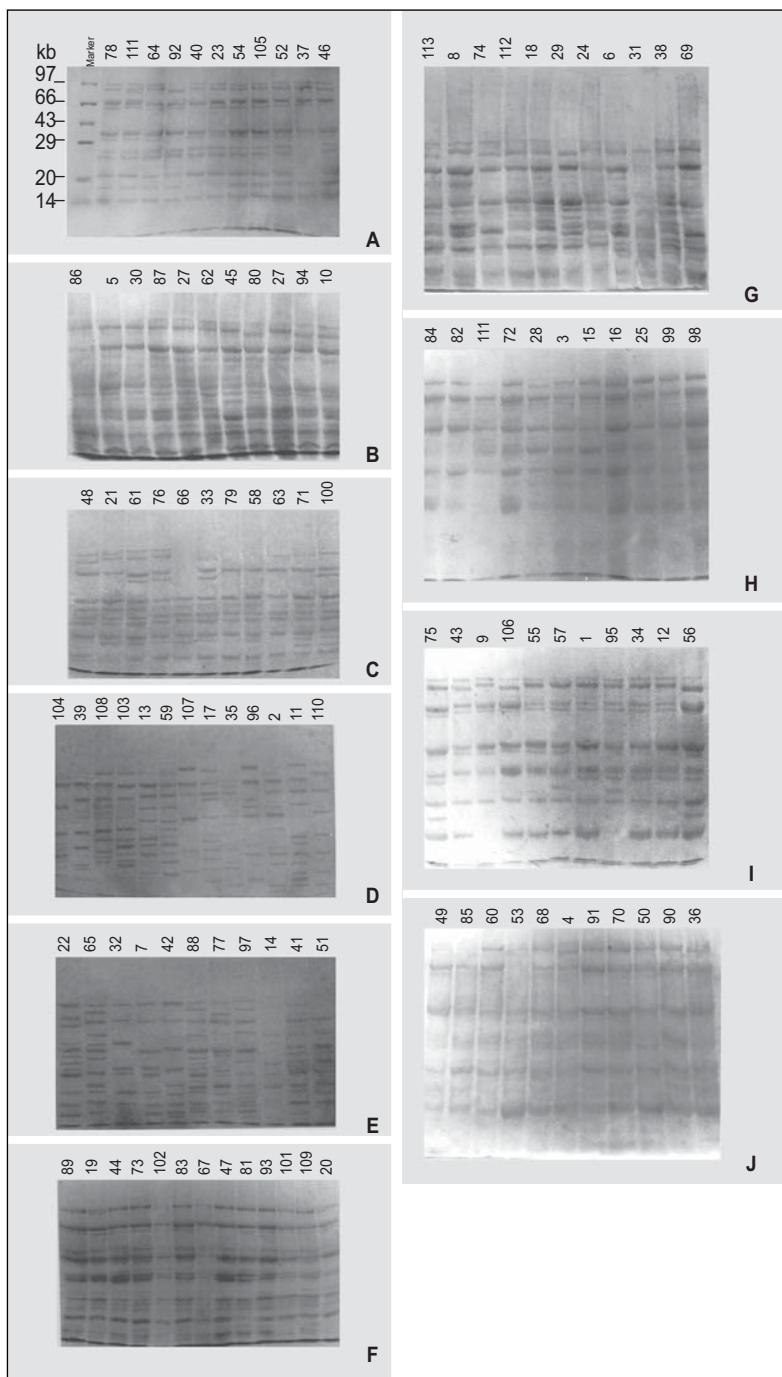


Fig. 1. Electropherogram of 113 genotypes of vegetable Pea. See Table 1 for legends

The banding patterns were characterized by 6 clear distinct zones viz., A, B, C, D, E and F. Zone A (around 97kDa) was nearest and F (around 14kDa) was farthest from the origin *i.e.* the point of protein sample application. The protein migrated from cathode to anode passing through separating gel. The protein bands were stacked

according to their molecular weight *i.e.* high molecular weight protein were located in upper region and low molecular weight proteins in the middle to lower regions of the gel, respectively (Table 2).

On the basis of molecular weight markers pattern, method used by Rosa and Jouve (1992) was followed

Table 1. Legend for Fig. 1.

S. No.	Genotype number	Genotype	S. No.	Genotype number	Genotype
Gel A			Gel F		
1.	78	Boach Selection	1.	89	Alderman Dwarf
2.	111	Alaska	2.	19	KS-245
3.	64	Waverplus	3.	44	Ecoli
4.	92	JP-4	4.	73	Early December
5.	40	NDVP-10	5.	102	Profino
6.	23	Cobric	6.	83	ELF
7.	54	Starcovert	7.	67	PMR-8
8.	105	P-388-1	8.	47	Borpeena
9.	52	PMR	9.	81	Bonneville
10.	37	PMR-7	10.	93	VP-8002
11.	46	KS-246	11.	101	Arkel
Gel B			12.	109	King
1.	86	VP-8902	13.	20	Bridger
2.	5	JP-83	Gel G		
3.	30	Dwarf Gray Sugar	1.	113	Frosty
4.	87	VRP-1	2.	8	Midivert
5.	26	PM-1	3.	74	Rover
6.	62	Primette	4.	112	PI-3
7.	45	Tuinya Pratapgarh	5.	18	PMR-3
8.	80	Sutton Early Giant	6.	29	Cobrette
9.	27	PMR-11	7.	24	Selection-23
10.	94	Sel-82	8.	6	GC-141
11.	10	PM-5	9.	31	VL-6
Gel C			10.	38	Alderman
1.	48	Sel-30	11.	69	NDVP-9
2.	21	Deleketesse	Gel H		
3.	61	PC-121	1.	84	Meethi Phali
4.	76	Lincoln	2.	82	PMR-13
5.	66	Stop	3.	26	PM-1
6.	33	VL-7	4.	72	GC-245
7.	79	GC-152	5.	28	PMR-18
8.	58	Sel-14-3-2	6.	3	Manova Sugar
9.	63	UD-3	7.	15	PMR-21
10.	71	Corona Imperette	8.	16	PMR-15
11.	100	P-88	9.	25	6588-1
Gel D			10.	99	KT-15-4-4
1.	104	Azad Pea-3	11.	98	KS-123
2.	39	NDVP-1	Gel I		
3.	108	Recette	1.	75	Multifreezer
4.	103	Progress	2.	43	KS-226
5.	13	DPP-62	3.	9	Thomas Laxton
6.	59	Harabona	4.	106	Lay long Progress
7.	107	Superlaska	5.	55	PRS-18-6
8.	17	VRP-2	6.	57	Little Marvel
9.	35	JP-171	7.	1	UU-12
10.	96	Victory Freezer	8.	95	PMR-12
11.	2	6587-1	9.	34	NDVP-25
12.	11	VP-7802	10.	12	Pioneer
13.	110	Green Gulf	11.	56	P-23
Gel E			Gel J		
1.	22	PMR-9	1.	49	PMR-17
2.	65	Waverex	2.	85	Meethi Phali
3.	32	Polerette	3.	60	NDVP-5
4.	7	PM-2	4.	53	UD-2
5.	42	Piourette	5.	68	E-6
6.	88	Frizette	6.	4	Vitalis
7.	77	Petit Breton	7.	91	VL-3
8.	97	J-506	8.	70	NLP
9.	14	Asauji	9.	50	PH-2
10.	41	Early Queen	10.	90	Mammoth Melting Sugar
11.	51	PMR-16	11.	36	Sel-93

Table 2. SDS-PAGE banding patterns for seed protein in 113 genotypes of vegetable pea classified into 28 groups

Zone Rf	Value	Groups																											
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
A ₁	1.0	+	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
A ₂	1.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	+	-	-	-	-	-
A ₃	1.5	-	-	-	+	-	+	-	-	+	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	+	-	-	-
A ₄	1.7	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
A ₅	2.0	+	-	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	+	-	+	-	-	-
A ₆	2.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
B ₁	2.5	-	+	-	-	-	+	+	-	+	+	-	+	-	+	+	+	-	+	-	-	-	-	-	-	+	-	-	-
B ₂	2.7	-	-	-	-	+	-	+	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
B ₃	2.9	-	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
B ₄	3.0	-	-	-	+	+	-	-	+	-	+	+	-	+	-	+	-	+	-	-	-	-	-	-	-	-	-	+	+
B ₅	3.2	-	-	-	-	-	-	+	-	-	-	-	-	+	-	-	-	+	-	+	-	-	+	-	-	-	-	-	-
B ₆	3.4	-	+	-	-	-	+	-	+	-	-	+	+	+	+	+	+	-	+	-	-	+	-	-	-	+	+	-	+
B ₇	3.6	-	-	-	-	-	-	+	+	+	+	-	+	-	+	+	-	+	-	-	-	+	-	-	-	-	-	+	-
B ₈	3.8	-	+	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	-
C ₁	4.0	+	-	-	-	-	-	-	-	+	+	-	-	-	-	+	+	+	-	+	-	-	+	+	-	-	-	-	+
C ₂	4.2	+	-	-	-	-	-	-	+	+	-	+	-	+	-	-	-	+	-	-	-	-	-	+	-	-	+	-	-
C ₃	4.5	-	-	+	+	+	-	-	-	+	+	-	+	-	+	+	-	-	+	-	-	-	+	-	-	+	-	-	-
C ₄	4.7	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	+	-	+	-	-	-	-	-	-	+	-	-
C ₅	5.0	-	-	+	+	+	+	-	+	+	+	-	-	+	-	+	-	-	-	-	+	-	-	+	-	+	+	-	-
C ₆	5.2	-	-	-	-	-	+	-	-	-	-	-	+	-	+	-	+	+	-	+	-	-	-	-	-	-	-	-	-
C ₇	5.4	+	-	-	-	-	-	-	-	-	-	-	+	-	+	+	-	-	-	-	-	-	-	+	-	-	-	+	-
C ₈	5.5	-	+	+	-	+	+	+	-	-	+	+	-	+	-	-	+	-	+	+	-	+	-	+	+	+	-	-	-
C ₉	5.8	-	-	-	-	-	-	-	-	+	-	-	+	+	+	+	-	-	-	-	-	+	-	-	-	-	-	-	+
C ₁₀	6.0	-	-	+	+	+	-	-	+	-	+	+	+	-	-	+	+	+	-	-	-	-	-	-	+	-	+	-	+
C ₁₁	6.2	-	-	+	-	-	-	-	+	-	-	+	-	+	+	+	-	+	-	-	-	-	-	-	-	-	-	-	-
C ₁₂	6.5	-	+	-	-	-	+	+	-	+	-	+	+	-	+	-	+	+	+	-	+	+	+	+	+	+	+	+	+
C ₁₃	6.7	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	+	-	-	-	-	-	-	+	-	-
C ₁₄	6.8	+	-	-	-	-	-	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
D ₁	7.0	-	-	-	+	+	-	-	+	-	-	+	+	-	+	+	+	-	-	+	-	+	+	+	+	+	-	+	+
D ₂	7.2	-	-	+	-	-	+	-	-	-	+	+	-	-	-	-	-	-	+	-	+	-	-	-	-	-	-	-	-
D ₃	7.4	-	-	-	-	-	-	-	+	+	-	-	+	+	+	+	+	+	-	+	-	+	+	-	-	+	+	-	-
D ₄	7.6	-	-	-	-	-	-	-	-	-	-	-	+	-	+	+	-	+	-	-	-	-	-	-	-	-	+	-	-
D ₅	7.8	-	+	-	-	-	-	-	-	-	-	+	-	+	-	+	-	-	-	-	-	+	-	-	-	-	-	-	-
D ₆	8.0	-	-	-	-	+	-	+	+	-	+	-	+	+	+	-	-	+	-	-	-	+	-	-	-	-	+	+	+
E ₁	8.2	-	-	-	-	-	-	-	-	-	-	+	-	+	+	+	-	+	-	+	+	-	+	-	-	-	-	-	-
E ₂	8.5	+	+	+	+	+	+	-	+	-	-	+	+	+	+	+	-	+	-	-	-	-	-	+	+	-	+	-	-
E ₃	8.8	-	-	-	-	-	-	-	-	-	-	+	-	+	-	+	-	+	-	-	-	-	-	-	-	-	-	-	-
E ₄	9.0	-	-	-	-	-	-	+	-	-	+	-	+	+	+	-	+	-	+	+	+	-	+	-	-	-	-	-	-
F ₁	9.2	-	-	-	-	-	-	-	+	+	-	-	-	+	+	+	-	+	-	-	+	-	-	-	-	-	+	-	-
F ₂	9.5	-	-	-	-	-	-	-	+	-	-	+	+	-	+	+	-	+	-	+	-	+	+	-	+	-	-	-	+
F ₃	9.7	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	+	+
F ₄	9.8	-	+	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
Total		7	9	9	9	10	11	11	13	13	14	15	16	17	18	20	11	19	11	11	8	9	9	10	6	9	14	7	10

for band differentiation, zone A representing the heaviest molecular weight protein was sub divisible into six distinct bands i.e. A₁, A₂, A₃, A₄, A₅ and A₆. Among these A₃ and A₅ were comparatively sharp bands. Similarly, zone B representing mostly thicker and dark bands, was sub divisible into eight bands i.e. B₁, B₂, B₃, B₄, B₅, B₆, B₇ and B₈. However, B₁, B₄ and B₆ were relatively dark bands. The next zone C representing dark to lighter bands with few faint bands was sub divisible into C₁, C₂, C₃, C₄, C₅, C₆, C₇, C₈, C₉, C₁₀, C₁₁, C₁₂, C₁₃, and C₁₄. The next zone D characterized by lighter to faint bands was sub divisible into D₁, D₂, D₃, D₄, D₅ and D₆. Similarly, zone E representing mostly sharp bands were sub divisible into E₁, E₂, E₃ and E₄. Among these, E₂ and E₃ were comparatively thicker and darker bands. The last zone F was characterized by comparatively lighter bands and was sub divisible into F₁, F₂, F₃ and F₄. Thus a total of 42 bands could be resolved in seed protein (Table 2).

The different bands of HMW (97-43 kDa) were used for calculation of similarity indices. Presence of bands was scored as 1 and its absence as 0 for all the genotypes. These data matrix were then entered into NTSYS-PC.

The grouping was carried out by unweighted pair group method using arithmetic averages (UPGMA) cluster analysis (Sneath and Sokal, 1973). The calculations were done using computer software package NTSYS-PC (Numerical Taxonomy and Multivariate Analysis System Programme) (Rohlf, 1993).

Results and Discussion

The seed protein of 113 pea lines was subjected to sodium dodecyl sulphate polyacrylamide slab gel electrophoresis. The results obtained in the present study demonstrated the existence of 42 protein bands located in six zones (A, B, C, D, E and F). Different protein electrophoretic patterns exhibited by 113 cultivars could be identified solely by the cultivar specific electropherogram (Fig. 1). On the basis of protein profile, 113 genotypes were classified into 28 groups. The genotypes within the group had similar protein banding pattern (Table 3).

The cultivars which were indistinguishable on the basis of simple identifiable morphological traits like growth habit; flower colour etc. could be distinguished on the basis of their electrophoretic patterns, example,

Table 3. Name of cultivars with in groups

Group	Cultivars
1.	6587-1, Asauji, Primette and NDVP-9
2.	Manova Sugar, Cobric, Dwarf Gray Sugar, Early Queen, VL-3, JP-4, Sel-82, Profino, Recette, Green Gulf, IP-3 and Frosty
3.	JP-83, VP-7802, UD-2, and PRS-18-6
4.	GC-141 and NDVP-5
5.	NDVP-1 and Ecoli
6.	P-23, Little Marvel, Progress, E-6, KS-246, Multifreezer, and NLP
7.	PMR-8 and Lincoln
8.	UU-12, VRP-2, PMR-3, PM-1, PMR-21, PMR-18, Sel-93, Alderman, NDVP-10, Tuinya Pratappgarh, Bridger, Borpeena, Piourette, PH-2, Sel-30, Deleketesse, UD-3, Waverex, PMR-11, Rover, PMR-13, Vitalette, VP-8902, P-88 and Azad Pea-3
9.	Cobrette, KS-245, VL-7, Stop, Petit Breton, KT-15-4-4, Sutton Early Giant, Victory Freezer and Waverplus
10.	PM-2, PMR-15, PMR-9, Starcovert, PMR-12 and P-388-1
11.	NDVP-25, Herabona, PC-121, ELF, VRP-1, Frizette, Boach Selection, Alderman Dwarf and Superlaska
12.	PM-5, Sel-23, VL-6, Polerette and J-506
13.	KS-226, PMR-17, VP-8002 and Arkel
14.	PMR, Corona Imperette, GC-245, GC-152, Bonneville, Lay Long Progress and King
15.	DPP-62
16.	Vitalis
17.	Midivert
18.	Thomas Laxton
19.	Pioneer
20.	6588-1
21.	JP-171
22.	PMR-7
23.	PMR-16
24.	Early December
25.	Meethi Phali
26.	Mammoth Melting Sugar
27.	KS-123
28.	Alaska

cultivars UU-12, Multifreezer, Piourette, Starcovert, Bonneville and IP-3 got separated which was not possible by morphological markers. Cultivar Meethi Phali with a specific characteristic of edible pod formed a separate group with 9 bands.

Some of the cultivars placed in the same group on the basis of their similar banding pattern were distinguishable by the intensity of staining of bands, for example, UU-12, VRP-2, PMR-3, PM-1, PMR-21, PMR-18, Sel-93, Tuinya Pratapgarh, PH-2, UD-3, PMR-11, PMR-13, Azad Pea-3 had a very dark and thick B₄ band as compared to KS-245, Alderman, NDVP-10, Bridger, Borpeena, Waverex, Rover, Vitalette and P-88 where this B₄ band was medium dark. Differences between accessions in the darkness and thickness of various bands are the most commonly reported types of variation, suggesting that the formation of many of the bands in the seed protein profile are under control of quantitative gene systems. This theory was supported by the study of Ladizinsky and Hymowitz (1979) and they also suggested that this kind of variation may be due to differential extraction or solubility of seed protein from different accessions.

Variation in band intensity observed within electropherograms of different groups may be attributed to large variation in the amount of various polypeptides present in the protein extract. Similar trends were observed in the protein-banding pattern of other leguminous crops like cowpea (Gomathinayagam and Ramaswary, 1994), fieldpea (Hussain *et al.*, 1988) and also pea (Mishra *et al.*, 1998).

Although, uniformity and uniqueness of seed protein profile are typical of plants, variation in the number of bands and their position in the profile have been reported, especially where great number of accessions were examined (Salmanowiz and Przybylska, 1992 and Singh *et al.*, 1994). There was pattern in grouping of genotypes cultivars UU-12, Multifreezer, Piourette, Starcovert, Bonneville and IP-3. Cultivar Meethi Phali related to agronomic traits and selected genotypes from various clusters are suggested to use in pea improvement program (Ghafoor and Arshad, 2008).

Cluster analysis (Fig. 2; Table 4), after quantifying the protein bands, using UPGMA procedure, indicated that broadly the germplasms were grouped into two clusters, KS-226, Harabona and Multifreezer in cluster I and rest 110 genotypes in cluster II. The cluster II again formed

12 small clusters having 50-100% similarity. Dwarf and early varieties KS-226, Multifreezer and Harabona were included in one cluster which was most distinct from other showing greater divergence from other cultivars. The above varieties showed greater internal homogeneity and were more distinct from the other varieties. Within this clusters genotypes Multifreezer and KS-226 were having 68% similarity and from this Harabona included with a branching having 48% similarity with the above two. This may be due to the fact that Multifreezer and KS-220 are received from Holland and Harabona must be split off from an earlier common ancestor to form the secondary gene pool. This study had been in agreement with the work of Labdi *et al.* (1996).

Similarly relatively higher similarity percentage indicated a closeness among the genotypes as perusal of result presented 100% similarity between Progress and Recette and Alderman and VL-6. The closeness might be due to common parentage as former three cultivars were released from Europe and VL-6 had parentage of European origin or confluence of similar genes from different parents in the development of varieties. Similar pattern had been reported by Mishra *et al.* (1998). The phylogenetic evolutionary tree developed from the analysis indicated that most of the pea varieties did not form distinct clusters; rather, the relatively close and small clusters of varieties were distributed within one broad cluster as can be seen in the phenogram obtained in cluster II with 12 groups of 110 varieties of pea. The relatedness of varieties in dendrogram were of mixed pattern as per their geographical distribution (Table 4). This may be due to the fact that till now different selection pressure must have been applied for different yield and yield related characters in different genotypes which caused the diverse expression of genes for those characters in genotypes. This need to the fact that formation of many bands in seed protein profiles are under control of quantitative gene systems and proteins are primary products of structural gene changes in coding base sequence will under many circumstances result in corresponding changes in the primary structure of protein. Even single amino acid substitution, deletion or addition can have marked effects on the migration of proteins under an electric field during electrophoresis (Ladizinsky and Hymowitz, 1979).

The similarity percentage varied between 50–100%. This corresponds with the fact that little genetic diversity found in pea used in study and most cultivars have the

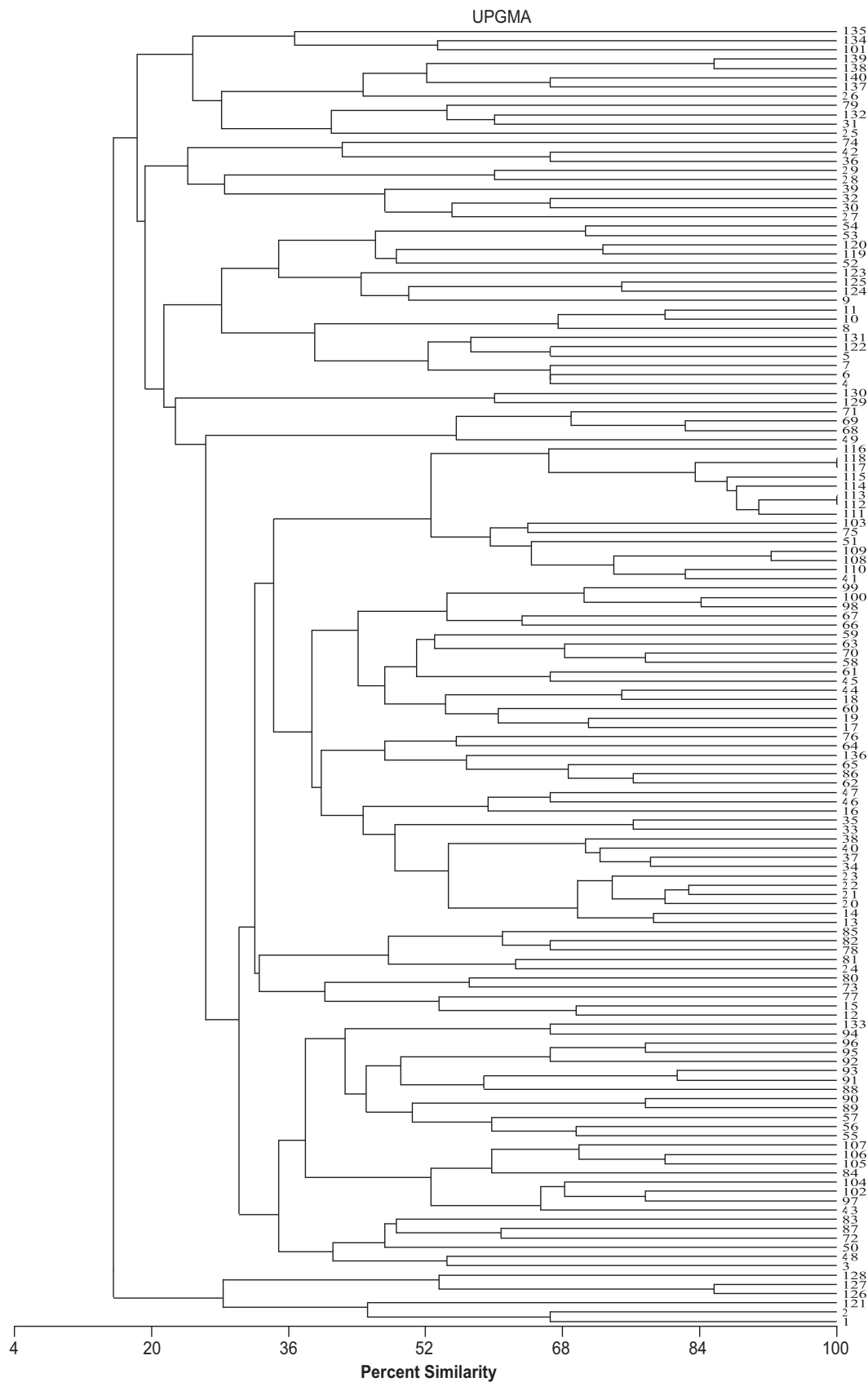


Fig. 2. Dendrogram generated based on seed protein bands of pea genotypes

Table 3. Arrangement of genotype in dendrogram

S. No.	Genotype No.	Genotypes	S. No.	Genotype No.	Genotypes
1.	82	PMR-13	58.	83	ELF
2.	97	J-506	59.	51	PMR-16
3.	15	PMR-21	60.	27	PMR-11
4.	84	Viodetti	61.	80	Sutton Early Giant
5.	86	VP-8902	62.	22	PMR-9
6.	91	VL-3	63.	94	Sel-82
7.	49	PMR-17	64.	78	Boach Selection
8.	28	PMR-18	65.	36	Sel-93
9.	72	GC-245	66.	102	Profino
10.	53	UD-2	67.	98	KS-123
11.	16	PMR-15	68.	25	6588-1
12.	3	Manoa Sugar	69.	66	Stop
13.	110	Green Gulf	70.	68	E-6
14.	54	Starcovert	71.	85	Meethi Phali
15.	23	Cobric	72.	99	KT-15-4-4
16.	13	DPP-62	73.	109	King
17.	40	NDVP-10	74.	101	Arkel
18.	107	Superlaska	75.	93	VP-8002
19.	17	VRP-2	76.	81	Bonneville
20.	34	NDVP-25	77.	44	Ecoli
21.	56	P-23	78.	19	KS-245
22.	12	Pioneer	79.	65	Waverex
23.	95	PMR-12	80.	42	Piourette
24.	55	PRS-18-6	81.	14	Asauji
25.	1	UU-12	82.	88	Frizette
26.	57	Little Marvel	83.	20	Bridger
27.	106	Lay Long Progress	84.	77	Petit Breton
28.	30	Dwarf Gray Sugar	85.	5	JP-83
29.	87	VRP-1	86.	41	Early Queen
30.	26	PM-1	87.	73	Early December
31.	64	Waver Plus	88.	89	Alderman Dwarf
32.	39	NDVP-1	89.	33	VL-7
33.	103	Progress	90.	79	GC-152
34.	108	Recette	91.	60	NDVP-5
35.	104	Azad Pea-3	92.	76	Lincoln
36.	69	NDVP-9	93.	21	Deleketesse
37.	38	Alderman	94.	61	PC-121
38.	31	VL-6	95.	37	PMR-7
39.	6	GC-141	96.	52	PMR
40.	113	Frosty	97.	105	P-388-1
41.	92	JP-4	98.	18	PMR-3
42.	29	Cobrette	99.	112	IP-3
43.	24	Sel-23	100.	74	Rover
44.	4	Vitalis	101.	32	Polerelte
45.	63	UD-3	102.	8	Midivert
46.	71	Corona Imperatte	103.	100	P-88
47.	62	Primette	104.	58	Sel-14-3-2
48.	45	Tuinya Pratapgarh	105.	70	NLP
49.	35	JP-171	106.	7	PM-2
50.	2	6587-1	107.	48	Sel-30
51.	46	KS-246	108.	11	VP-7802
52.	10	PM-5	109.	111	Alaska
53.	90	Mammoth Melting Sugar	110.	9	Thomas Laxton
54.	50	PH-2	111.	59	Harabona
55.	67	PMR-8	112.	43	KS-226
56.	96	Victory Freezer	113.	75	Multifreezer
57.	47	Borpeena			

Table 4. List of genotypes, their source and features

S.No.	Genotype	Source	Plant height	Growth	Flower colour	Foliage colour	Seed colour	Seed type
1.	UU-12	Pantnagar	Medium	Mid	W	YG	Green	Wrinkled
2.	6587-1	Jabalpur	Tall	Late	W	YG	Yellow	Smooth
3.	Manova sugar	Ludhiana	Medium	Mid	W	YG	Yellow	Smooth
4.	Vitalis	Holland	Tall	Late	P	YG	Green	Wrinkled
5.	JP-83	Jabalpur	Medium	Mid	W	YG	Yellow	Smooth
6.	GC-141	Gwalior	Tall	Early	W	G	Green	Wrinkled
7.	PM-2	Pantnagar	Dwarf	Early	W	G	Green	Wrinkled
8.	Midivert	Holland	Medium	Early	W	YG	Green	Wrinkled
9.	Thoms laxton	Etawah	Dwarf	Mid	W	DG	Yellow	Smooth
10.	PM-5	Pantnagar	Dwarf	Mid	W	DG	Green	Wrinkled
11.	VP-7802	Almora	Medium	Mid	W	G	Green	Wrinkled
12.	Pioneer	Etawah	Medium	Mid	W	DG	Green	Wrinkled
13.	DPP-62	N.Delhi	Dwarf	Mid	W	DG	Green	Wrinkled
14.	Asauji	Kalyanpur	Tall	Mid	W	YG	Green	Wrinkled
15.	PMR-21	Pantnagar	Dwarf	Early	W	DG	Green	Smooth
16.	PMR-15	Pantnagar	Medium	Mid	P	YG	Green	Smooth
17.	VRP-2	Varanasi	Medium	Mid	W	YG	Green	Wrinkled
18.	PMR-3	Pantnagar	Medium	Mid	W	G	Green	Wrinkled
19.	KS-245	Kalyanpur	Dwarf	Mid	P	G	Yellow	Wrinkled
20.	Bridger	Etawah	Medium	Mid	W	DG	Green	Wrinkled
21.	Deleketesse	Holland	Tall	Late	W	G	Green	Wrinkled
22.	PMR-9	Pantnagar	Medium	Mid	W	YG	Yellow	Smooth
23.	Cobric	Holland	Medium	Mid	W	G	Green	Smooth
24.	Selection-23	Pantnagar	Dwarf	Mid	W	G	Green	Wrinkled
25.	6588-1	Jabalpur	Tall	Mid	W	G	Yellow	Wrinkled
26.	PM-1	Pantnagar	Dwarf	Early	W	G	Green	Wrinkled
27.	PMR-11	Pantnagar	Medium	Late	W	G	Green	Wrinkled
28.	PMR-18	Pantnagar	Dwarf	Mid	W	DG	Yellow	Smooth
29.	Cobrette	Holland	Tall	Late	W	YG	Yellow	Smooth
30.	Dwarf gray sugar	Etawah	Tall	Late	P	YG	Green	Wrinkled
31.	VL-6	Almora	Medium	Mid	W	G	Yellow	Wrinkled
32.	Polerette	Holland	Medium	Mid	W	G	Green	Smooth
33.	VL-7	Almora	Dwarf	Early	W	G	Green	Wrinkled
34.	NDVP-25	Faizabad	Dwarf	Mid	W	G	Yellow	Wrinkled
35.	JP-171	Jabalpur	Dwarf	Mid	W	YG	Yellow	Wrinkled
36.	Sel-93	Jabalpur	Tall	Late	W	G	Yellow	Smooth
37.	PMR-7	Pantnagar	Medium	Late	W	YG	Yellow	Smooth
38.	Aldarman	England	Medium	Late	W	DG	Green	Wrinkled
39.	NDVP-1	Faizabad	Dwarf	Early	W	G	Yellow	Wrinkled
40.	NDVP-10	Faizabad	Dwarf	Mid	W	G	Green	Wrinkled
41.	Early queen	Ludhiyana	Dwarf	Mid	W	G	Green	Wrinkled
42.	Piourette	Faizabad	Medium	Mid	W	DG	Green	Wrinkled
43.	KS-226	Holland	Dwarf	Mid	W	G	Yellow	Smooth
44.	Ecoli	Kalyanpur	Tall	Mid	W	G	Yellow	Wrinkled
45.	Tuyina Pratapgarh	Lucknow	Dwarf	Early	W	G	Green	Smooth
46.	KS-246	Kalyanpur	Dwarf	Mid	W	YG	Green	Wrinkled
47.	Borpeena	Etawah	Medium	Mid	W	G	Green	Wrinkled
48.	Sel-30	N.Delhi	Dwarf	Early	W	YG	Yellow	Wrinkled
49.	PMR-17	Pantnagar	Dwarf	Early	W	G	Green	Wrinkled
50.	PH-2	Hissar	Dwarf	Mid	W	DG	Green	Wrinkled
51.	PMR-16	Pantnagar	Medium	Mid	W	G	Green	Wrinkled
52.	PMR	Pantnagar	Medium	Late	W	YG	Green	Wrinkled
53.	UD-2	Udaipur	Tall	Late	W	YG	Yellow	Wrinkled
54.	Starcovert	Holland	Medium	Mid	W	G	Green	Wrinkled
55.	PRS-18-6	Jabalpur	Dwarf	Mid	W	G	Green	Wrinkled
56.	P-23	Ludhiana	Dwarf	Mid	W	G	Green	Smooth
57.	Little Marvel	N.Delhi	Dwarf	Early	W	G	Green	Wrinkled
58.	Sel-14-3-2	Pantnagar	Tall	Late	W	G	Green	Wrinkled
59.	Herabona	Ludhiana	Dwarf	Early	W	G	Green	Wrinkled
60.	NDVP-5	Faizabad	Dwarf	Mid	W	G	Green	Wrinkled
61.	PC-121	Pantnagar	Dwarf	Mid	W	G	Yellow	Wrinkled
62.	Primette	Holland	Dwarf	Early	W	YG	Yellow	Smooth

Contd.

Table 4. Contd...

S.No.	Genotype	Source	Plant height	Growth	Flower colour	Foliage colour	Seed colour	Seed type
63.	UD-3	Udaipur	Dwarf	Early	W	YG	Yellow	Smooth
64.	Waverplus	Holland	Medium	Mid	W	DG	Yellow	Wrinkled
65.	Waverex	England	Dwarf	Mid	W	DG	Green	Wrinkled
66.	Stop	Holland	Dwarf	Mid	W	YG	Yellow	Wrinkled
67.	PMR-8	Pantnagar	Medium	Mid	W	YG	Yellow	Smooth
68.	E-6	Almora	Dwarf	Early	W	G	Green	Wrinkled
69.	NDVP-9	Faizabad	Dwarf	Early	W	G	Green	Wrinkled
70.	NLP	Etawah	Medium	Mid	W	DG	Green	Wrinkled
71.	Corona Imperette	Holland	Dwarf	Mid	W	G	Green	Wrinkled
72.	GC-245	Gwaliar	Dwarf	Mid	W	G	Yellow	Wrinkled
73.	Early December	N. Delhi	Dwarf	Mid	W	YG	Yellow	Wrinkled
74.	Rover	Holland	Dwarf	Mid	W	G	Green	Wrinkled
75.	Multifreezer	Etawah	Dwarf	Mid	W	YG	Green	Wrinkled
76.	Lincoln	Shimla	Medium	Late	W	YG	Green	Wrinkled
77.	Petit Breton	Holland	Dwarf	Mid	W	G	Yellow	Smooth
78.	Boach Selection	Solan	Medium	Mid	W	DG	Green	Wrinkled
79.	GC-152	Gwaliar	Tall	Late	W	YG	Yellow	Wrinkled
80.	Sutton Early Giant	Solan	Tall	Late	W	G	Yellow	Wrinkled
81.	Bonniville	Kalyanpur	Medium	Mid	W	YG	Green	Wrinkled
82.	PMR-13	Pantnagar	Dwarf	Mid	W	YG	Green	Smooth
83.	ELF	Holland	Medium	Mid	W	G	Yellow	Wrinkled
84.	Vitalette	Holland	Dwarf	Mid	W	G	Green	Wrinkled
85.	Meethi Phali	Ludhiana	Dwarf	Mid	W	G	Green	Wrinkled
86.	VP-8902	Almora	Dwarf	Mid	W	G	Yellow	Wrinkled
87.	VRP-1	Varanasi	Dwarf	Mid	W	YG	Yellow	Smooth
88.	Frizette	Holland	Medium	Mid	W	G	Green	Wrinkled
89.	Alderman Dwarf	Etawah	Dwarf	Mid	W	G	Green	Wrinkled
90.	Mammoth Melting Sugar	Etawah	Medium	Mid	P	YG	Green	Wrinkled
91.	VL-3	Almora	Dwarf	Mid	W	YG	Yellow	Wrinkled
92.	JP-4	Jabalpur	Medium	Late	W	YG	Green	Smooth
93.	VP-8002	Almora	Dwarf	Mid	W	G	Green	Wrinkled
94.	Sel-82	Hissar	Dwarf	Late	P	DG	Green	Wrinkled
95.	PMR-12	Pantnagar	Dwarf	Early	W	G	Green	Wrinkled
96.	Victory Freezer	Etawah	Medium	Mid	P	G	Green	Wrinkled
97.	J-506	England	Medium	Mid	W	G	Yellow	Smooth
98.	KS-123	Kalyanpur	Dwarf	Mid	W	YG	Yellow	Wrinkled
99.	KT-15-4-4	Katrain	Medium	Mid	W	G	Green	Wrinkled
100.	P-88	Ludhiana	Dwarf	Mid	W	G	Green	Wrinkled
101.	Arkel	Katrain	Dwarf	Early	W	G	Green	Wrinkled
102.	Profino	Holland	Dwarf	Early	W	G	Green	Smooth
103.	Progress	Etawah	Dwarf	Mid	W	YG	Yellow	Smooth
104.	Azad Pea-3	Kalyanpur	Dwarf	Mid	W	G	Green	Wrinkled
105.	P-388-1	Jabalpur	Medium	Late	W	G	Green	Wrinkled
106.	Lay Long Progress	Solan	Medium	Late	W	G	Green	Wrinkled
107.	Superlaska	Solan	Tall	Late	W	DG	Yellow	Wrinkled
108.	Recette	Holland	Dwarf	Mid	W	G	Yellow	Wrinkled
109.	King	Etawah	Dwarf	Mid	W	DG	Green	Wrinkled
110.	Green Gulf	Holland	Dwarf	Mid	W	YG	Yellow	Smooth
111.	Alaska	Etawah	Dwarf	Early	W	G	Green	Wrinkled
112.	IP-3	Etawah	Medium	Mid	W	DG	Green	Wrinkled
113.	Frosty	Etawah	Medium	Mid	W	DG	Green	Wrinkled

W = white YG = yellow green G = green P = purple DG = dark green

same ancestors. Similar results have been reported by Petr Samee and Vit Nasinec (1996) in 42 genotypes of *Pisum sativum* L. based on Jaccard's similarity coefficient.

Though considerable inter-variatal variability was found in the present study, most of the varieties showed no distinct patterns which would allow their characterization.

There were a few specific bands in each variety and most of them; although exclusive, appeared at such a low frequency that varietal characterization was not possible. Since pure seeds maintained by plant breeders were used in this study, the polymorphic protein patterns were considered to be representative of the varieties examined.

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Variability for Yield and Quality Traits in (Single-Cut) Forage Sorghum [*Sorghum Bicolor* (L.) Moench]

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An investigation was carried out using 62 diverse genotypes of forage sorghum to study the variability for yield and quality traits. Highly significant genotypic differences were found for all the traits studied. A wide range of variation was observed for days to 50% flowering, plant height, leaf length, leaf width, brix content, HCN content, green fodder yield/plant, dry matter yield/plant and dry matter (%), while moderate range was evident for tillers/metre row length, leaves/plant, leaf : stem ratio, and crude protein content. The genotypic coefficient of variation was high for green fodder yield/plant, dry matter yield/plant and HCN content which also manifested through high heritability and high genetic advance expressed as percentage of mean. Hence, phenotypic selection for these traits would be effective.

Key Words: Forage Sorghum, Genetic Advance, Heritability, Variability, White revolution

Introduction

Forage crops are important for the national economy since they form the nutritional base for our livestock population. In order to continue harnessing the fruits of White Revolution, emphasis on research relating to the improvement and management of forages is indeed very critical. With the increase in human population, the demand for animal products such as milk, meat and eggs in the human diet is increasing. The success of dairy and poultry programmes will largely depend on the availability of forages and feeds since almost 60-65% investment is accounted for these requirements.

A recent estimate indicates that there is a gap between total forage need and its availability by about 68% of green fodder and about 53% of dry forage. This deficit is likely to increase further because: (1) The area under forage crops is declining because of growing cereals and other cash crops to meet the increasing demand for food, (2) the animal population is also increasing every year by about 2%, (3) cultivable land is decreasing due to urbanization and industrial growth, and (4) forage crops in future are going to have competition from biofuel crops.

Sorghum [*Sorghum bicolor* (L.) Moench] locally known as Jowar, apart from grain, is widely used for forage production on account of its quick growth habit, quick recovery or regeneration after cutting or grazing and its ability to provide highly palatable

and nutritious fodder for cattle. The crop has wide range of adaptability over diverse climates and soils. Sorghum green fodder is one of the cheapest sources of feed for milch, meat and draft animals.

Selection of superior plants is the basis for crop improvement. The estimates of variability, heritability and genetic advance for the yield components and their correlations with yield are considered to be of great importance for improving the crop. Genetic variability is the pre-requisite for selection because selection can be effective only when the population shows variability within itself. The study of heritability, genetic coefficient of variation and genetic advance is imperative as high values of these parameters show that the additive gene action is involved in governing the characters which can be exploited through selection.

Material and Methods

The experimental material for the present investigation was comprised of 62 diverse fodder genotypes and three checks (Table 1) obtained from the Main Sorghum Research Station, Navsari Agricultural University, Surat (Gujarat); Forage Research Station, Anand Agricultural University, Anand (Gujarat); as well as sorghum research stations located in Marathawada Agricultural University, Parbhani (Maharashtra); Mahatma Phule Krishi Vidhyapeeth, Rahuri (Maharashtra) and in Dr. Punjabrao Deshmukh Krishi Vidhyapeeth, Akola (Maharashtra). The experiment was conducted in a

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Table 1. List of genotypes evaluated with its source

S. No.	Genotypes	Source	Sr. No.	Genotypes	Source
1.	Amruta	FRS, A.A.U., Anand	32.	SG-348	FRS, A.A.U., Anand.
2.	AKFR-89	SRS, P.D.K.V., Akola	33.	SG-356	FRS, A.A.U., Anand
3.	AKFSV-3	MSRS, N.A.U., Surat	34.	SG-416	FRS, A.A.U., Anand
4.	C-10-2	FRS, A.A.U., Anand	35.	SG-426	FRS, A.A.U., Anand
5.	COFS-29	FRS, A.A.U., Anand	36.	SG-441	FRS, A.A.U., Anand
6.	IS-23960	SRS, P.D.K.V., Akola	37.	SG-479	FRS, A.A.U., Anand
7.	IS-22450	SRS, P.D.K.V., Akola	38.	SG-507	FRS, A.A.U., Anand
8.	IS-23980	SRS, P.D.K.V., Akola	39.	SG-544	FRS, A.A.U., Anand
9.	IS-SGL87	SRS, P.D.K.V., Akola	40.	SG-570	FRS, A.A.U., Anand
10.	M-35-1	FRS, A.A.U., Anand	41.	SRF-187	MSRS, N.A.U., Surat
11.	Mp-Chari	FRS, A.A.U., Anand	42.	SRF-204-1	MSRS, N.A.U., Surat
12.	PKV-801	SRS, M.A.U., Parbhani	43.	SRF-207	MSRS, N.A.U., Surat
13.	PKV-809	SRS, M.A.U., Parbhani	44.	SRF-283	MSRS, N.A.U., Surat
14.	Ruchira	SRS, M.P.K.V., Rahuri	45.	SRF-285	MSRS, N.A.U., Surat
15.	S-1049	FRS, A.A.U., Anand	46.	SRF-286	MSRS, N.A.U., Surat
16.	SG-16	FRS, A.A.U., Anand	47.	SRF-288	MSRS, N.A.U., Surat
17.	SG-25	FRS, A.A.U., Anand	48.	SRF-289	MSRS, N.A.U., Surat
18.	SG-65	FRS, A.A.U., Anand	49.	SRF-311	MSRS, N.A.U., Surat
19.	SG-85	FRS, A.A.U., Anand	50.	SRF-312	MSRS, N.A.U., Surat
20.	SG-105	FRS, A.A.U., Anand	51.	SRF-314	MSRS, N.A.U., Surat
21.	SG-138	FRS, A.A.U., Anand	52.	SRF-315	MSRS, N.A.U., Surat
22.	SG-149	FRS, A.A.U., Anand	53.	SRF-319	MSRS, N.A.U., Surat
23.	SG-150	FRS, A.A.U., Anand	54.	SRF-322	MSRS, N.A.U., Surat
24.	SG-173	FRS, A.A.U., Anand	55.	SRF-324	MSRS, N.A.U., Surat
25.	SG-214	FRS, A.A.U., Anand	56.	SRF-1663	MSRS, N.A.U., Surat
26.	SG-230	FRS, A.A.U., Anand	57.	SSG-59-3	FRS, A.A.U., Anand
27.	SG-251	FRS, A.A.U., Anand	58.	SSG-59-3 (Brown glume)	SRS, P.D.K.V., Akola.
28.	SG-269	FRS, A.A.U., Anand	59.	SSV-84	SRS, M.A.U., Parbhani.
29.	SG-289	FRS, A.A.U., Anand	60.	GFS-3 (Check 1)	FRS, A.A.U., Anand
30.	SG-314	FRS, A.A.U., Anand	61.	GFS-4 (Check 2)	MSRS, N.A.U., Surat
31.	SG-316	FRS, A.A.U., Anand	62.	GFS-5 (Check 3)	FRS, A.A.U., Anand

FRS, A.A.U., Anand – Forage Research Station, Anand Agricultural University, Anand

SRS, P.D.K.V., Akola – Sorghum Research Station, Punjabrao Deshmukh Krushi Vidhyapeeth, Akola

MSRS; NAU, Surat – Main Sorghum Research Station, Navsari Agricultural University, Navsari

SRS, M.A.U., Parbhani – Sorghum Research Station, Marathwada Agril. University, Parbhani

SRS, M.P.K.V., Rahuri – Mahatma Phule Krushi Vidhyapeeth, Rahuri

Randomized Complete Block Design (RCBD) with three replications. Each genotype consisted of three rows each of two metre length spaced 30 cm apart from each other with a plant to plant distance of 10 cm. The experimental material was dibbled on 10th July 2008 at the College farm, NM College of Agriculture, Navsari Agricultural University, Navsari. The plant protection measures, irrigation, fertilizer schedule and other cultivation aspects were adopted as per recommended package of practices specific to the crop for South Gujarat Heavy Rainfall Zone (AES-III). From each plot in all the three replications, five randomly selected plants were tagged for recording the observations on days to 50% flowering, tillers per metre row length, plant height (cm), leaves per plant, leaf length (cm), leaf width (cm), leaf:stem ratio, brix content (%), hydrocyanic acid content (ppm), crude protein content (%), green fodder yield/plant (g), dry matter yield/plant (g) and dry matter (%). The mean values of data from the tagged plants were computed

and used for statistical analysis. The phenotypic and genotypic coefficients of variation (PCV and GCV, respectively) were calculated as per Burton (1952). Heritability (h^2) and expected genetic advance (GA) were calculated by the formula suggested by Allard (1960) while, Expected Genetic Advance in terms of per cent of mean (GA%) was calculated by the methodology proposed by Johnson *et al.* (1955).

Results and Discussion

Analysis of variance (Table 2) revealed highly significant differences among the genotypes for all the traits evaluated which indicated that there was considerable amount of genetic variability in the experimental material indicating the suitability of material under study.

Mean performance of each genotype for all the 13 traits evaluated is given in Table 3. Result revealed that wide range of phenotypic variation (Table 4) was observed for days to 50% flowering, plant

Table 2. Analysis of variance showing means square for 13 traits in forage sorghum

Source	D.F.	Days to 50% flowering	Tillers/ metre row length	Plant height (cm)	Leaves/ plant	Leaf length (cm)	Leaf width (cm)	Leaf: Stem ratio	Brix content (%)	HCN content (ppm)	Crude protein content (%)	Green fodder yield/plant (g)	Dry matter yield / plant (g)	Dry Matter (%)
Replications	2	1.04	0.49	1.39	0.08	4.46	0.04	0.001	0.01	24.70	0.05	7.46	30.38	10.23
Genotypes	61	297.01**	17.52**	2721.99**	8.42**	212.32**	3.94**	0.021**	7.06**	12744.09**	6.05**	18131.81**	2313.70**	186.92**
Error	122	1.56	0.68	352.73	0.20	7.70	0.07	0.002	0.08	21.00	0.06	326.21	26.89	32.57

** Significant at 0.01 p level

height, leaf length, leaf width, brix content, HCN content, green fodder yield/plant, dry matter yield/plant and % dry matter. This indicated that there is enormous scope for selection of desirable genotypes for higher fodder yield from the material evaluated. These results corroborated with the earlier findings reported in fodder sorghum by Agarwal (2004) and Choudhary *et al.* (2005) where in for days to 50% flowering, plant height, leaf length, leaf width, green fodder yield/plant and dry matter yield/plant. The traits tillers/metre row length, leaves/plant, leaf:stem ratio, crude protein content had moderate range of phenotypic variation. Agarwal (2004) and Choudhary *et al.* (2005) reported moderate range of variation for leaves/plant and crude protein content.

High magnitude of genotypic and phenotypic variances were recorded for days to 50% flowering, plant height, leaf length, HCN content, green fodder yield/plant, dry matter yield/plant and % dry matter. While for tillers/metre row length, leaves/plant, leaf width, leaf:stem ratio, brix content and crude protein content, the estimates of both the genotypic as well as phenotypic variances were low which suggested that the phenotypic variance in these traits was not the true reflection of their respective genotypic variance. Simultaneously, it was also found that all these characters had greater genotypic variance than phenotypic variance except for leaf:stem ratio, indicating that that these traits were least influenced by environment. Similar results were also reported for days to 50% flowering, plant height, leaf length and leaves/plant by Kaushik *et al.* (1996).

The estimates of GCV (%) and PCV (%) were comparatively high for green fodder yield/plant, dry matter yield/plant and HCN content, which indicated the presence of high amount of both the genotypic as well as phenotypic variability for these traits in the genetic material. Earlier, high estimates of GCV

(%) as well as PCV (%) were reported by Anup and Vijaykumar (2000), Agarwal (2004) and Kishore and Singh (2005) for green fodder yield/plant and dry matter yield/plant. The values of genotypic and phenotypic coefficients of variation were moderate for tillers/metre row length, leaves/plant, leaf width, leaf:stem ratio, crude protein content and % dry matter. Similar results were earlier reported in fodder sorghum for L:S ratio and crude protein content by Anup and Vijaykumar (2000); for tillers/metre row length, leaves/plant and crude protein content by Kishore and Singh (2005). The estimates of GCV (%) and PCV (%) were in low magnitude for days to 50% flowering, plant height, leaf length and brix content. Similar findings were also obtained in fodder sorghum for days to flowering and plant height by Anup and Vijaykumar (2000); for leaf length by and Kishore and Singh (2005).

A comparison of estimates of GCV (%) with their corresponding PCV (%) for different traits revealed that in general, the estimates of GCV (%) were close to the estimates of PCV (%) for all the characters evaluated except for leaves/plant. This indicated that except for leaves/plant, majority of the traits studied were least influenced by the environment. This result was in accordance with the findings of Agarwal (2004) for days to 50% flowering, leaf length, green fodder yield/plant, dry fodder yield/plant and crude protein.

The estimates of heritability in broad sense for different traits revealed that, the high values of heritability were observed for days to 50% flowering, tillers/metre row length, leaves/plant, leaf length, leaf width, leaf:stem ratio, brix content, HCN content, crude protein content, green fodder yield/plant and dry matter yield/plant. The higher estimates of heritability for these traits indicated that simple selection on the basis of phenotypic performance of genotypes would

Table 3. Mean performance of 62 genotypes of forage sorghum

S. No.	Genotypes	Traits												
		Days to 50% flowering	Tillers/ metre row length	Plant height (cm)	Leaves/ plant	Leaf length (cm)	Leaf width (cm)	Leaf: Stem ratio	Brix content (%)	HCN content (ppm)	Crude protein content (%)	Green fodder yield/ plant (g)	Dry matter yield/ plant (g)	Dry Matter (%)
1	Amruta	87.67	9.00	258.73	11.07	84.87	9.32	0.31	11.10	71.80	7.87	431.33	156.00	36.17
2	AKFR-89	76.67	10.00	144.30	8.47	66.93	4.09	0.21	11.97	110.13	5.71	151.33	38.00	25.06
3	AKFSV-3	76.67	10.67	208.13	7.33	64.60	4.63	0.43	11.03	38.42	5.67	170.67	32.00	18.81
4	C-10-2	58.00	11.33	187.33	7.07	63.80	4.85	0.34	11.33	220.07	6.38	165.33	32.00	19.37
5	COFS-29	59.67	11.67	193.20	5.93	57.20	3.23	0.30	11.67	76.48	3.39	71.00	19.33	27.22
6	IS-23960	76.00	11.00	241.33	9.13	80.87	5.38	0.27	12.33	112.80	6.24	189.33	39.50	20.85
7	IS-22450	79.00	7.67	173.00	10.47	70.27	5.05	0.34	11.60	124.75	4.01	123.33	42.60	34.50
8	IS-23980	83.33	9.33	264.40	11.33	69.93	5.24	0.37	10.70	74.23	7.33	202.00	73.00	36.11
9	IS-SGL87	75.00	12.67	185.93	7.87	64.60	3.63	0.52	11.40	90.47	4.20	156.00	33.00	21.24
10	M-35-1	88.33	10.00	210.00	11.73	76.13	5.26	0.36	11.00	35.20	6.80	246.00	68.00	27.66
11	MP-Chari	49.67	12.33	183.07	6.20	58.27	3.85	0.33	12.63	211.89	5.47	87.67	16.50	18.80
12	PKV-801	81.00	6.67	167.73	11.00	75.67	7.97	0.40	13.50	195.82	7.95	335.33	118.50	35.46
13	PKV-809	86.33	7.67	212.40	10.73	70.40	5.93	0.34	12.50	113.28	7.61	294.00	109.67	37.29
14	Ruchira	87.33	12.00	211.67	10.53	71.73	4.98	0.30	10.50	130.48	7.78	332.33	90.50	27.20
15	S-1049	50.33	12.33	185.67	7.20	62.27	4.69	0.43	13.00	246.10	7.41	79.33	24.17	30.55
16	SG-16	65.33	9.33	170.87	7.87	73.80	4.86	0.38	5.50	27.49	4.23	121.33	35.00	28.82
17	SG-25	65.67	9.33	184.33	8.13	64.73	4.06	0.40	12.20	32.48	4.35	134.00	39.33	29.36
18	SG-65	87.33	8.33	245.33	11.40	73.07	5.34	0.39	13.53	14.38	5.30	149.33	63.33	42.45
19	SG-85	86.33	5.33	199.07	11.53	84.13	7.08	0.41	11.00	126.33	6.68	226.00	96.00	42.47
20	SG-105	86.33	6.00	255.53	10.80	72.60	4.58	0.33	11.20	118.05	5.31	159.33	62.67	39.35
21	SG-138	73.00	6.33	177.07	9.27	57.27	4.39	0.41	12.30	142.06	6.17	172.00	54.00	31.36
22	SG-149	73.33	6.33	193.67	7.87	72.07	4.57	0.46	12.97	92.50	4.00	130.67	33.83	26.04
23	SG-150	76.00	7.00	228.73	11.47	68.87	4.30	0.23	13.00	140.79	6.08	172.00	55.33	32.24
24	SG-173	87.33	7.67	248.33	11.80	67.80	4.86	0.28	10.40	144.91	4.60	136.00	54.50	40.19
25	SG-214	85.00	4.33	200.93	10.53	65.33	6.45	0.42	11.00	175.87	6.04	209.33	65.00	31.03
26	SG-230	65.00	11.67	196.93	7.93	63.80	5.23	0.32	10.70	165.54	4.41	126.67	27.00	21.14
27	SG-251	72.67	8.00	201.50	8.20	66.20	4.75	0.24	13.77	172.71	5.96	154.67	56.20	36.29
28	SG-269	65.33	10.00	168.93	8.13	60.47	3.62	0.45	12.07	43.48	3.99	103.33	24.00	23.14
29	SG-289	76.67	7.67	217.27	9.80	70.20	5.00	0.27	12.47	236.84	6.47	209.33	79.67	37.99
30	SG-314	76.67	9.33	209.47	10.20	71.80	4.79	0.27	13.57	185.15	5.53	144.33	59.17	41.34
31	SG-316	63.67	8.33	176.80	7.40	54.67	3.25	0.41	12.27	225.65	3.63	90.00	21.17	23.57
32	SG-348	77.33	7.00	195.20	8.40	64.73	4.29	0.25	11.00	70.31	7.13	201.33	74.00	36.76
33	SG-356	67.33	12.00	190.00	7.00	52.60	4.60	0.29	12.03	180.37	4.06	90.00	32.33	35.97
34	SG-416	76.00	6.00	234.73	11.47	71.60	5.93	0.33	10.70	147.93	7.22	249.33	46.00	18.42
35	SG-426	76.00	11.00	231.13	9.60	66.20	5.34	0.35	11.47	96.06	6.73	221.67	46.83	21.18
36	SG-441	66.00	12.00	148.30	8.07	51.80	3.47	0.28	10.20	69.93	4.03	93.33	19.50	22.38
37	SG-479	76.00	7.33	210.80	9.80	63.60	7.76	0.19	11.00	214.16	7.71	316.67	77.17	24.84
38	SG-507	82.67	8.00	252.60	10.87	81.47	5.42	0.28	11.23	122.98	6.76	234.67	85.33	36.74
39	SG-544	67.00	8.33	216.80	7.60	74.40	5.77	0.34	12.67	75.36	6.75	212.67	54.17	25.57
40	SG-570	86.33	6.00	243.73	9.27	68.87	5.23	0.36	8.77	214.65	6.66	235.33	59.33	25.70
41	SRF-187	87.67	5.67	258.50	10.40	79.40	6.13	0.33	12.53	184.06	6.66	190.67	102.00	56.68
42	SRF-204-1	76.67	8.00	191.13	9.60	75.47	6.15	0.28	11.33	180.23	6.74	212.33	61.00	28.76
43	SRF-207	84.67	6.00	230.73	10.40	78.73	6.40	0.37	12.83	166.65	8.04	377.00	106.33	28.25
44	SRF-283	84.33	12.67	227.07	9.20	73.60	4.79	0.44	11.00	175.70	5.65	183.33	39.33	21.49
45	SRF-285	81.00	7.67	181.47	8.80	78.80	4.65	0.40	12.83	288.48	4.65	126.67	65.33	51.62
46	SRF-286	80.67	4.67	208.53	9.40	76.87	5.09	0.27	11.20	135.47	6.06	178.67	60.33	33.82
47	SRF-288	81.00	9.67	222.47	8.47	76.60	5.22	0.39	11.80	230.70	6.86	235.67	65.00	27.63
48	SRF-289	80.33	7.33	163.20	8.20	66.75	4.40	0.45	11.23	129.76	5.28	124.00	41.33	33.34
49	SRF-311	74.33	14.33	211.67	9.40	71.60	4.68	0.32	11.80	141.16	6.37	184.67	48.33	26.24
50	SRF-312	79.00	6.67	182.00	7.87	59.87	4.46	0.52	12.23	228.97	4.16	114.67	36.83	34.25
51	SRF-314	77.00	8.67	244.77	12.20	80.40	6.53	0.41	14.23	124.73	7.59	275.33	74.00	27.01
52	SRF-315	71.00	8.67	226.13	9.27	73.67	4.39	0.48	9.83	46.50	5.24	180.00	43.73	24.29
53	SRF-319	87.67	4.33	189.47	9.53	77.20	4.83	0.64	13.80	148.53	7.58	204.67	63.67	31.86
54	SRF-322	80.00	10.00	186.67	7.27	78.20	4.73	0.37	14.70	192.75	4.20	134.33	45.50	37.10
55	SRF-324	67.00	10.33	195.13	8.27	64.80	4.73	0.21	12.83	76.67	8.08	230.67	45.27	19.69
56	SRF-1663	77.00	5.67	180.40	7.67	70.07	4.43	0.26	10.53	85.83	6.45	183.33	58.27	31.77
57	SSG-59-3	66.00	11.00	195.00	6.20	59.27	2.94	0.26	12.00	73.68	3.85	68.67	17.77	27.91
58	SSG-59-3	66.00	11.00	162.91	7.13	63.00	3.48	0.30	11.13	163.32	3.83	82.67	24.17	33.54
(Brow glum)														
59	SSV-84	89.00	7.33	201.73	9.47	74.80	4.81	0.34	13.77	265.21	6.39	170.00	62.00	37.18
60	GFS-3	86.67	8.67	226.40	11.20	81.93	4.48	0.38	16.23	220.33	9.55	184.33	65.00	35.71
61	GFS-4	50.67	12.67	139.73	6.07	46.27	3.61	0.42	12.23	170.19	5.23	38.67	11.33	30.44
62	GFS-5	64.67	6.33	160.20	6.47	58.73	4.33	0.38	14.23	152.80	7.28	66.67	25.83	38.72
		0.72	0.47	10.84	0.26	1.60	0.15	0.024	0.17	2.65	0.14	10.43	2.99	3.30
	CD at 5%	2.02	1.33	30.36	0.72	4.49	0.42	0.068	0.47	7.41	0.40	29.19	8.38	9.22
	CV %	1.65	9.36	9.23	4.89	4.02	5.22	11.985	11.90	139.83	5.96	178.63	54.45	30.77

Table 4. Phenotypic range, General mean, Variance components, Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), Heritability (H^2 b) and Genetic advance (% of mean) for the traits studied at Navsari, Gujarat during 2008 rainy season

Characters	Phenotypic range	G.M.	σ^2 (P)	σ^2 (G)	σ^2 (E)	PCV (%)	GCV (%)	Heritability (%)	GA (% of mean)
Days to 50% flowering	49.67– 89.00	75.61	98.48	100.05	1.16	13.23	13.13	98.44	26.83
Tillers/metre row length	4.33– 14.33	8.78	5.61	6.29	0.68	28.57	26.99	89.27	52.53
Plant height (cm)	139.73–264.40	203.39	7898.75	1142.48	352.74	16.62	13.82	69.13	23.67
Leaves/plant	5.93– 12.20	9.08	2.74	2.94	0.20	18.88	18.23	93.28	36.28
Leaf length (cm)	46.27– 84.87	69.12	68.21	75.91	7.70	12.61	11.95	89.85	23.33
Leaf width (cm)	2.94– 9.32	4.97	1.29	1.36	0.07	23.45	22.86	95.04	45.71
Leaf:Stem ratio	0.19– 0.64	0.35	0.01	0.01	0.002	25.79	22.86	78.40	41.65
Brix content (%)	5.50– 16.23	11.90	2.33	2.41	0.08	13.05	12.82	96.50	25.94
HCN content (ppm)	14.38–288.48	139.83	4241.03	4262.03	21.00	46.68	46.57	99.51	95.70
Crude protein content (%)	3.39– 9.55	5.96	2.00	2.06	0.06	24.07	23.72	97.06	48.13
Green fodder yield/plant (g)	38.67–431.33	178.63	5935.20	6261.41	326.21	44.30	43.13	94.79	86.50
Dry matter yield/plant (g)	11.33–156.00	54.45	762.27	789.16	26.89	51.59	50.70	96.59	102.66
Dry Matter (%)	18.42– 56.68	30.77	51.54	84.02	32.57	29.79	23.31	61.23	37.57

also be more efficient in further improvement of these traits. Similar findings for high heritability estimates were also obtained for green fodder yield/plant and dry fodder yield/plant in fodder sorghum by Anup and Vijaykumar (2000); for days to 50% flowering and crude protein content by Kishore and Singh (2005). Moderate values of heritability were registered by plant height and % dry matter. This suggested that it was moderately influenced by environment and genetic enhancement through selection might be difficult due to masking effects of the environment on the genotypic effect. Moderate estimates of heritability revealed in the present investigation for plant height was earlier reported by Patil *et al.* (1996) and Kishore and Singh (2005) also.

Genetic advance expressed as percentage of mean [GA (% mean)] revealed that high estimates of genetic advance (% mean) were observed for green fodder yield/plant, dry matter yield/plant and HCN content. This indicated that inheritance of these characters were under the control of additive genes and selection would be rewarding for further improvement of these traits. High estimates of genetic advance (% mean) were reported for green fodder yield/plant and dry fodder yield/plant by Anup and Vijaykumar (2000) and Kishore and Singh (2005). The moderate estimates of genetic advance (% mean) were observed for tillers/ metre row length, leaf width, leaf:stem ratio and crude protein content indicating that these characters were under the influence of both additive as well as non-additive gene effects thereby suggesting that reciprocal recurrent selection would be effective for

further improving these traits. Moderate estimates of genetic advance were also manifested for L:S ratio and crude protein by Anup and Vijaykumar (2000); for leaf width and crude protein by Sankarpandian (2002); for tillers/metre row length and crude protein by Kishore and Singh (2005). Genetic advance (% mean) were low in magnitude for characters like days to 50% flowering, plant height, leaves/plant, leaf length, brix content and % dry matter suggesting that these traits were under the influence of non-additive genes, thus emphasizing the importance of heterosis breeding for exploitation of these non-additive genes. Earlier, Sankarpandian (2002) and Anup and Vijaykumar (2000) reported the similar results to this findings for days to 50% flowering and for leaves/plant, respectively.

High heritability coupled with high genetic advance (% mean) were observed for green fodder yield/plant, dry matter yield/plant and HCN content revealing that these characters can be improved by simple phenotypic selection as they are more likely to be controlled by additive gene action. Similar evidences were observed for green fodder yield/plant as well as dry fodder yield/plant by Anup and Vijaykumar (2000). In the present investigation the estimates of high heritability and moderate genetic advance (% mean) were observed for tillers/metre row length, leaf width, leaf:stem ratio and crude protein content emphasizing the role of both additive and non-additive gene action for these traits. Hence, recurrent selection or reciprocal recurrent selections are the best suited method for exploitation of both additive and non-additive genetic components. Similar findings were

reported by Anup and Vijaykumar (2000) for L:S ratio and crude protein by Sankarpandian (2002), while Kishore and Singh (2005) for leaf width and crude protein per cent. Further, high heritability coupled with low genetic advance (% mean) was exhibited by days to 50% flowering, leaves/plant, leaf length and brix content. This indicated that there is little scope for further improvement through selection for these traits due to the involvement of non-additive gene effect in the inheritance of these traits. These findings were in conformity with the earlier results of Anup and Vijaykumar (2000) for days to 50% flowering and leaves/plant. Plant height and % dry matter exhibited moderate heritability along with low genetic advance (% mean) indicating that these traits were under the influence of non-additive gene action. Earlier, Patil *et al.* (1996) and Kishore and Singh (2005) reported similar findings for plant height.

In the present investigation, considering the importance of genetic parameters like GCV, heritability and genetic advance (% mean) together, it is evident that green fodder yield/plant, dry matter yield/plant and HCN content are the most important traits in fodder in fodder sorghum improvement. Selection for these traits in the segregating generations would be fruitful for further genetic improvement in fodder sorghum.

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Ethnobotanical Evidences vis-à-vis Domestication Trends in “Drumstick Tree” (*Moringa oleifera* Lam.) in India

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Drumstick tree (*Moringa oleifera* Lam.) has gained importance as potential species in view of its multipurpose usage, well adaptability to dry and hot climates of north-western plains, central India and drier regions of peninsular India. It has been protected as multipurpose tree species and domesticated as a vegetable in different parts of India. In the present communication, this species has been reported for ethnobotanical evidences on the basis of diversity distribution pattern in India and trends towards domestication.

Key Words: Domestication trends, Drumstick tree, Ethnobotanical evidences, Genetic resources, Multi-purpose species, *Moringa oleifera*, Protected species, Semi-domesticated species, Uses, Wild species

Introduction

Drumstick tree (*Moringa oleifera* Lam.) (family Moringaceae; commonly called horse radish tree, ben-oil tree, West Indian Ben) has recently gained importance as a multipurpose tree with tremendous potential uses in the tropical and subtropical regions. It is a fast-growing tree which is resistant/tolerant to drought and most pests. This species can be propagated sexually or asexually and can thrive in poor soil. In India it is propagated generally through cuttings (1-2 m long), preferably from June to August. This species occurs wild in the sub-Himalayan tracts of northern India from the river Chenab eastwards to the Sarda and in the tarai tract of Uttarakhand, foothills of Himachal Pradesh and part of northern Uttar Pradesh in India (Ramachandran *et al.*, 1980; Joseph, 2007). The tree is widely cultivated and naturalized worldwide in the tropical and sub-tropical regions of the world (Morton, 1991).

The present day cultivated plants have been domesticated through the process of selection resulting in change of characters and bringing wild species under human management (Wilson, 1992; Diamond, 2002). Study of diversity distribution and ethnobotanical trends have provided evidences in understanding the process of selection for desirable traits. In *M. oleifera* information on ethnobotanical use as multipurpose species and a potential oilseed has pinpointed evidences in support of domestication (Jain, 1981; Jain *et al.*, 1990; Samant and Dhar, 1997) in the protected/semi-domesticated areas in the tribal belt of India. In any case,

the recorded information on its genetic resource value as potential species dates back to 400 years since its use for edible pods, seed oil, fodder and as medicine was known to the Indians (Watt, 1889). During the entire process, the cultivation must have resulted through series of selection from the wild types for desirable genotypes suitable for edible pods with more palatability (non-bitter forms), thus presenting a case of conscious folk domestication.

The published records have thrown light on the history of this little-known vegetable crop that was cultivated to a significant extent in south India. The earliest records (400 years old) of genetic resource use of *M. oleifera* are available in *Ain-i-Akbari* that lists the plant use as favourite pickles by the north Indians and as a commercial oilseed crop (Watt, 1889). This species was reported to be cultivated by the Dravidians (south Indians) in each and every home yard for exceptionally nutritious pods (Ramachandran *et al.*, 1980). How this species moved from from centre of origin to other parts of the Indian region remains unclear (Fuller, 2006). During the past two centuries it was introduced to other parts of the world mainly as an ornamental and multipurpose species (Morton, 1991; Folkard and Southerland, 1996). Presently, this species is cultivated nearly throughout the Old World Tropics and also found naturalised in many regions of the world.

M. oleifera still largely remains a minor cultivated species in marginal land and small farm holdings as source of vegetable for domestic use and also sold in the local markets of India. Reasons for neglect in the past in northern

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India were probably the socio-economic preference and plant growth. But owing to rich nutritional content of fruit, leaf and other plant parts, it deserves renewed attention particularly for improvement and commercial utilization in India. The present investigation envisages the trends towards domestication on the basis of diversity distribution pattern, ethnobotanical evidences and changes in useful plant characters. Information on valuable plant genetic resources and their uses in India is also briefly discussed.

Materials and Methods

A total of 216 accessions of *M. oleifera* collected from different phytogeographical regions of the country during 1976-2010 were considered for present work. The germplasm accessions were classified into cultivated, protected/semi-domesticated and the wild types represented from diverse agro-climatic conditions. Selected samples (41) of cultivated and wild types were studied for agro-morphological/botanical characters viz., tree habit, branching pattern, leaf characters, flowering period, traits of flower (colour) and fruits (pod shape, size, ribs, colour), number of seeds/pod, seed characters (wings, colour, ease of detachment), seed coat hardness (soft/hard), characters of seedlings, seed germination and oil contents. Observations were recorded using random samples (ten samples/per accession) of vegetative and reproductive parts. Comparison of morphological characters was done based on visual observations. Vouchers of herbarium specimen and seed samples (HS14244, 19907, 20281, 20282, 20285 and SS2893-2902) maintained in the National Herbarium of Cultivated Plants were used to validate the observations in present study. Analysis of information on diversity distribution pattern, ethnobotanical evidences and utilization of the species was done by the authors based on self-experience, non-formal interactions with local persons, farmers and experienced folks of the diversity regions and the published literature.

Result and Discussion

Botanical description

M. oleifera a deciduous perennial tree (height upto 12 m) is characterized by slender stem with brittle and corky bark, drooping branches and pale green and bi-tripinnate leaves. The flowers (2.5 cm diameter) are white-cream (rarely pink), honey scented, and borne in profuse axillary drooping panicles. The fruit (20-120 cm × 1.0-2.8 cm) is beaked capsule (also called pods), three valved, drooping,

turns brown on maturity, nine-ribbed, angles are more prominent on maturity, splitting into three parts when dry; seeds (ca 15-24) with placentation parietal, creamish white-brown with three, embedded in pith, membranous and semi-deciduous wings. The seeds are orthodox, produced in large quantity and have no dormancy period and loose viability within a short period of 2-3 months. Under north and eastern parts of the country, leaves are shed in December-January and new ones appear in March-May along with flowers followed by fruiting. However, in the southern part of the country flowers and fruits are produced throughout the year, July to September and March to April being two peak periods (Wealth of India, 1962).

The wild and domesticated types exhibited very little botanical distinction except pod/seed characters. Study of population of both showed range of variation in tree stature (erect-spreading, moderately loose canopy), leaflet size, shape (round, obovate), flower colour (pink, creamish-white with base dotted/streaked with yellow), fruit bearing (cluster, sparsely bearing), fruit length (small-thin, long-thick), colour of pericarp (pale green, green, dark green), fruit surface (striated or smooth), fruit tip (red or green) and taste of pulp (bitter, tasteless). The wild types usually have bitter/semi-bitter, hard and fibrous poor quality fruits (Arora and Pandey, 1996).

Diversity distribution and ethnobotanical use

To domesticate a species there must be: (a) genetic diversity, (b) availability of useful plants/interesting types, and (c) reproductive isolation of the varieties selected. Thus, Indian gene centre offers great biodiversity with enormous number of useful plants for domestication (Arora, 1991). The tribal belts are more often considered as the centre of diversity and origin of many of these multipurpose species holding an array of potential plant diversity ranging from wild, semi-wild and domesticated forms (Maheshwari, 1986). The selection pressure operates through unconscious and conscious means through necessity-based, ritual-based or tribal customs/culture and socio-economy based requirements evolving desired types (Arora, 1981; 1997).

In the areas of natural distribution *M. oleifera* occurs as a component of the mixed broad leaved/conifer forest along forest of sub-Himalayan tracts, and river side of Uttarakhand and Uttar Pradesh, and central Himalaya (Strachey, 1974; Ramachandran *et al.*, 1980; Gaur, 1999; Singh *et al.*, 2000; Bhattarai and Baral, 2006). This species is well represented under protected habitats in

the tribal dominated tracts of central India (parts of Bihar, Chhattisgarh and Simlipal region of Orissa) evidently exhibiting trends of semi-domestication/ protection (Duthie, 1960; Wood, 1977; Haines, 1978; Khanna *et al.*, 2005). In home gardens in South India (a probable area of domestication) it is commonly cultivated as a perennial but under commercial cultivation mostly as an annual tree. Self sown populations are also seen near areas of cultivation (Haridasan and Rao, 1985; Murthy and Venu, 2005).

The tree is mainly valued for edible pods used as vegetables and pickle. The leaves and flowers are used as vegetables and garnishing food; also sold in the market. Vegetable prepared from leaves is commonly recommended as a special food supplement for rich in iron and calcium (Wealth of India, 1962; Verma *et al.*, 1976). Dried leaves are used as condiments. Seeds are consumed after frying like peanuts and edible seed oil used for cooking. The flowers are good source of nectar for honey producing bees. The leaves, roots, flowers and seeds are used in folk remedies for tumours, abdominal tumours, rheumatism and venomous bites (Hartwell, 1967-1971); root as expectorant, mild diuretic, epilepsy, hysteria and stimulant in paralysis (Mughal *et al.*, 1999).

The oil is extracted from seeds (up to 40 per cent) and used for edible purposes, for illumination, cosmetics, soap and lubricant industry (Wealth of India, 1962; Burkill, 1966). The coagulating ability of the seed powder became important for water purification in arid regions (Morton, 1991). Leaves and twigs are used as fodder in many parts of India (Watt, 1889; Parker, 1918). The tree is used as fence and bark is a source of coarse fibre. The seed cake left after extraction of oil is valued as fertilizer.

Domestication trends and changes in useful characters

Response of wild species to domestication process is primarily dependent on the species behaviour to selection process rather than on its acceptability by the natives/local people where it occurs (Diamond, 2002). The plant is considered to have achieved the stage domestication when it reaches at its highest level of genetic modification and human aid is necessary for survival (Harlan, 1975). The process of domestication is likely to be facilitated with high responds to selection and market requirement than its production in natural population (Venturieri, 2001).

Wider adaptability of *M. oleifera* to different agro-climates, cultivation practices and ease to cultivation

practices has facilitated its selection for desirable traits during course of selection process. Despite long history of cultivation of *M. oleifera*, the wild types apparently do not much differ in gross morphological characters and propagation aspects except few characters. These facts probably suggested that the crop is still under evolutionary process and thus offers much scope for improvement/ selection for desirable traits.

During the selection process in domestication of cultivated plants distinct changes/modifications occur in a species leading to distinct types from their parental wild ones (progenitors); for example in cereals an unconscious selection of the non-shattering types got selected during preliminary planting by man (Zohary and Hopf, 2000; Venturieri, 2001; Diamond, 2002). The domesticated types grow outside the distributional range of their wild progenitors and have changed morphologically, physiologically and phenologically (Ladizinsky, 1998).

Folk domestication trends evidently exhibit protection mechanism, its gradual effect on enhancing the useful diversity and utilization based socio-economic structure and dependence on local useful genetic resources (Arora 1986; Pandey and Arora, 2004). In areas of natural distribution (foothills of the Himalaya, extending towards Pakistan in the west and central Himalaya and central parts) of *M. oleifera* rich variability in fruit types in wild/ protected and semi-wild populations, with minimal use of species was recorded (Arora and Pandey, 1996; Tiwari *et al.*, 2010). In protected/semi-domesticated populations this species was recorded for edible oil by Indian folks (Vishnu Mittre, 1981), for vegetable from pods and leaves by the Gonds and Santhals of Central India, fruit for pickle by tribals of eastern regions and north-eastern India (Jain, 1981; Arora, 1981; Chhetri, 2006) and edible leaves, flowers, fruit in Andaman and Nicobar Islands (Parker, 1918; Bhargava, 1981). However, in the southern states of India, especially in Tamil Nadu and Kerala, *M. oleifera* is frequently cultivated in homesteads as a vegetable crop and for multipurpose uses (Varalakshmi and Devaraju, 2007).

Cultivation of *M. oleifera* in India has been principally for vegetable and not for seed oils (Watt, 1889; Morton, 1991; Joseph, 2007). The wild populations hold more variability in genepool reservoir over the range of distribution of species. The traditional use as a multipurpose species by natives pinpointed accumulation of useful characters/attributes in the protected/semi-domesticated populations. Trend indicating dependence on the species

as locally available genetic resources in the tribal tracts of central and eastern region of India suggested of concentration of diversity, thus the priority areas for genetic resources collection and conservation. The diversity distribution pattern identified the following types of populations:

- Truly localized populations occur as wild trees in the areas of distribution (in western Himalaya and adjoining parts) with minimal plant use.
- Protected populations occur in new dwellings in the forested land, as patchy populations with shorter, hard and bitter fruits reported for multipurpose uses in parts of foot-hill region.
- Selected and semi-domesticated populations occur in community land/forested/ backyards of tribal dwellings in the central and western and eastern plains (Bihar, Upper Gangetic Plains, Orissa) and reported as multipurpose tree with diverse uses.
- Domesticated and improved cultivars grown in farmers field/ land mainly for vegetable purpose (in southern region).

Changes in qualitative and quantitative characters in wild and cultivated types were studied using selected types (41 accessions) (Table 1; Fig. 1 and 2).

Table1. Characters in wild and cultivated types in *M. oleifera*

S. No.	Characters*	Wild type	Cultivated type
1	Distribution and habitat	Foot-hills of Himalaya; forested area, near habitation	Mainly in southern region; home gardens, farmers field; sometimes as escape (self sown types)
2	Habit	Perennial; large sized (14 m) trees with broader stem	Perennial and annuals; tree with shorter height (12 m) with narrow stem
3	Mode of reproduction	Through seed	Through seeds and cuttings
4	Leaflets	Smaller (1.1x0.8 cm)	Leaves with pink tinge in petiole, comparatively larger sized leaflets (1.5x1.2 cm)
5	Leaf shedding	Leaf shedding after flowering	Tree bears leaves all throughout the growing period
6	Flowering and fruiting period	One time flowering (February- March); fruiting strictly after the flowering is over (March-May)	Fruiting and flowering simultaneously
7	Flower colour	Generally creamish-white but also pink	Creamish-white with yellow dots
8	Fruit	Fruits smaller (upto 50 cm), 1.0-1.5 cm diameter, cylindrical, tapering, generally borne in clusters of 15-20 fruits, thin walled, less fleshy with bitter	Fruits longer (upto 120 cm), up to 1.8 cm diameter, pale green or red tinged, angular-cylindrical, borne in clusters of 8-10 fruits, thick walled, fleshy with good taste
9	Seed	Smaller (22x11 cm), soft walled, spindle shaped, wings soft membranous, deciduous, seed coat white-ivory, kernel and seed coat normally soft; 15-20 seeds/fruit	Bigger (32x26 cm), three angled, kernel, wings hard smaller, kernel more mealy and seed coat hard, black-brown and persistent; over 25 seeds/ fruit
10	Seed dispersal	Valves split open widely upto the peduncle; seed shattering high	Splitting upto half length, less shattering (fruits still left on tree)
11	Palatability	Less palatable, bitter-semi-bitter	More tasty with mild aroma, improved palatability
12	Oil (%)	18- 24	Upto 20
13	Seedling	Thin with narrow leaflets	Stout with bigger leaflets

* Modified from Arora, 1991

Species selected through the process of conscious folk domestication have resulted in developing variation in useful characters as habit, seed yield, shattering of seeds and other economic traits among cultivated types such as *Moghania vestita* (for edible tubers in the Khasi and Jaintia tribal regions), *Digitaria cruciata* var. *esculenta* (minor cereal and as fodder species in the Khasi tribal region); *Coix lacryma-jobi* (for edible soft, thin-shelled, and easy hulling grain types, with bold seeds and high yield) and rice bean/*Vigna umbellata* (for edible grain pulse by tribals of north eastern Himalaya); *Inula racemosa* (for aromatic oil in Western Himalaya in the tribal region of Lahaul) (Singh and Arora, 1972; Arora, 1997; Arora *et al.*, 1980a and b).

Trends of domestication are evident through the study of distributional range (of cultivated types growing outside their wild progenitors) and change in morphological, physiological and phenological traits (Ladizinsky, 1998). Under domestication, all the characteristics of plant species for which the selections are made, exhibit distinct changes or modifications. In the present study wild *M. oleifera*, has prominently exhibited fruit characters such as smaller sized, lesser pulpy (poorer food reserves), bitter (defensive mechanism) and fruits borne in clusters with high splitting (adapted for dispersal). In the process of domestication these have shown a change in cultivated types (Table 1).



Fig. 1. Tree bearing pods (cultivated type on left and wild type on right side, bearing fruits in clusters) and seedling leaf in cultivated and wild type



Fig. 2. Characters of pod (wild type on left and cultivated on the right side) and seed (on left is wild type with narrow papery wing and white kernel; on right is cultivated type with broader and thicker wing and dark kernel) of *M. oleifera*

However, some traits (like tree bark, branching), seed germination, oil and protein contents in seed kernel, etc.) have shown a marginal distinction in the cultivated types from their wild ones. Further studies are desired to throw more light on changes in characters like thin seed coat and soft fruit wall in wild types to hard seed coat and hard fruit wall in cultivated types. Accumulation of the following useful characteristics/promising attributes were observed in cultivated types:

- Habit: relatively low height (facilitate harvest), flowering and fruiting throughout the year

and selection of leafy types (leafy vegetable and fodder yield)

- Economic part: big sized fruits, more pulpy, edible fruits (mesocarp), non-bitter fruits (improved quality); lesser fruit splitting, prolonged fruit availability period (economically viable), much variability in fruit size in cultivated types (selected types)
- Propagation: through seed as well as cuttings
- Protective mechanism: decrease in bitter com-

ponent in protected/ cultivated types (increased palatability)

Recent studies on domestication of indigenous fruit trees in Africa suggested that identification of trees combining a few, rather than many superior traits is preferable to create new cultivars specialised for a particular set of environment and for a set of traits for a single product. In *Choerospondias axillaris* (lapsi—a wild edible fruit), the combination of traits as pulpy fruits recombined with larger sweet types may be desirable to fetch high market of Nepal Himalayas (Paudel *et al.*, 2002). In *M. oleifera* also selecting rare genotypes with desirable traits (fruit, oil, ornamental use, etc.) maintaining broader genetic base in all other characteristics, thus, minimising the risk of pest and diseases, would be desirable.

Future Thrust

The wild species of no or minor importance today may assume major significance for tomorrow's generation. Since any kind of breeding work depends on the availability of genetic variability, the first step is collection of germplasm mainly from indigenous sources. In view of the account presented above, it is desirable to undertake detailed surveys, explorations and collection in diversity-rich areas for search of useful types. In view of considerable potential of *M. oleifera* for utilization as an oilseed, fodder and ornamental in the Indian context, this minor cultivated species deserves renewed attention for identification of desirable types. The following thrust areas have been pinpointed:

- Diversity assessment of entire moringa genepool (especially wild/protected and semi-domesticated population) for desirable traits and augmentation of germplasm in gene bank holdings.
- Identification of genotypes with desirable traits (relatively short statured plants with low gestation period, year round fruit bearing, clustered fruits bearing, higher pod yield, fleshy pods and tasty fruits, leafy types, showy flowered types with ornamental value); identification of ecotypes suitable for wide agro-climatic range, for industrial value with higher percentage of oil, etc.
- Validation of centre of origin, diversity, dispersal and domestication through modern tools.

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Genetic Diversity in Rice Accessions of Madhya Pradesh and Chhattisgarh

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Seventy-one rice accessions from Madhya Pradesh and Chhattisgarh were evaluated to study the diversity pattern among the genotypes. The genotypes were grouped into eight clusters. The distribution pattern indicated that maximum number of genotypes 17 was grouped into the cluster III followed by 12 each in cluster I and II. The mode of distribution of genotypes from different geographic regions into various clusters was at random, indicating no association between geographical distribution of genotypes and genetic divergence. The inter-cluster distance in most of the cases was higher than the intra-cluster distance, indicating wider genetic diversity among the accessions of different groups. The highest inter-cluster distance was observed between cluster VI and VIII (6.51) followed by cluster II & VII (5.56), showing wide diversity among the groups. The highest intra-cluster distance was observed for the cluster VII and the lowest for the cluster V. The genotypes in these clusters *i.e.* Tulsi Mala (cluster II), Kali Kamod (cluster VI), Shankar Jeera and Bhata Dubraj (cluster VII) and Lohandi and Til Kasturi (cluster VIII) can be used as potential donors for future hybridization programme to develop genotype with high grain yield.

Key Words: Genetic Divergence, Germplasm, Rice

Introduction

Rice is the staple food of India and occupies an area of 44.6 million ha. In eastern India the coverage area of rice is 26.8 million ha. However, the productivity is very low due to natural calamities. In order to meet out the food requirement of the increasing population, development of high yielding varieties becomes essential. Thus, in order to improve the productivity potential, a break through would be desirable by way of increasing biological efficiency through hybridization followed by the selection in which diverse parents are used. The importance of genetic diversity for selection of parents for recombination in an autogamous crop such as rice to recover transgressive segregants has also been repeatedly emphasized and therefore, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedure such as D^2 statistic. There is need to identify the genetically diverse accessions with desired genes for better utilization in crop breeding programme. Keeping these in view, 71 rice germplasm accessions of Madhya Pradesh and Chhattisgarh were evaluated with the objective to identify the genetically diverse genotypes for their further exploitation in rice improvement programme aimed at enhanced grain yield.

Materials and Methods

The experimental material consists of 71 rice germplasm accessions collected from Madhya Pradesh (21) and

Chhattisgarh (50) as given in Table 1. These genotypes were evaluated in a randomized complete block design with three replications during *Kharif* 2008-09 at Research Farm, IGKV, Raipur. Twenty-one-day-old seedlings from the nursery were transplanted. Each plot consisted of three rows of 2 m length. The spacing was maintained at 20×15 cm. The recommended agronomic practices were followed. Five plants from the middle row of each entry in each replication were randomly taken for recording observation on grain yield and thirteen yield attributing traits namely plant height (cm), panicle length (cm), ear bearing tillers, fertile spikelets/panicle, spikelet density, spikelet sterility (%), hundred seed weight (g), milling (%), kernel length (mm), kernel length: breadth (l/b) ratio, head rice recovery (%), harvest index (%) and grain yield/plant (g) were recorded. Mahalanobis (1928) D^2 statistic was employed to measure the genetic distance between the genotypes. The distance were estimated from the sample on the basis of P characters by the formula $D^2P = \sum_{i=1}^P (\Delta_i j) \Delta_i \Delta_j =$ where, Δ_{ij} is the reciprocal of (ij), the pooled common matrix *i.e.* error matrix; Δ_i is the difference in the mean value for i^{th} character and Δ_j is the difference in the mean value for j^{th} character. The genotypes were grouped into number of clusters by Tocher's method as described by Rao (1952).

Results and Discussion

A clear understanding of the extent of variability prevails for each trait in germplasm is essential for the improvement of characters through selection. Moreover, in hybridization

Table 1. Details of rice accessions use in present study

S.No.	Variety	Accession No.	Area of collection		
			Village	Block	District
1.	Laloo-14	L:90	Kolar	Antagarh	Bastar
2	Anterved	A:219	Ghana	Jabera	Damoh
3	Kadamphool	K:2209	Bandaji	Lohandiguda	Bastar
4	Vishnu Bhog	V:37	Naraki	Rajpur	Ambikapur
5	Kalimuchh	K:243	Vakia	Ghatigaon	Gwalior
6	Kubri Mohar	K:361	Arjuni	Bhatapara	Raipur
7	Loktimachhi	L:538	Chandragiri	Darbha	Bastar
8	Jata Shankar	J:380	Churtela	Dabhara	Bilaspur
9	Shri Kamal	S:1085	Nagpur	Manendragarh	Sarguja
10	Tulsi Prasad	T:186	Bardebhata	Kanker	Bastar
11	Atma Shital	A:26	Leda	Chhindgarh	Bastar
12	Waasmati	W:48	Khadora	Majholi	Sidhi
13	Banspatri	B:2357	Idagaon	Mainpur	Raipur
14	Badshsbhog	B:54	Kasoli	Gidam	Bastar
15	Shitalbhog	S:1684	Parakhariki	Kunkuri	Raigarh
16	Vishnubhog	V:26	Sirsi	Bhayathan	Sarguja
17	Chinoor	C:392	—	Barghat	Seoni
18	Dubraj	D:812	Kotma	Kotma	Shahdol
19	Ganga Balu	G:480	Bodalwali	Saraipali	Raipur
20	Ganga Prasad	G:280	Bishunpur	Batauli	Sarguja
21	Kala Jira	K:1456	Dohana	Kusmi	Ambikapur
22	Bhanta Phool	B:1091	Chaudal	Sidhi	Sidhi
23	Samund Chini	S:980	Kirwai	Fingeshwar	Raipur
24	Til Kasturi	T:264	Chiplawan	Pithora	Raipur
25	Tulsi Manjari	T:247	Abhanpur	Abhanpur	Raipur
26	Kari Gilas	Bd:1290	—	Charama	Bastar
27	Kapoor Sar	Bd:1364	—	Chhuriya	Rajnandgaon
28	Kali Kamod	Bd:680	Baroda	Patan	Jabalpur
29	Dhawara Sawa	D:716	Mudagaon	Devbhog	Raipur
30	Shukla Phool	Bd:384	—	Jaipur	Bilaspur
31	Samudra Fan	Bd:419	—	Pandaria	Bilaspur
32	Fundri	F:28	—	Antagarh	Bastar
33	Jau Phool	Bd:1362	—	Lailunga	Raigarh
34	Lahsun Bhog	L:985	—	Kunkuri	Bastar
35	Shonth	—	Jodhpur	Shoagpur	Shahdol
36	Jeera Shankar	J:4	Kalpi	Bijadandi	Mandla
37	Jeelo	J:29	Kheri	Narayan Gunj	Mandla
38	Shankar Jeera	S:59	Sangadi	Katangi	Balaghat
39	Tulsi Amrit	T:76	Pordi	Baihar	Balaghat
40	Badar Phool	B:96	Umatola	Baihar	Balaghat
41	Bhata Dubraj	B:131	Penderwain	Chhuikhadan	Rajnandgaon
42	Sevanti	S:156	Chanegaon	Balaghat	Balaghat
43	Kadam Phool	K:164	Khamaria	Balaghat	Balaghat
44	Badarpur	B:56	—	Baleoni	Mandla
45	Lohandi	L:60	—	Kusalpur	Dindori
46	Talsani	T:99	Jalda	Chada	Dindori
47	Badshah	B:799 I	Mirga	Tokapal	Bastar
48	Chini Kapoor	C:340	Jampara	Bhanupratappur	Bastar
49	Dudh Dhan	D:964	Jamuna	Anuppur	Bilaspur
50	Deshi Dubraj	D:104	Ghurkot	Uhhara	Bilaspur
51	Ganga Baru	G:845	Kumhrawand	Bakawand	Bastar
52	Jira	J:214 IV	Ronje	Gidam	Bastar
53	Dumar Phool	D:822	Bewatri	Kanker	Bastar
54	Jan Phool	J:339	Kalia	Bagicha	Raigarh
55	Rajim-14	R:170 IV	Rajim	Fingeshwar	Raipur
56	Samund Chins	S:980 I	Kirwai	Fingeshwar	Raipur
57	Sarsaraiya	S:428	Mendra	Udaipur	Ambikapur
58	Thakur Prasad	T:102 I	Kalabhajan	Odangi	Sarguja
59	Tulsi Bar	T:7 I	Jhakharpura	Devbhog	Raipur

contd

Table 1 contd...

S.No.	Variety	Accession No.	Area of collection		
			Village	Block	District
60	Tulsi Mala	T:305	Jarhadesh	Shankargarh	Ambikapur
61	Laxmi Bhog	L:359	Bada	Kusumi	Ambikapur
62	Sukra Phool	S:1072	Puri	Gharghoda	Raigarh
63	Bisun Bhog	B:666	Batwahi	Lunka	Sarguja
64	Banspaati	B:2130	Kirwai	Fingeshwar	Raipur
65	Chhatri	C:194	Benikheda	Patan	Jabalpur
66	Hahjira	S:1281	Tuktuli	Jashpurnagar	Raigrah
67	Shyam Jira	S:885	Suwarpara	Batauli	Sarguja
68	Kabri Moharai	K:2497	—	Kanker	Bastar
69	Harun Dubraj	H:253	Bilharikala	Chowki	Rajnandgaon
70	Kadam Phool	K:2512	—	Jagdulpur	Bastar
71	Lallu	L:218	Khaparbeda	Piparia	Hoshangabad

Table 2. Analysis of variance for thirteen quantitative traits in 71 rice genotypes

Source of variation	Mean squares		
	Replication	Genotypes	Error
D.F.	2	71	142
Plant height (cm)	0.050	527.05**	0.389
Panicle length (cm)	0.027	35.88**	0.287
Ear bearing tillers	0.394	4.6**	0.178
Fertile spikelets/panicle	1.250	6070.36**	0.193
Spikelet density	0.0039	13.12**	0.044
Spikelet sterility percent	0.078	215.06**	0.022
Hundred seed weight(g)	0.005	0.541**	0.010
Milling (%)	0.718	36.86**	0.406
Kernel length (mm)	0.032	1.41**	0.003
Kernel l/b ratio	0.004	0.55**	0.002
Head rice recovery (%)	0.531	122.2**	0.346
Harvest index (%)	12.60	49.2**	14.62
Grain yield/plant (g)	3.40	950.87**	12.11

** Significant at 1% level

Table 3. Distribution of rice genotypes into different clusters

Cluster No.	No. of Genotypes	Genotypes	Origin/Source
I	12	Jata Shankar, Chinoor, Dubraj, Ganga Prasad, Shonth, Jeelo, Dudh Dhan, Deshi Dubraj, Rajim-14, Tulsi Bar, Bisunbhog, Banspaati	Bilaspur (2), Seoni, Shahdol (3), Ambikapur (2), Mandla, Raipur (3)
II	12	Ganga Balu, Dhawara Sawa, Samudra Fan, Jauphool, Jeera shankar, Badshah, Chini Kapoor, Ganga Baru, Dumar Phool, Samund Chins, Tulsi Mala, Laxmibhog	Raipur (3), Bilaspur, Raigarh, Mandla, Bastar(4), Ambikapur (2)
III	17	Kubri Mohar, Badshahbhog, Kalajira, Samund Chini, Tulsi Manjari, Kapoor Sar, Fundri, Badar Phool, Sevanti, Kadam Phool, Badarpur, Sarsaraiya, Shahjira, Shyam Jira, Kabri Moharai, Harun Dubraj, Lallu	Raipur (3), Bastar (3), Ambikapur (3), Rajnandgaon (2), Balaghat (3), Mandla, Raigarh, Hosangabad
IV	6	Anterved, Kalimuchh, Banspatri, Kari Gilas, Talsani, Sukra Phool	Damoh, Gwalior, Raipur, Bastar, Dindori, Raigarh
V	9	Laloo-14, Kadam Phool, Atma Shital, Waasmati, Shital Bhog, Vishnu Bhog, Tulsi Amrit, Jira, Kadam Phool	Bastar (5), Sidhi, Raigarh, Ambikapur, Balaghat
VI	5	Vishnubhog, Loktimachhi, Shri Kamal, Tulsi Prasad, Kali Kamod	Ambikapur (2), Bastar (2), Jabalpur
VII	2	Shankar Jeera, Bhata Dubraj	Balaghat, Rajnandgaon
VIII	8	Bhanta Phool, Til Kasturi, Shukla Phool, Lahsun Bhog, Lohandi, Jan Phool, Thakur Prasad, Chhatri	Sidhi, Raipur, Bilaspur, Bastar,Dindori, Raigarh, Ambikapur, Jabalpur

programme where, selection of genetically diverse parent is important to set the wide array of recombinants, the knowledge of genetic diversity among the accessions is necessary. The analysis of variance indicated the existence of significant amount of variability among the genotypes for all the traits (Table 2).

The 71 genotypes were grouped into eight clusters by using D² statistic in such a way that the genotypes within a cluster had a small or low D² values than those of in between the characters. The composition of clusters has been presented in Table 3 and Fig. 1. Cluster III had the largest number of genotypes (17) followed by cluster I (12) and cluster II (12) whereas, cluster VII had minimum number of genotypes with two. The clustering pattern showed that genotypes collected from the same geotropic region got distributed in several clusters. It might be due to selection differential and/or genetic drift under diverse environmental conditions within same geographical region. This pattern of clustering further indicated that

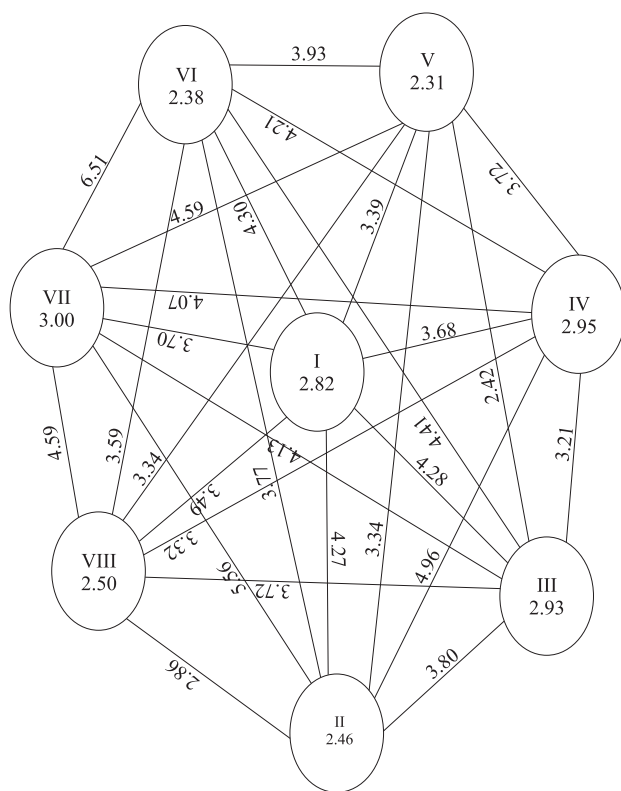


Fig. 1. Intra- and inter-cluster distance (D) in the rice germplasm

there was no association between geographical distribution of genotypes and genetic divergence.

The inter-cluster distance is higher than intra-cluster, indicating wide genetic diversity among the genotypes (Table 4). The inter-cluster distance varied from 6.51 to 2.42. The maximum inter-cluster distance was observed between clusters VI and VII (6.51) followed by clusters II and VII (5.56) and clusters II and IV (4.96). On the other hand, minimum distance was observed between clusters III and V (2.42), indicating close relationship between these clusters and hybridization among the genotypes of these clusters would not provide the encouraging results. The greater the distance between clusters, wider the genetic diversity between the genotypes. Highly divergent genotypes would produce a broad spectrum of variability in the subsequent generations enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants or high magnitude of heterosis. This would be useful in rice breeding programme. Sarawgi and Rastogi (2000) and Nayak *et al.* (2004) also found similar degree of diversity in rice.

Table 4. Intra-cluster (in bold) and inter-cluster distance for 13 characters in rice

Cluster	I	II	III	IV	V	VI	VII	VIII
I	2.82	4.27	4.28	3.68	3.39	4.30	3.70	3.49
II		2.46	3.80	4.96	3.34	3.77	5.56	2.86
III			2.91	3.21	2.42	4.41	4.13	3.77
IV				2.95	3.72	4.12	4.07	3.32
V					2.31	3.93	4.59	3.34
VI						2.38	6.51	3.59
VII							3.00	4.59
VIII								2.58

The maximum intra-cluster distance was observed for cluster VII (3.00) followed by cluster IV (2.95), cluster III (2.91) and cluster I (2.82). It was reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance (Bose and Pradhan, 2005). On the other hand, cluster V had minimum intra-cluster distance (2.31) with more than one genotype, indicating the unidirectional selection which might have been practiced in the past that could lead to uniformity with less deviation between the genotypes (Rajesh *et al.*, 2010).

The cluster mean and coefficient of variation were presented in Table 5. The coefficient of variation was highest in spikelet sterility percentage (19.44) and hundred seed weight (18.18) and lowest was recorded in milling percentage (2.83). The moderately high grain yield (20.19), hundred seed weight (1.80), spikelet density (8.25) kernel length (8.23) and harvest index (49.18) and kernel l/b ratio (3.73), head rice recovery (64.24) and ear bearing tillers (6.62) were recorded for cluster I whereas, cluster II exhibited highest mean value for fertile spikelets per panicle (180.96) and spikelet density (9.09) with better head rice recovery (67.66) and grain yield (18.08). Cluster IV showed highest kernel l/b ratio (4.15) with better kernel length (8.60), head rice recovery (64.98) and hundred seed weight (1.77). Likewise, cluster VII had highest hundred seed weight (1.83), milling percent (75.78), kernel length (8.95), head rice recovery (69.57) and harvest index (50.64) with good l/b ratio (4.01). Cluster VIII showed highest value for ear bearing tillers (8.12) and grain yield per plant (22.29) with better harvest index (49.46), head rice recovery (68.04) and kernel l/b ratio (3.44).

These observations suggested that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. Therefore, the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes.

The genotype Shankar Jeera in the cluster VII showed

Table 5. Character means in different clusters of rice genotypes

Cluster	Characters												
	1	2	3	4	5	6	7	8	9	10	11	12	13
I	100.7	19.94	6.62	153.2	8.25	10.20	1.80	71.95	8.23	3.73	64.24	49.18	20.19
II	117.8	23.91	7.92	180.9	9.09	15.45	1.06	75.49	5.91	2.90	67.66	44.09	18.08
III	105.5	22.52	6.85	101.1	5.65	20.59	1.32	73.93	6.71	3.18	66.11	42.22	13.29
IV	118.7	24.47	7.25	97.94	4.59	14.91	1.77	73.21	8.60	4.15	64.98	43.22	16.66
V	102.7	20.10	7.44	117.7	6.51	10.48	1.15	73.12	6.31	3.18	63.23	40.32	15.99
VI	134.8	25.91	7.70	160.2	7.31	15.04	1.27	69.27	6.88	3.30	57.60	43.46	19.36
VII	69.2	20.55	7.40	107.0	6.60	19.24	1.83	75.78	8.95	4.01	69.57	50.64	18.44
VIII	118.9	24.54	8.12	133.6	6.33	13.01	1.30	74.69	6.93	3.44	68.04	49.46	22.29
Grand mean	108.5	22.74	7.41	131.4	6.79	14.86	1.43	73.43	7.31	3.48	65.17	45.32	18.03
CV (%)	8.53	7.51	15.51	16.31	17.67	19.44	18.18	2.83	9.71	14.94	5.69	12.48	17.30
1. Plant height (cm)			5. Spikelet density			9. Kernel length (mm)			13. Grain yield/plant (g)				
2. Panicle length (cm)			6. Spikelet sterility (%)			10. Kernel l/b ratio							
3. Ear bearing tillers			7. 100-seed weight (g)			11. Head rice recovery (%)							
4. Fertile spikelets/panicle			8. Milling percent			12. Harvest index (%)							

Table 6. Desirable genotypes for different traits

S. No.	Characters	Desirable genotypes
1	Grain Yield/plant (g)	Lohandi (22.29), Ganga Baru (18.33), Shrikamal (16.5)
2	Ear bearing tillers	Til Kasturi (9.66), Laxmi Bhog (8.93) Shrikamal (8.12)
3	Fertile spikelets/panicle	Ganga Balu (195), Kali Kamod (144.66), Dumarphool (136.5)
4	Spikelet density	Tulsi Mala (10.0), Ganga Prasad (7.6), Shrikamal (6.33)
5	Hundred seed weight (g)	Shankar Jeera (2.65), Jeera Shankar (2.2), Kari Gilas (1.83)
6	Kernel length (mm)	Shankar Jeera (8.91), Anterved (8.7), Chini Kapoor (8.10)
7	Head rice recovery (%)	Shankar Jeera (72.13), Shukla Phool (68.36), Dumarphool (66.24)
8	Harvest index (%)	Bhata Dubraj (53.71), Lohandi (50.46), Laxmi Bhog (48.32)

the highest hundred seed weight, kernel length, milling percent and head rice recovery whereas, Bhata Dubraj of same cluster showed highest harvest index. The accession Lohandi in cluster VIII showed the highest performance by grain yield whereas, ear bearing tillers was maximum in Til Kasturi. The maximum fertile spikelet per panicle and spikelet density was found in Tulsi Mala of cluster II.

On the basis of divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of cluster VII, VIII, II and VI in varietal improvement programme. For bringing improvement in specific traits, genotypes like Lohandi of cluster VIII for grain yield per plant; Til Kasturi of cluster VIII for ear bearing tillers; Ganga Balu of cluster II for fertile spikelets per panicle; Tulsi Mala of cluster II for spikelet density; Shankar Jeera of cluster VII for hundred seed weight, kernel length and head rice

recovery; Bhata Dubraj of cluster VII for harvest index could be considered in rice improvement programme as shown by their *per se* performance (Table 6).

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Studies on Genetic Divergence in Basil (*Ocimum basilicum* L.) Germplasm

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The genetic diversity studies was conducted on 30 genotypes of basil comprising 20 exotic introductions and 10 indigenous collections representing from different phyto-geographical regions. The experiments were laid down during *kharif* season of 2004 and 2005 at National Bureau of Plant Genetic Resources (NBPGR), Experimental Station, Issapur, New Delhi. The genetic divergence for sixteen characters using Mahalanobis D² statistical analysis revealed the presence of considerable genetic diversity in the germplasm. These germplasm lines were grouped into seven clusters with variable number of genotypes. The intra-cluster distance ranged from 2.078 to 3.051. The maximum intra-cluster distance was observed in cluster VI and minimum in cluster I. The grouping of genotypes (intra- or inter-) were not consistent over the environments exemplify variations due to phyto-geographical regions.

Key Words: Basil, Genetic Divergence, Germplasm

Introduction

The genus *Ocimum* belongs to family Lamiaceae and 160 species are known to occur world wide. It is widely distributed and extensively grown throughout India (Pushpangadan and Bradu, 1995; Verma *et. al.*, 1998, Pandey and Chowdhary, 2002). *Ocimum basilicum* L., commonly known as basil, is one of the important medicinal and aromatic herb. Assessment of genetic diversity in germplasm collection can facilitate classification and identification of diverse genotypes with maximum utilization for specific traits. Superior genotypes can be used as parents for development of improved cultivar for specific traits like essential oil yield and quality and other traits of breeding importance. This requires a well established statistical tool to quantify the degree of genetic diversity among the available genotypes. Grouping of the genotypes based on the character association through multivariate analysis had been suggested by Mahalanobis (1936); Rao (1952) and Anderson (1957). The most simple and convenient method for assessment of the genetic diversity and grouping of genotypes is D² analysis. Genetically diverse parents are expected to produce physiologically and morphologically more efficient genotypes. Present study was therefore, aimed to estimate the quantum of genetic diversity for various agro-morphological and photo-chemical characters in germplasm collection of basil.

Materials and Methods

The experimental material of thirty accessions of *Ocimum* comprised 20 exotic introductions (USA-10, USSR-07, Poland 01, Hungary-01 and Germany-01) and 10 indigenous collections were collected by taking into consideration their place of origin (Madhya Pradesh-6, Gujarat-2, Andhra Pradesh-1 and Uttar Pradesh-1) to represent the maximum variability. The experimental material was grown in nursery and transplanted in a Randomized Block Design (RBD) with three replications during *Kharif* 2004 and 2005 at National Bureau of Plant Genetic Resources (NBPGR), Experimental Farm, Issapur, New Delhi. The NBPGR Experimental Farm (latitude 28°36'N, longitude 76°50'E) has semi-arid climate with average annual rainfall of 400 mm. The soil of the experimental field was sandy loam (pH 8.0). Three rows of each accession having 10 plants per row were transplanted with row to row and plant to plant spacing of 45 and 30 cm, respectively. Observations were recorded on five randomly selected plants in each genotype for sixteen characters viz., number of primary branches/plant, lamina length (cm), lamina width (cm), leaf-stem ratio, days to flower initiation, number of spikes/plant, spike length (cm), number of flower-whorls/spike, plant height (cm), fresh herbage yield/plant (g), dry herbage yield/plant (g), days to seed maturity, seed yield/plant (g), 1000-seed weight (g), essential oil content (%) and essential oil yield/plant (ml). Genetic divergence

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was estimated by utilizing Mahalanobis D^2 statistics as described by Rao (1952) and genotypes were grouped into different clusters.

Results and Discussion

Analysis of variance revealed significant differences among 30 genotypes for all the 16 characters studied. The D^2 values determining the genetic distances among the genotypes were computed and thirty genotypes were grouped into seven clusters. Clustering pattern of these genotypes, their cluster mean values and intra- and inter-cluster distances are depicted in Tables 1 to 5 respectively.

During *Kharif* 2004, it was observed that Cluster III has the maximum number of genotypes (9) followed by Cluster II (8), Cluster IV (5), Cluster I (4), Cluster VII (2), Cluster V (1) and Cluster VI (1). The maximum and minimum was recorded in intra cluster distance Cluster I (2.729) and Cluster VI (0.001) respectively. The maximum inter Cluster (D^2) value was observed between Cluster VI and Cluster V (10.685) followed by Cluster I and Cluster VI (9.275) and minimum inter cluster distance was observed between cluster I and cluster II (3.216). The cluster mean values when examined across the clusters

Table 1. Clustering pattern of 30 genotypes of basil in *Kharif* 2004

Cluster	Genotypes (no.)	Germplasm accession (s)
I	4	EC 388893, EC 388891, EC 387837, EC 388896
II	8	EC 388890, EC 388895, EC 387838, EC 388788, EC 338794, EC 338782, EC 338772, EC 338773
III	9	IC 326735, IC 336833, IC 344638, EC 174527, IC 201233, IC 211313, IC 326732, EC 388889, IC 338959
IV	5	IC 110267, IC 333332, EC 312264, EC 112548, EC 388887
V	1	EC 338775
VI	1	EC 338785
VII	2	IC 326711, EC 338776

Table 2. Clustering pattern of 30 genotypes of basil in *Kharif* 2005

Cluster	Genotypes (no.)	Germplasm accession (s)
I	2	EC 387837, IC 326732
II	3	EC 338785, EC 388891, IC 326711
III	4	IC 110267, EC 388890, EC 388788, EC 338773
IV	5	EC 388895, EC 388893, EC 387838, IC 326735, EC 112548
V	4	EC 338794, IC 333332, EC 338782, EC 388887
VI	2	EC 338775, EC 338776
VII	10	IC 336833, EC 312264, EC 338772, IC 344638, EC 174527, IC 201233, EC 388896, IC 211313, EC 388889, IC 338959

Table 3. Cluster mean values of 16 characters of 30 genotypes of basil

Character (s)	Cluster I		Cluster II		Cluster III		Cluster IV		Cluster V		Cluster VI		Cluster VII	
	2004	2005	2004	2005	2004	2005	2004	2005	2004	2005	2004	2005	2004	2005
Number of primary branches per plant	12.47	11.20	13.40	11.00	12.24	10.95	12.11	10.71	11.93	11.07	12.00	12.90	12.07	11.17
Lamina length (cm)	4.73	4.09	5.00	4.93	5.05	4.82	5.28	5.29	4.62	4.73	6.18	4.34	5.37	4.72
Lamina width (cm)	2.86	2.43	2.93	2.70	2.96	2.56	3.03	2.59	3.01	2.63	3.79	3.72	3.26	2.58
Leaf-stem ratio	1.33	1.06	1.04	1.05	0.80	0.92	0.76	1.06	1.73	0.85	1.21	1.46	1.25	0.87
Days to flower Initiation	61.75	64.00	61.53	70.78	64.68	61.67	65.64	62.27	74.00	68.08	62.27	62.50	72.90	63.67
Number of spikes per plant	61.90	76.47	63.33	72.33	59.96	73.55	60.47	78.51	93.93	80.97	52.20	63.80	54.30	79.52
Spike length (cm)	16.03	14.23	16.68	20.87	15.36	20.16	13.01	17.96	20.19	13.24	27.73	23.95	20.82	17.34
Number of flower-whorls per spike	13.00	12.23	12.80	14.13	12.10	13.37	11.68	12.45	12.20	11.72	16.80	13.03	12.00	12.91
Plant height (cm)	55.50	44.62	56.18	65.92	52.33	54.44	51.99	55.81	57.49	49.30	83.27	57.08	64.55	50.82
Fresh herbage yield per plant (g)	279.92	263.67	351.50	254.78	303.89	308.67	357.94	240.80	306.67	294.58	375.00	261.50	244.17	231.90
Dry herbage yield per plant (g)	58.49	55.56	72.79	52.94	64.11	63.85	76.14	50.17	63.58	62.65	79.48	55.06	51.35	48.99
Days to seed maturity	160.08	159.67	156.54	166.78	157.52	156.08	163.27	156.07	156.67	163.50	162.33	157.50	161.50	158.57
Seed yield per plant (g)	29.90	11.11	27.21	36.50	13.88	27.79	24.82	29.45	11.92	24.95	48.55	11.54	14.47	14.95
1000-seed weight (g)	1.45	1.28	1.44	1.69	1.30	1.36	1.46	1.51	1.21	1.52	1.66	1.45	1.68	1.32
Essential oil content (%)	0.22	0.28	0.19	0.20	0.17	0.19	0.21	0.17	0.19	0.18	0.13	0.18	0.18	0.17
Essential oil yield per plant (ml)	0.63	0.75	0.68	0.50	0.51	0.60	0.75	0.41	0.57	0.53	0.50	0.46	0.44	0.40

Table 4. Intra- and inter-cluster divergence D^2 values among seven clusters in Kharif 2004

Cluster	I	II	III	IV	V	VI	VII
I	2.729						
II	3.216	2.271					
III	3.619	3.360	2.534				
IV	4.151	3.341	3.808	2.716			
V	5.745	6.099	5.606	6.816	0.004		
VI	9.275	8.431	9.162	9.065	10.685	0.001	
VII	5.168	6.128	4.822	6.238	6.596	8.122	2.486

Table 5. Intra- and inter-cluster divergence D^2 values among seven clusters in Kharif 2005

Cluster	I	II	III	IV	V	VI	VII
I	2.078						
II	6.862	3.051					
III	4.813	5.194	2.968				
IV	5.976	4.730	3.823	2.597			
V	4.797	4.874	3.932	4.268	2.509		
VI	7.051	6.409	5.735	5.844	6.636	2.644	
VII	4.998	5.181	4.074	2.594	4.034	5.548	2.414

revealed that Cluster I had highest mean value for essential oil content (0.22%) and lowest for lamina width (2.86 cm) like-wise Cluster II had highest cluster mean value for number of primary branches/plant (13.40) and lowest for days to flower initiation (61.53 days) and days to seed maturity (156.54 days). No highest or lowest values were recorded in cluster III. Days to seed maturity (163.27 days) and essential oil yield/plant (0.75 ml) had highest leaf-stem ratio (0.76), spike length (13.01 cm), number of flower-whorls/spike (11.68) and plant height (51.99 cm) had lowest cluster mean values in cluster IV. In Cluster V leaf-stem ratio (1.73), days to flower initiation (74.00 days) and number of spikes/plant (93.93) had high cluster means and number of primary branches/plant (11.93), lamina length (4.62 cm), seed yield/plant (11.92 g) and 1000-seed weight (1.21 g) had low cluster mean values. Cluster VI had highest cluster mean for lamina length (6.18 cm), lamina width (3.79 cm), spike length (27.73 cm), number of flower-whorls/spike (16.80), plant height (83.27 cm), fresh herbage yield/plant (375.00 g), dry herbage yield/plant (79.48 g), seed yield/plant (48.55 g) and lowest value for number of spikes/plant (52.20) and essential oil content (0.13 %). Cluster VII showed highest cluster mean value for 1000-seed weight (1.68 g) and fresh herbage yield/plant (244.17 g) whereas dry herbage yield/plant (51.35 g) and essential oil yield/plant (0.44 ml) had lowest cluster mean values.

In Kharif 2005, it was observed that out of seven clusters, Cluster VII had highest number of genotypes

(10) followed by Cluster IV (5), Cluster III (4), Cluster V (4), Cluster II (3) and Cluster I (2) and Cluster VI (2) genotypes. Minimum and maximum intra-cluster distance was observed in cluster I (2.078) and Cluster II (3.051) respectively. The maximum inter-cluster value (D^2) was obtained between clusters I and VI (7.051) while minimum inter cluster value (D^2) was recorded between Clusters IV and VII (2.594). The highest mean value for essential oil content (0.28 %), essential oil yield/plant (0.75 ml) and lowest mean value for lamina length (4.09 cm), lamina width (2.43 cm), plant height (44.62 cm), seed yield/plant (11.11 g) and 1000-seed weight (1.28 g) were recorded in cluster I. The highest cluster mean values for days to flower initiation (70.78 days), number of flower-whorls/spike (14.13), plant height (65.92 cm), days to seed maturity (166.78 days), seed yield/plant (36.50 g) and 1000-seed weight (1.69 g) were recorded in Cluster II. Cluster III was characterized by maximum cluster mean value for fresh herbage yield/plant (308.67 g) and dry herbage yield/plant (63.85 g) and minimum for days to flower initiation (61.67 days). Maximum cluster mean value for lamina length (5.29 cm) and minimum cluster mean value for primary branches/plant (10.71), days to seed maturity (156.07 days) and essential oil content (0.17 %) were observed in Cluster IV. The highest cluster mean value in Cluster V was recorded for number of spikes/plant (80.97) and minimum cluster mean value for leaf-stem ratio (0.85), spike length (13.24 cm) and number of flower-whorls/spike (11.72). Cluster VI recoded high cluster mean for primary branches/plant (12.90), lamina width (3.72 cm), leaf-stem ratio (1.46), spike length (23.95 cm) where as minimum cluster mean value was recorded for number of spikes/plant (63.80). The lowest cluster mean values for fresh herbage yield/plant (231.90 g), dry herbage yield/plant (48.99 g), essential oil content (0.17 %) and essential oil yield/plant (0.40 ml) were observed in Cluster VII. The genetic divergence studied in *Ocimum* species by earlier workers demonstrated a clear relationship between clustering pattern and geographical distribution (Vieira *et al.*, 2001; Ahmad and Khalid, 2002; Vieira *et al.*, 2003; Sharma, 2005).

Genetic diversity is an important component for a plant breeding programme. The hybrids derived from genotypes of diverse origin generally display greater heterosis than those between closely related genotypes. In addition to facilitate the selection of divergent parent for hybridization, genetic divergence analyses measures the degree of diversification and determine the relative

proportion of each component character to the total divergence. The genotypes grouped together within a cluster are less divergent than the ones which are placed in different clusters. The clusters which are separated by the greatest distance show the maximum divergence. The genotypes which were grouped in a cluster were not consistent over the environments in all the seven clusters exemplifying great variations due to environments. Higher genetic variability is likely to be created when the crosses are made between selected parents from distant clusters than within cluster.

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SHORT COMMUNICATION

Genetic Variability for Hull Weight Ratio and their Inter-relationship with other Traits in Rice (*Oryza sativa* L.)**RK Sharma^{1*#} and Dinesh Kumar^{2*}**¹ Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora-263 601, Uttarakhand² Directorate of Seed Research, Mau-275 101, Uttar Pradesh

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Study on the variability and correlations for hull weight, grain weight, kernel weight, hull weight ratio (proportion of hull weight to grain weight) and kernel weight ratio (proportion of kernel weight to grain weight) in rice revealed substantial amount of variability. The broad sense heritability ranged from 66.6% for panicle length to 98.6% for 100-grain weight. Hull weight, kernel weight and grain weight had positively significant genotypic and phenotypic correlation among themselves. Hull weight ratio showed significantly negative correlation with grain weight and kernel weight. Distinct varietal differences for hull weight and grain weight ratios suggest the possibilities of breeding rice with lower hull weight ratio to further improve the marketable yield of rice.

Key Words: Correlations, Hull weight, Hull weight ratio, *Oryza sativa*, Rice

Photosynthetic efficiency of the crop plants to produce biomass and its partitioning to economic sink determine their yielding ability. In rice, hulled (dehusked) grains or kernels are used for human consumption; thus, they decide the marketable yield while husked grains account for farmers yield, respectively. For increasing the marketable yield potential in rice several approaches, such as, enhancing the grain density (Venkateswarlu *et al.*, 1986), reducing partitioning of dry matter to hull (Padmaja Rao, 1993) and selection for low hull weight ratio (Akita *et al.*, 1990) have been suggested. Low hull weight ratio indicated reduced partitioning of dry matter into husk, thus, indicative of increase in the marketable rice yield.

Thus, it was suggested to evaluate the possibility of breeding varieties for low hull weight/low hull weight ratio. Therefore, an attempt was made to examine the extent of variation for hull weight ratio and their relationship with other grain attributes to explore the possibility to breed for low hull weight ratio.

The experimental materials consisted of 60 early and medium duration elite cultures of rice, developed through recombination breeding involving genetically diverse parents of hill ecology. Thirty days old seedlings of these cultures were transplanted in well-puddled field during wet season at Experimental Farm, Hawalbagh (1250 m amsl) of VPKAS, Almora, using Randomized Block Design with

three replications. Each accession was grown in five-rows plots of 3 m length, with row-to-row and plant-to-plant distances 20 and 10 cm respectively. Recommended dose of fertilizer (*i.e.*, 50 kg N, 60 kg P and 40 kg K/ha as basal and subsequently two top dressing of 25 kg N/ha each at tillering and panicle initiation stages) was applied to raise the healthy crop. Observations were recorded on days to 50% flowering, days to maturity (plot basis), panicle length and grains/ panicle on five randomly selected plants from each plot. At harvest, matured panicles from the central row were threshed and 100-grains from the composite sample were manually dehulled. The grain weight, hull weight and kernel weight were used to compute hull weight ratio (hull weight divided by grain weight) and kernel weight ratio (kernel weight divided by grain weight). Mean values were used for statistical analysis. Different parameter of variability like phenotypic and genotypic coefficients of variability (PCV, GCV, and GA) and heritability were calculated as per Burton and De Vane (1953) and correlation coefficients were computed following Al-Jibouri *et al.*, (1958).

The analysis of variance showed highly significant differences among the genotypes for all the characters under study in-turn, showed the presence of substantial amount of genetic variability among the genotypes. Days to 50% flowering varied from 73.67 days (VL 94-3028) to 96.33 days (VL 95-3347) with a mean value of 89.9

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days. Genotypes VL 94-3028 and VL 95-3347 recorded minimum (105.67 days) and maximum (130 days) maturity duration with a mean value of 121.08 days. The average panicle length was found 24.10 cm, which varied from 19 cm (VL 91-1952) to 27 cm (VL 95-3336). Genotype VL 91-1762 showed highest number of grains/panicle (152.67) while VL 91-1952 showed the least number of grains/panicle (58.0) with a mean value of 124.78 in present set of genotypes. 100-grain weight ranged from 1.64 g (VL 93-3635) to 2.54 g (VL 93-3424) with a mean value of 2.034 g in the present set of cultures. Lowest (1.20 g) and highest (1.96 g) kernel weight were recorded in VL 91-1930 and VL 89-1171, respectively with mean value of 1.535 g. Genotypes like VL 89-1194 and VL 93-3424 exhibited the lowest (0.420 g) and highest (0.626 g) hull weight, respectively. With an average value of 0.249, the variation for hull weight ratio varied from 0.179 (VL 89-1171) to 0.286 (VL 90-1617). The kernel weight ratio ranged from 0.681 (VL 89-1196) to 0.821 (VL 89-1171) with a mean value of 0.751.

The estimates of PCV and GCV are quite close suggesting lower magnitude of the environmental influence on these traits except for grains/panicle (Table 1). The closeness of estimate for PCV and GCV for hull weight, kernel weight, grain weight and hull weight ratio revealed the least influence of environment on the expression of these traits. These findings are in agreement of the findings of several researchers. The grain weight was reported to be a stable character because the grain size is rigidly controlled by the size of the hull (Yoshida, 1981). Similarly the hull weight ratio is reported to be constant character by Padmaja Rao (1993). The estimates for heritability ranged from 66.6% for panicle length to 98.6% for 100-grain weight. The high heritability estimates observed for flowering and maturity duration, grain weight, hull weight kernel weight and hull weight and kernel weight ratio while moderate estimates were observed for panicle

length and grains/panicle. The genetic advance ranged from 5.242 (kernel weight ratio) to 26.89 (kernel weight). High heritability coupled with high genetic advance for kernel weight, grain weight, hull weight and hull weight ratio suggesting the preponderance of additive gene effects in the expression of these traits and offer scope for further improvement through selection. Moderate heritability estimates coupled with high genetic advance for grains/panicle and panicle length indicated that these could be due to non-additive gene effects and expression might be influenced by the non-genetic factors.

The perusal of genotypic and phenotypic correlations coefficients (Table 2) among the characters revealed that in general the magnitude of genotypic correlations is higher than that of phenotypic correlations suggesting that elimination of environmental effects further led to strengthen the genetic association. Hull weight had positively significant correlation with grain weight ($r = 0.7014^{**}$), kernel weight ($r = 0.566^{**}$), both at genotypic and phenotypic levels. Increase in weight of hull and kernel, with the increase in grain weight were also reported by Padmaja Rao (1993). The hull: grain weight ratio showed highly significant negative correlation with grain weight ($r = -0.548^{**}$) and kernel weight ($r = -0.684^{**}$). Chauhan (2000) also reported the similar findings. It implies that grain and kernel weight increased with the decreases in hull: grain weight ratio and rigorous selection for higher grain weight and kernel weight would result into correlated response for low hull weight ratio. Hull weight and hull weight ratio did not show significant relationship with flowering and maturity durations. No relationship between hull weight ratio with crop duration was also observed by Padmaja Rao (1993). She further reported that hull weight ratio *i.e.*, hull weight/grain weight was constant among the varied grain sizes, indicating that the hull thickness develops in a certain proportion (which is characteristic of a variety), and increases with the grain size.

Table 1. Range, mean and other genetic parameters for hull weight and related component characters

Character	Range		Mean $\pm$ SEM	PCV (%)	GCV (%)	Heritability (Broad sense)	Genetic advance (%)
	Min.	Max.					
Days to 50% flowering	73.67	96.33	89.90 $\pm$ 0.679	4.777	4.716	0.970	9.793
Days to Maturity	105.62	130.00	121.08 $\pm$ 0.725	3.658	3.609	0.973	7.3342
Panicle length (cm)	19.0	27.0	24.10 $\pm$ 1.076	7.720	6.298	0.666	10.585
Grains/panicle	58.0	152.67	124.78 $\pm$ 58.924	50.360	38.494	0.741	12.519
100-grain weight (g)	1.64	2.54	2.034 $\pm$ 0.0275	11.564	11.486	0.986	23.50
100-hull weight (g)	0.420	0.626	0.504 $\pm$ 0.012	9.898	9.599	0.941	19.177
100-kernel weight (g)	1.200	1.960	1.535 $\pm$ 0.027	13.288	13.170	0.982	26.890
Hull weight ratio	0.179	0.286	0.249 $\pm$ 0.006	8.360	8.017	0.920	15.836
Kernel weight ratio	0.681	0.821	0.751 $\pm$ 0.006	2.768	2.653	0.920	5.242

Table 2. Phenotypic (rp) and genotypic (rg) correlation coefficients between different characters in rice

Character		Maturity days	Panicle length	Grains / panicle	100-grain weight	100- hull weight	100- kernel weight	Hull wt ratio	Kernel wt. ratio
Days to 50% flowering	rg	0.9723**	0.2231	0.4416	0.0186	0.1585	-0.0164	0.1702	-0.1702
	rp	0.9622**	0.1808	0.3820	0.0214	0.1476	-0.0113	0.1514	-0.1514
Maturity days	rg		0.2281	0.2781	-0.0339	0.1090	-0.0654	0.1930	-0.1930
	rp		0.1883	0.1770	-0.0346	0.1006	-0.0647	0.1799	-0.1799
Panicle length	rg			0.6563**	0.1654	0.1629	0.1526	-0.0221	0.0221
	rp			0.5477*	0.1329	0.1234	0.1235	-0.0213	0.0213
Grains / panicle	rg				-0.1445	-0.2121	-0.1167	-0.0803	0.0803
	rp				-0.0384	-0.0451	-0.0333	-0.0105	0.0105
100-grain weight	rg					0.7207**	0.9861**	-0.5646**	0.5647**
	rp					0.7014**	0.9847**	-0.5481**	0.5481**
100-hull weight	rg						0.5956	-0.1591	-0.1592
	rp						0.5663**	0.2054	-0.2054
100- kernel weight	rg							-0.6924**	0.6925**
	rp							-0.6841**	0.6841**
Hull wt. ratio.	rg								-0.998
	rp								-0.999**

Table 3. Promising genotypes with low hull weight ratio and other characteristics

Genotype	Hull weight ratio	Hull weight (g)	Grain weight (g)	Kernel weight (g)	Grains/panicle	Panicle length (cm)
VL 89-1171	0.178	0.427	2.387	1.960	130.67	27.00
VL 91-2878	0.210	0.500	2.373	1.873	114.00	24.00
VL 93-3610	0.214	0.440	1.640	1.200	114.67	24.33
VL 88-971	0.222	0.440	1.987	1.547	133.33	23.33
VL 94-3148	0.230	0.513	2.227	1.713	105.33	24.00
VL 95-3336	0.231	0.526	2.280	1.753	144.67	27.00
VL 91-1990	0.231	0.473	1.847	1.453	115.33	23.00
VL 89-1167	0.232	0.567	2.160	1.880	110.00	25.67
VL 88-1044	0.234	0.440	1.880	1.440	106.67	23.00
VL 89-1194	0.235	0.420	1.787	1.367	104.00	24.00

The promising genotypes with low hull weight ratio (varied from 0.178 to 0.235) are listed in Table 3 along with other characteristics. Distinct varietal differences for hull weight and hull weight ratio observed among 60 genotypes suggested the possibility of breeding rice with lower hull weight and more kernel weight ratio. Utilization of these genotypes in recombination breeding could lead to improve marketable rice yield.

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SHORT COMMUNICATION

Evaluation of Fibre Quality Traits in *G. arboreum* Germplasm**RS Sangwan¹, SS Siwach¹, Ramesh Kumar^{2*} and Jal Singh¹**¹Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, Haryana²Central Institute for Research on Cotton Technology, Regional Station, Sirsa, 125 055, Haryana

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A total of 119 accessions of *Gossypium arboreum* of diverse origin were evaluated for 2.5% span length, uniformity ratio, micronaire value and fibre strength. FFS-44 had recorded 26.7mm 2.5% span length, 5.3 micronaire value and 20.2 g/tex fibre strength. CINA 329 had recorded micronaire value (5.0). The accession 35/5-B had recorded good fibre quality (26.6mm, 2.5% span length, 5.1 micronaire value and 17.9 g/tex fibre strength). Based on this study it is advocated that these lines could be used in further fibre quality improvement programme of *Gossypium arboreum*.

Key Words: 2.5% Span length, Fibre strength, *Gossypium arboreum*, Micronaire value, Uniformity ratio

Plant germplasm is the basic raw material for any crop improvement programme. The availability of genetic variability for desired traits are the first and foremost requirement for success of any breeding programme. Hence collection, maintenance, categorization and utilization of germplasm have special significance. The precise evaluation of genetic stock and dissemination of findings is of great importance for their utilization in breeding programme. The inherent quality characteristics of fibre produced on a cotton plant are mainly dependent on genetic make up of the variety. The systematic evaluated genetic resources of crop plays pivotal role in crop improvement. More than 90% of the cotton grown in the country goes into production of yarn (Iyer and Iyer, 1999). Hence, parameters crucial to trouble free processing should be given maximum importance while evaluating quality. These parameters include 2.5% span length, strength, fibre uniformity, fineness. Diploids are commonly known as *desi* cottons. The *desi* cottons are inherently resistant to sucking pests and cotton leaf curl virus disease. In the present study the germplasm lines were evaluated and identified for important fibre quality traits for *Gossypium arboreum* improvement.

The experimental material consisted of 119 accessions of *Gossypium arboreum* of diverse origin, grown in a single row of 6 m length at research area of Department of Plant Breeding, CCS Haryana Agricultural University, Hisar, during *Kharif* 2007. The spacing between rows was 67.5 cm and plants in a row were kept 30 cm apart. Recommended agronomic and plant protection measures

were adopted. The season by and large remained favourable for cotton crop. Observations were recorded on four important fibre characters i.e. 2.5% span length, uniformity ratio, micronaire value and fibre strength.

Desi cotton varieties like RG8, HD107, HD123, HD324, LD327, LD694 etc. and hybrids like AAH-1, CICR-2, Moti grown in north India have short staple length, coarse fibre and spin to less than 10 count's. Although, these varieties/hybrids have very good seed cotton yield potential. With the introduction of *G. hirsutum* cotton in India, research work on *desi* cotton suffered a set back. Work on quality improvement in *desi* cotton largely remained confined to few centers like Parbhani, Surat and Dharwad. The major aim of these researchers was to develop *desi* cottons on par with *G. hirsutum* with regard to their yield potential and fibre quality (Singh *et al.*, 2004). These efforts resulted in development of varieties like PA 255 and PA 402 from Parbhani (Maharashtra), MDL 2463 from Andhra Pradesh and DLSA 17 from Karnataka. These varieties have high productivity and superior fibre quality (Deshpande *et al.*, 2004). Earlier research work on cotton in these states remained concentrated on yield improvement whereas; improvement in fibre quality was given least priority. In the last few years efforts have been made to improve the fibre quality and to achieve this goal the germplasm had been enriched with good fibre quality lines from Central and Southern Zones. The fibre quality parameters of these *arboreum* lines were at par with local American cotton varieties or hybrids. Results obtained in the present investigation are presented and described as under:

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Fibre length: Among the various fibre properties of cotton that matters to a spinner, the fibre length is most important. Shorter fibre than a minimum length is difficult to be handled by the processing machines. Spinnability is basically decided by fibre length and its variability. Other factors being equal, long staple cottons give better spinning performance than shorter ones. Wide range of variability exists for fibre length in cotton (16 mm to 40 mm) (Narayanan *et al.*, 2004). Various fibre length parameters used in different countries may be mean length, effective length and span length. These are measured by several instruments like comb shorter, Fibrograph, High Volume Instrument. In addition to length, the uniformity of fibre length is also an important attribute. This is usually expressed in terms of co efficient of variation for fibre length. More uniform the fibre length, better will be the quality of yarn. The fibre length is generally measured as 2.5% span length. It is the length spanned by 2.5% of the fibre caught by the comb and termed as 2.5 % span length. In other words if the span length of a cotton sample is 25 mm, it means that only 2.5% of the fibres in the sample have length longer than 25 mm. In general 2.5% span length is about 10% higher than the mean fibre length obtained by comb sorter. For various purposes, it is common practice to group cottons into various categories based on staple length values. Classification of staple length is now based on 2.5% span length. Indian cottons based on span length are categorized into different groups as under:

Category	Range of 2.5 % span length (mm)	No. of germplasm lines
Short	20 mm or below	42
Medium	20.1–24.0	58
Medium long	24.1–27.0	19
Long	27.1–32.0	–
Extra long	32.5 mm and above	–

The 2.5% span length ranged from 15.5 mm (AC 3376) to 26.7 mm (FFS-44) with mean value of 21.1 mm (Table 1). On the basis of 2.5% span length the germplasm was grouped into different categories. Out of 119 germplasm lines, 42 lines had short fibre, maximum lines fall in medium fibre group i.e. 58 and medium long fibre category had 19 lines. No *arboreum* germplasm line had long and extra long 2.5% span length of fibre. Similar findings for 2.5% span length (17.46–26.4 mm) have also been reported by Pundhir *et al.*, 2004 in *G. arboreum* cotton. Promising genetic stock identified for span length are: FFS-44 (26.7mm), 35/5-B (26.6mm), 302 (26.2mm),

AKA 9410 (26.0 mm), D 462 P4 (25.8 mm), AKA 315-1 (25.8 mm), AKA 315 (25.8 mm), FFS-20 (25.5 mm), 0479 (25.0 mm). The genetic stock having 2.5% span length more than 24.0 mm along with other fibre quality traits are listed in Table 2.

Uniformity Ratio: The ratio of 50% span length to 2.5% span length expressed as per cent is called uniformity ratio (UR%). It gives an idea about fibre variability in a sample. The uniformity ratio (%) ranged from 48 to 53 with mean value of 52 (Table 1). Only five lines had the uniformity ratio below than 50. This indicated that in the present germplasm uniformity ratio is quite high. Although, Pundhir *et al.* (2004) in their studies reported slight wide range (45.0–53.5) for uniformity ratio that may be due to difference in the material or some environmental factors.

Fibre Fineness: It is also one of the important fibre characters in cotton. It plays a major role in deciding spinnable counts and yarn quality. If similar kind of yarn is spun from two different varieties of cotton, yarn spun from finer cotton will have a larger number of fibres in its cross section and hence they will be stronger and more uniform than that of coarse variety. Fineness may be denoted in various ways. Diameter, perimeter and area of cross section are dimensional measures of fineness. For practical purpose fineness is measured as mass per unit length (linear density) and denoted as gravimetric fineness is most suitable. Linear density is expressed in microgrammes/inch or as millitex which is weight of fibre in milligrammes or as millitex which is weight of fibre in milligrammes per kilometer.

The micronaire values ranged from 5.0 to more than seven. Fifty genotypes had micronaire value more than seven whereas; 46 genotypes fall in the range of 6.0 to 7.0 and only 23 germplasm lines had below than 6.0 (Table 1). These findings confirm the earlier studies (Singh *et al.*, 1988) where Pundhir *et al.* (2004) observed 5.1 to 8.0 micronaire value in *arboreum* cotton. Above observations indicated that the dominance of coarse material in the present genetic stock. Although, the efforts have been made to enrich the genetic stock with fine fibre genotypes. It has been noticed that with the passes of time good fibre lines slowly loose their fineness and ultimately fall in the medium fineness group. The main reason seems to be the environmental conditions of this zone are not favourable for the development of fine fibre. Germplasm lines with fine fibre traits identified are: CINA 329 (5.0), 35/5-B (5.1), PA 255 (5.3), FFS 44 (5.3), FFS 59 (5.3),

Table 1. Range and superior germplasm lines for different fibre quality traits

S.No.	2.5 % SL	Micronaire value	Tenacity (g/tex)	UR (%)
1	FFS-44 (26.7)	CINA 329 (5.0)	FFS-44 (20.2)	49 germplasm lines have UR (%) values 53
2	35/5-B (26.6)	35/5-B (5.1)	CAD 29 (19.9)	
3	302 (26.2)	PA 255 (5.3)	D 462-1-1 (19.7)	
4	AKA 9410 (26.0)	FFS 44 (5.3)	PA 255 (19.4)	
5	D 462 P4 (25.8)	FFS 59 (5.3)	FFS 98 (19.3)	
6	AKA 315-1 (25.8)	D 462-1-1 (5.4)	AKA 315 (19.2)	
7	AKA 315 (25.8)	302 (5.4)	AKA 210 (19.0)	
8	FFS-20 (25.5)	CAD 306 (5.6)	AH 11 (19.0)	
9	0479 (25.0)	AKA 315-1 (5.6)	AKA 315-1 (18.9)	
10	CINA 329 (24.9)	FFS 60 (5.7)	H476-5 (18.6)	
11	P489 (24.8)	H 476-5 (5.8)	CAD 306 (18.4)	
12	CAD 306 (24.6)	H 460 (5.8)	AC 3352 (18.0)	
13	AH 11 (24.6)	AC 3352 (5.8)	35/5-B (17.9)	
14	AKA 210 (24.5)	3031 (5.8)	P 489 (17.9)	
15	PA 255 (24.5)	FFS 98 (5.8)	FFS 69 (17.9)	
16	CINA 305 (24.3)	AH 11 (5.8)		
Min.	15.5	48	5.0	12.9
Max.	26.7	53	> 7.0	20.2
Mean	21.1	52.0	—	16.2

Values of a particular genotype are given in parentheses

Table 2. Best genotypes for 2.5% span length along with UR(%), micronaire value and tenacity

S No.	Name of germplasm line	2.5 % SL	UR (%)	Micronaire value	Tenacity (g/tex)
1	FFS-44	26.7	51	5.3	20.2
2	35/5-B	26.6	48	5.1	17.9
3	302	26.2	48	5.4	16.5
4	AKA9410	26.0	51	6.3	18.5
5	D 462 P4	25.8	52	5.8	19.2
6	AKA 315-1	25.8	50	5.6	18.9
7	AKA 315	25.8	52	5.8	19.2
8	FFS-20	25.5	52	6.3	18.4
9	0479	25.0	50	6.2	17.7
10	CINA 329	24.9	49	5.0	19.9
11	P489	24.8	52	6.4	18.7
12	CAD 306	24.6	52	5.6	18.4
13	AH 11	24.6	50	5.8	19.0
14	PA 255	24.5	49	5.3	19.4
15	AKA 210	24.5	50	5.9	17.9
16	CINA 305	24.3	51	6.2	19.7
17	FFS-98	24.2	52	5.8	19.3
18	FFS-18	24.2	51	6.5	18.1
19	BPS	24.2	51	6.6	17.9

D 462-1-1 (5.4), 302 (5.4), CAD 306 (5.6), AKA 315-1 (5.6) etc. Utilization of these lines for improvement in fibre fineness is advocated.

Fibre Strength or Tenacity: The durability of a textile material depends largely on mechanical strength of the fibre. In modern spinning systems like OE Rotor Spinning the fibre strength is most desirable parameter. In textile mills operations like spinning, winding, and weaving largely depends on the strength of the material, otherwise breaking leads to frequent stoppage of machine. Tenacity is the maximum specific stress that is developed in a tensile test taken to rupture. Tenacity is expressed as a force per unit linear density of the unstrained specimen. Commonly

used unit is grammes per tex.

The fibre strength (tenacity) ranged from 12.9 to 20.2 g/tex with a mean value of 16.2 g/tex indicated that the present germplasm stock had low fibre strength. In the present fibre quality norms more emphasis is given on fibre strength, the ratio of fibre strength over fibre length should not be less than 0.8. Most of the superior 2.5% span length lines also failed to meet out this norm. Out of total 119 germplasm lines 56 lines had the fibre strength less than 16 g/tex, 45 lines ranged between 16.1 to 18.0 g/tex and only 18 lines fall in the range of 18.1 and above for this character. These findings confirm the findings of Pundhir *et al.* (2004) also reported low fibre

strength range (15.1 to 19.9 g/tex) in *arboreum* cotton of North zone. The genetic stock lines, namely, FFS-44 (20.2), CAD 29 (19.9), D 462-1-1 (19.7), PA 255 (19.4), FFS 98 (19.3), AKA 315 (19.2), AKA 210 (19.0) may be utilized for development of varieties/hybrids with better fibre strength.

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SHORT COMMUNICATION

Components of Genetic Variances, Heritability and Genetic Advance in Maize Lines for Resistance to Northern Corn Leaf Blight in North-west Himalayas

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The study on components of variances, genetic advance and heritability of northern corn leaf blight (turicum leaf blight) was conducted at VPKAS, Almora during 1999-2001. Four susceptible (CM 128, V 327, V 128 and V 17) and two resistant inbred lines (V 335 and V 13) and their 15 F₁s, 15 F₂s, 15 BC₁s and 15 BC₂s, were generated for study of components of variances, genetic advance and heritability. Additive genetic variance (D), dominance (H) and environmental variance (E) were more in environment E₁ than in environment E₂ in most of the crosses which showed the importance of additive as well as non-additive components and also environmental variance. The broad and narrow sense heritability varied from cross to cross. However, their magnitude was higher in E₁ than E₂. The higher magnitudes of heritability estimates in E₁ were encouraging as it offered viable scope for selection in this environment. The estimates also revealed greater scope of genetic advance in E₁, nevertheless, high genetic advance expressed as percentage of mean were evident for turicum leaf blight in both environments. The results showed that all types of gene effects viz., additive, dominance and epistasis were operating in the crosses in controlling resistance to turicum leaf blight.

Key Words: Components of variances, Genetic advance, Heritability, Northern corn leaf blight

Turicum leaf blight (*Helminthosporium turicum* Pass or *Exserohilum turicum*) of maize, also known as northern corn leaf blight is the major foliar disease of maize in the plains of India and in Himalayan region, especially Jammu and Kashmir, Himachal Pradesh, Uttaranchal, Sikkim, Meghalaya, Tripura and Assam. The production of the maize in North-west Himalayas (Kumaun hills) of India is low as compared to the other areas of the country. Northern corn leaf blight is the major cause of low yield and may cause 28 to 91% yield losses of maize (Pant *et al.*, 2000; Singh *et al.*, 2004). Most of the maize cultivars, particularly early maturing, have been found highly susceptible.

Success of any crop improvement programme depends on the nature and magnitude of genetic variability available in the crop. The effectiveness of selection largely depends on the degree of heritability and genetic advance for traits under study. The present study was therefore undertaken to investigate heritability and genetic advance for turicum leaf blight to formulate appropriate breeding strategies for development of high yielding, early maturing and disease resistant maize cultivars suitable for the hilly areas. To reduce the loss from turicum leaf blight through selecting early maturing resistant maize material, an attempt has

been made to access the variability in present material of maize.

Four susceptible (CM 128, V 327, V 17 and V 128) and two resistant (V 335 and V 13) inbred lines were used to develop the F₁ crosses and their segregating generations. These lines, evolved under hilly environment were selected on the basis of their disease reaction and early maturity. These susceptible and resistant lines were crossed in all possible combinations (excluding reciprocals) to get 15 F₁ crosses during Rabi (Post-monsoon), 1998-99 at Vivekananda Parvatiya Krishi Anusandhan Sansthan (VPKAS). During Kharif (Monsoon), 1999, 15 BC₁s and 15 BC₂s were made along with the advancement of F₁ generation by bulk pollinations to obtain 15 F₂s. The 66 populations comprising 15 F₁s, 15 F₂s, 15 BC₁s, 15 BC₂s and 6 parents were grown in a complete randomized block design during Kharif 2000 (E₁) at the Experimental Farm of VPKAS, Almora and during Rabi 2000-01 (E₂) at Sihora Farm, Rudrapur, with two replications. Row-to-row spacing of 60 cm and plant-to-plant of 25 cm was maintained at both the locations. Recommended fertilizer dose of 160 Kg N, 60 Kg P₂O₅ and 40 Kg K₂O was applied to the crop at both the locations.

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Components of Variances for Reaction to Turcicum Leaf Blight: Additive (D), dominance (H) and environmental (E) components of variances were worked out following Mather (1949) and the estimates are presented in Table 1. Additive effects were higher in E_1 than E_2 in 10 crosses, viz., CM 128 $\times$ V 327, CM 128 $\times$ V 13, CM 128 $\times$ V 128, CM 128 $\times$ V 17, V 327 $\times$ V 335, V 327 $\times$ V 128, V 327 $\times$ V 17, V 335 $\times$ V 13, V 335 $\times$ V 128 and V 128 $\times$ V 17. The dominance effects were higher in E_1 than E_2 for 10 crosses and were lower in 5 crosses, viz., V 327 $\times$ V 13, V 335 $\times$ V 13, V 335 $\times$ V 17, V 13 $\times$ V 128 and V 13 $\times$ V 17. The environmental effects were also higher in E_1 than in E_2 for all the crosses, except in 2 crosses, CM 128 $\times$ V 327 and V 13 $\times$ V 17. The additive effects were higher in E_1 by 1.0 time, 3.3 times in 5 crosses, by 7.0 to 9.8 times in two crosses, by 19.5 and 19.6 times in two crosses and by 32.5 times in one cross CM 128 $\times$ V 17. Thus in environment E_1 , 10 crosses showed higher magnitude of additive gene effects than in E_2 . Like-wise the magnitude of dominance component was higher in E_1 than E_2 by 1.0 to 3.0 times in 10 crosses and was higher in E_2 by 1.1 to 3.5 times and by 21.5 times in one cross V 13 $\times$ V 128. Similarly the environmental component was higher in E_1 by 1.2 to 3.2 times in 13 crosses and was higher in E_2 by 1.1 to 1.3 times. On the basis of pooled analysis the magnitude of estimates of dominance component was higher than the additive component for all the crosses. These results indicated that both additive and dominant genetic variance were important in the inheritance of resistance to turcicum leaf blight. The magnitude of additive, dominance and environmental variances was higher in E_1 than in E_2 .

The ratio $(H/D)^{1/2}$ was more than 1.00 for all crosses in E_1 , and in pooled data and in 13 crosses in E_2 indicating over dominance for the trait. Only two crosses, namely CM 128 $\times$ V 128 and V 13 $\times$ V 128 in E_2 showed the above ratio below 1.00 indicating partial dominance. In a similar study Sharma *et al.* (2003) found that the resistance to maydis leaf blight was controlled by additive gene effects and inbreds CM 104, CM 105 and CM 206 were highly efficient in transferring resistance to their progenies.

Heritability and Genetic Advance for Reaction to Turcicum Leaf Blight: Estimates of heritability broad sense (bs) as well as narrow sense (ns) and genetic advance for turcicum leaf blight in 15 maize crosses in two environments are presented in Table 2. The estimates differed in two environments as well as for different crosses. The heritability (bs) in 15 crosses ranged from 35.42 to 84.44% in E_1 , 44.69 to 73.38% in E_2 and 39.03 to 64.99% on the basis of pooled analysis. The estimates of heritability (bs) were higher in 8 crosses in E_1 and in 7 crosses in E_2 . The heritability (ns) ranged from 4.0 to 50.0% in E_1 , 1.91 to 46.80% in E_2 and 3.40 to 68.60% in pooled data. Estimates of heritability (ns) were higher in E_1 than in E_2 in 10 crosses. The broad sense estimates were high to very high in both the environments, while narrow sense estimates ranged from very low to high in two environments. Furthermore, the estimates of both broad and narrow sense heritability varied in most of the crosses. Such variation was, however, more for heritability (ns) as compared to heritability (bs). Lerner (1958) has also reported that the heritability of a character may vary from one cross to another due to the extent of genetic

Table 1. Estimates of D, H and E components for reaction to turcicum leaf blight in E_1 , E_2 and pooled data

Crosses	Additive effects (D)			Dominance effects (H)			Environmental effects (E)		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
CM 128 $\times$ V 327	0.0469	0.0416	0.0187	0.1800	0.1316	0.1512	0.0528	0.0586	0.0288
CM 128 $\times$ V 335	0.0321	0.0725	0.0049	0.5179	0.3163	0.1522	0.1129	0.0347	0.0311
CM 128 $\times$ V 13	0.0242	0.0152	0.0416	0.2379	0.1471	0.1363	0.052	0.0361	0.0371
CM 128 $\times$ V 128	1.2035	0.0613	0.0416	0.856	0.2854	0.1363	0.0714	0.0376	0.0364
CM 128 $\times$ V 17	0.0423	0.0013	0.0416	0.3721	0.2061	0.1363	0.0592	0.0345	0.0333
V 327 $\times$ V 335	0.0704	0.0036	0.019	0.3483	0.192	0.0679	0.0787	0.0445	0.0283
V 327 $\times$ V 13	0.0638	0.1327	0.0681	0.4879	0.7834	0.2775	0.0755	0.047	0.035
V 327 $\times$ V 128	0.1402	0.0532	0.0136	0.3029	0.3022	0.176	0.0792	0.0481	0.0378
V 327 $\times$ V 17	0.064	0.0194	0.0397	0.3867	0.1416	0.1871	0.0817	0.0525	0.0291
V 335 $\times$ V 13	0.0354	0.0272	0.0429	0.3142	0.3498	0.1286	0.0929	0.0551	0.0289
V 335 $\times$ V 128	0.0279	0.004	0.0055	0.1562	0.1274	0.0771	0.0881	0.0406	0.0258
V 335 $\times$ V 17	0.0171	0.0898	0.0025	0.2025	0.4334	0.113	0.0767	0.0657	0.0271
V 13 $\times$ V 128	0.1742	0.4196	0.0874	0.0475	1.0226	0.3191	0.0752	0.0414	0.0276
V 13 $\times$ V 17	0.0102	0.3887	0.1151	0.3029	1.0575	0.3846	0.0574	0.075	0.0323
V 128 $\times$ V 17	0.0994	0.0101	0.0194	0.2387	0.1473	0.1677	0.0559	0.0393	0.0206

Table 2. Estimates of heritability and genetic advance for reaction to *turcicum* leaf blight in E₁, E₂ and pooled data

Crosses	Heritability broad sense (hbs)			Heritability narrow sense (hns)			Genetic Advance (GA)		
	E ₁	E ₂	Pooled	E ₁	E ₂	Pooled	E ₁	E ₂	Pooled
CM 128 × V 327	56.43	48.37	49.67	19.33	18.34	16.30	10.14	08.85	05.70
CM 128 × V 335	50.11	55.26	55.60	07.10	46.80	03.40	04.90	19.90	01.41
CM 128 × V 13	47.69	44.69	59.66	12.20	11.70	22.62	05.50	04.10	10.92
CM 128 × V 128	84.44	52.03	60.12	31.07	39.10	22.79	16.81	16.30	11.00
CM 128 × V 17	65.85	60.18	62.22	12.20	10.78	23.59	08.49	00.37	11.39
V 327 × V 335	39.74	52.81	48.34	27.00	01.91	17.31	12.70	00.88	05.80
V 327 × V 13	54.42	73.38	50.22	19.20	37.60	48.40	11.90	27.90	18.80
V 327 × V 128	64.81	50.46	57.32	31.16	27.40	07.69	24.51	12.50	03.57
V 327 × V 17	44.2	46.23	48.01	21.90	09.94	35.40	11.40	04.35	12.00
V 335 × V 13	50.89	64.71	64.99	09.36	08.71	26.02	05.98	05.70	12.41
V 335 × V 128	37.57	45.48	39.03	09.89	02.69	06.60	04.69	01.02	01.70
V 335 × V 17	35.42	49.16	52.08	07.20	34.80	02.22	03.00	18.00	00.79
V 13 × V 128	56.82	52.52	56.65	50.00	40.40	68.60	32.40	06.00	26.80
V 13 × V 17	55.15	48.28	54.49	4.00	13.40	08.12	02.20	73.10	32.90
V 128 × V 17	70.23	44.71	61.02	26.46	07.10	18.40	19.79	02.60	06.80

variance present in the parents. High heritability was also reported in the study conducted by Welz and Geiger (2000) for resistance to *turcicum* leaf blight. The genetic advance ranged from 2.20 to 32.40% in E₁, 1.02 to 73.10% in E₂ and 0.79 to 32.90% in pooled analysis. The genetic advance was relatively higher in E₁ in 11 out of 15 crosses. The broad and narrow sense heritability estimates were higher in more number of crosses in E₁ than in E₂ for reaction to *turcicum* leaf blight. The higher estimates of additive component of variance, heritability and genetic advance in E₁ environment indicated that selection for *turcicum* leaf blight is likely to be more effective in E₁ than in E₂ environment.

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SHORT COMMUNICATION

Genetic Variability of Blanket Flower (*Gaillardia pulchella*)**LN Mahawer^{1*}, HL Bairwa¹, AK Shukla² and Rajvir Sharma³**¹ Department of Horticulture, Maharana Pratap University of Agriculture and Technology, Udaipur-313 001, Rajasthan² Central Institute of Arid Horticulture, Bikaner-334 006, Rajasthan³ Division of Agronomy, Indian Agricultural Research Institute, Pusa Campus, New Delhi-110 012

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Seven genotypes of blanket flower were collected from Southern parts of Rajasthan through single plant selection sampling method. These were evaluated with respect to morphometric traits, floral yield attributes and flower shelf-life under ambient conditions for further utilization in crop improvement programmes to meet the future demand of floricultural industry. After screening seven genotypes of the open-pollinated seedlings of blanket flower maintained in the field repository, two lines *i.e.*, MPUAT GOPS-1 and MPUAT GOPS-3 were identified as most promising. MPUAT GOPS-1 has compact double flowers with yellow ray florets and flower yield ranges from 154.0 to 351.0 g/plant and obtained flower yield from 17.11 to 38.99 t/ha, mostly preferred by farmers. However, MPUAT GOPS-3 is a compact double flower with dark red ray florets and flower yield ranges from 174.6 to 328.0 g/plant and obtained flower yield from 19.39 to 36.44 t/ha. Further, MPUAT GOPS-5 and 7 are also promising with respect to flower yield and quality attributes.

Key Words: Blanket flower, Germplasm, Ray floret, Variability

Blanket flower also known as *Gaillardia* (*Gaillardia pulchella*) belongs to the family Asteraceae and is a native of Central Western United States of America. The genus *Gaillardia* has a basic chromosome number $X = 18$ and $2n = 36$ (Srivastava and Kandpal, 2006). The generic name *Gaillardia* was proposed in the honours of M. Gaillard, a French patron of botany. The genus has 12 species, out of which, three species *viz.* *G. amblyodon*, *G. aristata* and *G. pulchella* have played an important role in the evolution of varieties for horticultural importance. *Gaillardia* is an important commercial flower in Gujarat, Madhya Pradesh, Maharashtra and Rajasthan. It can be used for mixed borders, edging, as a loose flower or as a cut flower. *Gaillardia aristata* is suitable for dry land and requires low maintenance (Cox and Klett, 1984). The plant possesses brilliant, daisy-like flowers with single, semi-double or double forms. There are many unexplored regions for collecting blanket flower variability for further characterization and evaluation. Keeping this in view, an exploration was undertaken to collect and evaluate the variability of blanket flower for further use in crop improvement programmes.

In cross-pollinated crops, majority of seeds population are heterozygous in nature and growing of crop through seeds may result in large variability. The variation observed for all the important characters is suggestive of its use

in crop improvement programmes of this genus. Wider range of genetic variability in *Gaillardia* provides ample scope to evolve suitable genotypes or varieties possessing combination of valuable, adaptable characteristics under different environment. At the Department of Horticulture, MPUAT, Udaipur (Rajasthan) collections were made of the seeds of seven open-pollinated selections from Jaipur, Ajmer, Kota, Chittorgarh, Udaipur and Banswara district of Rajasthan during 2005-06 and evaluation was done during 2006-07 to 2007-08 for various parameters like vegetative growth, flower quality, yield and shelf-life (in moist muslins cloth) under ambient conditions. Further, 50 plants of each genotype were used for taking the observation on plant growth characteristics and flower yield attributes. Uniform package of practices was adopted for all the genotypes studied.

Data presented in Table 1 revealed that plant height varied in MPUAT GOPS-1 (60.0–76.0 cm) followed by MPUAT GOPS-5 (59.0–75.0 cm), while minimum in MPUAT GOPS-6 (45.0–63.0 cm). Maximum variability for number of branches/plant was recorded in MPUAT GOPS-1 (15.0–28.0) followed by MPUAT GOPS-5 (15.0–25.0) and minimum range *i.e.* 13.0–19.0 in MPUAT GOPS-4 (Mahawer *et al.*, 2009a). Maximum variability for number of flowers/plant was observed in MPUAT GOPS-1 (100.0–137.0) followed by MPUAT GOPS-3

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Table 1. Characteristics of different genotypes of blanket flower

Characters	MPUAT GOPS- 1	MPUAT GOPS- 2	MPUAT GOPS- 3	MPUAT GOPS- 4	MPUAT GOPS- 5	MPUAT GOPS- 6	MPUAT GOPS- 7
Plant height (cm)	60.0–76.0	58.0–68.0	53.0–73.0	58.0–75.0	59.0–75.0	45.0–63.0	50.0–65.0
No. of branches per plant	15.0–28.0	13.0–21.0	15.0–22.0	13.0–19.0	15.0–25.0	15.0–18.0	15.0–22.0
No. of flowers per plant	100.0–137.0	84.0–133.0	90.0–135.0	90.0–134.0	98.0–134.0	95.0–130.0	98.0–130.0
Flower diameter (cm)	4.6–6.0	4.9–5.3	5.4–5.8	5.3–5.7	5.6–6.0	5.0–5.8	5.4–5.8
Plant spread (cm ²)	60–72 x 60–72	58–70 x 55–70	52–72 x 50–70	57–70 x 60–67	55–69 x 55–70	50–60 x 52–62	52–65 x 55–65
Range weight per flower (g)	1.54–2.56	1.97–2.43	1.94–2.43	0.88–1.66	1.63–1.75	1.12–1.24	1.34–1.68
Yield per plant (g)	154.0–351.0	165.5–323.2	174.6–328.0	79.2–222.4	159.7–234.5	106.4–161.2	131.3–218.4
Yield per ha (t)	17.11–38.99	18.38–35.91	19.39–36.44	8.79–24.71	17.74–26.05	11.82–17.91	14.59–24.26
Colour of ray floret and type	Compact yellow double	Yellow petals, ray floret end, red brown tips	Fully dark red double type	Bicolour red petals yellow tips single type	Red petals ray floret end yellow tips semi-double	Fully yellow single type	Compact light yellow semi-double
Disc diameter (cm) with hair colour	1.9–2.2 yellow hairs with convex disc	1.5–1.8	1.7–1.9 coppery hairs flat disc	1.8–2.3 semi convex to fully convex	2.1–2.3 semi flat –fully convex	1.6–1.9 yellow hairs semi – fully convex	1.4–1.6 yellow hairs semi-fully convex
Number of teeth on ray floret	4–5	4–5	5–6	2–3	4–5	2–3	4–5
Flower duration(days)	110.0–120.0	80.0–95.0	90.0–100.0	70.0–90.0	90.0–95.0	80.0–95.0	85.0–95.0
Shelf life under ambient condition 25±2°C (hr)	10.0–12.0	6.0–8.0	10.0–12.0	Less than 2.0	7.0–8.0	Less than 2.0	6.0–8.0

(90.0–135.0), whereas lowest range was recorded in MPUAT GOPS-2 (84.0–133.0). A wide range of variation for flower diameter was recorded in MPUAT GOPS-1 (4.6–6.0 cm), narrow variation in MPUAT GOPS-3 (5.4–5.8 cm) and MPUAT GOPS-2 (4.9–5.3 cm). The wider plant spread variability was observed in MPUAT GOPS-1 (60.0–72.0 × 60.0–72.0 cm) and MPUAT GOPS-3 (52.0–72.0 × 50.0–72.0 cm), whereas lowest variation was recorded in MPUAT GOPS-6 (50.0–60.0 × 52–62.0 cm). The wider variation range was recorded for weight/flower in MPUAT GOPS-1 (1.54–2.56 g), MPUAT GOPS-3 (1.94–2.43 g), while narrow range i.e. in MPUAT GOPS-5 (1.63–1.75 g), 1.12–1.24 g in MPUAT GOPS-6 (Mahawer *et al.*, 2009b). Highest variation for flower yield per plant was noticed in MPUAT GOPS-1 (154.0–351.0 g) and MPUAT GOPS-3 (174.6–328.0 g), while lowest variation was recorded in MPUAT GOPS-6 (106.4–161.2 g). The highest variation for flower yield/hectare was observed in MPUAT GOPS-1 (17.11–39.99 t/ha), MPUAT GOPS-3 (19.39–36.44 t/ha) which were liked by farmers, while lowest variation was recorded from 11.82–17.91 t/ha in MPUAT GOPS-5 (Mahawer *et al.*, 2009a, b). The genotypes like MPUAT GOPS-1 have compact yellow ray florets with double type, MPUAT GOPS-3 have fully dark red ray florets with double type (more than three rows of ray floret/flower) and which are mostly desired by the farmers. The genotype MPUAT GOPS-5 has red petals ray florets ended with yellow tips with semi-double types and MPUAT GOPS-7 has light yellow ray florets with semi-double type of flowers (2–3 rows of ray floret per flower).

Among seven genotypes evaluated for disc diameter with hair colour, MPUAT GOPS-1 has disc diameter (1.9–2.2 cm) along with yellow hair on convex disc, MPUAT GOPS-3 has disc diameter (1.7–1.9 cm) with coppery hair with flat position disc in double types flower group. However, in semi-double types group, MPUAT GOPS-5 had disc diameter (2.1–2.3 cm) with semi-flat to fully convex disc with coppery color hair. The MPUAT GOPS-7 exhibited varied disc diameter (1.4–1.6 cm) with yellow hair along with semi to fully convex disc. In double type genotype, MPUAT GOPS-3, number of teeth on ray floret ranged from 5–6/ray floret, 4–5 in MPUAT GOPS-1, whereas, in semi-double type there were 4–5 teeth per ray floret in MPUAT GOPS-5 and 7. The desirable variability for number of teeth/ray floret ranged from 4–6 in semi-double to double type promising class. However, the desirable flower duration range was

recorded in MPUAT GOPS-1 (110–120 days), MPUAT GOPS-3 (90.0–100 days) in double type; in semi-double type in MPUAT GOPS-5 (90.0–95.0 days) and MPUAT GOPS-7 (85.0–95.0 days).

The variability for shelf-life of flower in seven genotypes was also recorded under ambient condition (in muslin cloth) at $25\pm 2^{\circ}\text{C}$. Out of seven genotypes, highest shelf- life was recorded in MPUAT GOPS-1 and MPUAT GOPS-3 (10–12 h) genotypes and these were most promising in double type group. In semi double genotype, MPUAT GOPS-5 exhibited medium range shelf-life variability (7.0–8.0 h) than double type genotypes.

It is concluded on the basis of evaluation for two years that genotypes, MPUAT GOPS-1, MPUAT GOPS-3 (for double type), MPUAT GOPS-5 and MPUAT GOPS-7 (for semi-double type), are promising germplasm. However, MPUAT GOPS-2, MPUAT GOPS-4 and MPUAT GOPS-

6 were not preferred by the farmers for commercial flower production though they have the capacity to tolerate adverse climatic condition. Therefore, these can be utilized in future breeding programmes.

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SHORT COMMUNICATION

Variability Studies in Some Quantitative Characters in Sunflower (*Helianthus annuus* L.)

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Twenty-two genotypes of sunflower were evaluated for sixteen different quantitative characters, revealed considerable amount of variability for all the characters. Variation at genotypic level was also quite high for most of the traits indicating sufficient scope for selection. The magnitude of GCV and PCV were comparatively higher for seed yield per plant leaf area, total weight of head and number of seeds per head as compared to other characters. The characters such as days to 50% flowering and oil content were less affected by environment showing a close correspondence between GCV and PCV, while characters such as leaf area, total weight of head, seed yield/plant and head diameter of sterile area were the most effected. High heritability estimates with low genetic advance was observed for days to 50% flowering implying less genetic gain if selected upon, while selection for seed yield per plant, leaf area, total weight of head and number of seeds per head possessing high GCV, moderate h^2 and high genetic advance as percent of mean in the material under study is expected to result in considerable genetic gains. Lowest values of GCV, h^2 and GA were observed for oil content, suggesting that this character can not be improved effectively by selection.

Key Words : Genetic advance, Genetic variability, Heritability

The exploitation of sunflower (*Helianthus annuus* L.) as a source of edible oil in India is receiving considerable thought for increasing the quantity of oil in the seeds of some promising strains after their successful introduction into this country from the Soviet Union. A need for improving and stabilizing the yield of this crop was felt by the breeders. Selection of superior varieties will be possible only when adequate variability exists in the gene pool. Therefore, an attempt was made in the present study to estimate genetic variability with the aid of genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as % of mean (GA).

Seeds of twenty two genotypes of sunflower viz., PZ-1570, EC370, PZ-1351, PC-317, PC-1569, PZ-D1603, PC-B1382, CMS-339B, PC-381, CMS-339A, EC336, PZ-1571, PCF-1604, PCA-1173, PZB-1141, PC-1520, PCB-1603, PZ-1040, PZ-1572, PC-160, PC-1603 and local selections were collected from the Division of Genetics, Indian Agricultural Research Institute (IARI), New Delhi. The material was evaluated in a Randomized Block Design experiment with three replications during rainy season 2005 at research farm of Kisan (PG) College,

Simbhaoli, Ghaziabad (UP). Each genotype was assigned to two row plots of 3 m length with inter and intra row spacing of 75 cm and 30 cm, respectively. Recommended cultural practices were followed to raise a healthy crop. The data was recorded on five randomly selected plants from each treatment on sixteen distinct morphological characters mentioned in Table 1. Data were subjected to analysis of variance (Panse and Sukhatme, 1967). GCV and PCV were estimated using the method suggested by Burton and Devane (1953). Genetic advance as percent of mean at 5%. Selection intensity was estimated according to the formula suggested by Allard (1960).

The analysis of variance revealed highly significant differences among the cultivars for all the characters (Table 1) which indicated the presence of considerable amount of diversity in the material selected for the study. The range of variation was maximum for leaf area (257.57–50.73), number of seeds per head (213.33–82.33), total weight of head (192.50–32.67) and plant height (131.90–69.70), while it was lowest in the case of stem diameter at top height (3.40–1.93), stem diameter at mid height (4.30–2.53) and head diameter of sterile area (3.87–1.10). Though, the comparison between characters is uncalled for, the results would apparently remain same

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Table 1. Analysis of variance (ANOVA) for sixteen quantitative characters recorded on 22 genotypes of sunflower

Source of variation	d.f.	D.F.	50 %	NL/P	PH	SDTH	SDMH	HD	HDSA	TWH	NS/H	PFS	100SW	SY/P	OC %	LL	LB	LA
Replication	2	13.921	35.503	605.000	0.246	0.951	4.432	2.972	3606.843	2664.750	64.734	22.753	55.156	102.518**	5.546	3.648	6.378	1886.062
Treatment	21	44.470**	19.909**	773.797**	0.392**	0.913**	5.776**	1.468**	5653.013**	4748.363**	82.856*	17.535**	102.518**	12.69	28.674**	22.342**	16.506**	6726.274**
Error	42	4.333	5.079	165.584	0.149	0.292	1.987	0.351	1048.463	826.285	42.216	2.952	12.69	3.955	4.016	3.104	1198.708	
** = Significant at p = 0.01 level																		
Character Code :																		
D.F. 50 % = Days to 50 % flowering																		
NL/P = Number of leaves/plant																		
PH = Plant height																		
SDTH = Stem diameter top height																		
SDMH = Stem diameter at mid height																		
HD = Head diameter																		
HDSA = Head diameter of sterile area																		
TWH = Total weight of head																		
NS/H = Number of seeds per head																		
PFS = Per cent filled seed																		
100 SW = 100 Seed weight																		
SY/P = Seed yield/Plant																		
OC % = Oil content percentage																		
LL = Leaf length																		
LB = Leaf breadth																		
LA = Leaf area																		

even after standardization with the corresponding means. It leads to say that there exists an association between mean values and the range. In other words, higher mean was associated with high range. It means, there is better scope for selection for number of seeds/head and total weight of head compared to others. The magnitude of PCV was higher than the GCV for all the characters studied which suggested that the apparent variation is not only due to the genotype but also due to the influence of environment. High PCV and GCV were observed for seed yield per plant (59.46 and 49.83) followed by leaf area (54.72 and 42.59), total weight of head (51.91 and 40.01) and number of seeds/head (34.71 and 27.17) which suggested greater genetic diversity among the genotypes and responsiveness of the attributes for making further improvement by selection. These characters also showed narrow differences between PCV and GCV which indicated their relative resistance to environmental variation. Genetic factors were predominantly responsible for the expression of these attributes and selection could be made effectively on the basis of phenotypic performance. Saravanan *et al.* (1996) and Patil *et al.* (1996) reported similar results. The lowest PCV and GCV values were observed for oil content (7.38 and 6.06) and percent filled seeds (10.28 and 5.07) which indicated low variability for these traits. A marked difference between PCV and GCV was observed for leaf area, total weight of head, seed yield/plant, head diameter of sterile area and head diameter suggesting the predominance of GXE interactions and genetic role of environment on the expression of these traits. This is in agreement with the earlier reports of Chaudhary and Anand (1987).

However, high variance values alone are not the determining factors of the expected progress that could be made in respect of quantitative traits (Falconer, 1981). It was suggested that the GCV together with the high h^2 estimates would give a better picture of the extent of genetic gain to be expected under selection. In the present study, high h^2 estimates was obtained for days to 50% flowering (76%). Similar results have been reported by Patil *et al.* (1996). However, in general, characters with high h^2 did not possess greater variability (high GCV). In other words, characters with high GCV showed moderate h^2 . Incidentally these characters also showed higher genetic advance as per cent of mean. Johnson *et al.* (1955) suggested that h^2 considered together with GA is more reliable in predicting the effect of selection than h^2 alone. Therefore, selection for seed yield/plant, leaf area, total

Table 2. Estimates of genetic constraints (for variability) for 16 characters in 22 genotype of sunflower

Characters	Range	Heritability (bs)	Genetic advance	Genetic advance over mean	Coefficient variability		Difference PCV-GCV
					GCV	PCV	
D.F. 50 %	50.83–64.67	0.76	6.55	11.90	6.65	7.65	1.00
NL/P	13.67–23.83	0.49	3.22	17.12	11.82	16.84	5.02
PH	69.70–131.90	0.55	21.76	22.64	14.81	19.97	5.16
SDTH	1.93–3.40	0.35	0.35	12.86	10.46	17.62	7.16
SDMH	2.53–4.30	0.42	0.60	17.91	13.58	21.08	7.50
HD	5.60–10.47	0.39	1.44	18.34	14.31	22.95	8.64
HDSA	1.10–3.87	0.51	0.90	35.43	23.99	33.45	9.46
TWH	32.67–192.50	0.59	62.21	63.54	40.01	51.91	11.90
NS/H	82.33–213.33	0.61	58.30	43.81	27.17	34.71	7.54
PFS	62.10–80.73	0.24	3.74	5.15	5.07	10.28	5.21
100SW	8.17–16.33	0.62	3.58	28.66	17.65	22.38	4.73
SY/P	4.00–22.90	0.72	9.45	86.06	49.83	59.46	9.63
OC %	43.37–54.43	0.68	4.86	10.26	6.06	7.38	1.32
LL	10.53–22.63	0.60	3.95	27.39	17.13	22.06	4.93
LB	6.43–16.17	0.59	3.34	35.34	22.37	29.12	6.75
LA	50.73–257.57	0.61	68.83	68.29	42.59	54.72	12.13

Table 3. Potent genetic donors in sunflower identified for seed yield and its component traits

Characters	Promising genotypes
Seed Yield/plant (g)>10.98	PCB-114, PC-1520, PZ-1569, PZ-381
100 seed weight (g)> 12.49	PZ-1572, PZ-1570, PZA-1173, PZ-1040
Total weight of head(g)> 97.91	PCB-114, PZB-1603, PCB-520, PZ-1569
Head Diameter >7.85	PZB-1603, PZ-381, PZ-1520
Oil Content(%) > 47.35	PZ-1570, PZ-1569, PZ-160, PZ-1603
Days to 50% flowering < 55.02	PZ-1040, PZ-1572, PCB-1382, PC-1351, PZ-1570

weight of head and number of seeds/head which possessed high GCV, moderate h^2 and high GA over mean in the material under study is expected to result in considerable genetic gains. While selection for days to 50% flowering where only h^2 was high is not expected to result in maximum genetic gains. Lowest values of GCV, h^2 and GA were observed for oil content suggesting that this character can not be improved effectively by selection.

Potent genetic donors were identified (Table 3) for high yielding potentials, bold seed size, total weight of heads, head diameter, high oil content and early flowering

in nature. These genotypes can also be utilized for general cultivation and in breeding programme for their useful traits.

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SHORT COMMUNICATION

Varietal Screening of Strawberry (*Fragaria x ananassa* Duch.) under Organic Production System for Fruit Quality and Yield in Mid-Hills of Sikkim Himalayas

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Experiments were conducted at ICAR Sikkim Centre, Tadong at an elevation of 1400 m amsl during 2006–09 to study the performance of 11 strawberry varieties in the mid-hills of Sikkim Himalayas. Observations on vegetative parameters, fruit quality and yield were recorded for the selected varieties. The highest fruiting stalk/plant (11.67) was recorded in Chandler followed by Ofra (10.87). Maximum number of runners were in Hasta and Etna (14 and 14, respectively). Fruits/inflorescence were highest in Seascab (7.67). Fruit diameter was highest in Blackmore (3.30 cm) followed by Ofra (3.16 cm) whereas the fruit length was longest in Ofra and Chandler (4.97 and 4.94 cm, respectively). Maximum fruit weight (20 g) was recorded in Ofra. Highest TSS (7.20%) and total sugar (6.18) were recorded in Elsanta. Lowest acidity (0.89 %) was observed in Chandler followed by Ofra and Selva. Highest yield (37.2 t/ha) was recorded in Ofra, and the maximum marketable yield and B:C ratio were recorded in Chandler (32.6 t/ha and 2.26, respectively).

Key Words: *Fragaria x ananassa*, Fruit quality, Fruit yield, Mid hills, Varietal screening, Sikkim

Sikkim is an entirely hilly state of India where settled agriculture is practiced in 10% of its total geographic area out of 14.9% cultivable area (Lama, 2007). Horticulture occupies a dominant position with mandarin, ginger and large cardamom as the main cash crops. Majority of farmers are categorized as small and marginal operating and also low input production system with low productivity and hence, resource poor. Strawberry can be easily cultivated up to 3000 m amsl elevation (Sharma, 2002) under open/protected conditions especially with the advantages of being a low volume, high value crop that can be expected to significantly increase the household level income. Among the fruit crops, strawberry gives the quickest return in the shortest possible time. Strawberry fruits are in great demand by fruit processing industries owing to its distinct flavour/aroma, richness in vitamin C and minerals. Although, strawberry is a crop of temperate regions of the world, its cultivation has been extended to subtropical regions of India (Sharma and Yamadagni, 2000). There is a considerable variation among different strawberry cultivars regarding their adaptability to a particular set of agro-climatic conditions (Sharma and Thakur, 2008). In strawberry cultivation, fruit quality in terms of morphology and chemical composition is of prime importance and is greatly influenced by the weather conditions. The quality of strawberry is determined by its taste, flavour, texture, size, shape, gloss and skin colour, storage and transportability (Mochizuki, 1991).

Strawberry has not been very popular as an alternate cash crop amongst the farmers of Sikkim owing to non-availability of location specific planting material and standardized package of practices. Therefore, suitable varieties need to be identified for different climatic conditions. In the present study, an attempt has been made to evaluate different strawberry varieties suitable for the mid-hill temperate region of Sikkim.

Eleven strawberry varieties viz., Ofra, Chandler, Selva, Hasta, Red Coat, Etna, Belruby, Seascab, Dana, Blackmore and Elsanta were evaluated during 2005–09 at ICAR Farm at Tadong, Gangtok, at an altitude of 1400 m amsl. The field experiments were laid out in a randomized block design with three replications, in a plot size of 2 x 3 m² with 20 plants of uniform health and vigour. The soil of the location is well drained with pH 5.3, O.C. 1.36%, available nitrogen-221.8 kg/ha (alk. KMnO₄), available P₂O₅-28.5 kg/ha (Bray P₁) and available K-194.7 kg/ha. Transplanting was done in the first week of September at the spacing of 30 x 45 cm and 15 t/ha fully rotten FYM and 5 t/ha neem cake was applied as basal dose. Regular drenching of plants with diluted cow urine @ 20 % was done after one month of transplanting at fortnightly interval.

Data was recorded for quality parameters with randomly selected 10 fruits/plant. Fruit length and breadth was measured with vernier callipers. The weight of the representative fruits of each variety was recorded. The

marketable yield was calculated by subtracting damaged fruits during or prior to harvest from the total fruit yield. Total soluble solids were recorded from the juice obtained from randomly selected fruits from all the varieties in each replication with the help of refractometer of 0–32°B range. Level of acidity was calculated by titration method. TSS/acid ratio was determined by dividing acidity with TSS values. Total sugars were determined by Shaffer-Somogyi micro method (Ranganna, 1991). The data were analysed statistically following the method of Panse and Sukhatme (1985). The mean of attributes were compared by paired 't' test and the standard error of mean (SEM) was calculated at 5% level of probability. Net profit of cultivation was calculated by subtracting cost of cultivation from gross profit and B:C ratio was estimated. The market price of the fruits was fixed @ Rs 100/kg.

The study revealed significant differences among the varieties for different traits such as fruiting stalk/plant, fruits/inflorescence, runners/plant, fruit diameter, fruit length, fruit weight, TSS, acidity, total sugar, yield and

marketable yield. Maximum number of fruiting stalks/plant were in Chandler (11.67) which was at par with Ofra (10.87) with significant difference in the fruit stalks of all other varieties. The minimum number of fruiting stalks/plant were in Blackmore (2.67) which was at par with Hasta (3.33). The highest number of fruits/inflorescence was observed in Seascab (7.67) which was at par with Blackmore, Elsanta, Ofra and Chandler while the lowest number of fruits/inflorescence was reported in Dana (3.23). Maximum number of runners was produced by Hasta and Etna (14) which were significantly higher than other treatments except Belruby (12.67). The minimum number of runners was seen in Blackmore (3.76). The highest fruit diameter was recorded for Blackmore (3.3 cm) and the lowest (2.12 cm) for Selva. The longest fruits were in Ofra (4.97 cm) and the shortest fruits were in Seascab (2.57 cm). Ofra (20.0 g) produced the heaviest fruits whereas Belruby produced fruits with lowest fruit weight (12.02 g). TSS was highest in Elsanta (7.20%) which significantly differed from the other varieties while

Table 1. Varietal performance of strawberry for yield attributing traits

Varieties	Fruiting stalks/plant	Fruits/inflorescence	Runners/plant	Fruit diameter (cm)	Fruit length (cm)	Fruit weight (g)
Ofra	10.87	7.12	4.00	3.16	4.97	20.00
Chandler	11.67	6.87	4.00	2.37	4.94	18.10
Selva	4.00	5.95	4.00	2.12	4.63	12.60
Hasta	3.33	5.50	14.00	2.57	4.13	14.20
Red Coat	7.00	6.10	11.33	2.36	4.16	16.06
Etna	4.00	5.95	14.00	2.33	3.43	10.00
Belruby	6.67	5.07	12.67	2.60	4.27	12.02
Seascab	6.00	7.67	4.67	2.23	2.57	14.01
Dana	8.00	3.23	5.00	2.83	4.27	11.50
Blackmore	2.67	7.35	3.67	3.30	4.33	15.10
Elsanta	7.00	7.10	4.33	2.55	3.97	19.00
SEM±	0.68	0.47	0.86	0.27	0.27	0.35
LSD ($P = 0.05$)	1.42	0.98	1.79	0.57	0.57	0.72

Table 2. Performance of strawberry varieties for fruit quality, yield and economics

Varieties	TSS %	Acidity %	Total Sugar (%)	TSS:acid Ratio	Yield (t/ha)	Marketable yield (t/ha)	Net profit (Rs in lakhs)	B:C Ratio
Ofra	6.30	0.96	3.67	6.56	37.20	26.70	16.70	1.67
Chandler	6.60	0.89	4.05	7.42	36.30	32.60	22.60	2.26
Selva	6.50	1.02	4.31	6.37	7.32	5.80	-4.20	-0.42
Hasta	6.10	1.21	4.11	5.04	7.74	6.10	-3.90	-0.39
Red Coat	6.20	1.15	4.00	5.39	18.96	15.20	5.20	0.52
Etna	6.70	1.06	4.92	6.32	8.16	5.85	-4.15	-0.42
Belruby	5.10	1.18	3.57	4.32	12.96	11.05	1.05	0.11
Seascab	5.30	1.16	3.14	4.57	12.66	9.85	-0.15	-0.02
Dana	6.20	1.25	4.34	4.96	12.30	9.40	-0.60	-0.06
Blackmore	5.70	1.15	3.16	4.96	17.34	14.60	4.60	0.46
Elsanta	7.20	1.20	6.18	6.00	27.60	22.60	12.60	1.26
SEM±	0.14	0.08	0.10	—	0.43	0.49	—	—
LSD ($P=0.05$)	0.29	0.17	0.22	—	0.89	1.02	—	—

the lowest was recorded in Belruby (5.10%). The findings of TSS are not in conformity with those of Singh *et al.* (2008) where TSS was to the tune of 12.8⁰B but similar to the findings of Sharma (2002) who reported TSS of 7.8⁰B in Chandler. Lower TSS content of the varieties may be due to the high relative humidity during the fruit growth, development and ripening period. The lowest acidity was recorded in Chandler (0.89%) and the highest in Dana (1.25%). Good quality fruit with higher TSS/acid ratio was in Chandler (7.42 %) followed by Ofra (6.56 %). Similar varietal differences in acidity were reported by Chandel and Badiyala (1996) and Singh *et al.* (2008). The highest total sugar was observed in Elsanta (6.18%) while the lowest was in Seascab (3.14 %). These findings on varietal differences in total sugar were similar to those reported by Mondal *et al.* (2001), Sharma and Thakur (2008) and Singh *et al.* (2008). The highest fresh fruit yield was recorded for Ofra (37.2 t/ha) which was significantly higher than all other varieties and the lowest was in Selva (7.32 t/ha). Among all the varieties, the highest marketable yield was observed in Chandler (32.60 t/ha) which was significantly different from other varieties. The lowest marketable yield was recorded in Selva (5.80 t/ha). These findings are in conformity with those reported by Mondal *et al.* (2001) and Sharma and Thakur (2008).

Cultivation cost of the strawberry production includes the cost of planting material, manure, field preparation, mulch material, packing material and the labour. Maximum net profit (Rs. 22.6 lakh/ha) was recorded for Chandler followed by Ofra (Rs. 16.7 lakh/ha) and Elsanta (Rs. 12.6 lakh/ha) whereas negative return was recorded for Selva, Hasta, Etna, Seascab and Dana. The highest B: C ratio was in Chandler (2.26) followed by Ofra (1.67) and

Elsanta (1.26). Financial loss in production was observed with Selva, Hasta, Etna, Seascab and Dana.

Chandler and Ofra were identified as the varieties that could be profitable under the mid-hill conditions of Sikkim. Both the varieties can be promoted amongst the resource poor farmers of the state which could considerably increase monetary benefits through strawberry cultivation at the household level.

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SHORT COMMUNICATION

Dendrobium lituiflorum* Lindl.– A Validation Report from Khasi Hills of Meghalaya*R Devadas^{1*}, D Barman and RP Medhi***National Research Centre for Orchids, ICAR, Pakyong-737 106, Sikkim*

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An unidentified flowering species belonging to genus *Dendrobium*, morphologically allied to *Dendrobium nobile* Lindl., was collected near lower Khasi hills of Meghalaya in 2007 and was characterized and discussed. Critical comparison was made with its allied group in the same geographical area of North East Hill (NEH) of India to distinguish from the others. Deciduous nature of pseudo-stems during flowering, dominant shining purple colour of sepals and petals, short peduncle traits and finally purple column colour as phenological markers, served as taxonomic identification traits for confirmation of this species as *Dendrobium lituiflorum* Lindl., from *D. nobile* Lindl., (also known as noble orchid).

Key Words: Characterization, *Dendrobium lituiflorum* Lindl., Wild species

The genus *Dendrobium* was established in 1799 by O. Swartz in *Nova Acta Regiae Societatis Upsaliensis*, which comprises 1,400 species distributed from India across to Japan, South to Malaysia, Indonesia and east to New Guinea, Australia, New Zealand and the Pacific Island (Lucksom, 2007). The beautiful species, *Dendrobium lituiflorum* Lindl., is similar to *Dendrobium nobile*, was native to the warm valleys throughout Arracan (presently a part of modern Myanmar) (James Veich and Sons, 1888). It was first reported in Burma during 1856, but also seen in Assam (at present, Asom, India), adjoining Khasi & Jaintia hills and Sikkim of India. This species first became known in British gardens in 1856 from the collections of late Mr. Robert Hanbury, at Poles, near Ware. The species name derived from *lituus*, “a sort of trumpet”, refers to the form of lip. Although John Lindley and John Dalton Hooker described the species taxonomically in 1856 and 1890 respectively, but the modern scholars often misquoted it because of its similarity and time of flowering like noble orchid and some times considered as variant of *D. nobile* Lindl. Even though, it is considered as a close ally with *D. nobile*, which is an endemic orchid species in North-East India and popularly recognized as the state flower of Sikkim, the taxonomical identity of both the species are different. Current species under report was collected (NRCO-Coll-1/2007) from the local vendors at lower Khasi hills of Meghalaya, as an ‘unidentified species’. It was studied for two consecutive years and characterized morphologically for validation of identity and application

in future research programmes. An effort was made critically to phenotypically distinguish the species from another with pictorial depiction. The major emphasis had been now given for multiplication of this species and collection for conservation in the capacity of ‘National Active Germplasm Site’ (NAGS) at ‘National Research Centre for Orchids’, ICAR, Sikkim under Germplasm Management Unit of Plant Breeding. Existence of this species in Khasi and Jaintia hills was earlier reported without depiction (Arora and Mukherjee, 1983) and current status of this species was reported as endangered, extremely rare and threatened category from north-east India (Chowdhery, 2001).

Taxonomical description used for identification of *D. lituiflorum*: Habit – epiphyte; Stem – long, slender, grayish white, pendulous with a knob-like base; Root – slender, whitish brown; Leaves – linear lanceolate, deciduous; Inflorescence - produced on older leafless stems, usually in pairs at the upper most joints of nodes on short and very large bracted peduncle; Flowers – deep purple, equal; Bract – white, scarious; Sepals – oblong lanceolate, acute, purple with much paler at the base; Petals – ovate oblong, broader, dark bright purple, mentum short saccate; Lip – white, convolute at the base with white and heavy purple transverse stripes, disc of limb/ mouth orbicular concave turned up like trumpet shaped puberulous edged with purple color and margins slightly recurved, dark purple central blotch at centre of lip, claw

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broad, convolute over column; Column – purple, short; Anther – velvety purple, pollinia – 4 (group of two), ca 0.2 cm long and orange yellow (Lindley, 1856; Grant, 1895; Hooker, 1890).

Evaluation and characterization: The species, was evaluated and characterized at this centre as per ‘Common Descriptors of Orchids’ developed. Data was collected on only few surviving and flowering plants of the collection. The colour pattern of qualitative characters was recorded with help of ‘Royal Horticultural Society’ (RHS) colour charts. The general descriptions for the morphological characters of the collection was based on mean data (quantitative) and expressivity of qualitative characters like color pattern was observed for two years at Pakyong, Sikkim (Altitude 1,300 m) location (summarized in Table 1). The comparative description of species, *D. lituiflorum* Lindl. and *D. nobile* Lindl., for identification and differentiation is shown in Table 2. The differences of the species with *D. nobile* (NRCO-Coll-NATP/PD/15-10.09.04 of Arunachal Pradesh and IC439518 of Sikkim) for plant and as well as flower configuration along with lip differences was depicted in Fig. 1.

The species being monopodial epiphyte, the growth in terms of height has been recorded with range of 25–40 cm

during the past two years. Pseudo-stem was long, slender with deciduous nature at the time of flowering. Young and emerging shoots arise from the base of older pseudo-stems. At growing stage, leaves were in alternate, linear-lanceolate, sheathed (3.2 cm), smooth, green, measuring 7.2 cm x 1.3 cm with sub-obtuse tip. Inflorescence were 3–4 per plant, un-branched (no rachis) raceme, peduncle with deep purple colour measuring short 0.47 cm embedded with base in translucent embricate sheaths. Pedicel is terete, smooth, deep purple colour measuring 3.6 cm x 0.25 cm with floral bracts measuring 2 cm x 0.8 cm. The floral bracts were observed to be scarious having smaller sized bracts inside measuring 1 cm x 0.5 cm.

Flowers sized ca., 3.5 cm x 6.0 cm, fragrant with shining purple sepals and petals (Fig. 1, b–2). The dorsal and lateral sepals were acute tipped measuring 3.85 cm x 1.0 cm, oblong-lanceolate shaped with moderately deep purple colour (RHS-N78 B). The basal end of lateral sepal in pair was adnate to the foot of column to form short conical blunt mentum. The petals were recorded a size of 3.6 cm x 2.1 cm, ovate-oblong shaped with deep purple colour with pale shading at base. The lip size recorded 3.2 cm x 1.8 cm having presence deep purple maroon blotch (RHS-N78 A) at centre surrounded by white disc. The trumpet shaped lip with convolute at the base with

Table 1. Major morphological characters of the collection, *D. lituiflorum* Lindl.

S. No	Characters	Observation
1	Plant height	37 cm
2	Number of leaves (new sprouted)	09
3	Leaf shape	Oblong-lanceolate, obtuse tipped
4	Leaf length	7.2 cm
5	Leaf width	1.3 cm
6	Rachis length	absent
7	Peduncle	Very short, with large bracted
8	Inflorescence type	Un-branched raceme
9	Position of flowers	Upper nodes
10	General appearance flower	Loose, spreading, incurved
11	Flower length in front view	3.5 cm
12	Flower breadth in front view	6.0 cm
13	Shape of sepals & petals	Oblong-lanceolate, acute tipped
14	Sepals size	3.85 cm x 1.0 cm
15	Color of sepals	Moderate deep purple color (RHS N78 B) #
16	Petal size	3.6 cm x 2.1 cm
17	Color of sepals	deep purple color (RHS N78 B) with pale at base #
18	Lip size	3.2 cm x 1.8 cm
19	Anterior lobe of lip	absent
20	Lip colour of throat	Deep purple botch (RHS N78 A) #
21	Column length	0.4 cm
22	Column colour of anther cap	Deep purple
23	Lip callus	present
24	Inflorescence emergence	February
25	Days to 1 st bud opening from inflorescence emergence	39 days
26	Days to 70 per cent flower withering from bud opening	21 days
27	Days to complete flower withering from bud opening	28 days

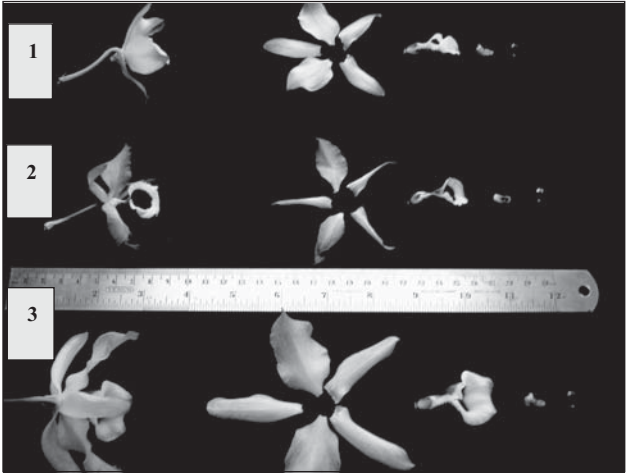
indicates RHS (Royal Horticultural Society) colour charts for verification

Table 2. Comparative description of *D. lituiflorum* Lindl and *D. nobile* Lindl. for identification and differentiation

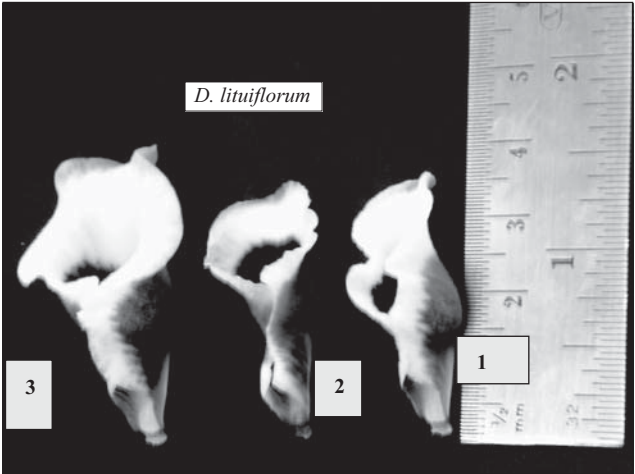
Characters	<i>Dendrobium lituiflorum</i> Lindl.	<i>Dendrobium nobile</i> Lindl.
Habitat	Epiphyte	Epiphyte or lithophyte
Pseudo-stem	Slender, long, pendulous, circular at base, more in number, white coloured, 15-24 nodes and nerved	Thicker, clustered, forming large clumps, laterally compressed, 7-12 nodes, thick at middle with tapering at ends, grooved and yellow with age, covered with old leaf sheath or blade
Leaves	Alternate, linear-lanceolate, leaf sheath with brownish spots	Distichous, oblong, apex unequally lobed
Inflorescence	Lateral, emerges from below nodes	Lateral, emerges from nodes in fascicles of 1-4 flowers below leaves
Rachis	Generally absent	Present
Peduncle	Very short covered with embricate sheaths	Short, terete, embedded in embricate sheaths
Pedice	3 cm long, dark purple	> 3.5 cm, whitish-purple
Flowers	Moderately deep purple, racemose, fragrant	Whitish-purple, sub-racemose, non-fragrant
Sepals	Thin, papery, deep purple to pale at base, spreading, 6-7 nerved,	Thin, fleshy, purplish-white, spreading, dorsal sepal erect
Petals	Oblong-lanceolate, broader, 4-5 nerved	Elliptic-ovate, broader, obtuse, 5-nerved
Lip	Curved like trumpet shaped, deep purple maroon blotch (RHS-N78 A) at center surrounded by white disc, mouth arbuticular, claw broad, convolute over column	Broadly ovate-oblong, base funnel shaped, lower half incurved, terminal half culcullate, acuminate tip, claw narrow
Column	Deep purple colour	Greenish colour
Mentum	Conical blunt	Broadly blunt



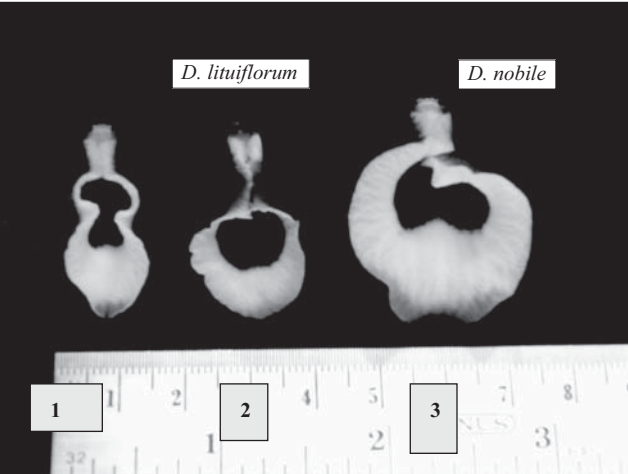
(a) Comparison of flowering plant of *D. lituiflorum* Lindl with *D. nobile* Lindl.



(b) Flower configuration of *D. lituiflorum* Lindl (2) and *D. nobile* Lindl. (1-Sikkim collection, 3-Arunachal Pradesh collection)



(c) Longitudinal view of lip of *D. lituiflorum* Lindl (2) and *D. nobile* Lindl. (1-Sikkim collection, 3-Arunachal Pradesh collection)



(d) Anterior view of lip of *D. lituiflorum* Lindl (2) and *D. nobile* Lindl. (1-Sikkim collection, 3-Arunachal Pradesh collection)

Fig. 1. Comparison of flowering plants of *D. lituiflorum* Lindl with *D. nobile* Lindl. with their flower configuration and lip differences

heavy purple transverse stripes having disc of limb/mouth orbicular in shape helped to clearly distinguish the species (Fig. 1, c and d). The column was small with purple colour serves as best phonological marker for quick identification (Fig. 1, b–2). The flowering traits like spike initiation, days to flower bud initiation, days to 1st flower opening (39 days) and days to 1st flower withering from bud opening (21 days) showed consistency for the two years.

The deciduous nature of pseudo-stems while flowering, dominant shining purple colour of sepals and petals, short peduncle traits and shape of lip from base helps for identification of this species. The shining purple colour of both sepals and petals look-alike flower colour and size of noble orchid (*Dendrobium nobile* Lindl.) are attributes of this species, that can be utilized in breeding programmes for developing new hybrids. This species can also be used as in-door planting and live hanging pots apart from *ex situ* conservation.

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geographical region of lower Khasi hills of Meghalaya, which we collected during 2nd Horticultural Congress (April 2007) held at Umiam, Meghalaya. Authors also thank Shri Dawa Bhutia and Shri Kunja Bihari Gupta for proper maintenance and multiplication of this species at NAGS.

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