

Traditional Crop Diversity in Kumaon Himalaya of Uttarakhand State – A Case Study

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Traditional crop diversity plays an important role for the sustenance of human life. In hilly areas, climatic conditions vary from place to place and the adaptability of crops also varies. In such complex system of hill farming, number of crops and their numerous varieties are one of the main components of sustainable development. These diverse crop groups and varieties play key role in diversifying the agriculture as well as ensuring food security. The present study was focused on the adaptability of crops and their varieties (both traditional and improved) on the parameters like altitude and irrigation water in the Kumaon Himalaya. Impact of irrigation on the loss of crops diversity and selection procedures of varieties is also discussed.

Key Words: Traditional crop diversity, Sustainable development, Kumaon Himalaya

Introduction

The Kumaon Himalaya lies between 28°29' to 30°41' N latitude and 79°32' to 81°11' E longitude. It is bordered by Kali river in the east towards Nepal and the districts Pauri and Chamoli of Garhwal region in the West. Tibet lies on the North and the Terai in the South. Physiographically, Kumaon Himalaya can be divided into the *Terai Bhabar*, the Sub-Himalayas or the *Sivaliks* or the foot hills, the lower Himalayas and the higher Himalayas. The higher Himalayan zone has a glaciated topography with many moraines, above 3000 m with ranges averaging 1850 msl and a width of above 50 km, it is highly rugged with difficult precipitous slopes. The lower Himalayas extend from West to East and are composed of granite and crystalline rocks. The sub-Himalayas or the *Sivalik* hills or the foot hills with an average height of 1225 msl is a chain of small hills. The elevation of *Bhabar* ranges between 300-600 msl from South to North.

The total geographical area of Kumaon region is 21,038 msl km of which 64.03% is under forest cover followed by crops 11.34%, meadows 4.67% and horticulture land 4.36%. The rest is under agricultural wasteland (1.95%) and wasteland (6.10%). The per capita agricultural land holding is very small (0.19 ha) in the entire Kumaon Himalaya. Around 21% area is irrigated and rest 79% is rainfed (Mehta, 2003). The farming system of the region is complex and interwoven with the natural resources like crops, livestock and forests. The great variation in topography and socio-economic factors has resulted in a diversity of farming system and mosaic

situations. Agriculture still remains the mainstay of the livelihood of the local communities in the hill region. This zone is mainly inherited by *Kumaonis* and a few tribal communities, viz., *Tharus*, *Boxas* and *Bhotiyas* residing in far flung areas, which are rich in their traditional cultures.

The entire Himalayan region is considered as one of the well known centres of crop diversity (Jain and Sastry, 1978; Arora, 1990; Khoshoo, 1992). A number of crops have been introduced in this region by early settlers. The introduction of new crops has created a huge diversity in crop plants, maintained through a variety of crop compositions, supported by enormous variations in the edaphic, topographic and climatic conditions (Pant, 2002). This vast wealth of crops and their numerous local varieties provide the subsistence needs to the local communities. These crops and their local varieties have become the integral part of socio-economy and culture. Growing a large number of crops and their varieties by an individual farmer is considered a symbol of respect in the region. Such kind of social respect encourages the farmers to grow and maintain more number of crops. '*Barahanaja*' (growing twelve crops together in a single field) was also once a very old tradition in the region to maintain the crop diversity. But due to demographic pressure and other socio-economic factors as well as industrial development in plains, farmers of this region have also started to adopt modern varieties and growing them by application of chemical fertilizers, pesticides, herbicides, etc. This has led to the erosion of traditional cropping system and crop genetic diversity in the region.

The Gazetteer of North-western provinces has mentioned a good account of crop plants cultivated in this Himalayan region and some varieties of paddy and wheat grown during the contemporary period (Atkinson, 1982).

A considerable amount of diversity in crops such as finger millet, wheat, paddy, etc. exists in this region. A large number of individual crop varieties were found suitable for various eco-niches (Tiwari and Das, 1995). Apart from the native crops, many useful crop species were also brought from outside by the inhabitants of the Kumaon hills. Important crops among these are foxtail millet, proso millet, buckwheat, horsegram, blackgram, greengram, cowpea, lablab bean, lentil, potato, maize, tomato, groundnut, *Cyclanthera pedata*, chilli, lai, etc. These crops have been adapted well in the climatic conditions of this region (Pant, 2002). Recently, Jardhari and Kothari (1995) and Maikhuri *et al.* (2001) have given an account of crop genetic resources of Garhwal hills and shown their concerns towards conservation of traditional crops and their landraces.

So far, very few studies have been conducted on the aspect related to availability of crops plants along the altitudinal gradients. Most of the workers have studied variation in availability of crops. Variation available in crop plants along different altitudinal zones are attributed to the factors such as environments, biodiversity conditions, temperature, amount of precipitation, soil moisture, thermal ranges, etc. (Maikhuri *et al.*, 1996a; 1996b; Palni *et al.*, 1998; Whittaker, 1970; Brookfield, 1973; Bailey, 1958 and Kawakita, 1956).

In the present study efforts have been made to have an idea about the availability of crop diversity along the altitudinal gradient and to find out the reasons of loss of crop diversity in different altitudes of the Kumaon hills.

Materials and Methods

In the present study, data were collected from primary sources with the help of a planned and structured interview schedule. Farmers/respondents were randomly selected from all the 33 development blocks of five districts (Nainital, Champawat, Almora, Bageshwar and Pithoragarh). Three villages were randomly selected from each development block. In each selected village, 5% households were randomly selected for interview. Lottery system was adopted for randomization. Thus, a total of 298 respondent farmers were sampled from 99 villages of 33 development blocks in five districts of Kumaon hills (Table 1). The respondents were interviewed

Table 1. District-wise number of development blocks, villages and respondents of the study

S.No.	Districts	No. of development blocks	No. of villages	No. of respondent households
1	Almora	11	33	100
2	Bageshwar	3	9	32
3	Champawat	4	12	31
4	Nainital	7	21	63
5	Pithoragarh	8	24	72
Total		33	99	298

thoroughly and their statements were recorded in the interview schedule. Thus, a multi-stage sampling method was employed for this study. The altitude of randomly selected villages were recorded by using Global Positioning System (GPS) instrument. During the survey of the region, observation method of data collection was also employed. A non-participant observation method was used to note down the availability of crop plants in the region.

Results and Discussions

The farming communities were dependent on a variety of crop plants available in the region for subsistence as well as to sustain their life. The number of crops grown in the entire Kumaon Himalaya were large. On the basis of their utility, these were divided into six major crop groups. There were 76 crops grown in the entire Kumaon hills. Maximum number of crops grown were under the category of vegetables (37) followed by pulses (12), cereals and pseudocereals (8), millets (7) and 6 each in oilseeds and spices (Table 2). In the cultivation system of Himalayan region, altitude plays an important role. The maximum number of crop plants (66) were being grown by the farmers in the mid-hills between 1000-2000 msl, while the minimum number of crops (39) are being grown in the higher hills above 2000 msl and followed by 44 crops in the foot hills upto 500 msl (Table 3).

Because of great variation in the topography, climatic conditions, agro-ecosystem, availability of natural resources and socio-economic and cultural dimensions in Kumaon hills, the farmers are bound to have choice to grow varieties of each crop in different agro-ecosystems to ensure production for subsistence. The number of traditional and high yielding varieties (HYVs) of major crops grown by farmers along the altitudinal gradients are of paramount importance in view of subsistence production.

Table 2. Availability of agricultural crops in the Kumaon hills

S.No.	Crop group (Nos.)	Name of crops	Percentage (%)
1.	Cereals and Pseudocereals (08)	Amaranth (<i>Amaranthus frumentacea</i>), Amaranth (<i>A. oleracea</i>), Barley (<i>Hordeum vulgare</i>), Barley (<i>H. himalensis</i>), Buckwheat (<i>Fagopyrum esculentum</i>), Buckwheat (<i>F. tataricum</i>), Maize (<i>Zea mays</i>), Paddy (<i>Oryza sativa</i>), Wheat (<i>Triticum esculentum</i>)	10.52
2.	Millets and minor millets (07)	Barnyard millet (<i>Echinochloa frumentacea</i>), Barnyard millet (<i>E. crusgalii</i>), Finger millet (<i>Eleusine coracana</i>), Foxtail millet (<i>Setaria italica</i>), Pearl millet (<i>Pennisetum typhoides</i>), Proso millet (<i>Panicum miliaceum</i>), Sorghum (<i>Sorghum bicolor</i>)	9.22
3.	Vegetables (37)	Aerial yam (<i>Dioscorea bulbifera</i>), Bell pepper (<i>Capsicum annum</i>), Bitter gourd (<i>Momordica charantia</i>), Bottle gourd (<i>Lagenaria sicerarea</i>), Brinjal (<i>Solanum melongena</i>), Cabbage (<i>Brassica oleracea</i> var. <i>capitata</i>), Carrot (<i>Daucus carota</i>), Cauliflower (<i>B. oleracea</i> var. <i>botrytis</i>), Chenopod (<i>Chenopodium album</i>), Chow-chow (<i>Sechium edule</i>), Colocasia (<i>Colocasia esculenta</i>), Colocasia (<i>C. roxburghii</i>), Cucumber (<i>Cucumis sativus</i>), Elephant ear cabbage (<i>Brassica juncea</i> var. <i>rugosa</i>), Elephant yam (<i>Amorphophalus campanulatus</i>), Faba bean (<i>Vicia faba</i>), Fenugreek (<i>Trigonella foenumgraecum</i>), French bean (<i>Phaseolus vulgaris</i>), Jackfruit (<i>Artocarpus heterophyllus</i>), Lablab bean (<i>Lablab purpureus</i>), Lepidium (<i>Lepidium sativa</i>), Okra (<i>Abelmoschus esculentus</i>), Onion (<i>Allium cepa</i>), Potato (<i>Solanum tuberosum</i>), Pumpkin (<i>Cucurbita moschata</i>), Pumpkin (<i>C. pepo</i>), Radish (<i>Raphanus sativus</i>), Ridge gourd (<i>Luffa acutangula</i>), Snake gourd (<i>Trichosanthes anguina</i>), Spinach (<i>Spinacea oleracea</i>), Sponge gourd (<i>Lufa cylindrica</i>), Sweet gourd (<i>Cyclenthera pedata</i>), Tomato (<i>Lycopersicon esculentum</i>), Tree tomato (<i>Cyphomendra betacea</i>), Turnip (<i>Brassica rapa</i>), Waxgourd (<i>Benincasa hispida</i>), Yam (<i>Dioscorea sagittata</i>)	48.69
4.	Pulses (12)	Blackgram (<i>Vigna mungo</i>), Chickpea (<i>Cicer arietinum</i>), Cowpea (<i>Vigna anguiculata</i>), Green gram (<i>V. radiata</i>), Horsegram (<i>Macrotyloma uniflorum</i>), Lentil (<i>Lens culinaris</i>), Pea (<i>Pisum sativum</i>), Pea (<i>P. sativum</i> var. <i>arvens</i>), Pigeon pea (<i>Cajanus cajan</i>), Rice bean (<i>Vigna umbellata</i>), Soybean (<i>Glycine max</i>), Soybean (<i>Glycine max</i>)	15.79
5.	Oilseeds (06)	Brown sarson (<i>Brassica juncea</i> var. <i>brown sarson</i>), Groundnut (<i>Arachis hypogaea</i>), Linseed (<i>Linum usitatissimum</i>), Perilla (<i>Perilla frutescens</i>), Sesame (<i>Sesamum indicum</i>), Yellow sarson (<i>Brassica juncea</i> var. <i>yellow sarson</i>)	7.89
6.	Spices and condiments (06)	Chilli (<i>Capsicum annum</i>), Coriander (<i>Coriandrum sativum</i>), Garlic (<i>Allium sativum</i>), Ginger (<i>Zingiber officinalis</i>), Hemp (<i>Cannabis sativa</i>), Turmeric (<i>Curcuma longa</i>)	7.89
Total (76)			100.00

Table 3. Altitude-wise crops grown by farmers of Kumaon for subsistence

S.No.	Crop groups	Altitude-wise No. of crops grown (Altitude in metres)				
		Up to 500	500-1000	1000-1500	1500-2000	2000-2500
1.	Cereals and pseudocereals	4	4	4	6	7
2.	Millets and minor millets	1	5	5	6	3
3.	Vegetables	26	33	36	32	17
4.	Pulses	5	9	9	9	5
5.	Oilseeds	3	6	6	6	2
6.	Spices and condiments	5	6	6	6	5
Total number of crops		44	63	66	65	39

The data revealed that the farmers in the Kumaon region were still growing a large number of traditional crops in their land holdings. The number of traditional crops were more in comparison to high yielding varieties. The farmers of lower altitude areas were mostly dependent upon high yielding varieties. With the increasing elevation, the number of traditional crops and their varieties also increase up to a certain altitude. In the cereal group, the number of crops were few, but number of

varieties in a crop were quite large. In case of paddy, more than one hundred landraces varieties are grown by farmers (Table 4 and 5). Likewise, wheat and finger millet also had many landraces/varieties under cultivation. In mid-hills also, number of crops and folk varieties of these crops were more. In the lower and higher hills, less number of traditional varieties were grown by the farmers in comparison to mid-hills. However, high yielding varieties were more in lower hills, followed by mid and

Table 4. Altitude-wise availability of number of traditional/folk varieties of some major crops in Kumaon hills

S.No.	Crops	No. of folk varieties at different altitudes (m asl)				
		Up to 500	500-1000	1000-1500	1500-2000	2000-3000
1.	Paddy (<i>Oryza sativa</i> L.)	0	18	61	52	27
2.	Wheat (<i>Triticum aestivum</i> L.)	0	5	10	14	13
3.	Finger millet (<i>Eleusine coracana</i> (L.) Gaerth.)	0	5	15	15	15
4.	Maize (<i>Zea mays</i> L.)	0	1	4	5	2
5.	Barnyard millet (<i>Echinochloa frumentacea</i> L.)	1	2	3	3	3
6.	Barley (<i>Hordeum vulgare</i> L.)	1	1	1	3	3
7.	Cowpea (<i>Vigna unguiculata</i> L.)	—	2	3	5	3
8.	Horsegram (<i>Macrotyloma uniflorum</i> Lam.)	—	2	2	2	2
9.	Black seeded soybean (<i>Glycine max</i> (L.) Merrill)	—	2	4	5	2
10.	Black gram (<i>Vigna mungo</i> (L.) Hepper)	1	1	2	2	2
11.	French bean (<i>Phaseolus vulgaris</i> L.)	—	2	3	4	4
12.	Pea (<i>Pisum sativum</i> L.)	0	2	2	3	1
13.	Lentil (<i>Lens culinaris</i> Medikus)	—	2	2	3	—
14.	Brinjal (<i>Solanum melongena</i> L.)	0	2	2	2	2
15.	Bottle gourd (<i>Lagenaria sicerarea</i> Molina (Standl. Ex.))	0	3	3	3	—
16.	Pumpkin (<i>Cucurbita moschata</i> Duch ex. Poir)	1	1	2	3	1
17.	Chillies (<i>Capsicum annuum</i> L.)	0	1	3	3	—
18.	Ridge gourd (<i>Luffa acutangula</i> (L.) Roxb.)	1	2	2	2	2
19.	Mustard (<i>Brassica juncea</i> L.)	2	2	2	2	2
20.	Potato (<i>Solanum tuberosum</i> L.)	—	2	2	3	1
Total		7	58	128	134	85

Table 5. Traditional varieties of major crops grown in Kumaon Himalaya

Crop	Name of traditional varieties
Paddy (<i>Oryza sativa</i> L.)	Akadi, Anjan, Askotia, Bagudhan, Bhatusanw, Bhadgar, Bhuria, Binduli, Bakul, Bakudhan, Bamkua, Banpas, Bantiya, Basmati, Boran, Chamadia, Chauria, Chhotia/Chhoti, Chinbhuri, Dalbadal, Dangazai, Dan naulia, Dansal, Dhania, Dhang, Dhaulia, Dotiyali, Dudh, Famkua, Gadalu, Gajazi, Gazala, Ghesu, Gid, Goldhan, Hat, Hayal, Jamai/Jamal, Janoli, Jawaan, Jhadua, Jhukai, Jiruli, Jolia, Jorhat, Jungledhan, Jungloi, Jyoli, Kaladhan, Kalasontu, Kalthunia, Kalisal, Kalijamali, Kalpara, Kapkoti, Kashmiri, Katyuri, Khardudh, Khasiyara, Khozia, Kimiti, Laldhan, Lali, Lahangi, Lathait, Lohin, Madguri, Maila, Makhur, Maltiya, Mangraj, Musmad, Masur, Nalu, Nandani, Nandhan, Naulia, Nauldudh, Paktauli, Parange, Parvati, Patoli, Pingau, Pyolia, Rajdhan, Rajmati, Rajula, Rakesia, Ramgarhi, Ram manua, Ram Sita, Rati, Rokhiyal, Sal, Sanwdhan, Simanjari, Silk, Sirmodia, Sokia, Sita, Sonti, Sontu, Sudia, Sunkhar, Suntola, Taoli, Teli, Thai, Thapachini, Thulbasmati, Timilia, Ud, Uskar.
Wheat (<i>Triticum aestivum</i> L.)	Bhati, Chanosi, Chotia safed, Chyud, Dapati, Dhang, Dhaulia, Dudgyun, Doldakhani, Dudh, Geruwa, Intor, Jhusia, Kanyari, Kavjhusi, Lalgeyun, Lalnoi, Mangraje, Munar, Naulia, Pothi, Rata, Syatgyun.
Finger millet (<i>Eleusine coracana</i> (L.) Gaerth.)	Adagdali, Ageti, Bagadi, Basuli, Bhati, Bhuria, Chhahmasi, Chhapariya, Chhiptalbhati, Dhuni, Dotiyali, Garhwali, Golmanua, Gunari, Jhakarua, Jhumaria, Kalamandua, Kataki, Kavnoi, Kodi, Kodya, Kunwi, Lalmanua, Lampadaliya, Lohariya, Lumadia, Maneri, Mutkiya, Nangihuni, Parvati, Pichheti, Putkiya, Pyoli, Sodia, Surai, Timasia.
Maize (<i>Zea mays</i> L.)	Angulighoga, Dhawal, Gorakhamakka, Lal, Pilimakki, Murali, Timasia.
Barley (<i>Hordeum vulgare</i>)	Kala jau, Safed jau, Uwa (naked)
Barnyard millet (<i>Echinochloa frumentacea</i> L.)	Bada, Chhahmasia, Chhotia, Ganaru, Manaru, Jhakru
Cowpea (<i>Vigna unguiculata</i> L.)	Kala, Safed, Lal, Chitkavari, Bhara.
Horsegram (<i>Macrotyloma uniflorum</i> Lam.)	Lal, Dhau, Bhura, Kala
Black seeded soybean (<i>Glycine max</i> (L.) Meritl.)	Kala chhota, Kalabada, Lal, Bhura, Hara
Black gram (<i>Vigna mungo</i> (L.) Hepper.)	Bhura, Kala, Hara
French bean (<i>Phaseolus vulgaris</i> L.)	Lal, Safed, Bhura, Kala, Chitkavare
Pea (<i>Pisum sativum</i> L.)	Safed, Cream, Bhure
Lentil (<i>Lens culinaris</i> Medikus)	Kala, Bhura, Cream
Brinjal (<i>Solanum melongena</i> L.)	Lamba kala, Lamba hara, Gole
Bottle gourd (<i>Lagenaria sicerarea</i> Molina)	Lamba, Gole, Madhyam chitkavara
Pumpkin (<i>Cucurbita moschata</i> Duch ex. Poir)	Lamba kadu, Golkadu, Nepali kadu
Chillies (<i>Capsicum annuum</i> L.)	Patali lal, Pili, Chhotigole
Ridge gourd (<i>Luffa acutangula</i> (L.) Roxb.)	Lamsi torai, Chhoti torai
Mustard (<i>Brassica juncea</i> L.)	Kali sarson, Pili sarson
Potato (<i>Solanum tuberosum</i> L.)	Gwaldam local, Lal alu, Safed alu, Naming, Dharchula local, Pahari gole (Gola)

high hills. Overlapping of crop varieties in different altitudinal zones was also observed (Table 6).

The study indicated that cultivation system in the Kumaon hills is dominated by traditional crop varieties. In all, 76.85% farmers were growing the age old folk varieties, while 23.15% farmers were growing high yielding varieties (Table 7). It is worth mentioning that the percentage of cultivation of traditional crop varieties was the lowest (30%) in the lower altitudinal zone (upto 500 m) and highest (91.25%) in the high altitudinal zone (2000-3000 m). With the increase in altitude, the number of traditional crop varieties also increased (Table 7). Contrary to this, the reverse pattern was observed in the use of HYVs. There was a high degree of positive correlation between the altitude and cultivation of traditional crop varieties (Table 7).

In the traditional agricultural system, seeds are kept and maintained by farmers themselves for next crop season, failing which, they arrange them from other sources. In the study area, the sources of seeds were local farmers and relatives, local market and government agencies (Table 8). It was evident that a large number of farmers (74.16%), still arranging the seeds from local/neighbouring farmers and relatives. Farmers also depended on local market for seeds as 17.12% seeds were procured from market sources. Government agencies had a very little role (8.72%) in distribution of seeds to the farmers in the region.

It is evident from Table 9 that with the increase in altitude, the irrigation facilities decreased. The availability of irrigation water varied, significantly ranging from 5% (>2000 msl) to 80% in the lower part of foot hills (upto 500 msl). Accordingly, introduction and farming of HYVs decreased in the entire hill zone. In the foot hills upto 500 m asl 80% HYVs and above 2000 msl 8.75% HYVs were big. A negative correlation was observed between the altitude and availability of irrigation water. The same correlation was also seen between altitude and cultivation of HYVs. There was a high degree of positive correlation between availability of irrigation water and cultivation of HYVs.

In terms of loss of agrobiodiversity, it was evident that the availability of irrigation water forced the farmers to replace the traditional crop varieties with the HYVs. The magnitude of loss of agrobiodiversity from the lower altitude to higher altitudes is shown in Table 9).

In the Kumaon hills, farmers inhabiting in different altitudinal zones cultivated different crops. The number

of crops also varied with the increase of elevation. Maximum number of crops were grown in the elevation zone between 500-1500 m asl. The variation in number of crops may be because of different factors such as environmental, bio-climatic, economic and cultural conditions (Maikhuri *et al.*, 1996a, 1996b and Palni *et al.*, 1998). Distribution of each species depends on its mode of genetic combination, physiology and life cycle pattern and its relationships to both physical environment and interaction with other species. Hence, the distribution of any two species may not be similar. The broadly overlapping and scattered centres of plant population along a gradient imply that most communities integrate continuously along environmental gradients, rather than forming distinct, clearly separate zones (Whittaker, 1978).

In the present study, the information was categorized as per the crop, viz., cereals and pseudocereals, millet and minor millets, vegetables, pulses, oilseeds and spices and condiments. The vegetable group contained largest number of crops followed by pulses, cereals and pseudocereals, respectively (Table 2). Further, the data were categorized according to different elevations. Maximum number of crops were grown in mid-hill zone between 1000-2000 msl (Table 3).

Mid-hills are the repository of crops and their numerous folk varieties, because of availability of water for irrigation as well as rainfall. In the rainfed condition, a large number of crops and varieties were grown in mixed cropping pattern in order to facilitate food security of farm households. Climatically, the mid-hills are neither too warm nor too cold, which suits to cultivation of more number of crops as compared to high hills and lower hills.

Other studies also supported our findings regarding availability of crop/plant species in different altitudinal zones attributed to micro-level environment and bio-climatic variables (temperature, precipitation, soil, moisture, etc.). The thermal ranges affect crop ranges in the hilly slopes (Brookfield; 1973; Bailey, 1958; 1960; 1977; Kawakita, 1956).

At present, traditional as well as improved varieties are under cultivation in Kumaon hills. Maximum number of traditional varieties are being grown in mid-hills between an altitude of 1000 and 2000 msl (Table 4). However, high yielding varieties (HYVs) were also grown by the farmers, but these were restricted to lower hills and valley zones only because of availability of irrigation water.

Table 6. Number of high yielding varieties grown in different altitudes in Kumaon hills

S.No.	Crops	No. of HYVs at different altitudes (m amsl)				
		Upto 500	500-1000	1000-1500	1500-2000	2000-3000
1	Paddy (<i>Oryza sativa</i> L.)	7	9	7	4	0
2	Wheat (<i>Triticum aestivum</i> L.)	5	4	3	0	0
3	Maize (<i>Zea mays</i> L.)	2	0	0	0	0
4	Soybean (<i>Glycine max</i> (L.) Merrill.)	2	2	1	1	1
5	Cowpea (<i>Vigna unguiculata</i> L.)	2	2	0	0	0
6	Black seeded soybean (<i>Glycine max</i> (L.) Merrill)	1	1	0	0	0
7	Lentil (<i>Lens culinaris</i> Medikus)	1	1	0	0	0
8	Brinjal (<i>Solanum melongena</i> L.)	1	1	0	0	0
9	Chillies (<i>Capsicum annum</i> L.)	1	1	0	0	0
10	Okra (<i>Abelmoschus esculentus</i> L. Moench.)	2	2	0	0	0
11	Potato (<i>Solanum tuberosum</i> L.)	0	0	0	2	2
Total		24	23	11	7	3

Table 7. Types of varieties grown by the respondent farmers in different altitudinal zones of Kumaon hills

S.No.	Altitude in metres	Type of varieties grown by farmers			
		Traditional varieties		High yielding varieties (HYVs)	
		No. of farmers	Percentage (%)	No. of farmers	Percentage (%)
1	Upto 500	1.5	30.00	3.5	70.00
2	500-1000	18	45.00	22	55.00
3	1000-1500	64	70.33	27	29.67
4	1500-2000	109	90.17	13	9.83
5	2000 and above	36.5	91.25	3.5	8.75
Total		229	76.85	69	23.15

Calculated chi-square value is 39.165 and table value at degree of freedom (d.f.) (r) = 4 is 9.488 at 5% level. Calculated value is > table value. Hence, the data is highly significant.

Table 8. Sources of seed material of the local farming communities of Kumaon Himalaya

S.No.	Sources of seed material	No. of farmers	Percentage (%)
1.	Local farmers and relatives	221	74.16
2.	Local market	51	17.12
3.	Government agencies	26	8.72
Total		298	100.00

Easy accessibility to improved and new technologies has changed the farming system from subsistence based to market oriented. The linking of rural areas with each other by the road transport also led to the higher degree of commercial farming. The cultivation of high value cash crops replaced low value subsistence crop cultivation in most of the areas. The subsistence crop farming continued only in marginal land on steep slopes, where irrigation facility was meagerly available (Jodha 1992). In this region, where irrigation facility is available, the farmers of villages of nearby markets grow the crops as per the needs of market, especially improved vegetables, by using external inputs. Hence, in lower altitude areas, the availability of irrigation and transport facilities encouraged the farmers to grow HYVs as compared to

Table 9. Availability of irrigation water and cultivation of high yielding varieties (HYVs) in different altitudinal gradients in Kumaon hills

Altitudinal gradients (m)	Availability of irrigation water (%)	Cultivation of HYVs (%)
Upto 500	80.00	70.00
500-1000	70.27	55.00
1000-1500	31.91	29.67
1500-2000	9.84	9.83
2000-2500	5.00	8.75

high altitude areas, where they faced adverse conditions and were bound to dwell upon subsistence agriculture containing good crop diversity of traditional varieties (Tables 7 and 9).

A steady shift from traditional agro-ecosystem to modern agro-ecosystem because of edaphic, topographic and climatic factors coupled with the tremendous selection pressure over centuries old cultivation system resulted into immense variations in traditional varieties suited to a particular area (Arora and Nayar, 1984). These varieties withstood the rigours of time, escaped the pressure of insect, pest, diseases and tolerated the adverse climatic conditions. They also possessed the desired agronomic

and genetic traits required to develop resistant varieties (Alteri, 1998; Anonymous, 1989; MC Neely *et al.*, 1990). However, the farmers of mid and high hilly areas were bound to cultivate maximum number of crops and their old traditional varieties. Change in traditional agro-ecosystem into modern agro-ecosystem and loss of agrobiodiversity was evident in the Himalayan region.

For traditional knowledge, women folk, old aged and illiterate people acquired good knowledge of crop varieties. In low input agriculture system, women had traditionally been the managers of germplasm (Sateesh, 1995). It was also observed in the hilly areas of Kumaon (Tiwari *et al.*, 1995). Women folk also played an important role in dissemination of the varieties (Ashby *et al.*, 1990). In ancient societies, old aged persons used to get respect because of knowledge, experience and legendary lore (Harlan, 1992). Due to long experience of cultivation of old traditional crops older generation acquired a lot of knowledge in comparison to younger generations. Modern literate society considers agriculture is meant for illiterate people. They are interested to seek off-farm jobs (Maikhuri *et al.*, 1996 a; Mulk, 1992).

The present study revealed that a large number of crops were grown in the Kumaon region. The adaptability of crops varied along the altitudinal zones. Farming communities were growing a large number of crops to fulfill their subsistence needs. Apart from a large number of crops, a large number of varieties of these crops were being grown in different types of soils, moisture regimes, eco-niches, altitudes, etc. Most of the crops grown in the entire hill region were traditional old varieties. These were very much suitable for production in adverse conditions also. These traditional crop plants and their varieties formed the base of subsistence for local inhabitants as well as for the sustainability in the production system. The cultivation of traditional crops and their varieties were the tools for on-farm/*in-situ* conservation of plant genetic resources in the region. It is noteworthy that the modernization of agriculture in the Central Himalaya is at the cost of the cultural heritage, which was preserved for centuries. In the valley areas, with availability of irrigation facilities, the farmers started cultivation of HYVs and pushed the traditional crops (millets, minor millets, coarse grain legumes, pseudocereals, etc.) towards marginal lands. With the marginalization and abandoning cultivation of traditional crops, farmers lost the unique wealth in the form of traditional knowledge associated with the cultivation of obsolete crops and varieties. In

addition, the region also lost the crop diversity as the farmers replaced their traditional varieties by growing HYVs. In the mid and high altitudes where crops are grown under natural precipitation regime, farmers should be encouraged to grow traditional cultivars. Keeping in view the natural and socioeconomic conditions, multi-disciplinary approach should be adopted to develop a viable farming system which could provide the food and economic security to the people of the region by using the local resources.

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Components of Genetic Variation in Yield Traits of Linseed (*Linum usitatissimum* L.)

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Ten diverse linseed parents were crossed in half diallel to estimate the components of genetic variation. It was revealed that non-additive genetic component contributed to the genetic expression of stem diameter, number of capsules per plant, number of tillers per plant, fibre strength and fibre fineness in both F_1 and F_2 generations. Some of the traits, viz., days to flower, plant height, technical plant height, days to maturity and fibre yield per plot displayed over dominance in the F_2 generation while days to maturity and fibre yield per plot expressed partial dominance in the F_1 generation.

Key Words: Sesame, Linseed, Genetic components, Seed yield, Oil content, Fibre yield

Introduction

The component analysis besides providing necessary information on the type of gene action governing different traits also determines the nature and magnitude of genetic variation present in the population and help in planning efficient breeding methodology. Various crop-breeding programmes are generally targeted to increase the productivity which requires consideration not only of yield but also of their components that have a direct or indirect bearing on economic yield. Breeders often select directly for seed and fibre yield to achieve yield improvement in linseed. The present study was therefore, undertaken with the objective to estimate the components of genetic variation for yield traits of linseed.

Materials and Methods

Ten parents of linseed having diverse geographical origin, viz., Shubhra (Mukta x K2), Garima (T-126 x Neelum), Shekhar (Laxmi-27 x EC1387), Janaki (New River x LC-216), J-23 (EC9882 x Heera), T 397 (T 491 x T-1193-1), Gaurav (Selection 3 x EC152), Belinca (Exotic Collection, Netherlands), Rasmi (Gaurav x Janaki), Nagarkot (New River x LC-216) were crossed in all possible combinations excluding reciprocals at CSA University of Agriculture and Technology, Kanpur, during *rabi* 2002. The 45 F_1 s, 45 F_2 s and 10 parents were sown in a Randomized Block Design with three replications having 10 m² plot size. Each plot had 6 rows of 5 m length with row to row distance of 30 cm. The observations were recorded for 13 traits, viz., days to flower, plant height (cm),

technical plant height (cm), days to maturity, stem diameter (mm), number of capsules per plant, number of tillers per plant, seed yield per plant (g), oil content (%), fibre length (cm), fibre strength (g/tax), fibre fineness (tax) and fibre yield per plot (kg). Components of genetic variation were worked out by following the approach of Hayman (1958).

Results and Discussion

The estimates of six genetic parameters, viz., D, H_1 , H_2 , F, h^2 and E along with their related statistics (Comstock and Robinson, 1948) are presented in Table 1.

The mean value of the degree of dominance (H_1/D)^{0.5} indicated over dominance for eight traits, viz., stem diameter, number of capsules per plant, number of tillers per plant, seed yield per plant, oil content, fibre length, fibre strength and fibre fineness in both F_1 and F_2 generations whereas, days to flower (50%), plant height, technical plant height, days to maturity and fibre yield per plot showed over dominance in F_2 generation only. Days to maturity and fibre yield per plot expressed partial dominance in the F_1 generation and significant h^2 for the characters also confirmed the importance of dominant gene action. Similar findings were reported by Swarnkar *et al.* (2005) and Polonetskaya *et al.* (2002) for plant height, days to flower, number of capsules per plant and number of tillers per plant. The proportion of genes with positive and negative effect ($H_2/4H_1$) was lesser compared to the theoretical value (0.25) in both F_1 and F_2 generations for all the characters, indicating that the positive and negative

Table 1. Estimates of genetic parameters $\hat{D}$, $\hat{F}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$, $\hat{E}$ and related statistics for 13 characters in 10 x 10 diallel cross of linseed

Genetic parameters and related statistics	Days to flower (50%)		Plant height		Technical plant height		Days to maturity		Stem diameter	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
$\hat{D}$	91.22	91.01**	326.95**3	26.30**	245.30**	245.12**	77.64**	77.77**	0.09 ±	0.09
	±5.70	±6.67	±14.71	±19.83	±8.62	±10.59	±5.33	±3.67	0.11	±0.06
$\hat{F}$	22.32	71.34*	21.83	124.43	40.88*	103.74*	12.79	51.87**	-0.12	0.32
	±13.15	±30.78	±33.94	±91.50	±19.90	±48.86	±12.30	±16.94	±0.26	±0.29
$\hat{H}_1$	66.70**	295.93**	168.95**	737.07**	149.90**	379.14**	47.60**	162.29**	1.18**	2.28**
	±12.13	±56.80	±31.31	±168.83	±18.36	±90.15	±11.35	±31.25	±0.24	±0.53
$\hat{H}_2$	51.31**	247.05**	134.39**	542.07**	126.38**	327.18**	35.61**	115.22**	0.98**	1.83**
	±10.31	±48.27	±26.61	±143.49	±15.60	±76.61	±9.65	±26.56	±0.20	±0.45
$\hat{h}^2$	2.05	40.81**	1.30	64.72*	33.37**	37.15**	0.46	22.17**	0.28*	0.09
	±6.90	±8.08	±17.81	±24.01	±10.44	±12.82	±6.46	±4.44	±0.14	±0.08
$\hat{E}$	1.10	1.31	1.62	2.27	1.83	2.01	0.50	0.37	0.03	0.03
	±1.72	±2.01	±4.43	±5.98	±2.60	±3.19	±1.61	±1.11	±0.03	±0.02
$(\hat{H}_1/\hat{D})^{0.5}$	0.85	1.80	0.72	1.50	0.78	1.24	0.78	1.44	3.56	4.92
$(\hat{H}_2/4\hat{H}_1)$	0.19	0.21	0.20	0.18	0.21	0.22	0.19	0.18	0.21	0.21
$[(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}/$	1.34	1.56	1.10	1.29	1.24	1.41	1.24	1.60	0.69	2.04
$[(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}]$										
$\hat{h}^2/\hat{H}_2$	0.04	0.17	0.01	0.12	0.26	0.11	0.01	0.19	0.28	0.05
r	-0.45	0.87	-0.88	-0.08	-0.14	-0.20	0.75	0.70	-0.30	0.58

Table 1. Contd.

Genetic parameters and related statistics	No. of capsules/plant		No. of tillers/plant		Seed yield/plant		Oil content		Fibre length	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
$\hat{D}$	504.26**	503.52**	0.38	0.38	0.92**	0.93**	1.53	1.54	33.76**	33.74**
$\hat{F}$	22.32	71.34*	21.83	124.43	40.88*	103.74*	12.79	51.87**	-0.12	0.32
$\hat{H}_1$	66.70**	295.93**	168.95**	737.07**	149.90**	379.14**	47.60**	162.29**	1.18**	2.28**
$\hat{H}_2$	51.31**	247.05**	134.39**	542.07**	126.38**	327.18**	35.61**	115.22**	0.98**	1.83**
	±10.31	±48.27	±26.61	±143.49	±15.60	±76.61	±9.65	±26.56	±0.20	±0.45
$\hat{h}^2$	2.05	40.81**	1.30	64.72*	33.37**	37.15**	0.46	22.17**	0.28*	0.09
	±6.90	±8.08	±17.81	±24.01	±10.44	±12.82	±6.46	±4.44	±0.14	±0.08
$\hat{E}$	1.10	1.31	1.62	2.27	1.83	2.01	0.50	0.37	0.03	0.03
	±1.72	±2.01	±4.43	±5.98	±2.60	±3.19	±1.61	±1.11	±0.03	±0.02
$(\hat{H}_1/\hat{D})^{0.5}$	0.85	1.80	0.72	1.50	0.78	1.24	0.78	1.44	3.56	4.92
$(\hat{H}_2/4\hat{H}_1)$	0.19	0.21	0.20	0.18	0.21	0.22	0.19	0.18	0.21	0.21
$[(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}/$	1.34	1.56	1.10	1.29	1.24	1.41	1.24	1.60	0.69	2.04
$[(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}]$										
$\hat{h}^2/\hat{H}_2$	0.04	0.17	0.01	0.12	0.26	0.11	0.01	0.19	0.28	0.05
r	-0.45	0.87	-0.88	-0.08	-0.14	-0.20	0.75	0.70	-0.30	0.58

Table 1. Contd.

Genetic parameters and related statistics	Fibre strength		Fibre fineness		Fibre yield/ plot	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
$\hat{D}$	6.18** ± 1.99	6.22** ± 1.09**	0.42** ± 0.07	0.41** ± 0.04	0.31** ± 0.02	0.31** ± 0.01
$\hat{F}$	-5.76 ± 4.59	-9.13 ± 5.04	0.20 ± 0.17	0.22 ± 0.17	0.02 ± 0.04	0.17* ± 0.06
$\hat{H}_1$	36.08** ± 4.23	78.23** ± 9.31	0.57** ± 0.16	1.15** ± 0.32	0.17** ± 0.04	0.57** ± 0.11
$\hat{H}_2$	28.14** ± 3.60	62.95** ± 7.91	0.50** ± 0.13	1.09** ± 0.27	0.14** ± 0.03	0.41** ± 0.09
$\hat{h}^2$	56.37** ± 2.41	19.32** ± 1.32	0.80** ± 0.09	0.07 ± 0.05	0.00 ± 0.02	0.01 ± 0.02
$\hat{E}$	0.81 ± 0.60	0.76** ± 0.33	0.00 ± 0.02	0.01 ± 0.01	0.01 ± 0.01	0.01 ± 0.00
$(\hat{H}_1/\hat{D})^{0.5}$	2.42	3.55	1.17	1.66	0.75	1.35
$(\hat{H}_2/4\hat{H}_1)$	0.20	0.20	0.22	0.24	0.19	0.18
$[(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}/$	0.68	0.66	1.53	1.38	1.08	1.50
$[(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}]$						
$\hat{h}^2/\hat{H}_2$	2.00	0.31	0.17	0.07	0.00	0.01
r	-0.76	-0.65	-0.44	-0.21	-0.08	0.33

r = correlation coefficient; * Significant at 5 per cent level; ** Significant at 1 per cent level.

alleles were distributed in a symmetrical manner across the parents.

The proportion of dominant and recessive genes was more than unity for most of the characters in both F_1 and F_2 generations, except for fibre length and strength which showed excess of dominant genes. However, this ratio was less than unity for stem diameter in F_1 denoting excess of recessive alleles in the parents.

The estimated ratio of (h^2/H_2) was less than unity for most of the characters in F_1 and F_2 generations except seed yield per plant in the F_1 generation. The characters having lesser value than unity indicated that at least one major gene was controlling their inheritance while the characters displaying values higher than unity were governed by more than one major gene. The coefficient of correlation (r) between parental order of dominance ($W_r + V_r$) and parental measurement (Y_r) was negative for most of the characters in both F_1 and F_2 generations. However, it was positive for days to maturity and number of capsules per plant. In F_1 generation, number of tillers per plant and in F_2 generation days to flower, stem diameter, seed yield

per plant and fibre yield per plot showed positive “ r ” values. The positive value of “ r ” indicated that negative genes were dominant for most of the traits. On the contrary, negative values showed that positive genes were mostly dominant for expression of these traits. The preponderance of non additive genetic variation for majority of characters may be exploited in breeding programme of linseed.

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Evaluation of Fodder Cowpea Genotypes for Tolerance to Semilooper (*Plusia nigrisigna* Wlk.)

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One hundred and sixty two accessions of fodder cowpea were screened against semilooper (*Plusia nigrisigna* Wlk.) under natural infestation conditions for four consecutive years. The mean incidence of semilooper ranged from 2.14-4.57% in promising genotypes EC24102-1 (2.14%), IL-1063 (3.89%), IL-05-08 (3.99%) and EC240884 (4.57%) as compared to 14.91-24.74% in the check lines. The entry EC24102-1 may be used as a donor for resistant breeding programmes.

Key Words: Cowpea, Pest tolerance, Semilooper

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] as a warm season annual leguminous fodder crop is mainly grown in Northern and Central India. It has a great potential for sustainable agriculture in marginal lands and semi arid regions of the country and is now rapidly spreading out to the entire country, because a number of new and better varieties have been released at national/zonal levels. The green cowpea fodder is rich in protein and forms an excellent mixture with maize, jowar, bajra and teosinte etc. considered as balance diet for animals for higher milk and meat production.

Cowpea is attacked by many insect-pests which are the principal limiting factor for its productivity throughout the country. The losses in green fodder yield were estimated to the tune of 30%. In Central India, the crop is severely damaged by the defoliator insects mainly, flea beetle (*Pagaria signata* Motsch), semilooper (*Plusia nigrisigna* Wlk.), tobacco caterpillar (*Spodoptera litura* F.) and various species of grasshoppers (*Hieroglyphus nigrarepletus* Bol., *Cantantopes pinguis* Stol., *Oedalius abruptus* Thun., *Acridida exaltata*, *Chrotogonus tachypterus* Blanch., *Atractomorpha crenulata* Fabr.). Among all these insects, maximum losses were caused by the semiloopers (Saxena *et al.*, 2002).

At present, the strategy is to develop pest and disease resistant varieties through breeding programmes (Hall *et al.*, 2003). Therefore, it is necessary to screen and identify insect-pest resistant genotypes, which could perform more or less uniformly under different environmental conditions (Graham *et al.*, 2003). Such genotypes are very useful for commercial fodder production.

The basic information on this important forage legume crop is meager. In view of this, the present investigation was envisaged to screen the forage cowpea genotypes against semilooper, which may be of great importance to initiate an effective crop improvement programme.

Materials and Methods

One hundred and sixty two accessions both exotic and indigenous were screened under natural infestation conditions for four years (2004-2007) in monsoon season against semilooper (*P. nigrisigna* Wlk.) at Central Research Farm of Indian Grasslands and Fodder Research Institute, Jhansi.

The accessions were kept unsprayed during the experiment. The materials were planted in Augmented Design with four control varieties, viz., Bundel lobia 1 (BL-1), Bundel lobia 2 (BL-2), UPC 5286 and local control (IGFRI 95-1). Two rows (3 m length) were assigned for each entry. Row to row distance was 60 cm, while distance between the entries was 100 cm. Out of 162 entries tested during 2004, 2005 and 2006, ten entries were selected and planted in replicated trial during *kharif* 2007.

Assessment of per cent leaf area damage was calculated using graph paper method. Ten central leaflets of fully opened leaf (third from top) from ten randomly selected plants were selected for injury estimation. The observations were taken three times (30, 45 and 60 days after sowing) during every crop season. The damage due to semilooper may be differentiated from the grasshopper damage as the semiloopers eat away the whole leaf area

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including the leaf veins and midribs while the grasshopper feed on the leaf lamina only.

The pest resistance percentage for entries was calculated using a formula derived from Abbott (1925).

$$\text{Pest resistance (\%)} = \frac{(\text{Pest incidence in check} - \text{Pest incidence in test entry})}{\text{Pest incidence in check}} \times 100$$

Pest Resistance/Susceptibility Rating (PRSR)	Pest Resistance (%)
1	100
2	99 to 75
3	74 to 50
4	49 to 25
5	24 to 10
6	9 to -10
7	-11 to -25
8	-26 to -50
9	> -50

The pest resistance percentage was then converted to 1 to 9 grading, based on the following scale and the low rating was the criteria of selection for resistant entries.

Results and Discussion

On the basis of data recorded during the year 2004 and 2005 the pest incidence of semilooper (*P. nigrisigna*) on test entries varied from 1.2 to 75.3 per cent as against 25%-30% in check lines (Table 1).

Seventy one lines were found better than the check. Out of which twenty six accessions were the best with the Pest Resistance/Susceptibility Rating value of 2. While 38 lines were at par with the check for the leaf area damage in the range of 22.5-32.6% (PRSR value of 5 and 6) and 53 lines were susceptible with leaf area damage in the range of 33.2-75.3% (PRSR value of 7, 8 and 9). The most susceptible lines were IL-2000-186, IL-99-38, IL-01-88, IL-05-29 and IL-390 (IL stands for Indigenous Legume).

The twenty six promising entries were selected for further testing in the year 2006. Entries EC24102-1, EC240884, IL-05-08 were found least susceptible (with 1.2-1.5% damage) followed by accessions IL-161-1, IL-05-12, IL-05-13 (damage in the range of 2.4-3.7%).

Observations recorded in 2006 (Table 2) showed that the leaf damage by semiloopers in entries ranged between 2.3-15.0 per cent (PRSR 2-5) compared to 15.8-24.3 per cent (PRSR 6 and 8) against check entries. A total of ten entries, viz., EC24102-1, EC240884, IL-05-08, IL-05-12, IL-05-13, IL-05-15, IL-55-1, IL-161-1, IL-1063, IL-1177-B were found superior with damage ranging between 2.3-4.2 per cent with PRSR value of 2. These entries were promoted for further screening for fourth and final year.

Table 1. Incidence of *P. nigrisigna* in evaluated gene pool of cowpea (2004 and 2005)

PRSR	Leaf area (damage %)	Accessions*
2	1.2-6.5	EC24102-1, EC48720, EC240564, EC240884, EC240887, EC244236, EC244979, IL-05-08, IL-05-12, IL-05-13, IL-05-14, IL-05-15, IL-156, IL-90, IL-55-1, IL-161-1, IL-178-4, IL-178-8, IL-179, IL-246, IL-380, IL-1063, IL-1177-B, IL-1182, IL-3152-1, IL-3178 (26)
3	8.1-14.7	EC240782, EC241023, IL-05-22, IL-99-98, IL-160-B, IL-177, IL-216-1, IL-370, IL-380-C, IL-867, IL-887, IL-893-1, IL-966, IL-1072-5, IL-2000-188, IL-2000-189, IL-4216, IL-14177-A (18)
4	15.1-22.4	EC240714, EC240809, EC240840, EC240898, EC244243, EC244310, IL-05-11, IL-05-17, IL-05-28, IL-99-69, IL-99-72, IL-99-73, IL-160-11, IL-181, IL-182, IL-380-A, IL-419-1, IL-449, IL-622, IL-792, IL-892, IL1093, IL-3177, IL-3192, IL-1471, IL-1721, IL-2000-183 (27)
5	22.5-26.7	EC120001, EC2440995, EC244217-1, EC244236, IL-05-06, IL-99-65, IL-144-A, IL-160-B, IL-812, IL-1050-3, IL-3138-B, IL-2000-182, IL-2000-187, IL-3155, IL-3168-A, IL-4170, IL-18720-A, BL-1(17+1)
6	27.0-32.6	EC240999, EC241037, EC244249, IL-05-03, IL-05-04, IL-05-07, IL-05-16, IL-05-18, IL-99-40, IL-160, IL-632, IL-893, IL-966-B, IL-1155-B, IL-1177, IL-3117, IL-3168-A, IL-2000-184, IVM-1, RA-1, RA-2, BL-2, UPC 5286, IGFR1 95-1 (21+3)
7	33.2-37.4	EC244223-1, EC24077, IL-05-23, IL-05-26, IL-921, IL-160-9, IL-210, IL-362, IL-1170-A (9)
8	38.0-44.2	EC240740, EC240800, IL-05-05, IL-05-19, IL-15-1, IL-99-2, IL-99-98-1, IL-131, IL-155, IL-372, IL-853, IL-892, IL-1057, IL-1156-1, IL-2000-179 (15)
9	45.3-75.3	EC240650, EC240842, EC244217, IL-01-88, IL-05-09, IL-05-21, IL-05-24, IL-05-25, IL-05-27, IL-05-29, IL-14, IL-99-34, IL-99-38, IL-99-171, IL-132, IL-153-1, IL-155-1, IL-160-A, IL-390, IL-416-4, IL-419-2, IL-886, IL-1014-1, IL-2000-178, IL-2000-180, IL-2000-186, IL-3157, IVM, UPC-870 (29)

*Figures in parentheses are number of entries+check

Table 2. Incidence of *P. nigrisigna* in selected entries of cowpea during 2006

PRSR	Leaf area damage (%)	Accessions*
2	2.3-4.2	EC24102-1, EC240884, IL-05-08, IL-05-12, IL-05-13, IL-05-15, IL-55-1, IL-161-1, IL-1063, IL-1177-B (10)
3	4.9-8.5	EC48720, EC240564, EC240887, IL-178-4, IL-246, IL-380, IL-3178 (7)
5	13.0-15.0	IL-05-14, IL-156, IL-3152-1, EC244236, EC244979 (5)
6	15.5-18.7	IL-90, IL-178-8, IL-179, BL-1 (3+1)
8	21.5-25.7	IL-1182, BL-2, UPC5286, IGFRI 95-1 (1+3)

* Figures in parentheses are number of entries+check

Table 3. Incidence of *P. nigrisigna* in selected entries of cowpea during 2007

PRSR	Leaf area damage (%)	Accessions*
2	1.6-2.4	EC24102-1, IL-1063 (2)
3	2.6-3.6	IL-05-08, EC240884 (2)
4	3.8-4.4	IL-05-12, IL-05-13, IL-05-15, IL-161-1, BL-1 (4+1)
7	7.8-21.6	IL-55-1, IL-1177-B, BL-2, UPC 5286, IGFRI 95-1 (2+3)

* Figures in parentheses are number of entries+check

Table 4. Incidence of *P. nigrisigna* in promising entries of cowpea

Accessions	Per cent leaf damage in different years			Mean
	2005	2006	2007	
EC24102-1	2.26	2.36	1.80	2.14
IL-1063	4.70	3.23	2.23	3.89
IL-05-08	5.53	3.63	2.80	3.99
EC240884	6.23	4.07	3.40	4.57
Bundel Lobia-1 (C)	24.67	15.80	4.27	14.91
Bundel Lobia-2 (C)	27.07	22.17	18.1	22.44
UPC 5286 (C)	26.83	21.97	19.33	22.71
IGFRI 95-1	30.13	24.30	19.80	24.74
(Local Control) CD (5%)	1.43	0.85	0.74	0.61

During the experimentation year 2007 the damage varied from 1.6–21.6 per cent (Table 3).

The entries EC24102-1 and IL-1063 were found least susceptible (1.6-2.4% damage) followed by IL-05-08 and EC240884 (2.6-3.6% damage). It is evident from the data presented in Table 4 that the mean leaf area damage in the test entry EC24102-1 was 2.14 and IL-1063 with 3.89 per cent damage (PRSR 2) and is statistically superior to the check entries.

Several fodder cowpea genotypes, viz., IL-118, IL-138, IL-148, EC24426, TUV 2287, TUV 2937 were reported as highly tolerant towards defoliator pests and semilooper damage (Shree Ram *et al.*, 1984; Pandey *et al.*, 1995). Similar trend of findings have also been endorsed by many workers (Mathur, 1995; Prasad *et al.*, 1996; Adebitan, *et al.*, 1997; Anku, *et al.*, 2000; Yadav and Dahiya, 2000; Bhadauria *et al.*, 2001; Kohali, 2002; Singh and Verma, 2002). They reported wide range of diversity and responsiveness in percentage of damage in various genotypes of cowpea caused by semilooper.

This study has identified four genotypes viz., EC24102-1, IL-1063, IL-05-08 and EC240884 which have consistent tolerance towards semilooper damage and thus could be used in breeding programmes as pest resistance donors.

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Genetic Variability, Heritability and Correlation Study for Nutritional Quality Traits in Tomato

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Thirty five genotypes of tomato were evaluated under midhills conditions in the Experimental Farm, Hawalbagh, VPKAS, Almora during Kharif 2007. Significant variation with regard to textural {pericarp thickness, skin firmness, total soluble solids (TSS)}, nutritional {phosphorus (P), potassium (K), iron (Fe), zinc (Zn), copper (Cu), manganese (Mn) and titrable acidity (TA)} and functional (Vitamin 'A', Vitamin 'C' and lycopene) traits were recorded in the genotypes of tomato. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. High heritability was recorded for Vitamin 'A', lycopene, iron, calcium, pericarp thickness, skin firmness, Vitamin 'C' and TSS whereas, low heritability was observed in case of titrable acidity and phosphorus content in fruits. The genotypic correlations were higher than the corresponding phenotypic for few important quality traits indicating inherent relationship among the nutritional quality traits. Both positive and negative correlations were observed among the traits under study.

Key Words: Tomato, Variability, Correlation, Textural and nutritional quality traits

Introduction

Tomato (*Lycopersicon esculentum* Miller) is an important commercial crop of the world used as raw salad and in processed forms like puree, paste, ketchup, juice, etc. Tomato soup is good remedy for patients suffering from constipation and very good appetizer (Kalloo *et al.*, 2001). It is universally treated as 'Protective Food' since it is a rich source of minerals, vitamins and organic acids. India is the fourth largest producer in the world after China, the USA and Turkey. During 2005-06, the area and production of tomato in the country was about 534.5 thousand ha and 9361.8 thousand metric tonnes, respectively (NHB, 2006), while in Uttarakhand the corresponding figures were 79.97 hundred ha and 86.87 thousand metric tonnes. In North-western Himalayan states, tomato has long cultivation season (March to October) as a summer rainy season and treated as an off-season crop, hence fetches high premium price from the market of North Indian plains. Tomato fruits start coming from hills to the market in the month of mid April to October as during this period tomato fruit supply is poor in the markets, because of restricted tomato cultivation in North Indian plains, poor fruit set during summer (Nandpuri *et al.*, 1971) and leaf curl disease in rainy season restrict the tomato cultivation in Plains.

Exploring natural biodiversity as a source of novel alleles to improve the productivity, adaptation, quality and nutritional value of crop is of prime importance in 21st century breeding programme (Fernie *et al.*, 2006). Novel and fast techniques are required for screening biodiversity

quickly for important textural and functional properties of tomato. Ahrens and Huber (1990) demonstrated a method of firmness determination using physiological attributes. Storability of tomato is of prime concern in terms of consumer preference and breeders choice. Tomato is called a fruit, which has a fleshy pericarp and soluble solids inside. It is very difficult to measure the fruit firmness by using a hand-operated penetrometer device. Although there is considerable literature on measurement of fruit firmness, very little information is available on storage capacity and germplasm variability for the purpose of quality breeding (Wu and Abbott, 2002). Measurement of tomato firmness with different techniques, viz., universal testing machine, acoustic firmness sensor were reported (Holt, 1970; Ketelaere *et al.*, 2004). Pericarp thickness is considered to be very important criteria among breeders for selecting cultivars and it relates to storage capacity. Textural quality of tomato is influenced by firmness of flesh. Flesh firmness is the ratio between pericarp and locular tissue, and skin toughness (Batu, 1998; Lana *et al.*, 2007). Change in firmness is correlated with textural characteristics of tomatoes which relate to colour, shape and flavour. The degree of fruit firmness has been used as an indication of fruit quality (Burton, 1982). However, firmness may be the final index by which the consumer decides to purchase tomatoes (using finger to test tomato firmness) at the time of selection (Gormley and Egan, 1978; Kader *et al.*, 1978). The aim of the present work was to investigate the

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relationship between textural properties such as pericarp thickness and fruit firmness and TSS with nutritional quality traits in order to fasten the screening procedure of tomato germplasm for quality breeding programme.

Materials and Methods

Sampling

Thirty five lines of tomato comprising open pollinated varieties (4), lines (6) and exotic materials (25) from Taiwan were planted in Randomized Block Design in *kharif* season (June–September), 2007, at experimental farm, Hawalbagh (29°36' N, 79°40' E and 1250 m above msl). Tomato fruits were harvested from the experimental field at red (ripe) stage. Fruits from three replicates of 35 lines each were analyzed for different attributes.

Instruments

Estimation of Vitamin 'A' and Vitamin 'C' content in tomato fruits was done by HPLC system (Shimadzu, Japan). For the estimation of potassium, a flame photometer (Systronics 128, India) and for other minerals like iron (Fe), zinc (Zn), copper (Cu), manganese (Mn) an atomic absorption spectrophotometer (Analytik Jena AG, Germany) was used. Phosphorus (P) was estimated photometrically via development of the phospho-molybdate complex. Tomato firmness was measured using Texture Analyzer-XT2i (Stable Micro Systems Ltd., Godalming, UK).

Textural Analysis

Pericarp thickness of tomato was measured using Vernier calliper (Mitutoyo, Japan) after cutting into slices. Tomato fruits firmness was measured using 2 mm cylindrical probe with 50 kg load cell. To obtain a good estimation of fruit texture, measurements were made on four places of fruits from each replicate, and three replicates were carried out. Firmness is the peak force during penetration, which is related to the strength of the flesh under penetration. At harvest TSS were determined in juice in three replicates of two fruits. TSS was measured using a digital refractometer (SR-05A; Sipcon, India)

Chemical Analysis

Titrate acidity (TA) in percentage was determined in juice after extraction in water in three replicates of two tomatoes. TA (%) was measured by titration with 0.1 N NaOH and expressed as citric acid equivalent.

Lycopene was estimated after extraction in acetone, followed by partitioning with petroleum ether. The ether extract was pooled after three extractions, followed by

washing with sodium sulfate solution. The extract was measured at 503 nm in spectrophotometer for the lycopene content.

Tomatoes were analyzed for nutrient parameters after di-acid digestion (HNO_3 : HClO_4 ; 10:4 v/v). The K content was determined by flame photometry, while Fe, Zn, Cu and Mn contents were analyzed by using an atomic absorption spectrophotometer. Phosphorus (P) was estimated photometrically via development of the phospho-molybdate complex (Tausky and Shorr, 1953).

Statistical Analysis

The genotypic and phenotypic coefficient of variation, heritability (broad sense) were calculated by standard statistical procedure given by Burton and DeVane (1953) and Johnson *et al.* (1955). The genotypic and phenotypic correlation coefficient was calculated by a method described by Singh and Choudhary (1979).

Results and Discussion

Significant variation with regard to all quality traits was recorded in the lines of tomato. Wide variation (0.27-1.14 mg 100 g⁻¹) was observed for Vitamin 'A' content in evaluated tomato lines, Vitamin 'C' content in tomato lines ranged from 12.0-86.0 mg 100 g⁻¹, consistent with the report by Franke *et al.* (2004). Lycopene content in evaluated genotype of tomato ranged from 0.58-4.92 mg 100 g⁻¹, consistent with previous reports (Thompson *et al.*, 2000). Among textural attributes, pericarp thickness and total soluble solid ranged between 1.41-4.87 mm and 2.0-4.0%, respectively, consistent with earlier reports (Saltveit, 2005). Skin firmness ranged from 273.7-611.7 g, consistent with previous report (Powell *et al.*, 2003, Mizrach, 2007). Titratable acidity in tomato juice ranged from 0.12-0.50 %. Phosphorus, potassium, Iron, zinc, copper and manganese content in tomato fruit ranged between 33.35-53.17 mg 100 g⁻¹, 228.8-371.15 mg 100 g⁻¹, 611-1772.2 g 100 g⁻¹, 67.76-154.9 g 100 g⁻¹, 9.39-40.53 g 100 g⁻¹ and 108.55-197.3 g 100 g⁻¹, respectively.

A perusal of data (Table 1) revealed that phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed high for almost all the traits under study except phosphorus, potassium and manganese content in fruits. These results indicated that traits showing the higher magnitude of coefficient of variation offer a better opportunity for improvement through selection. These results are in broad conformity to those of Manohar *et al.* (1981) and Meena *et al.* (2003).

Table 1. Range, Mean, Variance, Coefficient of variation, Heritability (broad sense) and Genetic Advancement for different quality traits in tomato lines

Traits	Range	Mean	Variance		Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance (5%)
			Genotypic	Phenotypic	Genotypic	Phenotypic		
Vit-A (mg/100 g)	0.27-1.14	0.61	0.050	0.050	36.347	36.394	99.7	0.459
Vit-C (mg/100 g)	12.00-86.00	40.26	419.462	479.726	50.875	54.407	87.4	39.451
Lycopene (mg/100 g)	0.58-4.24	1.99	0.657	0.691	40.599	41.633	95.1	1.629
Pericarp thickness (mm)	1.41-4.87	3.19	0.675	0.678	25.766	25.831	99.5	1.688
Skin firmness (g)	273.7-611.7	439.84	7328.128	7760.694	19.467	20.033	94.4	171.360
TSS (%)	2.0-4.0	2.89	0.347	0.411	20.766	22.579	84.6	1.117
Titric acid (%)	0.12-0.50	0.29	0.006	0.015	27.674	42.517	42.4	0.108
P (mg 100 g ⁻¹)	33.35-53.17	39.90	19.868	43.367	11.173	16.508	45.8	6.215
K (mg 100 g ⁻¹)	228.8-371.15	276.95	1082.010	1250.397	11.904	12.797	86.5	63.034
Fe (µg 100 g ⁻¹)	611-1772.2	918.23	45140.450	45523.550	23.141	23.239	99.2	435.828
Zn (µg 100 g ⁻¹)	67.76-154.90	116.52	648.534	730.978	21.856	23.204	88.7	49.414

The high heritability coupled with high genetic advance was recorded in skin firmness, Vitamin 'C', Cu, Fe, K, Zn and Mn content in fruits indicating the involvement of additive gene action for expression of these traits. Therefore, selection based on phenotypic performance of these traits would be more effective to select better lines. Johnson *et al.* (1955) has suggested that traits with high heritability coupled with high genetic advance would respond to selection better than those with high heritability and low genetic advance. Heritability is not an exact parameter because it could be high even when genetic advance is very low. However, expected genetic gain can be high only if the genetic variance is high (Allard, 1960). Burton (1953) suggested that GCV along with heritable estimates would give a better picture of the amount of progress expressed by phenotypic selection.

The assessment of genetic potentiality of important quality traits and their association is of paramount importance to carryout the effective selection for marking genotype with desired quality traits. Correlation coefficient of important quality traits were estimated at genotypic and phenotypic levels (Table 2).

In the present study, the genotypic correlation coefficients were significantly higher in magnitude than their respective phenotypic ones for few of the associations. Indicated that in these associations there was inherited relationship between the traits under study and environment had not played much role in reducing their actual association. From these associations, it appeared that Vitamin 'C' was significantly and positively

correlated with zinc content in fruit while it was significantly and negatively correlated with pericarp thickness and skin firmness. Significant and positive correlation was found among Vitamin 'A', titrable acidity and phosphorus content in fruit. Lycopene was significantly and positively correlated with potassium content in fruit. Pericarp thickness was positively correlated with skin firmness and phosphorus content in fruit similarly positive correlation was also found between skin firmness and phosphorus content in fruit. TSS was found positively correlated with phosphorus content in fruit whereas, titrable acidity was found negatively correlated with potassium content in fruit. Among nutrients, phosphorus was significantly and positively correlated with zinc and copper content in fruit, zinc had also positive correlation with copper whereas, potassium was found negatively correlated with manganese content in fruit. Result of the present study will help in selection of genotypes in nutritional quality improvement program of tomato.

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Table 2. Genotypic (r_g) Phenotypic (r_p) correlation coefficient among different quality traits in tomato lines

Traits		Vit-A	Vit-C	Lycopene	Pericarp thickness	Skin firmness	TSS	Titric acid	P	K	Fe	Zn	Cu	Mn
		(mg/100 g)			(mm)	(g)	(%)	(%)	(mg 100 g ⁻¹)		(µg 100 g ⁻¹)			
Vit-A (mg/100 g)	r_g	1.000	-0.020	-0.139	-0.008	0.177	-0.192	0.414*	0.402*	-0.135	-0.177	0.146	0.240	0.122
	r_p	1.000	-0.003	-0.128	0.009	0.163	-0.177	0.287	0.305	-0.126	-0.177	0.138	0.234	0.110
Vit-C (mg/100 g)	r_g		1.000	0.281	-0.355*	-0.333*	-0.257	0.126	-0.016	0.300	0.124	0.485**	0.215	0.057
	r_p		1.000	0.307	-0.325*	-0.353*	-0.208	0.158	0.237	0.260	0.116	0.431**	0.198	0.038
Lycopene (mg/100 g)	r_g			1.000	-0.080	-0.136	-0.187	-0.069	0.018	0.424*	-0.196	0.173	-0.008	0.029
	r_p			1.000	-0.076	-0.145	-0.164	0.002	0.116	0.389*	-0.188	0.155	-0.002	0.027
Pericarp thickness (mm)	r_g				1.000	0.492**	0.239	-0.054	0.376*	-0.239	0.135	0.019	0.135	0.054
	r_p				1.000	0.477**	0.216	-0.037	0.259	-0.226	0.135	0.021	0.132	0.048
Skin firmness (g)	r_g					1.000	0.322	0.275	0.361*	-0.172	0.017	0.079	0.034	-0.296
	r_p					1.000	0.315	0.114	0.128	-0.162	0.020	0.055	0.029	-0.274
TSS (%)	r_g						1.000	0.143	-0.038	-0.449**	-0.133	-0.246	-0.114	0.091
	r_p						1.000	0.077	-0.009	-0.390*	-0.125	-0.240	-0.130	0.077
Titric acid (%)	r_g							1.000	0.049	-0.361*	-0.072	0.060	-0.079	0.341*
	r_p							1.000	0.228	-0.232	-0.055	-0.013	-0.050	0.187
P (mg 100 g ⁻¹)	r_g								1.000	-0.151	0.266	0.676**	0.541**	-0.062
	r_p								1.000	-0.099	0.178	0.433**	0.357*	-0.060
K (mg 100 g ⁻¹)	r_g									1.000	-0.089	0.113	-0.119	-0.447**
	r_p									1.000	-0.084	0.098	-0.092	-0.301
Fe (µg 100 g ⁻¹)	r_g										1.000	0.315	0.099	-0.039
	r_p										1.000	0.292	0.101	-0.046
Zn (µg 100 g ⁻¹)	r_g											1.000	0.623**	-0.129
	r_p											1.000	0.569**	-0.093
Cu (µg 100 g ⁻¹)	r_g												1.000	-0.031
	r_p												1.000	-0.029
Mn (µg 100 g ⁻¹)	r_g													1.000
	r_p													1.000

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

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Screening of Sorghum Germplasm against Earhead Bugs with Morphological Characters

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One hundred and fifty sorghum genotypes collected from different sources were screened for earhead bug infestation during 2001-2002 and 2002-2003 on the basis of their population buildup in panicle. The screened sorghum genotypes were then segregated into 5 groups on the basis of different morphological plant characteristics imparting resistance to sorghum panicle and it was found that grain weight, length and breadth of panicle was inter related with mean number of bugs present on panicle. The lowest test weight was observed in RSU 158 (7.80 g) and maximum in AKENT 16 (43.58 g) and showed positive correlation ($r = 0.290$) with earhead bug population. Least panicle length was observed in genotype SRF 2102 (10.34 cm) and it was maximum in early SDSL 92131 (14.90 cm) and shown positive correlation ($r = 0.123$) with pest incidence and least panicle breadth was observed in genotypes ISCU 708 (2.5 cm) and maximum in SDSL 92131 (22.5 cm) and shown positive correlation ($r = 0.465$) with pest build up. Thus, morphological characters could be one of the tool of selection while selecting sorghum genotypes for earhead bug resistance for improvement programme which need further confirmation to understand the resistance in sorghum against bugs.

Key Words: Sorghum, Earhead bug resistance, Germplasm screening

Introduction

The genus *Sorghum* belongs to the family Poaceae and includes both cultivated and wild species for grain, fodder, feed, syrup, commercial and other purposes. All the cultivated forms are grouped under single species *Sorghum bicolor* (L.) Moench. The crop originated in Eastern Africa, is presently grown in all six continents extending about 40° on either side of the equator.

Africa and Asia, which produce one third of the grain crop, insect, mites and other pests have taken their toll. Insect-pests continue to compete with human beings for the sorghum crop, and knowledge of both old and new pests has accumulated at a faster rate in the recent years as the crop has received increasing attention (Young and Teetes, 1977). In these areas the use of insecticides has generally not been found economically feasible, because of insecticides being costly for farmers with limited resources. There are over 150 insect species known to damage sorghum from germination to crop harvest (Seshu Reddy and Davies, 1979). *Calocoris angustatus* is most important species in India and *Eurystylus immaculatus* in West Africa. Damage results from bugs sucking juices from the immature developing grains, resulting in shrivelling of grain thereby affecting both yield and quality (Wood and Stark, 1972).

Compared to temperate zones, insect problem in the tropics are generally more severe and this is particularly

so in the case of sorghum, the world's fourth most important cereal. Recommendations for integrated pest management (IPM) in sorghum in different parts of the world involve cultural practices, natural enemies, host-plant resistance (HPR) and management through insecticides. The statement of Wilson and Huffakar (1976) reflects much of a paradigm upon which IPM is built "biological control, together with plant resistance are the core around which pest control in crops and forests should be built". In this context, HPR assume a central role in our efforts to increase production and productivity of sorghum.

HPR does not involve any direct costs to the farmers, it is environment friendly, and is compatible with other components of pest management. Insect resistant cultivars should yield more than the susceptible cultivars in the presence of pests (Doggett *et al.*, 1970).

Materials and Methods

For screening, one hundred and fifty sorghum genotypes having different plant characters and maturity period were procured from different sources and the trials were laid in 2001-2002 and 2002-2003 *kharif* season in forage research area with row to row and plant to plant spacings of 50 cm and 10-12 cm, respectively in Randomized Block Design in three replications and a plot size of 3 row length. Recommended agronomic practices were followed to raise the healthy crop except plant protection.

All these selected sorghum genotypes including IS 18551, DJ 6514 and IS 2205 as resistant check, while ICSV 1, CSH 5 and CSH 9 as susceptible checks were grown for screening against earhead bugs. For recording the incidence of the head bugs, fifteen plants, *i.e.*, 5 plants per replication from each genotype were selected. At initiation of 50 per cent flowering, number of head bugs present on each panicle were counted from 15 panicles at weekly intervals till the harvest of the crop.

For investigations on morphological characters associated with population buildup, one hundred and fifty sorghum genotypes screened and clustered into five groups on the basis of infestation by sorghum earhead bugs. Morphological characters observations were recorded at maturity and for recording the morphological parameters, in each genotype 5 plants were selected randomly per repeat. The size, *i.e.*, length and breadth of earhead of each individual sorghum genotype was measured with the help of half metre rod. To get the test weight of each sorghum genotype, the 1000-grains were counted manually and then their weight was recorded on electronic balance (AFCOSET FX-300: The Bombay Burmah Trading Corporation Ltd.).

Results and Discussion

Morphological characters, *viz.*, 1000-grain weight (test weight), length and breadth of panicles were categorized into different groups. The results on these parameters are presented below:

1000-Grain Weight (Test weight)

One hundred and fifty sorghum genotypes were categorized into 5 different groups on the basis of 1000-grain weight (Table 1). Category-1 comprised of only 2 sorghum entries, namely, RSU 158 and AKENT 14 and in these two sorghum genotypes mean grain weight was 7.80 g and 8.58 g, respectively. In category-II, there were forty sorghum genotypes, in which the mean grain weight varied from 12.10 g to 19.80 g with an overall mean of 17.07 g. The mean grain weight was maximum (19.80 g) in genotype BT 623 and the minimum (12.10) in genotype SPV 1567. Category-III comprised maximum (86) number of sorghum genotypes and these genotypes had average grain weight of 23.96 g and the mean number of bugs/ 5 panicles was 12.24. In this category least (20.11 g) test weight was recorded in genotype SRF 203 and maximum (29.68 g) 1000-grain weight was recorded in sorghum genotype RSE 9744. In Category-IV average 1000-grain weight was 34.01 g, and least (30.23 g) mean

Table 1. Sorghum genotypes categorized on the basis of 1000-grain weight

S. No.	Sorghum genotype	Grain weight* (g)	Mean no. of earhead* bugs/ 5 panicles
0.0-10.0 g – Grain weight			
1.	RSU 158	7.80	1.0
2.	AKENT 14	8.58	9.0
	Average	8.09	5.0
10.1-20.0 g – Grain weight			
3.	SPV 1567	12.10	12.3
4.	SU 699	12.92	1.2
5.	DSFR3	13.16	8.5
6.	DJ 6514	13.36	6.0
7.	DSFR 2	13.62	11.6
8.	SRF 2102	14.00	12.8
9.	SPV 1581	14.04	16.3
10.	RSU 202	14.71	5.3
11.	SPV 1576	15.08	8.4
12.	ICSV 711	15.88	5.2
13.	RSE 9728	16.23	23.1
14.	SPV 1570	16.26	9.3
15.	SPV 1579	16.33	15.4
16.	ICSV 714	16.72	5.4
17.	168-II-112	16.86	4.0
18.	GD 65174-1	17.08	0.0
19.	ICSV1	17.22	23.0
20.	IS 18551	17.30	3.7
21.	SPV 1577	17.34	11.1
22.	SR 770-2	17.68	23.2
23.	SPV 1568	17.72	19.1
24.	AKENT 8-3	17.80	3.8
25.	IS 2205	17.84	8.2
26.	SPV 1580	17.85	0.0
27.	CSH 7	17.89	26.9
28.	SR 2460-1	18.12	15.8
29.	GD 65195	18.26	7.6
30.	GMSB 69	18.43	8.1
31.	SRF 1665	18.68	15.5
32.	SR 1048-1	18.76	15.1
33.	CSH 5	18.83	23.7
34.	SU 700	19.02	11.4
35.	SPH 1355	19.18	19.8
36.	SPH 1280	19.20	8.4
37.	SPV 1574	19.44	6.7
38.	27 B	19.52	23.9
39.	CH 3	19.53	15.2
40.	AKENT 10-1	19.56	23.1
41.	SPH 1354	19.72	19.0
42.	BT X 623	19.80	11.8
	Average	17.07	10.42
20.1 – 30.0 g – Grain weight			
43.	SRF 203	20.11	19.0
44.	CSV 457	20.12	11.6
45.	AKMS 14-A	20.34	12.5
46.	DSFR5	20.52	25.6
47.	SPV 1573	20.56	0.0
48.	ICSV 708	20.76	17.2
49.	CSH 14	20.76	17.6
50.	SPV 1565	20.90	8.5
51.	CSH 17	20.94	19.5
52.	SFCR 1047	21.14	4.4
53.	RSV 204	21.16	15.1
54.	SR 2458	21.20	29.0
55.	SPH 1374	21.36	27.1

S. No.	Sorghum genotype	Grain weight* (g)	Mean no. of earhead* bugs/5 panicles
56.	GMSB 4	21.45	7.9
57.	SPV 1571	21.46	19.9
58.	SPH 1375	21.48	4.6
59.	GMSB 76	21.50	4.1
60.	CSH 16	21.57	15.9
61.	CSV 15	21.71	16.3
62.	SPV 1575	21.72	16.5
63.	GMSB 5	21.76	8.2
64.	296 B	21.77	15.8
65.	SPV 1578	21.86	21.8
66.	SPH 1350	21.88	8.6
67.	GMSB 15	22.06	8.5
68.	CSH 9	22.28	24.0
69.	GD 65019	22.3	15.4
70.	ICSV 700	22.42	3.9
71.	168 UU 1006	22.44	4.4
72.	SU 663	22.47	15.6
73.	ICSV 112	22.48	8.2
74.	SR 1436	22.53	16.1
75.	SFCR 1143	22.64	22.8
76.	IS 2312	22.79	22.4
77.	200-1011	22.80	17.6
78.	SDSL 92131	22.84	0.0
79.	SPV 1569	22.92	12.3
80.	RSE 9715	22.92	3.8
81.	SR 833-2-3	22.96	19.2
82.	CSV 16	22.98	13.6
83.	200 IU 1005	22.98	19.1
84.	SPH 1353	23.03	18.0
85.	IS 22893	23.06	3.8
86.	200 UU 1011	23.26	15.4
87.	ICSV 745	23.44	9.1
88.	IS 2269	23.48	4.0
89.	168-II-108	23.66	7.9
90.	SPH 1183	23.78	4.1
91.	SFCR 1070	24.12	22.7
92.	SPV 1562	24.18	16.0
93.	Khwang Pahawang	24.24	0.0
94.	IS 6566	24.27	8.1
95.	GSSV 312	24.34	7.5
96.	SPH 1334	24.62	11.0
97.	IS 25596	24.82	0.0
98.	ICSV 93046	24.98	7.5
99.	168-IU-1021	25.02	13.9
100.	168-II-122	25.07	7.8
101.	SPV 1605	25.08	4.3
102.	AKENT 10-2	25.24	4.4
103.	SPV 1563	25.26	16.6
104.	GMSB 131	25.44	8.0
105.	IS 20016	25.66	0.0
106.	IS 2123	25.74	7.7
107.	IS 11119	25.74	7.6
108.	RSU 283	25.82	3.8
109.	IS 112	25.82	18.6
110.	168 UU 1022	26.02	7.7
111.	IS 1044	26.46	11.5
112.	IS 4663	26.51	8.4
113.	IS 2122	26.52	9.9
114.	AKENT 15	26.56	3.8
115.	ICSV 705	27.05	4.0
116.	GD 65055	27.16	10.0
117.	RSE 9741	27.18	6.5
118.	SFCR 1105	27.48	23.1
119.	RSE 9745	27.58	9.2

S. No.	Sorghum genotype	Grain weight* (g)	Mean no. of earhead* bugs/ 5 panicles
120.	296-A	28.16	26.5
121.	SFCR 1111	28.28	30.9
122.	SPH 1335	28.30	16.0
123.	463-A	28.76	3.9
124.	SU 45	28.98	12.5
125.	SPH 1352	29.16	6.1
126.	SRF 2549	29.43	25.7
127.	SU 52	29.58	12.0
128.	RSE 9744	29.68	24.1
Average		23.96	12.24

30.1-40.0 g – Grain weight

S. No.	Sorghum genotype	Grain weight* (g)	Mean no. of earhead* bugs/ 5 panicles
129.	RSE 9727	30.23	12.2
130.	SPH 1372	30.32	12.7
131.	SR 2460	30.34	12.1
132.	GD 65040	30.52	11.4
133.	SR 2704	32.38	12.4
134.	AKENT 7-1-1	32.48	5.9
135.	GD 65004	32.58	15.2
136.	SR 2459	32.90	26.7
137.	ICSV 717	33.62	17.7
138.	GD 65022	34.16	11.3
139.	ICSR 93034	34.58	17.5
140.	SPH 1349	35.40	8.6
141.	S-35	35.48	15.5
142.	GD65006	36.64	15.3
143.	SPH 1376	37.16	11.8
144.	SPH 1341	37.18	20.1
145.	SPH 1347	37.64	20.1
146.	SPH 1329	38.70	13.8
Average		34.01	14.46

40.1-50.0 g – Grain weight

S. No.	Sorghum genotype	Grain weight* (g)	Mean no. of earhead* bugs/ 5 panicles
147.	Amarnath	40.06	15.6
148.	NT 52	40.72	17.1
149.	Swati	43.26	17.0
150.	AKENT 16	43.58	8.2
Average		41.90	14.47
S.E.±		2.28	

*Grain weight and mean number of earhead bugs/ 5 panicles are mean of 3 replications

grain weight was observed in genotype RSE 9727 and the maximum (38.70 g) 1000-grain weight was recorded in genotype SPH 1329 with mean numbers of bugs per 5 earheads in this category were 12.46 bugs/ 5 panicle. Category-V consisted of only four genotypes, *i.e.*, Amarnath, NT 52, Swati and AKENT 16 with mean 1000-grain weight 40.06, 40.72, 43.23 and 43.58 g, respectively and the average mean grain weight of 41.90 g and the mean number of bugs/ 5 panicles varied from 8.2 (AKENT 16) to 17.1 (NT 52). The correlation ($r = 0.290$) between mean number of bugs/ 5 panicles and 1000-grain weight was positive.

Length of Panicle (cm)

On the basis of panicle length (cm), one hundred and fifty sorghum genotypes were categorized into 5 groups with

length ranging from 0.0 to 10.0, 10.1 to 15.0, 15.1 to 20.0, 20.1 to 25.0 and 25.1 to 30.0 cm into group 1, 2, 3, 4 and 5, respectively (Table 2). In Category-I, *i.e.*, (0.0 to 10.0 cm length), no sorghum entry was included. While Category-II included twenty, Category-III included sixty two, Category-IV included fifty three and Category-V included fifteen sorghum genotypes (Table 2). In Category-II, the least (10.34 cm) panicle length was observed in genotype SRF 2102, it was maximum (14.90 cm) in entry SPV 1568.

In Category-III, genotypes AKENT 15, had the least (15.11 cm) panicle length and it was maximum (19.91 cm) in entry 168-II-108. In Category-IV, entry SPV 1580 had the least (20.10 cm) panicle length and it was maximum (24.88 cm) in genotype GD 65004. In Category-V, genotype 296-A had the smallest panicle length (25.22 cm) and entry SDSL 92131 had maximum (28.96 cm). The average panicle length in Category-I, II, III, IV and V was 13.63, 17.21, 22.11 and 27.06 cm with mean number of bugs/ 5 panicles was 10.26, 12.69, 13.21 and 11.87, respectively. Length of panicles showed a positive correlation ($r = 0.123$) with pest incidence.

Breadth of Panicle (cm)

One hundred and fifty sorghum genotypes were categorized on the basis of breadth of panicle into 5

Table 2 . Sorghum genotypes categorized on the basis of length of panicle

S. No.	Sorghum genotype	Panicle length* (cm)	Mean no. of earhead* bugs/ 5 panicles
0.0-10.0 cm – Panicle length		NIL	
10.1 -15.0 cm - Panicle length			
1	SRF 2102	10.34	12.8
2	SRF 1665	12.00	15.5
3	SU 45	12.29	12.5
4	BT X 623	12.47	11.8
5	GSSV 312	12.56	7.5
6	ICSV 717	13.39	17.7
7	RSE 9715	13.67	3.8
8	DSFR2	13.72	11.6
9	AKENT 8-3	13.78	3.8
10	ICSV 708	13.85	17.2
11	RSU 158	13.92	1.0
12	AKMS 14-A	14.16	12.5
13	IS 2205	14.30	8.2
14	SR 2460-1	14.35	15.8
15	SPV 1605	14.36	4.3
16	SPV 1579	14.50	15.4
17	ICSV 714	14.50	5.4
18	RSU 202	14.77	5.3
19	IS 2269	14.84	4.0
20	SPV 1568	14.90	19.1
Average		13.63	10.26

S. No.	Sorghum genotype	Panicle length* (cm)	Mean no. of earhead* bugs/ 5 panicles
15.1-20.0 cm – Panicle length			
21	AKENT 15	15.11	3.8
22	200 IU 1005	15.33	19.1
23	SRF 2549	15.34	25.7
24	IS 2122	15.51	9.9
25	RSE 9727	15.53	12.2
26	AKENT 10-1	15.79	23.1
27	DSFR 5	15.83	25.6
28	SPV 1562	16.20	16.0
29	ICSV 705	16.33	4.0
30	IS 112	16.40	18.6
31	SU 700	16.67	11.4
32	SR 2458	16.76	29.0
33	GMSB 69	16.81	8.1
34	SRF 203	16.83	19.0
35	SPH 1183	16.70	4.1
36	SR 2460	17.11	12.1
37	SPV 1563	17.20	16.6
38	SPH 1352	17.33	6.1
39	DSFR-3	17.35	8.5
40	SR 770-2	17.36	23.2
41	SU 699	17.43	1.2
42	IS 18551	17.52	3.7
43	RSV 204	17.66	15.1
44	463-A	17.67	3.9
45	GMSB 76	17.69	4.1
46	CSV 457	17.77	11.6
47	SPH 1280	17.90	8.4
48	AKENT 10-2	18.00	4.4
49	ICSV 93046	18.10	7.5
50	SFCR 1047	18.24	4.4
51	SPV 1576	18.30	8.4
52	RSE 9744	18.33	24.1
53	GMSB 5	18.33	8.2
54	IS 22893	18.36	3.8
55	ICSV 700	18.39	3.9
56	IS 6566	18.48	8.1
57	CSH 9	18.50	24.0
58	SPH 1349	18.52	8.6
59	27 B	18.55	23.9
60	DJ 6514	18.60	6.0
61	CSV 16	18.65	13.6
62	SPH 1350	18.66	8.6
63	SR 1048-1	18.66	15.1
64	ICSV 745	18.70	9.1
65	SFCR 1143	18.72	22.8
66	CSH 14	18.73	17.6
67	ICSV 711	19.17	5.2
68	IS 2312	19.20	22.4
69	SR 1436	19.23	16.1
70	IS 11119	19.28	7.6
71	168 UU 1006	19.31	4.4
72	SPV 1571	19.40	19.9
73	CSH 17	19.47	19.5
74	GD 65055	19.47	10.0
75	200 UU 1011	19.47	15.4
76	CSV 15	19.60	16.3
77	RSE 9728	19.62	23.1
78	ICSV 112	19.63	8.2
79	CSH 7	19.66	26.9
80	AKENT 14	19.77	9.0
81	GMSB 15	19.80	8.5
82	168-II-108	19.91	7.9
Average		17.96	12.69

S. No.	Sorghum genotype	Panicle length* (cm)	Mean no. of earhead* bugs/ 5 panicles
20.1-25.0 cm – Panicle length			
83	SPV 1580	20.10	0.0
84	GD 65019	20.23	15.4
85	SR 833-2-3	20.33	19.2
86	SU 663	20.37	15.6
87	168-II-112	20.38	4.0
88	SPV 1569	20.40	12.3
89	GMSB 4	20.45	7.9
90	GD 65195	20.49	7.6
91	SPH 1375	20.50	4.6
92	SPH 1334	20.50	11.0
93	SFCR 1070	20.53	22.7
94	SPH 1329	20.66	13.8
95	168 IU 1021	20.69	13.9
96	RSE 9745	20.73	9.2
97	SPV 1574	20.80	6.7
98	SR 2704	20.81	12.4
99	GMSB 131	20.83	8.0
100	SPV 1567	20.90	12.3
101	SFCR 1105	20.93	23.1
102	SPV 1565	21.10	8.5
103	IS 4663	21.36	8.4
104	SU 52	21.47	12.0
105	SPH 1374	21.50	27.1
106	SFCR 1111	21.63	30.9
107	SPV 1581	21.66	16.3
108	SPH 1335	21.83	16.0
109	RSU 283	21.84	3.8
110	200-1011	21.90	17.6
111	SPV 1570	22.30	9.3
112	168 UU 1022	22.53	7.7
113	IS 2123	22.54	7.7
114	GD 65174-1	22.54	0.0
115	SPV 1575	22.60	16.5
116	IS 1044	22.70	11.5
117	168 II 122	22.73	7.8
118	SPV 1577	22.90	11.1
119	CH 3	23.12	15.2
120	SPH 1354	23.33	19.0
121	CSH 16	23.35	15.9
122	GD 65040	23.40	11.4
123	296-B	23.48	15.8
124	SPH 1355	23.50	19.8
125	SPH 1376	23.66	11.8
126	ICSR 93034	23.78	17.5
127	SPH 1353	23.83	18.0
128	SPV 1578	24.00	21.8
129.	S 35	24.13	15.5
130.	CSH 5	24.16	23.7
131.	SPV 1573	24.20	0.0
132.	SR 2459	24.32	26.7
133.	GD 65006	24.57	15.3
134.	AKENT 7-1-1	24.88	5.9
135.	GD 65004	24.88	15.2
Average		22.11	13.21

25.1-30.0 cm – Panicle length

136.	296-A	25.22	26.5
137.	SPH 1347	25.50	20.1
138.	GD 65022	25.51	11.3
139.	Swati	25.91	17.0
140.	SPH 1341	26.5	20.1
141.	Amarnath	26.52	15.6
142.	SPH 1372	26.66	12.7
143.	NT 52	26.82	17.1

S. No.	Sorghum genotype	Panicle length* (cm)	Mean no. of earhead* bugs/ 5 panicles
144.	ICSV-1	27.16	23.0
145.	AKENT 16	27.55	8.2
146.	RSE 9741	28.13	6.5
147.	IS 25596	28.24	0.0
148.	Khawang Pahwang	28.39	0.0
149.	IS 20016	28.91	0.0
150.	SDSL 92131	28.96	0.0
Average		27.06	11.87
S.E. $\pm$		1.42	

*Panicle length and mean number of earhead bugs / 5 panicles are mean of 3 replications

different categories (Table 3). Category-I included seventy six entries and the average breadth of these genotypes was 4.17 cm and mean number of bugs/ 5 panicles were 7.23 bugs. Least (2.5 cm) panicle breadth was observed in genotype ICSV 708 and maximum (5.0 cm) panicle breadth was observed in genotype SFCR 1047. In Category-II, a total of seventy sorghum genotypes were included and the least (5.1 cm) panicle breadth was observed in genotypes IS 2123, SPV 1578, CSH 17 and SFCR 1070 and maximum (9.6 cm) panicle breadth was observed in entry SPH 1329, having mean panicle breadth of 6.42 cm and the mean number of bugs/5 panicles was 13.85 bugs. In Category-III, only 2 genotypes SPV 1573 and GD 65174-1 were included with panicle breadth of 11.4 and 14.7 cm, respectively. In this category the mean panicle breadth was 13.05 cm and with no bugs/ population. Category-V also included two entries, Khawang Pahawang and SDSL 92131 with panicle breadth of 20.1 and 22.5 cm, respectively, having mean panicle breadth of 21.3 cm with no bugs presence. No sorghum genotype was included in Category-IV. It is concluded that as the breadth of panicle increases from a certain level, either there was a reduction in bug population or it was negligible. Breadth of panicle and the mean number of bugs/ 5 panicles exhibited a positive correlation ($r = 0.465$).

The grain weight, length and breadth of panicle and mean number of bugs present on panicle seems to be inter-related with each other. Similar results have earlier been reported by Sharma (1985), who observed that small grains covered by hairy glumes hindered oviposition by females in comparison to those which had bigger size grain. He also observed that lesser the 1000-grain weight, smaller will be the grain size and lesser will be the population of earhead bugs. As for length and breadth of panicle are concerned, it is already well established by many workers that size of panicle matters in deciding the number of head bugs as in case of *C. angustatus*, Sharma

Table 3. Sorghum genotypes categorized on the basis of breadth of panicle

S. No.	Sorghum genotype	Panicle breadth* (cm)	Mean no. of earhead* bugs/ 5 panicles
0.0 – 5.0 cm – Panicle breadth			
1	ICSV 708	2.5	17.2
2	ICSV 714	2.6	5.4
3	AKENT 8-3	2.8	3.8
4	SRF 2102	2.9	12.8
5	SPV 1605	3.2	4.3
6	DSFR2	3.3	11.6
7	AKMS 14-A	3.4	12.5
8	IS 22893	3.5	3.8
9	SPV 1576	3.5	8.4
10	IS 6566	3.5	8.1
11	IS 112	3.5	18.6
12	27-B	3.5	23.9
13	RSU 202	3.6	5.3
14	ICSV 112	3.6	8.2
15	296-B	3.6	15.8
16	SR 2458	3.6	29.0
17	IS 11119	3.8	7.6
18	SPV 1579	3.8	15.4
19	SU 700	3.8	11.4
20	RSE 9727	3.8	12.2
21	ICSV 745	3.9	9.1
22	ICSV 93046	3.9	7.5
23	GMSB 5	3.9	8.2
24	SPV 1562	3.9	16.0
25	SR 1436	3.9	16.1
26	GD 65019	4.0	15.4
27	AKENT 10-1	4.0	23.1
28	SRF 1665	4.0	15.5
29	RSU 283	4.1	3.8
30	168-UU-1006	4.1	4.4
31	GMSB 131	4.1	8.0
32	SU 52	4.1	12.0
33	AKENT 15	4.2	3.8
34	463-A	4.2	3.9
35	168-II-112	4.2	4.0
36	GMSB 76	4.2	4.1
37	IS 4663	4.2	8.4
38	GD 65195	4.2	7.6
39	SU 663	4.2	15.6
40	CSV 457	4.2	11.6
41	SR 770-2	4.2	23.2
42	CSH 7	4.2	26.9
43	SDH 1352	4.3	6.1
44	SU 699	4.3	1.2
45	RSE 9745	4.3	9.2
46	SR 2460-1	4.3	15.8
47	CSH 3	4.3	15.2
48	168-IU-1021	4.3	13.9
49	SR 2460	4.4	12.1
50	IS 1044	4.4	11.5
51	RSE 9715	4.5	3.8
52	168-II-108	4.6	7.9
53	RSU 158	4.7	1.0
54	ICSV 700	4.9	3.9
55	SPH 1280	4.7	8.4
56	SR 1048-1	4.7	15.1
57	CSH 14	4.7	17.6
58	SPV 1567	4.7	12.3

S. No.	Sorghum genotype	Panicle breadth* (cm)	Mean no. of earhead* bugs/5 panicles
59	SPV 1571	4.7	19.9
60	GSSV 312	4.8	7.5
61	GD 65055	4.8	10.0
62	GMSB 4	4.8	7.9
63	SPV 1575	4.8	16.5
64	SPV 1577	4.8	11.1
65	CSV 16	4.8	13.6
66	SPV 1568	4.8	19.1
67	SRF 203	4.8	19.0
68	168-II-122	4.9	7.8
69	CSH 16	4.9	15.9
70	SR 2704	4.9	12.4
71	296-A	4.9	26.5
72	RSE 9728	5.0	23.1
73	ICSR 93034	5.0	17.5
74	168-UU-1022	5.0	7.7
75	GMSB 69	5.0	8.1
76	SFCR 1047	5.0	4.4
Average		4.17	7.23
5.1 – 10.0 cm – Panicle breadth			
77	IS 2123	5.1	7.7
78	SPV 1578	5.1	21.8
79	CSH 17	5.1	19.5
80	SFCR 1070	5.1	22.7
81	SPV 1574	5.2	6.7
82	SPH 1375	5.2	4.6
83	ICSV 705	5.2	4.0
84	SU 45	5.2	12.5
85	AKENT 10-2	5.3	4.4
86	ICSV 711	5.3	5.2
87	DSFR3	5.3	8.5
88	200-UU-1011	5.3	15.4
89	SPH 1183	5.4	4.1
90	AKENT 14	5.4	9.0
91	GD 65006	5.4	15.3
92	SPV 1570	5.6	9.3
93	CSV 15	5.6	16.3
94	GD 65004	5.6	15.2
95	SR 2459	5.6	26.7
96	DJ 6514	5.7	6.0
97	SPH 1334	5.7	11.0
98	GD 65040	5.7	11.4
99	AKENT 7-1-1	5.8	5.9
100	SPV 1565	5.8	8.5
101	SPV 1569	6.0	12.3
102	200-1011	6.0	17.6
103	GD 65022	6.0	11.3
104	SR 833-2-3	6.0	19.2
105	AKENT 16	6.1	8.2
106	GMSB 15	6.1	8.5
107	IS 18551	6.2	3.7
108	IS 2269	6.2	4.0
109	SPH 1349	6.2	8.6
110	S-35	6.2	15.5
111	SPH 1350	6.3	8.6
112	SPV 1563	6.3	16.6
113	SPH 1335	6.3	16.0
114	SPH 1376	6.3	11.8
115	SPH 1341	6.3	20.1
116	SRF 2549	6.4	25.7
117	SPH 1374	6.4	27.1

S. No.	Sorghum genotype	Panicle breadth* (cm)	Mean no. of earhead* bugs/ 5 panicles
118	NT 52	6.5	17.1
119	SFCR 1143	6.6	22.8
120	Amarnath	6.7	15.6
121	SPH 1354	6.7	19.0
122	SPH 1347	6.7	20.1
123	Swati	6.8	17.0
124	SPH 1355	6.8	19.8
125	SFCR 1105	6.8	23.1
126	RSE 9741	6.9	6.5
127	SFCR 1111	6.9	30.9
128	200-IU-1005	7.0	19.1
129	CSH 9	7.0	24.0
130	SPH 1353	7.1	18.0
131	SPH 1372	7.2	12.7
132	RSE 9744	7.2	24.1
133	SPV 1580	7.2	0.0
134	RSV 204	7.3	15.1
135	ICSV 717	7.3	17.7
136	CSH 5	7.3	23.7
137	IS 2205	7.6	8.2
138	DSFR 5	7.7	25.6
139	ICSV-1	7.8	23.0
140	BT X 623	7.9	11.8
141	IS 2312	8.0	22.4
142	IS 2122	8.2	9.9
143	SPV 1581	8.7	16.3
144	IS 20016	8.7	0.0
145	IS 25596	8.7	0.0
146	SPH 1329	9.6	13.8
Average		6.42	13.85
10.1 – 15.0 cm – Panicle breadth			
147	SPV 1573	11.4	0.0
148	GD 65174-1	14.7	0.0
Average		13.05	–
15.1 – 20.0 cm – Panicle breadth			
		NIL	
20.1 – 25.0 cm – Panicle breadth			
149	Khawang Pahawang	20.1	0.0
150	SDSL 92131	22.5	0.0
Average		21.30	–
S.E. ±		0.937	

* Panicle breadth and mean number of earhead bugs/ 5 panicles are mean of 3 replications

and Lopez (1994a) recorded that the number of *C. angustatus* increased with increase in size of panicle in susceptible cultivars. They also observed more panicle breadth in loose type of earheads resulting in lesser population of bugs.

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Analysis of Molecular Diversity and Differentiation of Red and White Kernel Rice Varieties

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Colour of the rice kernel is an important characteristic in commerce. Rice kernels having white colour are preferred in the national and international markets. The red colour of the kernels is preferred by consumers in some regions of India particularly in the southern state, Kerala. Therefore, development of varieties with specific kernel colour is an important breeding objective. A number of red and white kernel varieties have been bred. No systematic attempt has been made to understand the extent of diversity within and between these two distinct phenotypic classes. In the present study, RAPD markers were employed to analyze the genetic relationship among 20 varieties of each kernel colour classes and to identify marker (s) that can be used to differentiate the red and white kernel types from each other. The genetic diversity analysis among red and white kernel rice varieties using different DNA amplicons grouped 40 varieties into two major clusters. The maximum diversity was observed between two red kernel varieties, i.e., 'Ptb 5' and 'Jyothi' followed by distance between two white kernel varieties 'Rohini' and 'Ptb 14', and two red kernel varieties 'Remanika' and 'Jyothi'. These varieties may be selected as parents for hybridization programme. DNA pooling strategy was adopted to identify molecular marker(s) for kernel colour. A total number of 145 random decamer primers were screened to identify highly polymorphic well-resolved specific bands for kernel colour. OPC-12₁₂₀₀ was indicated as a putative molecular marker for red kernel colour and OPK-14₁₀₀₀ as a putative molecular marker for white kernel colour in rice.

Key Words: Rice, Kernel colour, RAPD marker, Jaccard's similarity index, Cluster analysis

Introduction

As kernel aroma and kernel elongation, colour of the rice kernel is also an important characteristic in commerce. Rice kernels having white colour are preferred in the national and international markets. The red colour of the kernels is preferred by consumers in some regions of India particularly in the southern state, Kerala. Therefore, development of varieties with specific kernel colour is an important plant breeding objective. Even though a number of red and white kernel varieties have been bred, no systematic attempt has been made to understand the extent of diversity within and between these two distinct phenotypic classes. Study of germplasm diversity has significant impact on the improvement of crop plants. It is necessary to investigate the genetic diversity in rice germplasm in order to broaden the genetic variation in future rice breeding. Morphological traits can be used for assessing genetic diversity, but they are very often influenced by the environment. Similarly, isozyme analysis represents only a part of the genome.

The use of molecular markers for the evaluation of the genetic diversity is receiving lot of attention. The development of PCR has allowed the introduction of the RAPD (Random Amplified Polymorphic DNA) approach (Williams *et al.*, 1990) to the molecular analysis of the genome. The RAPD technique has several advantages such as a relatively unbiased portion of the genome sampled, simplicity of use, lower cost and the use of a small amount of plant material (Fritsch *et al.*, 1996). Chaudhury *et al.* (2001) employed RAPD analysis for identification and classification of aromatic rice genotypes. Phong *et al.* (2001) demonstrated existence of somaclonal variation in rice plants regenerated from callus which survived the desiccation treatment using RAPD method. Xie *et al.* (2000) investigated the genetic diversity of three salinity tolerant rice varieties using RAPD. Identification of a linked marker to a specific trait of interest is imperative in molecular marker aided selection programme. Identification of a molecular marker linked with rice kernel colour will be useful for rice breeders for the selection of desirable progenies from the segregating population at the seedling stage. A study was under taken with an objective to differentiate red and

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white kernel rice varieties and to identify putative RAPD marker(s) associated with kernel colour in rice. In this study, RAPD markers were employed to analyze the genetic relationship among 20 varieties of each kernel colour classes and to identify marker(s) that can be used to differentiate the red and white kernel types from each other.

Materials and Methods

Plant Material

Forty rice varieties were procured from Kerala and Gene bank of NBPGR, New Delhi. The pedigree and characters of the varieties are given in (Table 1).

Twenty varieties were red kernel type and 20 were white kernel type. Seeds of these varieties were germinated and grown under aseptic conditions at about 30°C in green house of NBPGR, New Delhi.

DNA Extraction

Three weeks old seedlings were taken for the isolation of genomic DNA following the protocol of Doyle and Doyle (1990). The DNA was quantified using TKO 100 Fluorometer (Hoefer, San Francisco, CA).

Preparation of Bulk DNA and RAPD Analysis

DNA pooling can be an effective strategy for detecting genetic marker differences among groups of individuals with similar genotypes or phenotypes (Michelmores *et al.*, 1991). DNA bulks were constituted by mixing equal amount of (5 ng μ l⁻¹) DNA from 10 different varieties each having the same kernel colour. Thus, there were two DNA bulks of white kernel coloured rice and two DNA bulks of red kernel coloured rice. Initially DNA bulks of red kernel colour and white kernel colour were used as target DNAs for RAPD analysis. A total number of 145 random decamer primers (from Operon Technology Inc., Alameda, California, USA) (primer kits A to Z) were screened to identify highly polymorphic well-resolved specific bands for kernel colour. The repeatability of those primers, which showed polymorphism among bulks, was tested. Those primers, which showed repeatability with respect to polymorphic bands in red and white bulks, were used to screen individual rice varieties, which formed the red and white bulks.

PCR Conditions

PCR was performed in a 0.2 ml reaction tube. Each 25 μ l reaction mixture consisted of 10x assay buffer 2.5 μ l, 12.5 ng templates DNA, and 0.2 mM each deoxy

nucleotide triphosphate (dNTP), 5 μ M of 10-mer primer and 1.0 unit *Taq* DNA polymerase. PCR reactions were performed in a Perkin Elmer 9600 Thermal Cycler programmed for 40 cycles of standardized cycling conditions. The each cycle consisting of, denaturation 94°C for one minute, primer annealing at 35°C for one minute, primer extension at 72°C for two minutes and final extension at 72°C for 5 minutes. Amplified DNA products were separated on a 1.6% agarose gel, using loading dye, in 1X TAE buffer and stained with ethidium bromide. The amplification products were visualized and photographed under UV light using Polaroid 667 film.

Data Analysis

The PCR products were scored as present (1) or absent (0) for each primer-genotype combination and used to compute the measures of genetic distance for all pairs or individuals. The data entry was done into a binary data matrix as discrete variables. The statistical analysis was carried out using NTSYS software (version 2.1) (Rohlf, 1993). Pair-wise comparisons of samples were used to estimate Jaccard's similarity coefficients (GS): $a/(n-d)$, where a = number of positive coincidences, n = total sample size, and d = number of negative coincidences. Genetic distances (GD), between pairs of lines were estimated as $GD = 1-GS$. Jaccard's similarity coefficients were used to generate dendrogram using Unweighted Pair Group Method with Arithmetic Average (UPGMA) (Sneath and Sokal, 1973) and relationships between accessions were depicted in the dendrogram.

Results and Discussion

Level of Genetic Diversity

Thirteen RAPD primers used for DNA profiling of 40 rice varieties, which included 20 red kernel and 20 white kernel varieties, amplified 126 different reproducible bands (Table 2).

Number of bands per primer ranged from 1 (OPU-11 and OPU-9) to 17 (OPK-01), the average bands per primer being 9.07. The size of the amplicon varied 0.25 kb to 5 kb. Out of 126 bands that were scored, 72.2% bands were found to be polymorphic. Maximum numbers of polymorphic bands were detected with the primers OPK-01, OPK-14 and OPU-10. The average number of polymorphic bands per primer was 7.

Based on information generated from thirteen RAPD primers on forty varieties of rice, cluster analysis was performed. The genetic diversity of 40 rice varieties revealed by 13 primers is depicted in dendrogram (Fig. 1).

Table 1. Pedigree and specific characters of rice varieties

S.No.	Name of varieties	Kernel colour	Pedigree	Other specific characters
1	Ptb 14	white	Pure line selection from Maskathi	Photo insensitive
2	Ptb 15	white	Pure line selection from Kavunginpoothala	Photo sensitive
3	Ptb 16	white	Pure line selection from Kavunginpoothala	Photo sensitive, moderately resistant to sheath blight
4	Rohini	white	Ptb 10/IR 8	Photo insensitive
5	Aswathy	white	Ptb 10/Dee-Geo-woogen	Photo insensitive
6	Triveni	white	Annapoorna (TN-1 x Ptb10)/Ptb 15	Photo insensitive
7	Suvarnamodan	white	Pure line selection from ARC 11775	Photo insensitive, drought tolerant, moderately resistant to blast
8	Swarnaprabha	white	Bhavani/Triveni	Photo insensitive, moderately resistant to blast, stem borer and drought but, susceptible to sheath blight and bacterial blight
9	Jayathi	white	Triveni/IR 2061	Photo insensitive, moderately resistant to blast and blight
10	Neeraja	white	IR 20/IR 5	Photo insensitive, resistant to blast, sheath rot, neck blast and leaf folder but susceptible to sheath blight
11	Suraksha	white	Sasyasree/CR57-MR1523	Resistant/tolerant to blast and bacterial leaf blight
12	IR 36	white	IR1561-228-1-2/IR 1737//CR94-13	Resistant/tolerant to blast and bacterial leaf blight
13	Pranava	white	Vikram/Benong 3	Resistant/tolerant to blast
14	Akasi	white	IR8/N22	—
15	Ajaya	white	IET 4141/CR98 – 7216	Resistant/tolerant to blast and bacterial leaf blight
16	IR 8	white	Peta/Dee-geo-woo-gen	Resistant/tolerant to blast
17	Vivekdhan 62	white	China 4/BG 367 – 4	Resistant/tolerant to blast and stem borer
18	Triguna	white	Swarnadhan/RP1579 -38	Resistant/tolerant to brown plant hopper and gall midge
19	Kannagi	white	—	—
20	TRY-1	white	BR 153-2B-10-1-3/	—
21	Jyothi	Red	Ptb 10/IR 8	Photo insensitive, moderately resistant to BPH but susceptible to blast and blight.
22	Sabari	Red	Annapoorna (TN-1xPtb10)/IR 8/2	Photo insensitive
23	Bharathy	Red	Ptb 10/IR 8	Photo insensitive, moderately resistant to blast
24	Mattatriveni	Red	Reselection from Triveni	Photo insensitive, moderately resistant to BPH but susceptible to blast and blight.
25	Kairaly	Red	IR 36/Jyothi	Photo insensitive, moderately resistant to blast, sheath blight, gall midge and leaf folder
26	Kanchana	Red	IR 36/Pavizham	Photo insensitive, moderately resistant to blast, brown spot and ungro virus
27	Aathira	Red	BR 51-46-1/Cul.23332-2	Photo insensitive, moderately resistant to blast, sheath blight, BPH and gall midge
28	Aiswarya	Red	Jyothi/BR 51 – 46 -1	Photo insensitive, moderately resistant to blast, sheath blight, BPH and gall midge
29	Bhadra	Red	IR 8/Ptb 20	Photo sensitive, resistant to BPH but susceptible to sheath blight
30	Asha	Red	IR 11-66/Kochuvithu	Photo insensitive, moderately resistant to sheath blight, sheath rot, bacterial blight and BPH
31	Pavizham	Red	IR 8/Karivenel	Photo insensitive, moderately resistant to sheath blight, sheath rot, stack burn and BPH
32	Karthika	Red	Triveni/IR 1539	Photo insensitive, moderately resistant to sheath blight, sheath rot, bacterial blight and BPH
33	Aruna	Red	Jaya/ptb 33	Photo insensitive, moderately resistant to sheath blight, brown spot, bacterial leaf blight, gall midge, stem borer and BPH
34	Makom	Red	ARC 6650/Jaya	Photo insensitive, moderately resistant to sheath blight, sheath rot, brown spot, gall midge, stem borer, BPH and leaf folder
35	Remya	Red	Jaya/ptb 33	Photo insensitive, resistant to BPH, moderately resistant to sheath blight, sheath rot, blast and gall midge
36	Kanakom	Red	IR 1561/Ptb 33	Photo insensitive, highly resistant to BPH, moderately resistant to sheath blight, sheath rot, bacterial leaf blight, blast, stem borer and gall midge
37	Remanika	Red	Mutant of MO1	Photo insensitive, resistant to BPH, moderately resistant to gall midge biotype 5
38	Ptb 5	Red	Pure line selection from Velutharikayama	Photo insensitive, moderately resistant to major pests and diseases
39	Ahalya	Red	Ptb10/TN1/TN 1	Photo insensitive
40	Hraswa	Red	IR 8/T140	Photo insensitive, suited to summer crop with lift irrigation and for areas requiring extra short duration varieties due to water scarcity or flash floods

Table 2. Details of nature of bands produced by 13 random primers with 40 (20 white and 20 red kernel coloured) rice genotypes

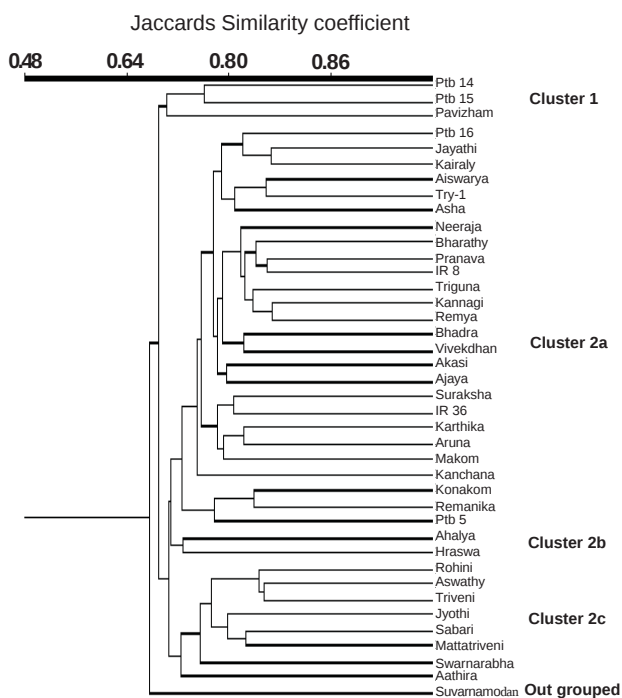
S.No	Primer	Nature of bands			Size range of bands(bp)	% Polymorphism
		Monomorphic (number)	Polymorphic (number)	Total bands (number)		
1	OPC-12	4	4	8	320-1750	50
2	OPK-01	4	13	17	350-5000	76
3	OPK-14	2	12	14	350-5000	86
4	OPM-10	4	9	13	375- 2500	69
5	OPM-13	2	11	13	400-1900	85
6	OPM-15	3	8	11	250-2200	73
7	OPN-02	6	0	6	450-1400	0
8	OPN-05	5	5	10	500-2400	50
9	OPQ-02	0	11	11	625-2500	100
10	OPU-09	1	0	1	400	0
11	OPU-10	0	12	12	400-3500	100
12	OPU-11	1	0	1	500	0
13	OPU-15	3	6	9	800-2500	67

Jaccard's similarity coefficient estimated on the basis of all the 13 primers ranged from 0.67 to 0.87 with an average of 0.72. The maximum similarity was observed between the varieties 'Jayathi' and 'Kairaly' and between 'Kannakam' and 'Remya' with 88% similarity index. But they are different in their kernel colour. This indicated that the clustering pattern was generated irrespective of kernel colour. The most genetically distant varieties revealed from genetic distance measurement are 'Ptb 5'

and 'Jyothi' (0.43) followed by 'Rohini' and 'Ptb 14' (0.41), and 'Remanika' and 'Jyothi' (0.41). The distant group varieties are of same kernel colour. These divergent varieties can be used as parents for recombination breeding without disturbing kernel colour. At 72% similarity index, the 40 rice varieties were grouped into two major clusters, and the variety 'Suvarnamodan' was out grouped. 'Suvarnamodan' is a drought tolerant high yielding variety with moderate resistance to blast disease.

In cluster 1 'Pavizham'—a photo insensitive, short bold grained, high yielding variety, moderately resistant to sheath blight, brown plant hopper, sheath rot and stack burn was grouped with 'Ptb 14' and 'Ptb 15'. Remaining thirty-six varieties were grouped together in cluster 2. This cluster can be further subdivided into three sub clusters. In sub cluster 2a twenty six varieties were grouped but grouping was neither based on kernel colour nor pedigree.

In sub cluster 2b, two varieties of red kernel colour namely, 'Hraswa' and 'Ahalya' were grouped together. 'Hraswa' is an extra short duration, high yielding variety suited to summer crop with lift irrigation and for areas requiring extra short duration varieties due to water scarcity or flash floods. 'Ahalya' is a photo insensitive high yielding variety with long bold grain. The variety 'Ptb 10' was one of the parents/ancestral parents for all the eight varieties that were grouped in sub cluster 2c. 'Ptb 10' is a variety from Kerala which is resistant to the pests, brown plant hopper, gall midge and stem borer and have high photosynthetic efficiency. This indicated that some of the varieties were clustered based on pedigree. The diversity analysis indicated that there is much

**Fig. 1: Dendrogram generated for 40 rice genotypes (20 red kernel coloured and 20 white kernel coloured) using RAPD markers**

diversity among the varieties which could not be differentiated based on kernel colour. Several other factors might have played major role in the pattern of clustering.

Differentiation of Red and White Kernel Rice Varieties

Out of 145 RAPD primers used for screening DNA bulks, to identify highly polymorphic well-resolved specific bands for kernel colour, 13 RAPD markers showed repeated consistent difference between DNA bulks of white kernel rice and red kernel rice. When these polymorphic primers were used to analyze individual varieties of red and white bulk, the DNA profile with the primer OPC-12 showed that the amplicon of 1200 bp was totally absent in the 1st set (Fig. 2A) as well as in the 2nd set (10 individual varieties) with white kernel colour varieties (Fig. 2B), but same amplicon (OPC-12₁₂₀₀) was amplified in 60% of individual varieties of red kernel colour in the 1st set (Fig. 2A) and 40% of individual varieties of red kernel colour in the 2nd set (Fig. 2B). Considering both sets together, there was complete absence of this RAPD marker in white kernel coloured rice varieties and presence of this marker in 50% of rice varieties with red kernel colour. The varieties, which showed presence of band for red kernel colour, were 'Jyothi', 'Sabari', 'Bharathi', 'Mattatriveni', 'Kairaly', 'Aiswarya', 'Karthika', 'Remya', 'Remanika' and 'Hraswa'.

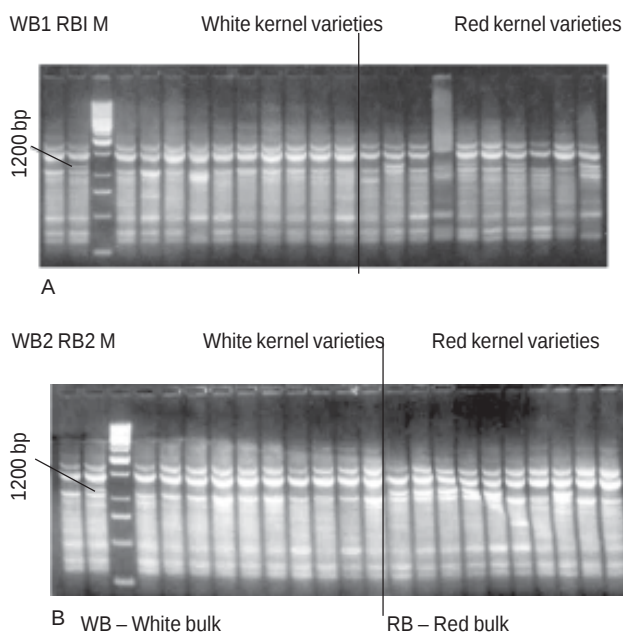


Fig. 2(A&B): Specific marker for red kernel colour revealed by the decamer primer OPC-12

The DNA profile with primer OPK-14 showed a bright thick amplicon of 1000 bp in 50% of 1st set 10 individual of varieties with white kernel, which was totally absent in the 1st set of 10 individual varieties of red kernel colour (Fig. 3A). Similar result was observed with the 2nd set in which 30% of white kernel varieties amplified bright thick amplicon of same size which was absent in all red kernel coloured individuals with similar thickness and brightness (Fig. 3B). Considering both sets together, there was complete absence of bright thick amplicon of 1000 bp in 20 red kernel colored rice varieties and present in 40% of rice varieties with white kernel color. The varieties, which showed presence of band for white kernel colour were 'Ptbi 14', 'Ptbi 15', 'Suvarnamodan', 'Swarnaprabha', 'Neeraja', 'Suraksha', 'Triguna' and 'Kannagi'.

Complete absence of molecular marker OPC-12₁₂₀₀ in all white kernel coloured varieties, and absence of thick bright amplicon of size 1000 bp with the primer OPK-14 in all red kernel coloured varieties indicated that the character kernel colour in rice may not be controlled by a single gene. The variation in red kernel viz., deep red, brownish red and light red (Fig. 4) also emphasized that the character kernel colour in rice might be controlled by more than one gene or alleles. Amplification of separate molecular markers, through RAPD, which is a dominant molecular marker leads to the inference that each red and

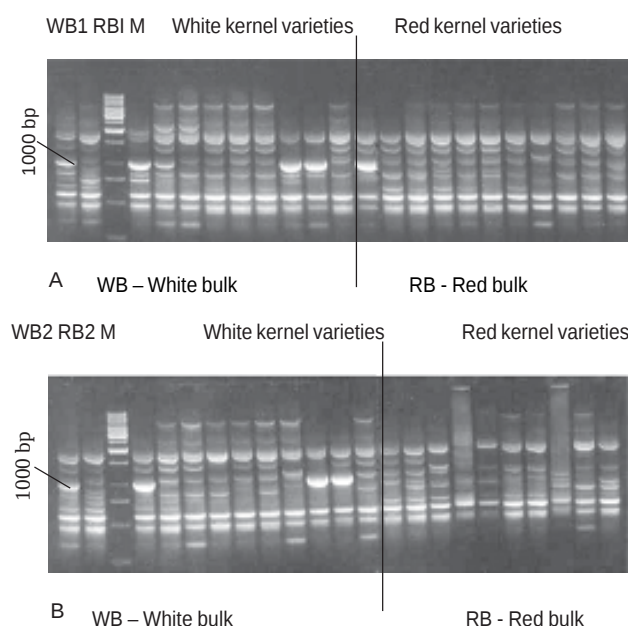


Fig. 3(A&B): Specific marker for white kernel colour revealed by the decamer primer OPK-14

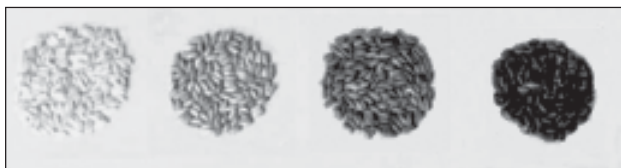


Fig. 4: Colour variation of rice kernel

white kernel colour, which is believed to be dominant and recessive character respectively, was separately controlled by more than one gene. Recessive forms of genes controlling red colour is not the only factor for the production of white kernel colour. The evolutionary process might have changed the recessive form of gene controlling red kernel colour into dominant in behaviour. The present result from molecular studies support the results of Vanaja (1999) based on F_2 segregation analysis for kernel colour in rice.

Segregation pattern of kernel colour in rice in F_2 generations of 19 crosses studied by Vanaja (1999) revealed that one dominant inhibitory gene and another colour gene appeared to be responsible for the inheritance. Gene governing red kernel colour found to exhibit inhibitory epistatic gene action over white kernel colour. Within the red kernel colour there was variation as light red, yellowish red and deep red both in F_2 generations and in back cross generations. The segregation ratio for red colour and white colour suggested that, each red and white colour may be separately controlled by two or more sets of major genes and there may be action of minor genes also. Among the dihybrid modified mendelian ratios, the phenotypic ratio 13:3 was found to fit in majority of the segregating populations, which suggested predominance of inhibitory type gene interaction.

Present investigation revealed lack of correspondence between molecular based RAPD markers and red kernel colour. More divergent types were found within red kernel colour class than white kernel colour class. The study also identified two molecular markers that can be used to differentiate the red kernel types from white kernel types and so can be used for transfer of this trait when these

varieties are used as donors for kernel colour in breeding programmes. However, the kernel colour is not controlled by single gene and thus additional efforts are needed to validate these markers using a large germplasm set.

Acknowledgements

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Evaluation of Hot Pepper (*Capsicum annuum* L.) Germplasm of Diverse Origin for Various Horticultural Characters

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A set of thirty three genotypes of hot pepper collected from Punjab, Rajasthan and AVRDC (Asian Vegetable Research and Development Centre) Taiwan were evaluated for various horticultural characters. The material was sown in a complete randomized block design with three replication during 2002-03. The observation were recorded on plant height, fruit length, number of seeds per fruit, number of fruit per plant, fruit yield per plant, fruit weight, number of branches per plant, days to first fruit harvest, chlorophyll content, capsaicin content, ascorbic acid content, colouring matter, resistance to fruit rot, virus complex. Analysis of variance indicated significant genotypic differences for all the characters which showed presence of wide variability in the material. Genotypes Punjab Lal, S-99-3, S-5, Punjab Guchhedar, S-12-1 and S-103 provided higher yield per plant (563.75g, 555.57g, 553.10g, 540.23g, 521.33g, 516.13g) respectively. Punjab Lal and S-12-1 were resistant to fruit rot, virus complex while Punjab Guchhedar, S-99-3 and S-103 were resistant to fruit rot and moderately resistant to virus complex. Genotypes S-2530, S-2, S-5, S-99-3 and S-30 were significantly superior to check varieties for colouring matter. Similarly, S-99-3 and S-5 were also identified for high capsaicin coupled with high yield and could be utilized for the genetic improvement of hot pepper for yield and quality characters.

Key Words: Hot pepper, Chilli, Yield, Quality

Introduction

Hot pepper (*Capsicum annuum* L.) belongs to family Solanaceae, is one of the most valuable commercial spice crop of India. It is grown for export as well as for domestic market. It is widely used in preparing different dishes, pharmaceuticals and in beverage industries throughout the world. It is mainly grown for red fruits, used as spice in powdered form, as medicine and also in pickles of many kinds. Dry chilli powder, soup, sauces, ketchup and oleoresin are its important processed products. Its fresh green fruits used as salad are a rich source of vitamin C and A. The important quality characters in chilli are pungency and red colour in fruits. India is the largest producer of chilli in world but productivity is very low as compared to other countries namely Japan and Korea due to attack of many diseases particularly viral diseases (virus complex). The important virus which attack chilli crop and cause significant losses are *Cucumber mosaic virus* (CMV), *Leaf curl virus* (LCV) and *Tobacco mosaic virus* (TMV) (Horvath, 1986). The improvement in any character through selection depends upon the magnitude of genetic variability present in the germplasm, so information on genetic variability in yield and quality characters is of vital importance in any breeding programme. Improvement in fruit yield which is an important character may be achieved through selection of one or more direct or indirect components. Therefore, present study was undertaken to evaluate the chilli

genotypes for yield, quality character and tolerance to various diseases viz. fruit rot and viruses.

Materials and Methods

The present investigation entitled "Evaluation of hot pepper germplasm of diverse origin for various horticultural characters" was conducted at Vegetable Research Farm and Biochemistry Laboratory, Department of Vegetable Crops, Punjab Agricultural University, Ludhiana during 2002-03. Ludhiana is situated at a latitude of 30°-54'N and longitude of 75°-48'E and at a mean height of 247 meters above sea level. This place is characterized by very hot and dry summer (April to June) followed by hot and humid period and cold winters during December to January. The average rainfall of the area is 600 mm, most of which is received during the monsoon season. A composite soil sample from 0-15 cm depth was taken before transplanting from the experimental field whose physico-chemical properties were as follows : soil texture-loamy sand; soil pH-8.5; organic carbon-0.18%; electric conductivity(mmhos/cm)-0.20. The experiment comprised thirty three genotypes of chilli collected from Punjab and Rajasthan states of India and Asian Vegetable Research and Development Centre (AVRDC) Taiwan including three check varieties (Punjab Guchhedar, Punjab Lal, and Punjab Surkh) were grown in a Randomized Complete Block Design. The genotypes and their sources are given in (Table 1).

The seeds of these genotypes were grown in nursery in first week of November and transplanted in the field during the second week of March. A distance of 60 cm and 30 cm was maintained between rows and plant respectively. Recommended agronomic and plant protection practices were followed to raise healthy crop. Eight plants per plot in each replication were planted and data were recorded on five randomly taken plants per plot in each replication. The observation were recorded on plant height (cm), fruit length (cm), number of seeds per fruit, fruit weight (g), number of branches per plant, number of fruits per plant, days to first fruit harvest, fruit yield per plant (g), fruit rot (%), virus complex (%), colouring matter (ASTA units by Rosebrook *et al.*, 1968), ascorbic acid content (mg/100g) by AOAC (1975), chlorophyll content of green fruits (mg/g) by Anderson and Bourdman (1964) and capsaicin content (%) by Bajaj and Kaur (1979). The

analysis of variance for randomized complete block design was calculated by the formulas given by Allard (1960).

Results and Discussion

The Analysis of Variance carried out for different character under study revealed highly significant differences among genotypes for all the characters. Mean value and range for each character under study are presented in (Table 2).

The varietal means for different characters are given in Tables 3(a) and (b). Fruit length varied from 3.83-9.90 cm and genotype S-5 possessed the maximum fruit length. Plant height varied from 60.37 to 117.57 cm. The maximum plant height recorded in genotype S-86-1. Number of seeds were found maximum in S-59. Fruit weight varied from 1.07 to 6.15 g with a mean of 3.74 g. Maximum fruit weight was recorded in S-3-1 which was

Table 1. List of genotypes of diverse origin under study

S.No.	Genotypes	Characters	Origin
1	S-1	medium ht; medium sized & less pungent fruit	Kapurthala, Punjab
2	S-2	tall plant; medium sized, less seeded & dark green fruit	Bathinda, Punjab
3	S-3	medium ht; small sized & less pungent fruit	Bathinda, Punjab
4	S-4	medium ht; small sized, heavily seeded & less pungent fruit	Kapurthala, Punjab
5	S-5	small ht; long sized, highly pungent & dark red fruit at maturity	Kapurthala, Punjab
6	S-6	tall plant; small & less seeded fruit	Bathinda, Punjab
7	S-8	small ht; small & less pungent fruit	Kapurthala, Punjab
8	S-13	small ht; long & less pungent fruit	Kapurthala, Punjab
9	S-23	small ht; medium sized & highly pungent fruit	Kapurthala, Punjab
10	S-24	medium ht; long & less pungent fruit	Bathinda, Punjab
11	S-30	small ht; long & dark red fruit at maturity	Bathinda, Punjab
12	S-35	tall and highly branched plant; less pungent fruit	Kapurthala, Punjab
13	S-59	small ht; medium sized & heavily seeded fruit	Bathinda, Punjab
14	S-86	medium ht; medium sized, less pungent & light green fruit	Bathinda, Punjab
15	S-103	small ht; medium sized & moderately pungent fruit	AVRDC, Taiwan
16	S-1-1	tall plant; long & dark green fruit	Jaipur, Rajasthan
17	S-3-1	medium ht; long & less pungent fruit	Bathinda, Punjab
18	S-5-1	medium ht; small & highly pungent fruit	Bathinda, Punjab
19	S-8-1-2 ²	small ht; small & heavily seeded fruit	AVRDC, Taiwan
20	S-12-1	small & highly branched plant; less pungent fruit	Bathinda, Punjab
21	S-30-1	medium ht; medium sized & dark green fruit	AVRDC, Taiwan
22	S-33-1	medium & highly branched plant; small & less pungent fruit	Kapurthala, Punjab
23	S-86-1	tall plant; long & less pungent fruit	Bathinda, Punjab
24	S-99-3	small ht; highly pungent & dark red fruit at maturity	Bathinda, Punjab
25	S-99-4	tall & highly branched plant; dark green fruit	Kapurthala, Punjab
26	S-106-1	small ht; medium sized & highly seeded fruit	AVRDC, Taiwan
27	S-108-2	small ht; small & light green fruit	AVRDC, Taiwan
28	S-370-2-1	tall; medium sized & dark green fruit	AVRDC, Taiwan
29	MS 12	medium ht; small sized & pungent fruit	Kapurthala, Punjab
30	S-2530	medium ht; medium sized & dark red fruit at maturity	Kapurthala, Punjab
31	Punjab Guchhedar	medium ht; medium sized fruits borne in cluster picked without stalk	Kapurthala, Punjab
32	Punjab Lal	small ht; small, erect & more pungent fruit	Kapurthala, Punjab
33	Punjab Surkh	small ht; long & dark red fruit at maturity	Kapurthala, Punjab

AVRDC = Asian Vegetable Research and Development Centre

Table 2. Mean and Range of different characters in hot chilli.

S.No.	Character	Range	Mean
1.	Plant height (cm)	60.37–117.57	81.75
2.	Fruit length (cm)	3.83–9.90	6.58
3.	Number of seed/fruit	17.27–71.33	37.62
4.	Fruit weight (g)	1.07–6.13	3.74
5.	Number of branches/plant	4.00–8.67	6.01
6.	Number of fruits/plant	28.63–514.37	135.65
7.	Fruit yield/plant (g)	166.07–563.73	378.63
8.	Chlorophyll content (mg/g)	0.11–0.70	0.35
9.	Days to first fruit harvest	70.00–95.00	90.65
10.	Capsaicin (%)	0.30–0.91	0.57
11.	Ascorbic acid (mg/100g)	99.90–140.50	123.39
12.	Colouring matter (ASTA units)	83.36–216.36	145.52
13.	Virus complex (%)	6.06–52.76	17.64

followed by S-24 (6.0 g), S-1-1 (5.97 g), S-86-1 (5.90 g) and S-8-1-2 (5.33 g). Number of branches per plants possessed mean value of 6.01 with range of 4.00-8.67 and maximum number of branches per plant found in Punjab Guchhedar.

Mean value for number of fruits per plant was 135.65 while this character varied from 28.63 to 514.37. The maximum number of fruits per plant was found in Punjab Lal followed by Punjab Guchhedar and S-5-1. Fruit yield varied from 166.07-563.73 g with mean value 378.63 g. Maximum fruit yield was found in Punjab Lal (563.73 g) followed by S-99-3 (555.56 g), S-5 (553.10 g), Punjab Guchhedar (540.23 g), S-12-1 (521.33 g) and S-103 (516.13 g). Similar type of variability was recorded in fruit yield, fruit length, number of fruit per plant by Khurana *et al.* (2003) and Kumar *et al.* (1999). Mean value for chlorophyll content was 0.35 mg/g with range from 0.11-0.70 mg/g. Maximum chlorophyll content was recorded in S-99-4. There was no incidence of fruit rot in any genotype under field conditions. There were ten genotypes viz. Punjab Lal, Punjab Surkh, S-2530, S-1, S-12-1, S-23, S-30-1, S-59, S-106-1, S-370-2-1 which were having less than 10% virus complex. Punjab Surkh was found to be early maturing than other genotypes. Capsaicin content varied from 0.30-0.91% with mean value 0.57%. The genotypes S-99-3 and Punjab Lal were statistically on par for capsaicin content. Ascorbic acid varied from 99.90–140.50 mg /100 g. Maximum ascorbic acid content found in S-24 (140.50mg/100 g) and S-13 (140.40mg/100g). Kumar *et al.* (2003) also found wide variability in ascorbic acid content in 30 chilli genotypes. The range of colouring matter was 83.36–216.36 ASTA units with a mean value of 145.52. Maximum colouring matter was found in S-2530 (216.37 ASTA units) followed

Table 3. Mean values of different genotypes for various traits

Genotypes	Days to first fruit harvest	Capsaicin (%)	Ascorbic acid (mg/100g)	Colouring matter (ASTA units)	Virus complex (%)
S-1	95.00	0.33	130.77	145.43	6.06
S-2	95.00	0.50	130.60	215.47	16.06
S-3	85.00	0.48	121.17	96.50	17.76
S-4	95.00	0.46	128.63	152.37	36.40
S-5	95.00	0.90	108.20	210.53	26.93
S-6	95.00	0.68	127.83	175.50	18.63
S-8	95.00	0.45	120.47	151.17	24.36
S-13	94.67	0.59	140.40	164.20	26.93
S-23	95.00	0.80	136.43	145.27	8.70
S-24	95.00	0.30	140.50	100.70	52.76
S-30	94.67	0.46	101.50	210.27	17.63
S-35	95.00	0.50	135.93	145.30	17.50
S-59	80.00	0.75	116.80	151.13	6.76
S-86	80.00	0.47	104.87	97.17	19.03
S-103	88.00	0.58	125.40	86.10	18.13
S-1-1	95.00	0.45	138.97	164.33	16.53
S-3-1	95.00	0.40	115.90	150.23	18.43
S-5-1	95.00	0.85	141.17	151.10	26.93
S-12-1	86.00	0.35	136.07	85.50	8.00
S-30-1	95.00	0.48	131.13	151.87	9.33
S-33-1	95.00	0.45	108.97	149.33	17.73
S-86-1	91.67	0.43	131.37	101.80	25.46
S-99-3	85.00	0.92	114.90	210.43	16.63
S-99-4	95.00	0.48	125.00	163.87	18.63
S-106-1	87.00	0.54	115.43	101.73	8.40
S-108-2	95.00	0.48	120.07	99.30	17.36
S-8-1-2	88.00	0.48	124.47	206.17	15.33
S-370-2-1	95.00	0.47	115.57	153.40	8.59
MS 12	95.00	0.90	135.90	96.87	18.46
S-2530	88.00	0.61	104.77	216.37	7.80
Punjab Lal	83.33	0.91	99.90	92.43	8.50
Punjab Guchhedar	80.00	0.86	116.50	83.37	18.53
Punjab Surkh	70.00	0.65	126.33	177.17	7.80
CD (p=0.05)	1.83	0.02	1.89	17.02	1.74

Note: There was no incidence of fruit rot on any of the genotypes. It did not appear under natural epiphytotic conditions.

by S-2 (215.46 ASTA units), S-5 (210.53 ASTA units), S-99-3 (210.43 ASTA units) and S-30 (210.26 ASTA units).

Genotypes Punjab Lal, S-99-3, S-5, Punjab Guchhedar, S-12-1 and S-103 provided higher yield per plant respectively. Punjab Lal and S-12-1 were resistant to fruit rot, virus complex while Punjab Guchhedar, S-99-3 and S-103 were resistant to fruit rot and moderately resistant to virus complex. Genotypes S-2530, S-2, S-5, S-99-3 and S-30 were significantly superior to check

varieties for colouring matter. Similarly, genotypes S-99-3 and S-5 were also identified for high capsaicin content, yield and quality characters. The results indicated the availability of the genotypes possessing the desirable horticultural characteristics and the breeder can make use of them in production of new cultivars with outstanding horticultural characters.

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Studies on Variability, Heritability and Genetic Advance for Quantitative Characters in Rice (*Oryza sativa* L.)

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Genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance for eleven characters in one hundred and fifty genotypes including five check varieties of rice were studied. The analysis of variance revealed that there were highly significant differences for all the characters except leaf width and 100-seed weight among the genotypes. The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were high for all the characters except days to 50% flowering and panicle length. Heritability and genetic advance were high for all the characters except days to 50% flowering and panicle length, which had moderate genetic advance along with high heritability indicating the involvement of additive type of gene action in controlling these characters.

Key Words: Rice, Genetic variability, Heritability, Genetic advance

Introduction

Rice is the staple food for 65% of the global population and forms the cheapest source of food, energy and protein. In India, rice is cultivated by different methods under diverse environmental conditions. To meet the food demand of the growing population and to achieve food security in the country, the present production levels need to be increased by 2 million tonnes every year, which is possible through heterosis breeding and other innovative breeding approaches. To increase the present levels of heterosis for yield, there is a need to identify and utilize genetically divergent parents for inter and intra sub-specific crosses in rice. A systematic evaluation and characterization of germplasm lines not only helps in identification of superior and genetically divergent germplasm lines but also provides information on the utility of the genetic resources. Characterization of accessions provides the information on morphological and agronomic aspects of the material that is essential for the gene bank management. Therefore, the present investigation was undertaken to study the genetic variability for yield and its component characters in various rice germplasm lines.

Materials and Methods

A field experiment was conducted with 145 genotypes of rice collected from 13 villages in Lohandiguda, 7 villages

in Bakawand, 5 villages in Darba, 3 villages in Tokapal, 10 villages in Bastanar, 2 villages in Pharsgaon, 2 villages in Kondagaon, 11 villages in Keskal and 5 villages in Baderajpur blocks of Chhattisgarh along with five check varieties Jaya, Mandya Vijaya, Prasanna, Rasi and Vasumathi in a Randomized Block Design with three replications. Thirty days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and plants, respectively. Five representative plants for each genotype in each replication were randomly selected to record observations on plant height (cm), leaf length (cm), leaf width (cm), total tillers per plant, productive tillers per plant, panicle length, grains per panicle, spikelet fertility and single plant yield. Days to 50% flowering were computed on plot basis. Seed weight (g) was recorded by weighing 100 grains of each cultivar. The mean data after computing for each character was subjected to standard methods of analyses of variance following Panse and Sukatme (1957). Phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (broad sense) and genetic advance as percentage of mean were estimated by the formulae suggested by Burton (1952) and Johnson *et al.* (1955).

Results and Discussion

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. Thus the primary objective of germplasm conservation

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is to collect and preserve the genetic variability in indigenous collection of crop species to make it available to present and future generations.

The analysis of variance indicated the existence of highly significant differences among genotypes for all the characters studied except leaf width and 100-seed weight (Table 1). A wide range of variation was observed in the rice germplasm for all the quantitative characters and yield (Table 2). However, widest range of variability was recorded for grains per panicle (73.81 to 297.23) followed by plant height (78.33 to 155.43 cm). The range of variation obtained for leaf width (0.68 to 1.45 cm) and 100-seed weight (1.42–3.60 g) was least when compared to all the other characters.

Grains per panicle and plant height exhibited high genotypic and phenotypic variances, followed by spikelet fertility and days to 50% flowering. Similar results were obtained earlier by Sawant *et al.* (1994) and Deb Choudhary and Das (1998).

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for plant height, leaf length, days to 50% flowering, grains per panicle and spikelet fertility indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. The magnitude of PCV was higher than the corresponding GCV for the characters like leaf width, total tillers per plant, productive tillers per plant, panicle length, 100-seed weight and single plant yield suggesting the influence of environment on the expression of these traits.

Table 1. Analysis of variance for different traits in rice germplasm

S. No.	Character	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.=149)	Error (d.f.=258)
1.	Days to 50% flowering	1.78	206.12**	1.02
2.	Plant height (cm)	6.98	568.60**	1.81
3.	Leaf length (cm)	7.16	87.86*	2.58
4.	Leaf width (cm)	0.014	0.07	0.01
5.	Total tillers per plant	5.17	22.95**	1.89
6.	Productive tillers per plant	3.19	11.69**	1.07
7.	Panicle length (cm)	8.43	15.05**	1.05
8.	Grains per panicle	8.86	3440.24**	7.14
9.	Spikelet fertility (%)	5.62	329.87**	0.59
10.	100-grain weight (g)	0.29	0.40	0.02
11.	Single plant yield (g)	4.61	50.76**	1.01

** Significant at 1 per cent level

* Significant at 5 per cent level

The characters like total tillers per plant, productive tillers per plant, grains per panicle and single plant yield showed high PCV and GCV estimates. Sinha *et al.* (2004) also recorded similar observations for total tillers per plant, productive tillers per plant and single plant yield. Low PCV and GCV estimates were obtained for days to 50% flowering and panicle length. These results are in conformity with those obtained for days to 50% flowering by Sinha *et al.* (2004) and panicle length by Patil *et al.* (2003).

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. In the present study, all the characters exhibited high heritability, which ranged from 62.56 to 99.46 % (Table 2). The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. The genetic advance expressed as a percentage of mean ranged from 17.34 to 49.54 and the important characters like productive tillers per plant (49.54), single plant yield (46.87) and grains per panicle (45.74) recorded higher estimates.

Based upon variability and heritability estimates, it could be concluded that improvement by direct selection in rice is possible for traits like productive tillers per plant and grains per panicle. In general, the character that shows high heritability with high genetic advance are controlled by additive gene action (Panse and Sukatme, 1957) and can be improved through simple or progeny selection methods. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance. In the present investigation, high heritability along with high genetic advance was noticed for all the traits except panicle length and days to 50% flowering, which had moderate magnitude of genetic advance. The characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadia, 2005).

In the present study, eleven superior genotypes, viz., IC114085, IC114126, IC114341, IC114612, IC114847, IC115114, IC115208, IC5738, IC5743, IC115757 and IC115909 were found to be potential enough to be used as parents in heterosis breeding. These genotypes recorded highest values for one or the other yield contributing

Table 2. Range, mean, genotypic and phenotypic variance components, coefficient of variability, heritability and genetic advance for different traits in rice germplasm

S. No.	Character	Range	Mean	Variance components		Coefficient of variability		Heritability (%)	Genetic advance	Genetic advance as per cent of mean
				Geno- typic	Pheno- typic	Geno- typic	Pheno- typic			
1.	Days to 50% flowering	69.0-113.0	89.83	68.37	69.39	9.20	9.27	98.52	16.91	18.82
2.	Plant height (cm)	78.33-155.43	115.70	188.93	190.74	11.88	11.94	99.05	28.18	24.35
3.	Leaf length (cm)	26.02-50.35	38.86	28.43	31.01	13.72	14.33	91.66	10.52	27.05
4.	Leaf width (cm)	0.68-1.45	1.15	0.02	0.03	12.52	15.83	62.56	0.23	20.40
5.	Total tillers per plant	7.30-20.21	13.14	7.02	8.91	20.17	22.73	78.72	4.84	36.85
6.	Productive tillers per plant	3.23-13.36	6.86	3.54	4.61	27.44	31.31	76.82	3.40	49.54
7.	Panicle length (cm)	17.13-28.87	23.17	4.67	5.72	9.32	10.33	81.54	4.02	17.34
8.	Grains per panicle	73.81-297.23	151.88	1144.37	1151.51	22.27	22.34	99.38	69.47	45.74
9.	Spikelet fertility (%)	52.39-97.35	86.18	109.76	110.35	12.16	12.19	99.46	21.52	24.97
10.	100-grain weight (g)	1.42-3.60	2.46	0.13	0.15	14.66	15.70	87.21	0.69	28.20
11.	Single plant yield (g)	6.19-26.17	17.37	16.58	17.60	23.44	24.15	94.21	8.14	46.87

characters and hence their utilization in combination breeding may help in generating high yielding varieties/hybrids by pyramiding all the favourable genes.

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Assessment of Genetic Diversity of *Woodfordia fruticosa* (L.) Kurz in Himachal Pradesh using Isozyme Polymorphism

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Woodfordia fruticosa (L.) Kurz (Lythraceae) is a rare woody shrub, the dried flowers of which are used as an important drug to treat various human disorders. Genetic variation of thirty genotypes of *W. fruticosa* was investigated using nine enzyme systems. Isozyme analysis of eight enzymes revealed considerable and very useful polymorphism among thirty genotypes from ten sites of Himachal Pradesh. Allele frequency in the thirty genotypes ranged from 0.5 to 1.00 and at all polymorphic loci only two alleles could be identified. On the basis of dendrogram the thirty genotypes were separated into two clusters. Cluster I included genotypes from Mandi, Hamirpur and Bilaspur districts, whereas Cluster II included genotypes from Solan and Sirmour districts. Polymorphism in the selected genotypes was found to be 34.5 per cent.

Key Words: *Woodfordia fruticosa*, Genetic markers, Isozymes, Polyacrylamide gel electrophoresis

Introduction

Woodfordia fruticosa Kurz. of the family Lythraceae, commonly known as Fire flame bush, Shiranjitea, Dhai, Dhataki, Dawi, is a plant of tropical and sub-tropical region. The plant is found in majority of South-East Asian countries—Malaysia, Indonesia, Sri Lanka, China, Japan, Pakistan and Tropical Africa. The plant is reported to be present throughout India upto an altitude of 1500 m. It is a leafy shrub about 3.5 m high and it is attracting the attention of floriculturist due to its brilliant red flowers. The plant is a well known forest produce that has long been in regular demand amongst practitioners of traditional medicines in different South-East Asian countries. In India, it is a much used medicinal plant in Ayurvedic and Unani systems of medicines (Chopra *et al.*, 1956). Although all parts of this plant possess valuable medicinal properties, there is a heavy demand for the flowers, both in domestic and international markets specialized in the preparation of herbal medicines. According to the Indian systems of medicine, this flower is pungent, acrid, cooling, toxic, alexiteric, uterine sedative, antihelmentic, and is useful in dysentery, leprosy, erysipelas, blood diseases, leucorrhea and menorrhagia. Many marketed drugs comprise flowers, fruits, leaves and buds mixed with pedicels and thinner twigs of the plant (Nadkarni, 1954; Chopra *et al.*, 1956). The use of bark, leaves, fruits and flowers in tanning industry are well known in the Indian subcontinent (Chadha, 1976). The flower produces red dye that is being used throughout

India for dyeing of fabrics or as an adjunct/mordant. Presently, genetic conservation of medicinal and aromatic plants has become of paramount importance because of ruthless extraction by upcoming biotechnology and pharmaceutical industry. For efficient conservation and management of medicinal plant diversity, the genetic composition of species collected from different phytogeographical regions of Himachal Pradesh need to be assessed. Therefore, it is important to study *W. fruticosa* at genetic and molecular levels for conservation and management of genetic diversity.

Keeping in view the importance of this medicinal plant species, it was considered appropriate to assess the genetic variability of the germplasm of *W. fruticosa* using molecular markers.

Molecular methods provide valuable tools for reliable and precise identification of plants at any stage of their growth and development. Isozymes offer the most reliable single gene markers (Arulsekar and Parfitt, 1986) and polymorphism at enzyme loci has been shown to be stable under a number of environmental conditions. Virtually any plant tissue can be analyzed for isozymic studies for cultivar identification (Torress, 1983). Moreover, results obtained with isozymes are easily repeatable and can be obtained without carrying out field experiments; this saves money, time and space. In the present study, 30 genotypes of *W. fruticosa* were analysed using isozyme analysis to estimate their genetic diversity.

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Materials and Methods

Thirty genotypes of *W. fruticosa* were selected from ten sites of five districts, viz., Mandi, Hamirpur, Bilaspur, Solan and Sirmour of Himachal Pradesh, which have been assigned code numbers as shown in Table 1. These sites were chosen on the basis of reported places of occurrence during the survey (Fig. 1).

Nine enzyme systems investigated were Peroxidase (PER), Acid phosphatase (ACP), Aspartate amino transferase (AAT), Esterase (EST), Catalase (CAT), Malate dehydrogenase (MDH), Alcohol dehydrogenase (ADH), Phosphorylase (PPH) and Alkaline phosphatase (ALP).

Table 1. Geographical location of selected ten sites and the sample codes of *W. fruticosa*

S. No.	Sites	Districts	Site code	Sample code	Altitude (m)
1.	Harabagh	Mandi	S ₁	W ₁ ; W ₂ ; W ₃	1100-1369
2.	Jogindernagar		S ₂	W ₄ ; W ₅ ; W ₆	
3.	Anu	Hamirpur	S ₃	W ₇ ; W ₈ ; W ₉	785
4.	Awahdevi		S ₄	W ₁₀ ; W ₁₁ ; W ₁₂	
5.	Ghumarwin	Bilaspur	S ₅	W ₁₃ ; W ₁₄ ; W ₁₅	350-670
6.	Bhararighat		S ₆	W ₁₆ ; W ₁₇ ; W ₁₈	
7.	Nauni	Solan	S ₇	W ₁₉ ; W ₂₀ ; W ₂₁	1365-1400
8.	Kandaghat		S ₈	W ₂₂ ; W ₂₃ ; W ₂₄	
9.	Rajgarh	Sirmour	S ₉	W ₂₅ ; W ₂₆ ; W ₂₇	900-3994
10.	Dhanech		S ₁₀	W ₂₈ ; W ₂₉ ; W ₃₀	

Sample Preparation

Fresh, young and green leaves were excised from 30 genotypes of *W. fruticosa* and then stored in liquid nitrogen till further use. Three hundred mg of leaf material was washed thoroughly and ground in prechilled pestle and mortar containing 1.5 ml Chase extraction buffer pH 7.5 (Chikkadevaiah and Nandinik, 2003). The homogenate was filtered through two folds of muslin cloth and then centrifuged at 20,000 rpm for 20 minutes at 4°C. The supernatant was taken and stored at -20°C till further study.

Electrophoresis

Electrophoresis was carried out for nine enzyme systems using miniVE electrophoretic and electrotransfer unit (Amersham Biosciences). The electrophoretic tank buffer was prechilled to 4°C to provide passive cooling. Two tray buffer systems were used for resolution of nine enzyme systems. First, tray buffer used was Lithium borate (lithium hydroxide 12 g, boric acid 118.9 g, distilled water 10.0 l and pH 8.3) as described by Scandalios (1969) and gel buffer used was Tris citrate (trizma base 62.0 g, citric acid 14.6 g, distilled water 10.0 l and pH 8.3) and this system was used for Peroxidase (PER), Esterase (EST), Aspartate amino transferase (AAT), Malate dehydrogenase (MDH) and Alcohol dehydrogenase (ADH). Second tray buffer used was Sodium borate (sodium hydroxide 20.0 g, boric acid 185.5 g, distilled water 10.0 l and pH 8.0) and gel buffer was Tris citrate (trizma base 121.1 g, citric acid 0.2 M, distilled water 10.0 l and pH 8.8) as described by Fowler and Morris (1977). This system was used for Acid phosphatase (ACP), Catalase (CAT), Alkaline phosphatase (ALP) and Phosphorylase (PPH).

Polyacrylamide gel electrophoresis was carried out to separate various isozymes due to its high resolving power, transparency and chemical inertness. Anionic system (Davis, 1964) was used for different enzyme systems. The gels were cast on the modules along with combs, which were removed after solidification and then these modules were placed in tank filled with tray buffer. The gentle inward pressure to both the tabs and locks into the lower notch were made to make contact between the gels and tray buffer. Thirty enzyme extracts were loaded in each



Fig. 1: Map showing ten selected sites of *Woodfordia fruticosa* in Himachal Pradesh

well with the help of a micropipette along with a drop of tracking dye (0.2 per cent bromophenol blue) in one well to work out the relative mobility (RM) values. Electrophoresis was carried at a constant current of 25 mA and 250 V till the marker dye reached the other end.

The bands of the enzyme activity were revealed by immersing the gels in specific histochemical stains. Staining recipes for ADH and AAT used were as described by Shaw and Prasad (1970). Staining of MDH was done according to Shaw and Koen (1968) while the methods of Scandalios (1969) were employed for EST and ACP. Staining procedures of Graham *et al.* (1964) were employed for PER. Staining of CAT was done according to Conkle *et al.* (1982) and methods of Tanksley and Orton (1983) were employed for PPH and ALP.

The genotypes were determined from the banding patterns obtained for each isozyme. In enzyme systems with multiple loci, the locus with greatest anodal migration was designated as I. Similarly, the fastest isozyme at a locus was represented by 'a' being controlled by allele 'A' (Mowrey *et al.*, 1990). The numbering of the additional loci and alleles within an enzyme system progressed sequentially in cathodal direction. The genotypes on the basis of isozymes were compared for each locus to assess genetic variability.

Different genetic parameters were obtained by analysing the data. The allele frequency was calculated as the proportion of a particular allele present at a given locus. Other genetic parameters studied to differentiate the genotypes included the proportion of polymorphic loci (Nei, 1975), the polymorphic index (Allard *et al.*, 1978), the average and effective number of alleles per locus (Crow and Kimura, 1970) and the observed (h_o) and expected heterozygosity (h_e), according to Nei (1975). The observed and expected heterozygote frequencies were compared using F-statistics (Wright, 1965). The inter-relationships of genotypes could be found on the basis of the following parameters.

Similarity index was calculated according to Hunter and Kannenberg (1971) based on presence or absence of bands. The identical bands in the particular enzyme system were rated as zero. If the two individuals differed for the presence or absence of a band within the same locus, these were given a rating of one. Thus, a diversity index comprised of cumulative ratings obtained in all the enzyme systems for each pair of the genotypes. Dendrogram was constructed from genetic distance values by the unweighted pair group arithmetic average

(UPGMA) method and NTSYS-pc software version 2.0 to analyse the patterns of genotype relatedness.

Results and Discussion

In the present investigation, eight enzyme systems out of the nine were found to be polymorphic in nature. Only three (AAT, PPH, MDH) were found to produce informative markers, which were able to differentiate amongst the ten sites, whereas the alkaline phosphatase enzyme system showed monomorphic banding pattern. The qualitative description of these three enzymes is depicted in the form of zymograms.

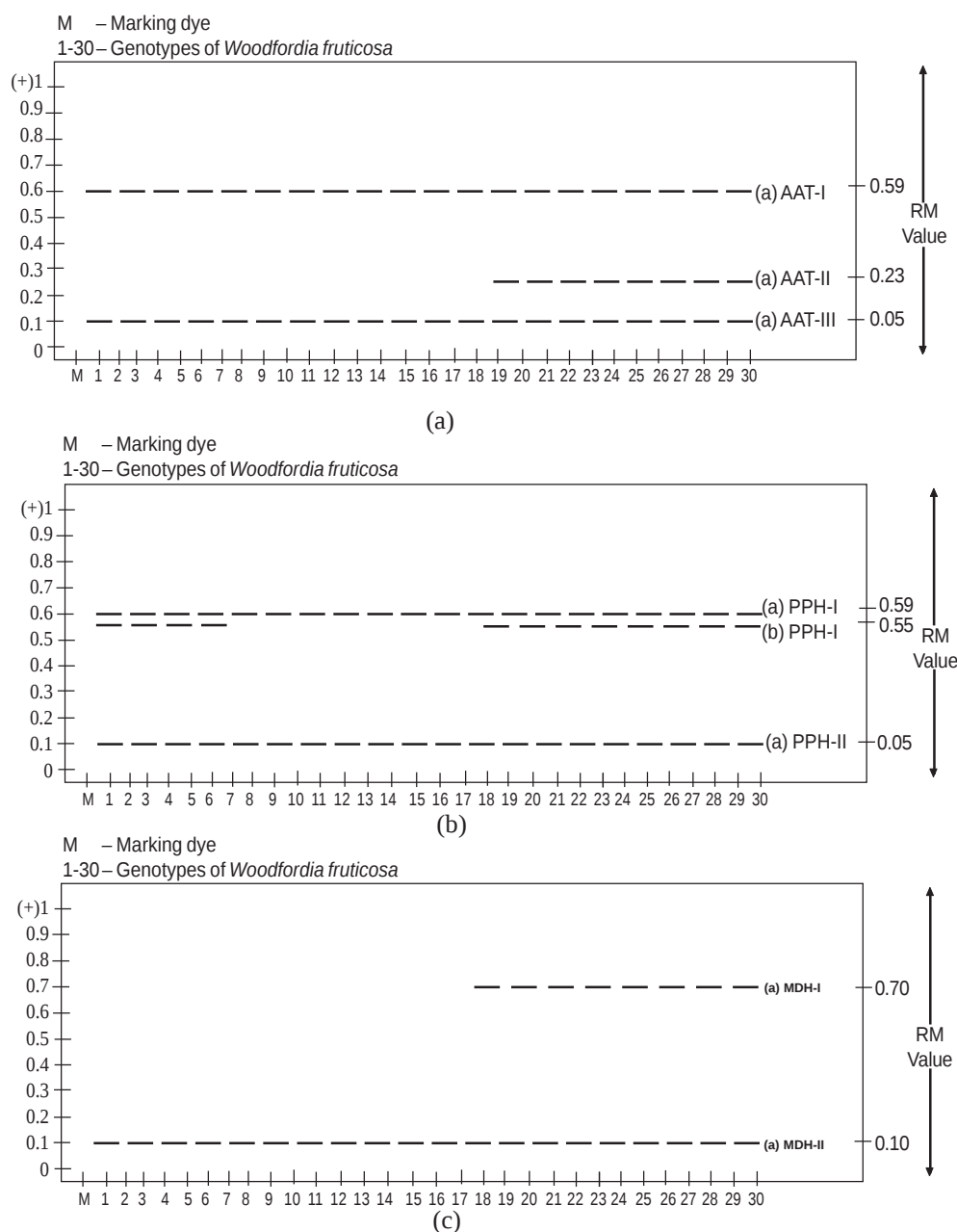
Isozymic Banding Patterns

Isozyme phenotypes of different enzyme systems have been described as under:

Aspartate amino transferase (EC2.6.1.2): Isozymic pattern of aspartate amino transferase with thirty genotypes produced three zones of enzyme activity (Fig. 2a). The most anodal zone locus AAT I displayed single band AAT Ia at RM value of 0.59. In the second zone locus AAT II showed a single band AAT IIa at RM value of 0.23 and was polymorphic in nature. It was present in genotypes from Nauni and Kandaghat of Solan district and Dhanech and Rajgarh sites of Sirmour district. The third zone locus AAT IIIa was found to be monomorphic and was present in all the thirty genotypes at the RM value of 0.05.

Phosphorylase (EC 2.4.1.1):- Two zones of enzyme activity were detected in phosphorylase enzyme system (Fig. 2b). The most anodal zone displayed a locus PPH I with two bands. PPH Ia at the RM value of 0.59 was present in all the thirty genotypes whereas PPH Ib was found to be polymorphic in nature and was present in the genotypes from Harabagh and Jogindernagar sites of Mandi district, Nauni and Kandaghat sites of Solan district and Rajgarh and Dhanech sites of Sirmour district. This band was present at the RM value of 0.55. The second zone locus PPH II showed single band PPH IIa at the RM value of 0.05 in all the thirty genotypes.

Malate Dehydrogenase (EC 1.1.1.37):- Malate dehydrogenase enzyme system displayed a banding pattern with two zones of enzyme activity (Fig. 2c). The locus MDH I showed a single band MDH Ia at the RM value of 0.70 in the genotypes from Nauni and Kandaghat sites of Solan district and Rajgarh and Dhanech sites of Sirmour district. The second zone locus MDH II showed single band MDH IIa at the RM value of 0.10 in all the thirty genotypes and thus was monomorphic in nature.



1-3 - Harabagh 4-6 - Jogindernagar 7-9 - Anu 10-12 - Awahdevi 16-18 - Bhararighat
 19-21 - Nauni 22-24 - Kandaghat 25-27 - Rajgarh 13-15 - Ghumarwin 28-30 - Dhanech

Fig. 2: Isozymic patterns of (a) Aspartate amino transferase, (b) Phosphorylase, and (c) Malate dehydrogenase

Genetic interpretation studies revealed that a total of 24 isozyme loci were scored, coding for nine enzyme systems in thirty genotypes of *W. fruticosa*. The number of loci coding for individual enzyme ranged from 1 to 4 and a total of 24 alleles were identified in the present investigation (Table 2). Allele frequency varied between 0.5 to 1.0, respectively (Nei, 1975) depending upon

whether a locus displayed heterozygous or homozygous conditions. Various monomorphic loci identified were PER I, AAT I, AAT II, AAT III, ACP I, ACP II, ACP III, CAT I, CAT II, CAT III, EST III, ADH II, ADH III, ALP I, ALP II, ALP III, PPH II, MDH I, MDH II. The polymorphic loci identified were PER IIA, PER IIB, PPH Ia, PPH Ib, EST Ia, EST Ib, EST IIA, EST IIB, ADH Ia

and ADH IIB. A locus was considered polymorphic if the frequency of the most common allele was not more than 0.99 (Nei, 1975). The proportion of polymorphic loci varied from 0.83 for Mandi district, 0.20 for genotypes from Hamirpur, Bilaspur and Solan districts and 0.187 for genotypes from Sirmour district. In the present study, the average number of alleles per locus varied from 0.95 for genotypes from Mandi district upto 1.00 for genotypes from Sirmour district. Expected heterozygosity ranged from 0.0416 to 0.062. F-Statistics showed negative values, depicting more heterozygosity than the observed values (Table 2). Goncharenko *et al.* (1994) also obtained negative values of Wright Fixation showing excess of heterozygosity between *Populus sylvestris* populations. However, such observations obtained in the present study may be biased due to very small sample size. Nei (1975) observed that in order to reduce the sampling error of

heterozygosity a large number of loci rather than a large number of individuals per locus must be examined and to study allele frequency distribution also, large number of individuals must be examined.

Genetic Relation

Isozyme polymorphism data was analysed considering all the bands obtained from nine enzymes. According to the dendrogram thirty genotypes were divided into two major clusters (Fig. 3). The upper cluster demarcated the genotypes into two sub clusters. The first one consisted of genotypes from Mandi district, whereas cluster included genotypes from Hamirpur and Bilaspur districts. The lower bifurcation divided the genotypes of Solan and Sirmour into two sub-sub clusters. In the present investigation, total number of isozyme bands obtained were 29 and the RM value ranges from 0.03- 0.95 for

Table 2. Genetic variation parameters among thirty genotypes of *W. fruticosa*

Parameters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Total no. of loci	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
Total no. of alleles	23	23	23	23	23	23	21	21	21	21	21	21	21	21	21
Proportion of polymorphic loci	0.083	0.083	0.083	0.083	0.083	0.083	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
Polymorphic index	0.0416	0.0416	0.0416	0.0416	0.0416	0.0416	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
Average no. of alleles per locus	0.95	0.95	0.95	0.95	0.95	0.95	0.87	0.87	0.87	0.87	0.87	0.87	0.87	0.87	0.87
Effective no. of alleles per locus	0.043	0.043	0.043	0.043	0.043	0.043	0.42	0.42	0.42	0.42	0.42	0.42	0.42	0.42	0.42
Mean observed heterozygosity (h_o)	0.083	0.083	0.083	0.083	0.083	0.083	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
Expected heterozygosity (h_e)	0.0416	0.0416	0.0416	0.0416	0.0416	0.0416	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020
F-statistics	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1

Table 2. Contd.

Parameters	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Total no. of loci	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
Total no. of alleles	21	21	21	21	21	21	21	21	21	24	24	24	24	24	24
Proportion of polymorphic loci	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.187	0.187	0.187	0.187	0.187	0.187
Polymorphic index	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.062	0.062	0.062	0.062	0.062	0.062
Average no. of alleles per locus	0.87	0.87	0.87	0.87	0.87	0.87	0.87	0.87	0.87	1.00	1.00	1.00	1.00	1.00	1.00
Effective no. of alleles per locus	0.42	0.42	0.42	0.42	0.42	0.42	0.42	0.42	0.42	0.044	0.044	0.044	0.044	0.044	0.044
Mean observed heterozygosity (h_o)	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.187	0.187	0.187	0.187	0.187	0.187
Expected heterozygosity (h_e)	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.062	0.062	0.062	0.062	0.062	0.062
F-statistics	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1

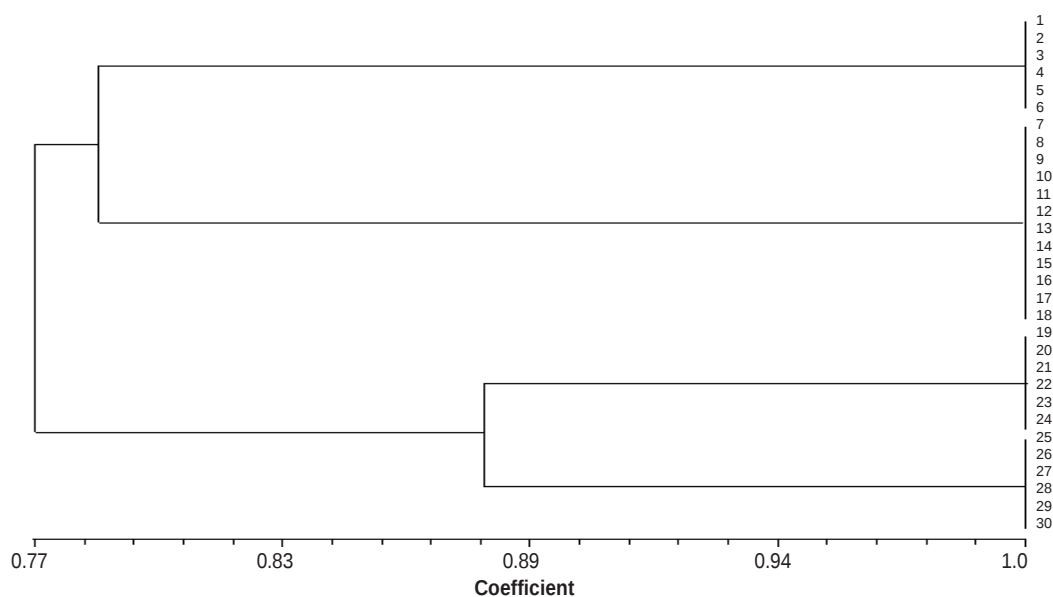


Fig. 3: Dendrogram showing genetic relatedness among 30 genotypes of *Woodfordia fruticosa*

thirty genotypes (Table 3). Only in five loci of the total twenty four studied show polymorphism that was not sufficient to characterize the individual genotypes.

Table 3. Summary of isozyme analysis obtained from thirty genotypes of *W. fruticosa*

Total number of enzyme studied	9
Total number of isozyme bands	29
Polymorphic isozyme bands	10
RM value range	0.03-0.95
Percent polymorphism	34.48 %

Genetic analysis based on isozyme analysis of thirty genotypes from the ten sites of Himachal Pradesh indicates low genetic variability of *W. fruticosa* germplasm. To the best of our knowledge this is the first report of isozyme polymorphism in *W. fruticosa*.

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Genetic Diversity Studies in Ash Gourd [*Benincasa hispida* (Thunb.) Cogn.] from Northern India

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The genetic diversity, clustering pattern and ordination (principal components) analyses were undertaken in 26 ash gourd accessions. The accessions showed significant inter-population differences and wide variation for quantitative and qualitative morphological descriptors observed. Low level of difference between the magnitude of PCV and GCV indicated that the descriptors were least influenced by environment and are genetically controlled. High heritability coupled with high genetic advance was observed for descriptors such as primary branches, fruits/plant and fruit weight/plant. These accessions were grouped into four major clusters. The clusters were homogenous within themselves and heterogeneous among each other. Cluster IV was the most distinct with more primary branches, higher individual fruit weight, more fruits/plant and highest fruit weight/plant. The PCA in general confirmed the groupings obtained through cluster analysis. PCA revealed four informative components accounting for 67.71% variance. PC1 was related with petiole length, node number at which first female flower appears and yield contributing descriptors like primary branches, fruit length, fruit width and fruit weight.

Key Words: Ash gourd, *Benincasa hispida*, Germplasm evaluation, Cluster analysis, Principal component analysis, Diversity analysis

Introduction

Ashgourd [*Benincasa hispida* (Thunb. Cogn.)], also popularly known as wax gourd, white pumpkin or winter melon has been under cultivation in India since ancient times. Among the cucurbits, ash gourd/wax gourd is considered a prized vegetable because of its high nutritional value, long storage life and good transport qualities, besides its medicinal properties. The young leaves, flowers and both immature and mature fruits are consumed. The mature fleshy fruit is either eaten raw or cooked as vegetable marrow or 'candied' as sweetmeat popularly known as 'petha'. It is a good source of carbohydrate, vitamin A, vitamin C and minerals like iron and zinc (Randhawa *et al.*, 1983 and Sureja *et al.*, 2006). An enzyme extracted from ash gourd juice can be used in place of calf rennet for producing cheddar cheese (Gupta and Eskin, 1977). It is also used to treat a variety of ailments in ayurvedic and naturopathy systems of medicine (Ramesh *et al.*, 1989).

Ash gourd is a monotypic genus and no wild or related species are reported. De Candolle found it wild on the sea shore of Java and later it spread Northwards to Japan, Central America and West Indies. There are reports suggesting that cultivated forms might have originated in South East Asia. Indo-China region is the centre of diversity for ash gourd (Rubatzky and Yamaguchi, 1997).

Indian cultivars were the earliest wax gourds introduced to Europe (Robinson and Decker-Walters, 1999).

In spite of its economic importance, no systematic efforts have so far been made to assess the genetic diversity of ash gourd germplasm. In India, the National Bureau of Plant Genetic Resources (NBPGR) has the responsibility of managing genetic resources of crop plants and their wild relatives. The present study was therefore undertaken to estimate the diversity present in the germplasm accessions with the objective of their potential use in crop improvement.

Materials and Methods

Twenty-six accessions of ash gourd germplasm representing diverse types from specific agro-ecological niches of ash gourd growing areas of Uttar Pradesh were used for the present study. These comprise 21 accessions from Eastern Uttar Pradesh, three from Orissa and one each from Jharkhand and Gujarat. Majority of these accessions were collected in the recent past under the National Agricultural Technology Project on Plant Biodiversity which was operational at NBPGR from 1999-2002. The germplasm accessions were grown in Complete Randomized Block Design (RBD) with two replications in three hills per accession and two plants per hill during 2002-03 at Vegetable Experimental Farm, Division of Vegetable Crops, IARI, New Delhi with a

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channel to channel spacing of 6 m and hill to hill spacing of 1 m. Data were recorded on a set of distinct 20 qualitative and 12 quantitative morphological descriptors (Table 1) following the minimal descriptors (Srivastava *et al.*, 2001). Data for quantitative descriptors were recorded on four randomly selected competitive individuals per accession and subjected to Analysis of Variance (ANOVA).

The different variability parameters as well as the heritability (broad sense, H^2_{bs}) and genetic advance (GA) as per cent of mean were calculated using Statistical Package for Agricultural Research (SPAR) programme developed at the Indian Agricultural Statistics Research Institute (IASRI), Pusa Campus, New Delhi, India.

The frequency distribution for quantitative and qualitative descriptors was computed and the phenotypic frequencies were also analyzed by the Shannon-Weiner Diversity Index (H') in order to estimate the diversity of each descriptor (Weaver and Shannon, 1949).

$$H' = -\sum_{i=1}^n p_i \log_e p_i$$

where, p_i is the proportion of the accessions in the i^{th} class of n -class descriptors.

Correlation between quantitative descriptors were computed for identification of descriptors of breeding importance.

Classification (cluster) and ordination (principal components) analyses were also performed. Skewed data on quantitative descriptors were transformed before multivariate analysis. Ward's minimum variance clustering method was used to classify accessions in discrete clusters (Sneath and Sokal, 1973). Principal components analysis was performed using quantitative descriptors. The statistical analysis was carried out using INDOSTAT statistical package developed at the INDOSTAT Services, Hyderabad, India.

Results and Discussion

The ANOVA (Table 2) showed significant differences as well as wide variation for all the quantitative descriptors studied. The variability parameters, heritability (H^2_{bs}) and genetic advance (GA) for 12 quantitative descriptors and frequency distribution for 20 qualitative descriptors are presented in Table 3. The difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low for all the descriptors. This

Table 1. List of descriptors studied

Quantitative descriptors		
1	PB	Primary branches
2	PL	Petiole length (cm)
3	NFFF	Node number at which first female flower appears
4	DFFF	Days to 50% flowering
5	PDL	Peduncle length (cm)
6	RF	Ridges/fruit
7	FL	Fruit length (cm)
8	FWD	Fruit width (cm)
9	FWT	Fruit weight (Kg)
10	FPP	Fruits/plant
11	SPF	Seeds/fruit
12	FWP	Fruit weight/plant (Kg)
Qualitative descriptors		
13	Early plant vigour: (3=Poor 5=Good 7=Very Good)	
14	Plant growth habit (3=Short vine 5=Medium vine 7= Long vine)	
15	Stem pubescence (1=Smooth 2=Pubescence)	
16	Stem shape (1=Rounded 2=Angular)	
17	Tendrils (0=Absent 1=Present)	
18	Tendrils type (1=Coiled 2=Straight)	
19	Tendrils branching (1=Unbranched 2= Branched)	
20	Leaf margin (1=Entire 2=Serrate 3=Multifid)	
21	Leaf size (3=Small 5= Medium 7=Large)	
22	Leaf pubescence nature (3=Soft 5= Intermediate 7= Hard)	
23	Leaf pubescence density (0=No hairs 3=Sparse 5=Intermediate 7=Dense)	
24	Sex type (1=Monoecious 2=Gynodioecious 3=Andromonoecious 4=Hermaphrodite 5=Androecious 6=Dioecious)	
25	Peduncle shape (3=Round 5=Smoothly angled 7=Sharply angular)	
26	Fruit shape (1=Cylindrical 2=Spindle type 3=Round)	
27	Fruit skin colour (3=Light green 5=Intermediate 7=Dark green)	
28	Fruit skin lustre (3=Matty 5= Intermediate 7=Glossy)	
29	Fruit pubescence density (0=No hairs 3=Sparse 5= Intermediate 7= Dense)	
30	Fruit ridge (rib) Shape (1=Superficial 2=Rounded/Grooved 3= Intermediate 4= Deep grooved)	
31	Stem-end fruit shape (1=Depressed 3=Flattened 5=Rounded 7=Pointed)	
32	Blossom-end fruit shape (1=Depressed 3=Flattened 5=Rounded 7=Pointed)	

indicates that the descriptors were least influenced by environment and are controlled genetically. The phenotypic coefficient of variation for six descriptors namely, primary branches, petiole length, fruit weight, fruits/plant, seeds/plant and fruit yield/plant were in excess of 20% signifying skewed distribution, both positive and negative. Similar results were also observed in ash gourd by Singh *et al.* (2002). H' revealed presence of diversity (≥ 0.40) in respect of primary branches, petiole length, days to 50% flowering, fruit width, fruit weight, seeds/fruit, early plant vigour, plant growth habit, fruit skin colour and fruit ridge (rib) shape. The estimates of genotypic coefficient of variation (GCV) alone may not be adequate for selection. Hence, heritability estimates should also be considered (Burton, 1952). The descriptors viz. primary branches, node number at which first female

Table 2. Analysis of Variance for different descriptors studied

Source of Variation	df	PB	PL	NFFF	DFFF	PDL	RF	FL	FWD	FWT	FPP	SPF	FWP
Replication	1	1.86	1.24	6.11	64.69	0.55	1.61	3.5	5.92	0.14	1.44	29473.92	1.04
Treatment	25	21.70**	28.06**	101.53**	78.49**	6.66**	1.37**	45.50**	13.18**	2.11**	19.63**	139633.92**	267.10**
Error	25	1.38	3.87	3.73	3.77	0.85	0.39	1.53	2.20	0.26	0.32	30946.33	13.11
Total	51	11.35	15.68	51.72	41.59	3.69	0.89	23.13	7.65	1.16	9.81	84195.69	137.38

** Significant at $p = 0.01$

Table 3. Range of variation in quantitative descriptors and predominance of qualitative descriptors of the ash gourd collections

Descriptors	Range	Mean	H ²	GCV (%)	PCV (%)	H ² _{bs}	GA as per cent of mean
Primary branches	6.0 - 18.0	11.5 ± 0.5	0.46	27.8	29.6	88.1	53.8
Petiole length (cm)	10.2 - 29.0	17.7 ± 0.6	0.44	19.6	22.3	75.7	35.2
Node number at which first female flower appears	33.0 - 66.3	45.6 ± 1.0	0.37	15.3	15.9	92.9	30.4
Days to 50% flowering	58.0 - 86.0	70.8 ± 0.9	0.42	8.6	9.1	90.8	16.9
Peduncle length (cm)	6.9 - 17.1	9.8 ± 0.3	0.38	17.4	19.8	77.5	31.6
Ridges/fruit	4.5 - 8.5	6.7 ± 0.1	0.33	10.4	13.9	56.0	16.0
Fruit length (cm)	28.8 - 51.7	36.1 ± 0.7	0.39	13.0	13.4	93.5	25.8
Fruit width (cm)	15.1 - 27.5	19.1 ± 0.4	0.40	12.3	14.5	71.4	21.4
Fruit weight (Kg)	2.0 - 6.3	3.6 ± 0.2	0.42	27.0	30.5	78.4	49.3
Fruits/plant	1.0 - 12.5	3.8 ± 0.4	0.36	81.2	82.5	96.8	164.5
Seeds/fruit	267.5 - 1538.0	836.8 ± 40.2	0.41	27.9	34.9	63.7	45.8
Fruit weight/plant	2.5 - 56.9	13.2 ± 11.7	0.30	85.6	89.9	90.6	167.8
Early plant vigour	Poor (3), Good (13), Very Good (10)		0.42				
Plant growth habit	Short vine (3), Medium vine (11), Long vine (12)		0.42				
Leaf size	Small (3), Medium (16), Large (7)		0.39				
Leaf pubescence nature	Soft (3), Intermediate (20), Hard (3)		0.30				
Leaf pubescence density	Sparse (4), Intermediate (18), Dense (4)		0.36				
Fruit shape	Cylindrical (21), Spindle type (2), Round (3)		0.27				
Fruit skin colour	Light Green (13), Intermediate (7), Dark green (6)		0.45				
Fruit skin lustre	Matty (14), Intermediate (12)0.30						
Fruit pubescence density	Sparse (19), Intermediate (4), Dense (3)		0.33				
Fruit ridge (rib) shape	Rounded/Grooved (11), Intermediate (3), Deep grooved (12)		0.42				
Stem-end fruit shape	Depressed (14), Rounded (12)0.30						
Blossom-end fruit shape	Depressed (6), Rounded (20)0.23						

flower appears, days to 50% flowering, fruit length, fruits/plant and fruit yield/plant showed high broad sense heritability (>80%) whereas petiole length, peduncle length, ridges/fruit, fruit width, fruit weight and seeds/fruit showed medium heritability (50-80%). Genetic advance over mean is the measure of genetic gain over mean. Higher genetic advance over mean was observed for descriptors namely, primary branches, fruit weight, fruits/plant, seeds/fruit and fruit yield/plant. High heritability along with high genetic advance (per cent of

mean) is more helpful in establishing close relationship between genotypes and phenotypes (Johnson *et al.*, 1955). High heritability coupled with high genetic advance was observed for primary branches, fruits/plant and fruit yield/plant indicating the influence of additive gene effects; hence, selection will be effective for genetic improvement. Similar results for primary branches and fruit yield/plant were also observed in bottle gourd (Singh and Kumar, 2002). High heritability and low genetic advance were observed for node number at which first female flower

Table 4. Correlation matrix for quantitative descriptors

Descriptors	PB	PL	NFFF	DFFF	PDL	RF	FL	FWD	FWT	FPP	SPF	FWP
PB	1.00	0.15	0.13	0.13	0.06	-0.03	0.22	0.40**	0.22	-0.01	-0.07	0.03
PL		1.00	0.39**	-0.21	-0.20	0.17	0.41**	0.50**	0.30*	-0.21	0.31*	-0.10
NFFF			1.00	0.05	-0.01	0.01	0.01	0.24	0.37**	-0.05	0.29*	0.09
DFFF				1.00	-0.18	-0.14	-0.14	-0.18	0.03	-0.21	0.11	-0.10
PDL					1.00	0.01	-0.14	0.08	-0.16	0.05	-0.22	-0.07
RF						1.00	-0.09	0.24	-0.01	0.12	0.19	0.15
FL							1.00	0.57**	0.25	-0.15	-0.17	-0.10
FWD								1.00	0.46**	-0.14	0.12	-0.03
FWT									1.00	0.07	0.18	0.38**
FPP										1.00	0.29*	0.91**
SPF											1.00	0.36**
FWP												1.00

*, ** significant at $p = 0.05$ and 0.01 respectively.

appears, days to 50% flowering and fruit length indicating the influence of non-additive gene effects. These results are in conformity with the findings of the earlier workers in ash gourd (Singh *et al.*, 2002) and ridge gourd (Prasad and Singh, 1989).

Correlations between important descriptors are presented in Table 4. The fruit yield/plant was positively and significantly correlated with fruit weight, fruits/plant and seeds/fruit. Number of primary branches was positively and significantly correlated with fruit width where as petiole length was positively and significantly correlated with node number at which first female flower appears, fruit length, fruit width, fruit weight and seeds/fruit. Node at which first female flower appears was positively and significantly correlated with fruit weight and seeds/fruit. Fruit length and fruit width was positively and significantly correlated with fruit width and fruit weight respectively. Fruits/plant was positively and significantly correlated with seeds/fruit. Positive and significant correlation between fruit weight/plant and number of fruits/plant and in between fruit length and fruit width was also reported in ridge gourd (Prasad and Singh, 1989). Correlations between important descriptors help in selection of desirable types, if high correlations exist or are established by breeding techniques between complex descriptors like yield that has a low heritability with other simply inherited component descriptors.

Ward's clustering technique clearly defined and characterized the clusters based on morphological descriptors. The accessions were grouped into four clusters based on distance ranges for the tree shown in Figure 1. Clusters I, II, III and IV comprised 9, 8, 7 and 2

accessions, respectively. The maximum inter cluster distance (6.24) was observed in between cluster I and IV (Table 5). Cluster means of different quantitative descriptors and predominance of qualitative descriptor states for individual clusters are presented in Table 6. Critical examination of the clusters revealed that clusters were homogeneous within themselves and heterogeneous between each other based on the major descriptors. Cluster IV was most distinct from other three clusters as evident from inter cluster distances (Table 6). This cluster is characterized by accessions having more primary branches, shortest peduncle length, more ridges/ fruit, higher fruit weight, more fruits/plant, more seeds/fruit, highest fruit yield/plant, more early plant vigour, medium to long vine length, medium leaf size, soft to intermediate leaf pubescence nature, sparse to intermediate leaf pubescence density, cylindrical fruit shape, green to dark green fruit skin color, matty fruit skin lustre, dense fruit pubescence, rounded/grooved fruit ridge (rib) shape with rounded blossom end fruit shape. Cluster I was characterized by accessions having long petiole, higher node number at which first female flower appears, greater fruit length and width, good to very good early plant vigour, medium to long vine, medium to large leaf size, intermediate to hard leaf pubescence nature and matty to

Table 5. Inter and Intra cluster (underlined) distances

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	<u>4.23</u>	5.04	4.99	6.24
Cluster II		<u>4.28</u>	4.55	5.68
Cluster III			<u>3.66</u>	6.03
Cluster IV				<u>5.31</u>

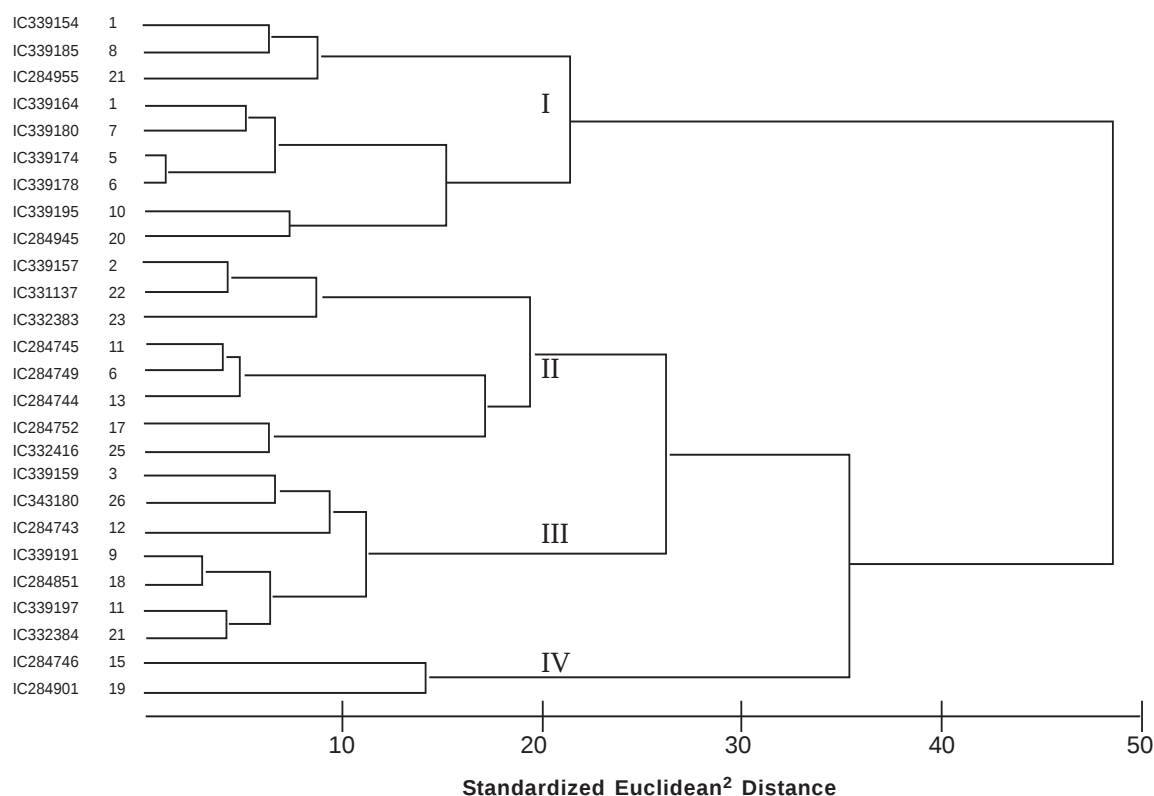


Fig. 1: Ward's Minimum Variance Dendrogram

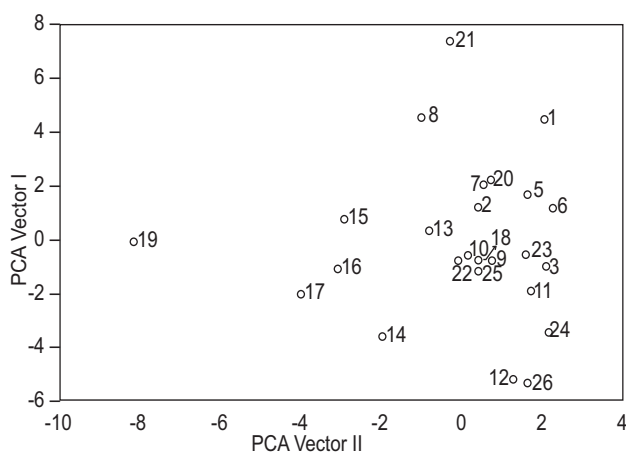
Table 6. Means of quantitative descriptors and predominance of qualitative descriptors' states in different clusters

Descriptors	Cluster I	Cluster II	Cluster III	Cluster IV
Primary branches	12.64	12.42	8.43	12.92
Petiole length (cm)	21.62	15.73	15.40	16.10
Node number at which first female flower appears	48.97	45.10	40.93	48.67
Days to 50% flowering	69.22	68.19	73.93	77.00
Peduncle length (cm)	9.26	10.96	9.74	7.84
Ridges/fruit	7.08	6.27	6.57	7.58
Fruit length (cm)	38.55	35.65	35.12	30.53
Fruit width (cm)	21.43	18.41	17.34	17.14
Fruit weight (Kg)	3.71	3.59	3.08	4.53
Fruits/plant	2.16	6.16	1.90	8.75
Seeds/fruit	936.90	762.79	664.58	1285.47
Fruit yield/plant (kg)	7.99	19.18	5.82	38.10
Early plant vigour	Good to very good	Poor to very good	Poor to very good	Good to very good
Plant growth habit	Medium to long vine	Short to long vine	Short to long vine	Medium to long vine
Leaf size	Medium to large	Small to medium	Medium to large	Medium
Leaf pubescence nature	Soft to hard	Soft to intermediate	Soft to hard	Soft to Intermediate
Leaf pubescence density	Sparse to Dense	Sparse to Dense	Sparse to Dense	Sparse to Intermediate
Fruit shape	Cylindrical to round	Cylindrical to round	Cylindrical and round	Cylindrical
Fruit skin colour	Light to dark green	Light to dark green	Light to dark green	Green to dark green
Fruit skin luster	Matty to intermediate	Matty to intermediate	Matty to intermediate	Matty
Fruit pubescence density	Sparse to Dense	Sparse to intermediate	Sparse	Dense
Fruit ridge (rib)	Rounded/grooved to deep	Rounded/grooved to deep grooved	Rounded/grooved and grooved	Rounded/grooved deep grooved
Blossom-end fruit shape	Depressed and rounded	Depressed and rounded	Depressed and rounded	Rounded

Table 7. Eigen values, cumulative variance of the first four principal components (PCs) and factor loading between PCs and descriptors studied

	PC1	PC2	PC3	PC4
Eigen value	2.87	2.39	1.52	1.34
Percent of variance	23.94	19.91	12.68	11.19
Cumulative variance	23.94	43.85	56.52	67.71
Descriptors	Factor loadings			
Primary branches	0.41	0.14	0.11	0.57
Petiole length (cm)	0.81	0.11	-0.06	-0.37
Node number at which first female flower appears	0.55	-0.15	-0.37	-0.02
Days to 50% flowering	-0.14	0.12	-0.72	0.36
Peduncle length (cm)	-0.21	0.04	0.53	0.07
Ridges/fruit	0.18	-0.31	0.22	-0.59
Fruit length (cm)	0.59	0.39	0.31	0.18
Fruit width (cm)	0.83	0.21	0.30	0.01
Fruit weight (Kg)	0.68	-0.23	-0.15	0.35
Fruits/plant	-0.08	-0.88	0.31	0.23
Seeds/fruit	0.34	-0.60	-0.44	-0.33
Fruit weight/plant (Kg)	0.11	-0.91	0.15	0.29

intermediate fruit skin lustre. Cluster II was characterized by accessions having less number of days to 50% flowering, small to medium leaf size, soft to intermediate leaf pubescence, matty to intermediate fruit skin lustre, sparse to intermediate fruit pubescence density. Cluster III was characterized by lowest node number at which first female flower appears, lowest seeds per fruit, sparse to intermediate leaf pubescence density, matty to intermediate fruit skin lustre, sparse fruit pubescence density, rounded/grooved and deep grooved fruit ridge (rib) shape. The minimum intra-cluster distance was recorded for cluster III (3.66) followed by cluster I (4.23) and cluster II (4.28).

**Fig. 2: 2D Principal Components Scatter Plot**

Principal components analysis performed on quantitative descriptors revealed that the first four most informative components accounted for 67.71% variance (Table 7). It also presented the descriptors with greater weightings in each of the four principal component axes. Characteristics of each Principal Component were determined on the basis of estimated factor loadings. Descriptors with greater weightings were petiole length, node number at which first female flower appears, yield contributing descriptors like primary branches, fruit length, fruit width, and fruit weight in PC1; fruit length in PC2; peduncle length, ridges/fruit, fruit length, fruit width and fruits/plant in PC3; primary branches, days to 50% flowering, fruit weight and fruit yield/plant in PC4.

The scatter plot of PC scores of first two PC axes is presented in Figure 2. The Principal Components Analysis (PCA) in general confirmed the groupings obtained through cluster analysis. A few distinct accessions could be marked. In some cases the pairs of accessions originating from the same locations fall into tight groups within clusters whereas in other accessions from the same location, are far apart in ordination.

The multivariate analysis might be effective in indicating high yielding accessions in different clusters which could be usefully intercrossed. The PCA ordination revealed that while the scatters of points for the clusters have a central focus, there are significant outliers to some groups. This presumably comes from the third PC. The outliers and central clusters provide the opportunity to identify representatives from the central as well as outliers for use in breeding.

The present study helped in understanding the diversity in the accessions studied and indicates the need for evaluating large number of accessions so as to identify desired germplasm for crop improvement. Being a potential crop of the future, collection programmes from major ash gourd growing areas as well as non-traditional areas should be planned along with introduction from South East Asian and South Asian countries like China.

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Micropropagation of Bael [*Aegle marmelos* (L.) Corr.] – An Indigenous Medicinal Fruit Tree of India

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A protocol for micropropagation of bael [*Aegle marmelos* (L.) Corr.] was developed. Bael (family Rutaceae) is an indigenous medicinally important fruit of India. The nodal explants of 30 year old tree were used to initiate cultures. Two cytokinins, viz., 6-benzylaminopurine (BAP) and kinetin (Kn) were used in varied concentration (0.1-2 mg/l) for shoot multiplication. BAP (2 mg/l) was found better than Kn, where a 3-fold increase in the number of shoots was recorded in 4 weeks. A synergistic influence of cytokinin and auxin was also observed in the present study. A combination of 0.5 mg/l BAP and 0.1 mg/l IAA induced the formation of maximum number (4.5) of shoots (2.5 cm). For rooting of *in vitro* shoots, different auxins, namely, NAA, IAA and IBA (0.1-2 mg/l) were tested. IAA (0.01 mg/l) was found better than NAA and IBA. It was concluded that elite cultivars of bael can be micropropagated, without undergoing callus phase, using the BAP (0.5 mg/l) plus IAA (0.1 mg/l) for shoot multiplication and IAA (0.1 mg/l) for rooting, to produce true-to-type *in vitro* plants. The *in vitro* raised plantlets were acclimatized with 30% success.

Key Words: *Aegle marmelos*, Bael, *In vitro*, Medicinal fruit tree, Nodal segment, Micropropagation

Introduction

Bael [*Aegle marmelos* (L.) Corr.], a member of family Rutaceae, is an important indigenous fruit of India. Bael fruit is valued for its curative properties, which make this tree one of the most useful medicinal plants of India. The leaves of the tree are traditionally used as sacred offering to 'Lord Shiva' according to Hindu custom. It grows throughout the Indian peninsula as well as in Sri Lanka, Pakistan, Bangladesh, Burma, Thailand and most of the South-East Asian countries.

The ripe fruit is a laxative whereas unripe fruit is prescribed for diarrhea and dysentery. It is in great demand from native systems of medicine such as Ayurveda (Kirtikar and Basu, 1975; Wealth of India, 1985). Various chemicals such as alkaloids, coumarins and steroids have been isolated and identified from different parts of the tree such as leaves, wood, roots and barks (Roy, 1985). The bael fruit is one of the most nutritious fruit. According to Gopalan *et al.* (1971), 100 g of fresh fruit pulp contains 61.5 g water, 1.8 g protein, 0.39 g fat, 1.7 g minerals, 31.8 g carbohydrate, 55 mg carotene, 0.13 mg thiamine, 1.19 mg riboflavin, 1.1 mg niacin, and 8 mg vitamin C. No other fruit has such a high content of riboflavin.

Bael is usually propagated by seeds and can be also propagated by budding on 1 or 2 years old rootstock. Budding in the month of June-July favoured best results (Singh *et al.*, 1976). The conventional methods of propagation are time-consuming and due to

heterozygosity, the seed progeny is not true-to-type. Earlier studies were taken up to develop micropropagation protocol with the various explants such as axillary bud (Kumar and Seenii, 1998; Mishra *et al.*, 2008), cotyledonary nodes (Arumugam and Rao, 1996; Nayak *et al.*, 2007) and leaves from *in vitro* seedlings (Islam *et al.*, 1993) and met with limited success. There is a strong need to produce true-to-type micropropagated plants from mature trees of *A. marmelos* to ensure the supply of quality planting materials (Islam *et al.*, 1993). Therefore, the present study was taken up with objective to develop a micropropagation protocol using nodal explants from the field-grown mature tree.

Materials and Methods

Plant Material

The nodal explants were collected from a 30 year old tree grown in the nursery of NBPGR, New Delhi.

Culture Medium

The nutrient medium used for the study was MS (Murashige and Skoog, 1962), with 0.8% bacto-agar and 3% sucrose (Qualigens Fine Chemicals). The pH of the media was adjusted to 5.8 using 0.1 N NaOH or 0.1 N HCl. The media was poured into culture tubes (20 ml/tube). The culture tubes (25 mm x 150 mm, Borosil, India) were closed with polypropylene caps and autoclaved for 15 minutes at 121°C at 1.06 kg cm⁻² pressure.

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Culture Initiation

The nodal explants were cut to the size of 2-3 cm, all leaves were removed and washed under running tap water for 30 minutes. The explants were then washed with Tween 20 for 5 minutes, followed by a washing with distilled water. Explants were surface sterilized with 0.1% mercuric chloride (HgCl_2) and washed thoroughly with sterile distilled water. Nodal segments were trimmed to the size of 1.5-2.0 cm, bearing single axillary bud, and inoculated on to the MS basal medium (with no growth hormone). The established cultures were further sub-cultured on the same medium to raise sufficient stock material for experiments.

Shoot Multiplication

For shoot multiplication experiments, shoots with single node were cultured on MS media (AEG0-AEG8) supplemented with different growth regulator alone, i.e., BAP (0.1, 0.5, 1, 2 mg/l), kinetin (0.1, 0.5, 1 and 2 mg/l) and a combination of BAP (0.5 mg/l) and IAA (0.1 mg/l).

Rooting

Four-week-old cultures of bael were used for rooting experiments. *In vitro* shoots of about 0.5-1 cm size were transferred (1 shoot/ tube) on rooting medium (AEG0-AEG12) containing different concentrations of NAA (0.1, 0.5, 1, 2 mg/ l), IAA (0.1, 0.5, 1, 2 mg/ l), and IBA (0.1, 0.5, 1, 2 mg/ l). Medium without auxin was used as control.

Acclimatization

Rooted plantlets of 8-week-age were taken out of the culture tubes, washed thoroughly and planted in the plastic pots containing sterile soilrite. The pots were covered with polythene.

Culture Conditions

The cultures were kept at $25 \pm 1^\circ\text{C}$ and 16 h photoperiod under 40 $\mu\text{mol/m}^2\text{s}$ light, which was provided by 40 Watt cool day light fluorescent lamps adjusted 30 cm high from the culture tubes.

Observation and Statistical Analysis

Observations were taken every week. Data were recorded on shoot parameters, namely, number of shoot, shoot length, number of nodes, presence or absence of callus. The observations on root parameters include root initiation, number of roots, root length and presence and absence of callus. A total of 12 tubes (single node per

tube) were inoculated for each treatment ($n=12$). Data are presented as percentage and mean. Mean values of treatments were compared using the Least-Significant-Difference Test. Significance is stated at $P \leq 0.05$.

Results and Discussion

Culture Initiation

The contamination-free cultures showed axillary buds swelling as the first response. Bud break occurred in 50% explants in 4 weeks.

Shoot Multiplication

The cultures showed single shoot in almost all media including the basal (AEG0), used as control. The average shoot number increased from 1 to 2.9 in AEG4 followed by AEG3 (2.4) and AEG2 (2) (Table 1). The BAP was better than kn in terms of mean number of shoot per culture. The highest number of shoots with kn was 1.7 (AEG7) followed by 1.5 (AEG8) after 4 weeks of subculture. The cultures showed about 3-fold shoot multiplication on BAP (2 mg/l).

The mean shoot length was not significantly different but ranged from 0.7 cm in AEG3, AEG4 medium to 0.9 cm in AEG0, AEG1 and AEG2 (BAP) medium after 4 week and 0.8 cm AEG5, AEG6 medium to 1 cm in AEG8 medium after 4 week. The shoots started growing from the 1 week and gradually reached to their maximum by 4th week. Kn and BAP were more or less equally effective as seen by the mean of shoot length after 4 weeks. However, a significantly high number of shoots (4.5) with 2.5 cm shoot length were produced on AEG9 medium

Table 1. Effect of various cytokinins in MS media on shoot multiplication of *A. marmelos* after 4 weeks of subculture

Medium code	Cytokinin conc. (mg/l)	4 week growth	
		Mean shoot no	Mean shoot length (cm)
AEG0	BAP 0	1.9 ^{bc}	0.9 ^b
AEG1	BAP 0.1	1.4 ^c	0.9 ^b
AEG2	BAP 0.5	2.0 ^{bc}	0.9 ^b
AEG3	BAP 1	2.4 ^b	0.7 ^b
AEG4	BAP 2	2.9 ^b	0.7 ^b
AEG5	Kn 0.1	1.4 ^c	0.8 ^b
AEG6	Kn 0.5	1.4 ^c	0.8 ^b
AEG7	Kn 1	1.7 ^{bc}	0.9 ^b
AEG8	Kn 2	1.5 ^c	1 ^b
AEG9	BAP 0.5+ IAA 0.1	4.5 ^a	2.5 ^a

The values are mean ($n=12$); Mean in a category followed by different letters are significantly different at $P < 0.05$

with a combination of BAP (0.5 mg/l) and IAA (0.1 mg/l) (Table 1).

The shoot initiation was observed without the formation of callus in nodal segments, ensuring direct shoot formation in all the treatments. The results of the present findings show low rate of shoot multiplication on cytokinin medium when used alone. The low rate of shoot production was reported earlier in the callus induced shoot cultures of *A. marmelos* (Varghese *et al.*, 1993). Repeated sub-culturing of nodes from shoot cultures may help to achieve continuous production of callus-free, healthy shoots through further subculture cycles. A synergistic influence of cytokinin and auxin was observed when a combination of them was tested in the present study. Combination of 0.5 mg/l BAP and 0.1 mg/l IAA induced the formation of maximum number (4.5) of stout and long (2.5 cm) shoots.

Rooting

Shoots formed grew uniformly and could be harvested in four weeks for rooting. The cultures showed no rooting in media used for shoot induction or multiplication, which shows the requirement of auxins to root *in vitro* shoots. Different concentration of NAA (0.5 mg/l), IAA (0.1 mg/l) and IBA (1 mg/l) were required to induce formation of one to three roots in 3 weeks at a frequency (number of shoots rooted) of 10%, 50% and 10%, respectively (Table 2). Roots were normal, *i.e.*, straight, white, thick and healthy in all the cultures (Fig.1).

Table 2. Effect of various auxins in MS media on root parameters of *A. marmelos*

Medium code	Auxins conc. (mg/l)	Root frequency (%)	Root no per shoot	Mean root length per shoot (cm)	Root condition
AEGR0	–	0 ^c	0	0	–
AEGR1	NAA 0.1	0 ^c	–	–	–
AEGR2	NAA 0.5	10 ^b	1	0.5	normal
AEGR3	NAA 1	0 ^c	–	–	–
AEGR4	NAA 2	0 ^c	–	–	–
AEGR5	IAA 0.1	50 ^a	3	1.5	normal
AEGR6	IAA 0.5	0 ^c	–	–	–
AEGR7	IAA 1	0 ^c	–	–	–
AEGR8	IAA 2	0 ^c	–	–	–
AEGR9	IBA 0.1	0 ^c	–	–	–
AEGR10	IBA 0.5	0 ^c	–	–	–
AEGR11	IBA 1	10 ^b	1	0.9	normal
AEGR12	IBA 2	0 ^c	0	0	–

The values are mean (n=10); Mean in a category followed by different letters are significantly different at P<0.05

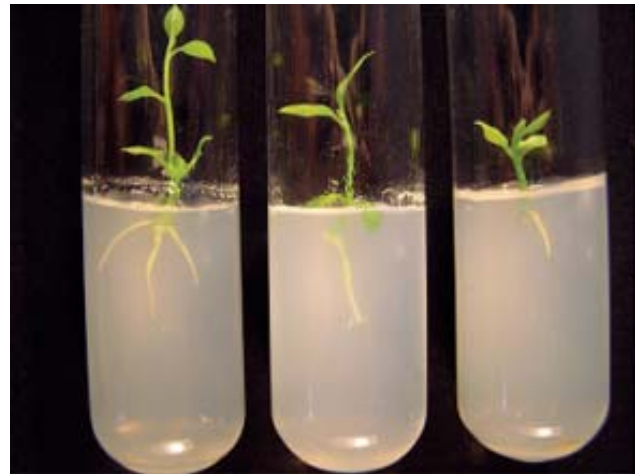


Fig. 1: Four weeks old cultures of *Aegle marmelos*: Plantlets are on medium MS + IAA, MS + IBA, MS + NAA (from left to right)

Acclimatization

Well rooted shoots were transferred into the pot. Only 30% plants could be successfully established in the soil in the present study. However, in the other study, a high rate of establishment was recorded among the rooted plants raised in the presence of IAA (70%) and IBA (90%) compared to NAA (40%) after hardening (Islam *et al.*, 1993).

Successful micropropagation has been easily achieved with seed derived explants of *A. marmelos* (Islam *et al.*, 1993) and other explants. In the earlier report, regarding stem segments of mature trees (Varghese *et al.*, 1993), the formation of a limited number of shoots was preceded by extensive callus formation. The present study showed that the shoot multiplication and rooting without the callus formation is possible in bael and that ensures true-to-type micropropagated plants. Thus, it is concluded that elite cultivars of bael can be micropropagated using a combination of BAP and IAA for shoot multiplication and IAA for rooting.

Acknowledgements

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Studies on the Medicinal Compound L-Dopa in *Mucuna pruriens* Bak.

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Fifty *Mucuna* germplasm accessions were augmented through introduction, exchange and exploration activities of National Bureau of Plant Genetic Resources (NBPGR), New Delhi. L-Dopa contents in *Mucuna* seeds were estimated as per cent/ gram of dry seed on an UV Spectrophotometer at 280 nm. The L-Dopa contents varied significantly in different accessions and ranged between 1.51 to 6.29 %. The minimum L-Dopa contents were recorded in accession number IC471873 and the maximum in IC385843. Out of 50 *Mucuna* accessions analyzed, L-Dopa contents varied significantly between 2-4.5% per gram of dry seeds in 45 accessions. Comparatively higher L-Dopa contents were recorded in the accessions IC385843, IC391885, IC83195, IC471875 and IC396648 with 6.3%, 5.8%, 5.2%, 4.9% and 4.6%, respectively. The present study validates the possible exploitation of five *Mucuna* germplasm for their pharmacological properties mainly the L-Dopa.

Key Words: *Mucuna*, Germplasm, Seeds, L-Dopa contents

Introduction

The genus *Mucuna* has a wide distribution in tropical and subtropical regions of the world. In India, 14 species are widespread over most of the subcontinent in bushes and hedges, dry-deciduous, low forests and throughout the plains of India (Sastry and Kavathekar, 1990; Singh *et al.*, 1996).

All the parts of *Mucuna* contain valuable medicinal properties (Pandey, 1998, 1999; Caius, 1989) and there is a heavy demand of *Mucuna* in Indian drug market. After the discovery that *Mucuna* seeds contain L-Dopa, an anti-Parkinson's disease drug, its demand in international market has increased many fold (Daxenbichler *et al.*, 1971, 1972; Lorenzetti *et al.*, 1998; Farooqi *et al.*, 1999) and demand has motivated Indian farmers to start commercial cultivation. Besides medicinal properties, *Mucuna* fixes nitrogen and is used as a green manure and cover crop.

Mucuna pruriens Bak. belongs to family Fabaceae, commonly known as Velvet bean, is one of the popular medicinal species and is constituent of more than 200 indigenous drug formulations. Seeds contain L-Dopa, glutathione, lecithin, gallic acid, glycosides, nicotine, prurenine, prurenidine, dark brown viscous oil (Ghosal *et al.*, 1971, Szabo and Tebbett, 2002). It is source of minerals (Rastogi and Mehrotra, 1991a, b; Singh *et al.*, 1995). According to Ayurveda, seeds are astringent, laxative, anthelmintic, aphrodisiac, alexipharmic and tonic. In particular, the seeds and the roots of *M. pruriens* are used in the system of medicine as effective nerve tonic

and aphrodisiac. It has diuretic property and consequently is used in kidney ailments and dropsy. The seeds contain L-Dopa (L-3, 4-dihydroxy phenylalanine), which is the active principle responsible for the treatment of Parkinson's disease and hypertension (Dollery, 1999; Moffat, 1986; Spratto and Woods, 1996; Szabo and Tebbett, 2002). In addition, the seeds have fats, sterols, alkaloids and other amino acids.

Of all these, the L-Dopa is the main active principle. A large number of analytical procedures have been reported in literature for the extraction, isolation and estimation of L-Dopa in the seeds. Considerable research work has also been done to produce L-Dopa through tissue culture (Brain, 1976; Huizing *et al.*, 1985; Wichers *et al.*, 1985) but it has not gone on commercial scale for industrial purpose. Considering the importance of this genus, attempts have been made throughout the world to screen and identify high L-Dopa yielding lines (Pieris *et al.*, 1980; Lubis and Sastrapardha, 1981; Bammi and Gangadhar Rao, 1982) for their commercial cultivation.

Materials and Methods

Plant Material

Fifty *Mucuna* germplasm accessions were selected from exotic and indigenous collections of National Bureau of Plant Genetic Resources (NBPGR), New Delhi and through explorations. The germplasm accessions represented 12 Indian states and eight exotic collections representing four species of *Mucuna*, namely, *M. utilis* Wall. ex. Wight, *M. panaba*, *M. pruriens*, *M. prurita*

and others as *Mucuna* species. The details of NBPGR accession numbers, *Mucuna* species, and place of collection are given in Table 1.

L-Dopa Estimation in *Mucuna* Seeds

L-Dopa contents in *Mucuna* seeds were estimated following the method described by Brain (1976) with some modifications. Standard curve of L-Dopa was plotted using pure L-Dopa AR (Sisco Research Lab) concentration 10 to 100 µg/ml on an UV/Vis Spectrophotometer (Hitachi U1500). The stock solution of L-Dopa was prepared using 15 mg of L-Dopa AR in a test tube and 3 ml of 0.1 N HCl was added to it. The solution was heated in a boiling water bath for 15 minutes. Cooled down to room temperature and added 3 ml of ethanol. Shaked for 10 minutes with hand and centrifuged at 2000 rpm for 10 minutes. Supernatant was aspirated and volume raised up to 15 ml. Finally, the solution was filtered through Whatman micro-filter (0.22 micron porosity) and diluted with ethanol so as to obtain 10, 20, 30, 40, 50, 60, 70, 80, 90, and 100 µg/ml concentrations of L-Dopa.

The absorption was read at 280 nm and standard curve was plotted taking L-Dopa concentration on X-axis and optical density at Y-axis.

Extraction and Estimation of L-Dopa

The *Mucuna* seeds were crushed in pastel mortar and seed coats were removed. Further, the seeds contents were powdered and taken in to 18 x 150 mm test tubes. The L-dopa was extracted from the 0.5 g powdered seed. Three replications were maintained for each germplasm accession. To 0.5 g powdered seed, 3 ml of 0.1 N HCl was added and kept in boiling water bath for 15 minutes. The test tubes were allowed to cool down to room temperature before adding 3 ml of absolute ethanol. The test tubes were then vigorously shaken for 10 minutes and centrifuged at 2000 rpm for 10 minutes. Supernatant was aspirated using 1000 µl micropipette. Finally, the volume was raised up to 15 ml. The solution was then filtered through Whitman membrane filter (0.22 micron porosity). The solution was diluted 1:10 with ethanol before reading A_{280} .

Calculation

The OD for 100 µg was taken as standard.

$$\text{L-Dopa / 100 } \mu\text{l solution (A)} = \frac{100 \times X}{Y} \text{ (in } \mu\text{g)}$$

$$\text{So, L-Dopa / ml solution (B)} = A \times 10 \text{ (in } \mu\text{g)}$$

$$\text{So, L-Dopa in 15 ml Solution (0.5 g seeds) (C)} = B \times 15 \text{ (in } \mu\text{g)}$$

$$\text{So, L-Dopa content in 1 g seed (D)} = C \times 2 \text{ (in } \mu\text{g)} = C \times 2/10^{-6} \text{ g}$$

$$\text{So, Per cent L-Dopa content} = 100 \times D \text{ (in g)}$$

Where,

$$X = A_{280} \text{ for sample}$$

$$Y = A_{280} \text{ for 100 } \mu\text{g L-Dopa}$$

Results and Discussion

The standard curve prepared using pure L-Dopa with 10 to 100 µg/ml for quantification of L-Dopa in *Mucuna* seeds is shown in Figure 1. Almost straight line of the standard curve at recommended wave length of 280 nm validated the precise quantification of L-Dopa in seeds of *Mucuna* accessions analyzed. The L-Dopa contents were finally estimated as percent/gram of dry seed. The L-Dopa contents varied significantly in different accessions and ranged between 1.51 to 6.29%. The minimum L-Dopa contents were recorded in accession number IC471873 and the maximum in IC385843.

Of the 50 *Mucuna* accessions analyzed, L-Dopa contents varied significantly between 2-4.5 % per gram of dry seeds in 46 accessions. Comparatively higher L-Dopa contents were recorded in the accessions IC385843, IC391885, IC83195, IC471875 and IC396648 with 6.3%, 5.8%, 5.2%, 4.9% and 4.6%, respectively (Table 1, Fig. 2). All these five high L-Dopa yielding *Mucuna* accessions can be exploited for extraction of L-Dopa contents.

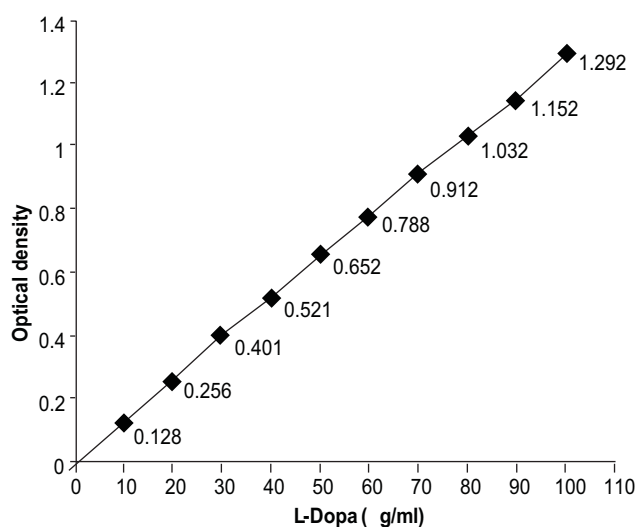
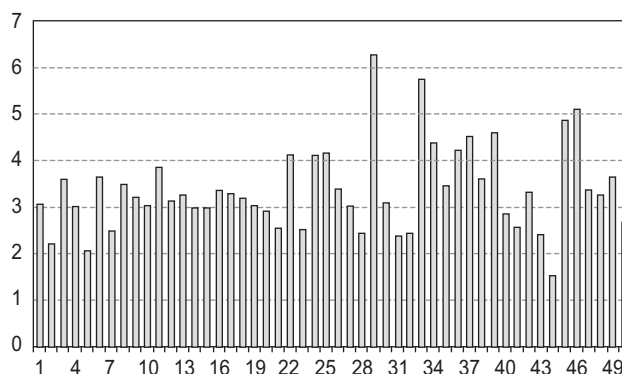


Fig. 1: Standard curve of L-Dopa

Table 1. *Mucuna* germplasm accessions with L-Dopa content per gram of seed

S. No.	Accession No.	Species	Collection Place	L-Dopa content per gram seed
1	EC030	<i>M. pruriens</i>	Australia	3.05
2	EC13047	<i>M. pruriens</i>	USSR	2.21
3	EC144945	<i>M. pruriens</i>	Italy	3.61
4	EC169813	<i>M. pruriens</i>	Nigeria	3.02
5	EC1842	<i>M. pruriens</i>	Australia	2.07
6	EC1842-A	<i>M. pruriens</i>	Australia	3.63
7	EC25334	<i>M. pruriens</i>	Kenya	2.49
8	EC4475	<i>M. pruriens</i>	Australia	3.48
9	IC127363	<i>M. pruriens</i>	NBPGR, HQ	3.21
10	IC15809-A	<i>M. pruriens</i>	Palaman/Bihar	3.04
11	IC21992	<i>M. utilis</i>	Madhya Pradesh	3.85
12	IC21996-A-1	<i>M. utilis</i>	Madhya Pradesh	3.15
13	IC21998	<i>M. utilis</i>	Madhya Pradesh	3.26
14	IC241679	<i>M. pruriens</i>	NBPGR, HQ	2.98
15	IC241680	<i>M. pruriens</i>	Kerala	2.99
16	IC241682	<i>M. pruriens</i>	Palaghat/Kerala	3.35
17	IC25333	<i>M. pruriens</i>	Mizoram	3.29
18	IC25333-2	<i>M. pruriens</i>	NBPGR, HQ	3.20
19	IC25333-A-1	<i>M. pruriens</i>	NBPGR, HQ	3.01
20	IC25334-2	<i>M. pruriens</i>	NBPGR, HQ	2.91
21	IC2534-2	<i>M. pruriens</i>	NBPGR, HQ	2.53
22	IC260046	<i>M. pruriens</i>	Kerala	4.12
23	IC260707	<i>M. pruriens</i>	Salem/Tamil Nadu	2.52
24	IC265577	<i>M. pruriens</i>	Kerala	4.11
25	IC296846	<i>M. pruriens</i>	Karnataka	3.64
26	IC296847	<i>M. pruriens</i>	Karnataka	2.67
27	IC326953	<i>M. utilis</i>	Solan/Himachal	4.17
28	IC33243	<i>M. pruriens</i>	Madhya Pradesh	3.38
29	IC369144	<i>M. pruriens</i>	Jharkhand	3.01
30	IC385841	<i>M. prurita</i>	Jharkhand	2.43
31	IC385843	<i>M. prurita</i>	Jharkhand	6.29
32	IC385844	<i>M. pruriens</i>	Godda/Jharkhand	3.10
33	IC385925	<i>M. prurita</i>	Jharkhand	2.39
34	IC385926	<i>M. prurita</i>	Jharkhand	2.44
35	IC391885	<i>M. pruriens</i>	Orissa	5.76
36	IC391899	<i>M. pruriens</i>	Orissa	4.38
37	IC391941	<i>M. pruriens</i>	Orissa	3.45
38	IC392241	<i>M. prurita</i>	Jharkhand	4.22
39	IC392835	<i>M. pruriens</i>	Orissa	4.51
40	IC392850	<i>M. pruriens</i>	Orissa	3.60
41	IC396648	<i>M. prurita</i>	Narmada/ Gujarat	4.60
42	IC43993	<i>M. pruriens</i>	Kerala	2.85
43	IC471869	<i>M. pruriens</i>	NBPGR, HQ	2.56
44	IC471870	<i>M. pruriens</i>	NBPGR, HQ	3.33
45	IC471872	<i>M. pruriens</i>	NBPGR, HQ	2.42
46	IC471873	<i>M. pruriens</i>	NBPGR, HQ	1.51
47	IC471875	<i>M. pruriens</i>	NBPGR, HQ	4.87
48	IC83195	<i>M. prurita</i>	Narmada/ Gujarat	5.12
49	IC83298	<i>M. pruriens</i>	NBPGR, HQ	3.37
50	IC16993-A	<i>M. pruriens</i>	Manipur	3.25
	CD			0.30

**Fig. 2: L-Dopa per cent per gram of seed in fifty accessions of *Mucuna***

In a survey of over 1000 plant species from 160 families, only *Mucuna* seed was found to contain L-Dopa at $> 0.5\%$ with concentrations between 3.1 and 6.7% indicated (Daxenbichler *et al.*, 1971, 1972). Other studies have reported as much as 9% L-Dopa contents in some *Mucuna* seeds, and as little as 1.5% in the seeds of *M. gigantea* which grows wild in southern India (Rajaram and Janardhanan, 1991). Less than 1% of the administered dose of L-Dopa actually enters the brain where it is converted to dopamine in the basal ganglia (Dollery, 1999; Moffat, 1986). Currently in the treatment of Parkinson's disease L-Dopa is almost always prescribed in a drug regimen with a peripheral deoxycarboxylase inhibitor to prevent loss of L-Dopa by the enzyme L-aromatic amino acid decarboxylase (LAAD) that begins in the internal mucosa. The presence of LAAD increases the amount of L-Dopa available to the brain by 75-80% (Jancovic and Caine, 1987), thereby decreasing the dosage necessary to achieve therapeutic effect.

L-Dopa itself has very little pharmacological effect, since it is rapidly converted to dopamine. Most side effects arise directly from dopamine's activity as a neurotransmitter involved in the regulation of heart, vascular system, digestive tract, and excretory system, rather than from its well-known effect on receptors in the brain (Dollery, 1999; Standaert and Young, 1996). With the limitation in mind, the inadvertent ingestion of L-Dopa as a result of consuming *Mucuna* that has not been adequately prepared could have serious consequences (Infante *et al.*, 1990).

Therefore, the possibility of raising *Mucuna* as a cash crop for its L-Dopa contents must be addressed and it may prove to be an affordable alternative for patients suffering from Parkinson's disease (Kempster

and Wahlqvist, 1994; Manyam and Sanchez-Ramos, 1999). The present study validates the possible exploitation of five promising *Mucuna* germplasm accessions for their pharmacological properties especially L-Dopa content.

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SHORT COMMUNICATION

Expression of Heterosis and Combining Abilities (Gca & Sca) in Inter-Specific Crosses of Tomato (*Lycopersicon esculentum* Mill. syn. *Solanum lycopersicum* L.)**G Himanshu¹, N Rai^{*2}, RK Singh¹ and DB Singh¹**¹ Crop Improvement Division, Indian Institute of Vegetable Research, Jakhni, Shahanshahpur, Varanasi-221305, Uttar Pradesh, India² Allahabad Agriculture Institute–Deemed University Allahabad, Uttar Pradesh, India**Key Words: Heterosis, Combining ability and Interspecific hybrids**

Interspecific crosses among wild and cultivated lines of tomato revealed that wild line EC520061 was the best combiner for plant height, number of primary branches and pericarp thickness, EC528372 for the days to 50% flowering, seeds/fruit and number of locules, EC521080 for maximum fruit set (%) and fruits/plant, EC520049 for the total soluble solids and yield/plant. High specific combining ability coupled with high heterosis were recorded in cross combinations, Hisar Anmole x EC520061 for plant height and primary branches; Kashi Vishesh x EC521080, Punjab Chhuhara x EC521080 and Kashi Anupam x EC528372 for fruits/plant and locules/fruit; Kashi Anupam x WIR-3957 for seed/fruit; Hisar Anmole x EC520049 and Punjab Chhuhara x EC528372 for the total soluble solids and yield/plant.

Tomato is grown in almost all parts of country (India), covering large area with high production (Sadhankumar *et al.*, 2007). Tomato is good source of vitamins and minerals. There are several species of tomato but only the fruits of two species, namely, *Solanum lycopersicum* (*Lycopersicon esculentum*) and *S. pimpinellifolium* are edible. Most of the *Solanum lycopersicum* based cultivars though they are high yielder are highly susceptible to abiotic and biotic stresses. However, wild species like *S. pimpinellifolium*, *S. habrochaites*, *S. cerasiformae*, *S. chilense*, *S. chmielewskii* and *S. peruvianum* have smaller fruit size but superior number of fruits with resistance/tolerance to several stresses. Keeping in view the importance of wild species of tomato, twenty-four crosses were made to know extent of heterosis, combining ability and gene action using wild species as one of the parent.

Four *Solanum lycopersicum* varieties namely, Punjab Chhuhara, Hisar Anmole, Kashi Anupam and Kashi

Vishesh as female parents and six testers of different wild species, viz., EC521080 (*S. pimpinellifolium*), EC520061 (*S. hirsutum*, syn. *S. habrochaites*), WIR-5032 (*S. chilense*), EC520049 (*S. chmielewskii*), EC528372 (*S. cerasiformae*) and WIR-3957 (*S. peruvianum*) were crossed in line x tester mating design at Indian Institute of Vegetable Research, Varanasi, during the year 2005-2006 to generate inter-specific F₁'s. Twenty four F₁s along with their parents were transplanted in Randomized Block Design (RBD) with three replications at spacing of 60 cm x 45 cm in plot size of 4.5 x 3.7 m during spring-rabi in 2006-2007. Ten plants in each replication were randomly selected from both parents and F₁s for recording data on plant height (cm), number of primary branches, days to flowering (50%), fruit set (%), fruits number/plant, fruit yield/plant (kg), seed number/fruit, locules number/fruit, pericarp thickness(mm) and total soluble solids(TSS). The mean data was statistically analysed to know the extent of heterosis (over best parent) and combining abilities (gca and sca) as per procedure given by Kempthorne (1957).

The extent of heterosis over the better parents of 24 crosses for yield and quality traits is presented in Table 1 and revealed that cross combinations Hisar Anmole x WIR-5032 and Kashi Anupam x WIR-5032 exhibited high and positive heterosis for plant height. Kumar *et al.* (1995) also reported similar finding in tomato. As regards number of primary branches, the positive and high heterosis was in Hisar Anmole x EC520061. Negative heterosis for early flowering and maturity is considered as a desirable feature for early yield. Negative and significant heterosis was recorded in cross combination Hisar Anmole x EC520061 and Punjab Chhuhara x EC520061. Negative heterosis for days to flowering was also reported by Premalakshme

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Table 1. Mean performance of heterosis over better parent and mid parent

Characters	Crosses	Mean	Heterosis for BP (%)
Plant height	Hisar Anmole × WIR-5032	186.73	59.74**
	Kashi Anupam × WIR-5032	161.61	38.29*
	Hisar Anmole × EC520061	280.53	31.38**
	Kashi Vishesh × EC520061	273.77	28.21*
Number of primary branches	Hisar Anmole × EC520061	25.47	81.04**
	Kashi Vishesh × EC520049	15.50	65.48**
	Punjab Chhuhara × EC520049	14.00	49.47**
	Kashi Anupam × EC520049	13.67	45.91**
Days to 50% flowering	Hisar Anmole × EC520061	21.00	-33.68**
	Punjab Chhuhara × EC520061	21.00	-33.68**
	Hisar Anmole × WIR-5032	21.00	-30.77**
	Punjab Chhuhara × WIR-5032	21.00	-30.77**
Per cent fruit set	Hisar Anmole × EC521080	87.07	24.38**
	Kashi Vishesh × EC521080	82.10	17.29**
	Punjab Chhuhara × EC521080	80.17	14.52*
	Kashi Anupam × EC521080	77.77	11.10
Number of fruits/plant	Kashi Vishesh × EC520049	255.47	42.22*
	Kashi Anupam × EC528372	135.60	13.31
	Punjab Chhuhara × EC528372	117.13	-2.12
	Hisar Anmole × EC528372	112.83	-5.68
Fruit yield/plant (Kg)	Hisar Anmole × EC520049	4.47	244.70**
	Hisar Anmole × EC521080	1.85	43.41**
	Hisar Anmole × WIR-3957	1.78	37.98**
	Kashi Anupam × WIR-5032	2.71	5.03**
Number of locules/fruit	Kashi Vishesh × EC520061	2.00	-62.50**
	Hisar Anmole × EC521080	2.00	-60.00**
	Hisar Anmole × EC520061	2.00	-60.00
	Hisar Anmole × EC5032	2.00	-60.00**
Pericarp thickness (cm)	Kashi Anupam × EC520049	.32	62.50**
	Kashi Anupam × WIR-3957	.37	31.25**
	Hisar Anmole × WIR-3957	0.43	30.00**
	Kashi Vishesh × EC528372	0.40	25.00**
Number of seeds/fruit	Kashi Vishesh × EC520061	35.43	-76.44**
	Hisar Anmole × EC520061	29.80	-74.80**
	Kashi Anupam × EC520061	43.73	-71.86**
	Kashi Vishesh × WIR-3957	49.63	-66.99**
Total soluble solids (%)	Kashi Vishesh × WIR-3957	5.73	30.30**
	Hisar Anmole × WIR-3957	5.50	25.00**
	Hisar Anmole × EC520049	5.83	20.6**
	Kashi Anupam × EC520061	6.13	12.20**

* Significant at 0.05% level, **Significant at 0.01% level

et al. (2006) in tomato. Maximum fruit set (%) was recorded in cross combination Hisar Anmole × EC521080 and Kashi Vishesh × EC521080. Whereas, number of fruits per plant, one of the major component for yield, was the highest in Kashi Vishesh × EC520049. Highest heterosis for yield per plant was observed in cross combination Hisar Anmole × EC520049. The wide range of heterosis observed for yield is attributed to the genetic diversity of the parents used in hybrid combinations. In tomato, lesser number of locules in fruit which showed negative heterosis in cross combination Kashi Vishesh × EC520061, is considered desirable for good shape index. The negative heterosis

over better parents for this trait was also reported by Singh *et al.* (2008) which is in consonance with our findings. Heterosis over better parents for increase in pericarp thickness was recorded in cross combinations Kashi Anupam × EC520049 and Kashi Anupam × WIR-3957. Negative heterosis for number of seeds was recorded in cross combination Kashi Vishesh × EC520061. The highest heterosis for total soluble solids was recorded in Kashi Vishesh × WIR-3957.

Table 2 shows both combining abilities effect (gca and sca) indicating EC520061, EC521080, EC528372 and EC520049 were good general combiners for yield and quality contributing character. This suggests that parent

showing high sca and yield may be due to their high gca for number of fruits. Premalakshme *et al.* (2006) have also reported high sca for fruit yield due to high gca for number of fruits per plant. Specific combining ability in present investigation exhibited that the cross combinations Kashi Anupam × EC521080 and Hisar Anmole × EC520061 had high positive sca effect as well as high degree of heterosis for plant height, while, Hisar Anmole × EC5210061, Kashi Anupam × WIR-3957, Kashi

Anupam × EC520061, Kashi Vishesh × EC528372, Punjab Chhuhara × EC528372, Punjab Chhuhara × EC521080, Kashi Anupam × WIR-3957, Kashi Anupam × WIR-3957, Hisar Anmole × EC3957 and Hisar Anmole × EC520049 for number of primary branches, days to 50% flowering, per cent fruit set, fruit width, fruit length, number of fruits/plant, number of seeds/fruit, number of locules, pericarp thickness and fruit yield/plant, respectively. The crosses viz. Punjab Chhuhara × EC528372, Kashi Vishesh × WIR-

Table 2. General combining ability and Specific combining ability effect of the 10 parents and 24 F₁'s yield and quality traits

Parents and crosses	Plant height (cm)	No. of primary branches	Days to 50% flowering	Fruit set (%)	No. of fruits/plant	No. of seeds/fruit	No. of locules/fruit	Pericarp thickness (cm)	TSS (%)	Fruit/plant (kg)
Female Line										
Punjab Chhuhara	-15.96**	-1.03**	-0.50	-1.29	15.09**	-3.44**	-0.29*	0.02	-0.13	-0.27**
Kashi Vishesh	14.04*	0.52	1.50	-0.65	10.32**	-2.28*	0.15	-0.01	0.15	0.28**
Kashi Anupam	-12.47*	-0.26	0.50	-0.98	-18.75**	4.29**	0.15	0.00	-0.03	-0.19*
Hisar Anmole	14.38**	0.77*	-1.50	2.93	-6.66*	1.42	-0.01	-0.01	0.01	0.18*
Tester male										
EC521080	-9.38	-2.13**	-1.50	6.70*	94.06**	8.21**	0.21*	-0.01	0.04	0.45**
EC520061	70-62*	5.89**	1.50	-2.35	39.99**	-29.11**	-0.29**	0.07**	0.34**	-0.26**
WIR-5032	-19.62**	-1.74**	1.50	-0.90	-2.91	-5.49**	-0.04	0.00	-0.29**	-0.23**
EC520049	-14.88**	0.14	0.00	4.12	-20.94**	-5.87**	0.21*	-0.04*	0.38**	0.95**
EC528372	-22.52**	0.94**	-1.50	-3.37	-90.93**	21.65**	-0.46**	0.06**	-0.35**	-0.45**
WIR-3957	-4.23	-1.22**	0.00	-4.20	-19.28**	10.61**	-0.21*	0.05**	-0.11	-0.46**
SE (GCA) Line	2.46	0.17	0.00	1.33	1.44	0.49	0.05	0.00	0.05	0.05
SE (GCA) Tester	3.17	0.22	0.00	1.72	1.86	0.64	0.06	0.01	0.07	0.04
Punjab Chhuhara × EC521080	-3.12	-214**	0.50	-0.32	155.20**	-11.52**	0.21	0.00	-0.22	1.03**
Punjab Chhuhara × EC520061	11.85*	-0.29	-2.50	9.97**	-45.76**	21.20**	0.29*	0.05**	-0.02	-0.41**
Punjab Chhuhara × WIR-5032	-10.74	1.60**	-2.50	-2.47	-14.26**	-27.32**	-0.04	-0.02	-0.23	0.25
Punjab Chhuhara × EC520049	21.49**	1.26**	5.00	-0.73	-35.40**	16.72**	0.21	0.02	-0.23	-0.61**
Punjab Chhuhara × EC528372	-20.28**	-0.26	0.50	-8.51**	-8.71*	1.34	-0.46**	0.02	0.80**	0.15
Punjab Chhuhara × WIR-3957	0.80	-0.15	-1.00	2.06	-15.06**	-0.42	-0.21	-0.07**	-0.10	0.08
Kashi Vishesh × EC521080	-7.75	2.29**	-1.50	0.98	-31.57**	19.52**	0.10	-0.04**	-0.20	0.26
Kashi Vishesh × EC520061	16.95**	-1.35**	1.50	-16.70**	45.74**	4.20**	-0.15	-0.02	0.00	0.77**
Kashi Vishesh × WIR-5032	-30.68**	-2.29**	1.50	-1.35	-29.93**	12.82**	-0.15	0.01	0.16	-0.80**
Kashi Vishesh × EC520049	7.09	1.20**	-3.00	6.86*	64.40**	-2.47*	0.10	0.05**	-0.87**	-0.61**
Kashi Vishesh × EC528372	1.12	-0.88*	-1.50	9.09**	-43.64**	4.04*	0.43**	0.05**	0.35**	0.91**
Kashi Vishesh × WIR-3957	13.27*	0.43	3.00	1.12	-4.9	-29.70**	-0.32**	-0.04**	0.59**	-0.52**
Kashi Anupam × EC521080	24.23**	-0.47	-0.50	-3.03	-88.64**	-2.55*	-0.24*	0.02	0.18	-0.95**
Kashi Anupam × EC520061	-52.17**	-3.53**	2.50	10.42**	40.67**	-3.47*	-0.15	0.08**	0.71**	0.43*
Kashi Anupam × WIR-5032	21.60**	2.03**	2.50	-1.62	51.17**	13.58**	0.15	0.00	-0.47**	1.57**
Kashi Anupam × EC520049	14.73*	0.16	-2.00	-0.71	-2.20	-10.68**	-0.24*	-0.06**	0.77**	-0.53**
Kashi Anupam × EC528372	6.70	1.97**	-0.50	0.22	43.59**	-29.6**	-0.57**	-0.06**	-0.21	-0.45**
Kashi Anupam × WIR-3957	-15.09*	0.11	-2.00	-5.28	-44.59**	32.78**	0.68**	0.02	-0.97**	-0.06
Hisar Anmole × EC521080	-13.36*	-0.01	1.50	2.36	-34.99**	-5.45**	-0.07	0.03	0.24	-0.34*
Hisar Anmole × EC5210061	23.38**	5.17**	-1.50	-3.69	-40.65**	-13.53**	0.01	-0.11**	-0.69**	-0.79**
Hisar Anmole × EC5032	19.85**	-1.34**	-1.50	5.44	-6.98*	0.92	-0.32**	0.01	0.53**	-0.52**
Hisar Anmole × EC520049	-43.32**	-2.61**	0.00	-5.42	-26.79**	-3.57**	-0.07	-0.01	0.33*	1.75**
Hisar Anmole × EC528372	12.45*	-0.83*	1.50	-0.80	8.77**	24.88**	0.60**	-0.01	-0.91**	-0.61**
Hisar Anmole × EC3957	1.03	-0.39	0.00	2.10	100.65**	-2.65*	-0.15	0.10**	0.49**	0.50**
SE ±	5.50	0.38	0.00	2.98	3.23	1.11	0.11	0.01	0.12	0.1577

* Significant at 0.05% level and **Significant at 0.01% level

3957 and Hisar Anmole x WIR-5032 were found the best specific combiners as well as exhibited high heterosis over best parent for TSS.

Thus present findings suggest that among wild species the lines EC520049, WIR-5032, EC528372 and EC521080 may be used as male parent for obtaining high yield along with better quality (TSS) F_1 's.

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SHORT COMMUNICATION

Collection and Characterization of *Allium* Species from Himachal PradeshVD Verma¹, K Pradheep¹, Anil Khar², KS Negi^{*3} and JC Rana¹¹ National Bureau of Plant Genetic Resources, Regional Station, Shimla-171004, Himachal Pradesh, India² National Research Centre for Onion and Garlic, Rajgurunagar-410505, Pune, Maharashtra, India³ NBPGR, Regional Station, Bhowali-263132, Nainital, Uttarakhand, India

A total of 56 accessions including 12 wild and cultivated *Allium* species were collected from Lahaul & Spiti, Kinnaur, Chamba and Shimla districts of Himachal Pradesh and were characterized using IBPGR descriptors. Poor establishment was noticed in *A. humile*, *A. carolinianum* and *A. auriculatum* indicating their poor adaptation to changed habitat. Collected population of wild *Allium* species showed genetic variation within the species for characters such as bulb shape, pungency, 100-seed weight etc.

Key Words: *Allium*, Wild species, Collection, Characterization, Himachal Pradesh

The genus *Allium* considered under the family Alliaceae, is one of the largest genera of more than 700 species distributed throughout the world (Kim *et al.*, 2001). Nearly all *Allium* crops originate from the main centre of *Allium* species diversity which stretches from the Mediterranean basin to Central Asia and beyond. Indian gene centre is fairly rich in wild species (about 30) mostly confined to Himalayas. Negi and Pant (1992) and Pandey and Pandey (2005) reported occurrence of wild *Allium* species in Himalayas. Wild *Allium* species are the good source of flavonols (Horbowicz and Kotlinska, 2000). Many are used in Western Himalaya as spice/condiment in curries, as vegetable and bulbs for seasoning salads since time immemorial. Knowledge on biosystematic relationship of wild *Allium* species occurring in Himalaya is sparse, which is a thrust area since wild relatives can offer novel traits for crop improvement. Apart from this, few species have potential as new crops of culinary, therapeutic and medicinal value. Hence, efforts were made to collect and characterize the *Allium* germplasm.

A total of 56 accessions of wild and cultivated *Allium* species were collected from Lahaul & Spiti, Kinnaur, parts of Chamba and Shimla (Churdhar Peak) districts of Himachal Pradesh in two explorations at seed maturity stage, i.e. during August-September 2005 and 2006 (Fig.1). These comprised 11 species namely, *Allium schoenoprasum* L. (10), *A. fistulosum* L. (3), *A. carolinianum* DC. (syn. *A. blandum*) (11), *A. griffithianum* Boiss (6), *A. tuberosum* Rottl. ex Spreng (2), *A. consanguineum* (syn. *A. stracheyi* Baker) (4), *A. przewalskianum* Regel (syn. *A. jacquemontii* Baker)

(4), *A. humile* Kunth (syn. *A. govanianum* Wall. ex Baker) (1), *A. auriculatum* Kunth (2), *A. sativum* L. (12) and *A. ampeloprasum* L. (1). Their occurrence, vernacular name and biological status are furnished in Table 1. The cultivated species *A. sativum*, *A. schoenoprasum*, *A. fistulosum* and *A. ampeloprasum* were found in kitchen garden and farmers' fields and wild species at acute slopes of dry rocky mountains. One accession, namely, serpent garlic, botanically *A. sativum* var. *ophioscordon* (Link) Doll. was also collected from kitchen gardens in Koksar (Lahaul & Spiti). Sympatric association of different wild *Allium* species was observed, but no hybrid derivatives/swarms, indicating their cross-incompatible nature.

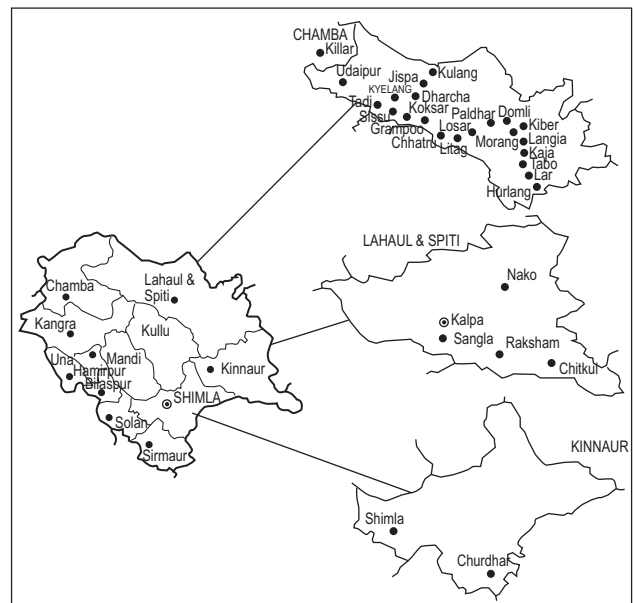


Fig. 1: Collection of wild *Allium* species in Shimla, Kinnaur and Lahaul and Spiti

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Table 1. *Allium* species collected from high hills and alpine region of Himachal Pradesh

Species	Vernacular name	Collection site	Biological status	Altitude (m)
<i>Allium schoenoprasum</i> L.	Chung, Rechong, Koche, Dhum, Keer	Koksar, Kangsar, Kuring, Udaipur (Lahaul)	Cultivated; semi wild	1890-4060
<i>A. fistulosum</i> L.	Japani onion, Chong, Chuwang	Chal Thang (Lahaul & Spiti), Kuring (Lahaul)	Cultivated; semi-wild	3115-3850
<i>A. carolinianum</i> DC. (Syn. <i>A. blandum</i> Wall.)	Laut, Arum	Shego, Kungti Gumpah, Morang, Losar (Spiti), Ranguo (Lahaul)	Wild	3540-4560
<i>A. griffithianum</i> Boiss.	Neolagu, Keer	Adargu (Spiti), Pangi (Chamba), Raksham (Kinnaur)	Wild	2660-3490
<i>A. tuberosum</i> Rottl. ex Spreng	Zimu, Jangli piaz	Bhavanagar (Kinnaur), Tabo (Spiti)	Semi-wild	1620-3300
<i>A. auriculatum</i> Kunth	Shillim	Chhicham (Spiti)	Wild	3850-4190
<i>A. consanguineum</i> Kunth (Syn. <i>A. stracheyi</i> Baker)	Keer	Kadunala, Shour (Chamba), Baspa dam, Sangla, Raksham (Kinnaur)	Wild	2420-2770
<i>A. humile</i> Kunth (Syn. <i>A. govanianum</i> Wall. ex Baker)	Duna	Chureshwar (Shimla)	Wild	3430
<i>A. przewalskianum</i> Regel (Syn. <i>A. jacquemontii</i> Baker)	Pharna	Nako, Maling (Kinnaur)	Wild	3370-3470
<i>A. ampeloprasum</i> L.	Chinese lahsun	Chitkul (Kinnaur)	Cultivated	3350
<i>A. sativum</i> L.	Gopa, Lahsun	Koksar (Lahaul), Kinnaur dt.	Cultivated	2260-3284

Present study was carried out at Experimental Farm, NBPGR Regional Station, Phagli, Shimla (31° 05' 924" N latitude, 77° 09' 580" E longitude; 1924 msl) for two consecutive years 2006 and 2007 using IBPGR descriptors (IBPGR, 1982). Nursery was raised from seeds for all species except *A. ampeloprasum* and *A. sativum* (for which cloves were used) during March in raised beds and after 45 days, the seedlings were transplanted in the field. For each accession, two rows of 2 m length with the spacing of 40 cm x 20 cm was adopted. Important qualitative and quantitative characteristics (mean and range values) of wild *Allium* species are depicted in Table 2. Collected populations of wild *Allium* species showed genetic variation within the species for characters such as bulb shape, pungency, 100-seed weight for instance, in *A. consanguineum*, 100-seed weight ranged from 0.70 to 2.83 g. All plants of *A. humile* degenerated after 35 days of transplanting under Shimla conditions. Poor establishment accompanied with poor seedling vigour was evident in *A. carolinianum* and *A. auriculatum* also indicating their poor adaptation to changed habitat. It was noticed that *A. carolinianum* was susceptible to white rot (*Sclerotium cepivorum*) while all the other species were free from disease symptoms at field level.

In *A. fistulosum*, three accessions showed clear-cut differences in plant stature i.e., dwarf, medium and tall. Although seed germination in wild *Alliums* was poor, *A. tuberosum* recorded nearly 70 per cent germination. High tillering capacity was noticed in *A. schoenoprasum* and *A. tuberosum*. The seeds of wild *Allium* species were conserved in National Gene Bank after characterization.

Cultivated and wild species of *Allium* possesses onion and garlic like odour, pungency and antioxidative properties in leaves and bulbs. Mostly wild *Allium* species are cold tolerant and drought resistant. In *A. fistulosum*, resistance to white rot (*Sclerotium cepivorum*) (Anon., 1985) and anthracnose (*Colletotrichum gloeosporioides*) (Galvan *et al.*, 1997) was reported. Taxonomically *A. cepa*, *A. fistulosum* and *A. schenoprasum* belong to subgenus *Rhiziriduem* while *A. ampeloprasum* and *A. sativum* under subgenus *Allium* (Hanelt *et al.*, 1992). Kim and Chae-YongAm (2003) reported that hybridization between *A. fistulosum* and *A. cepa* lead to local Korean cultivars such as Samcheung-Pa and Soekkori-Pa. Successful interspecific hybrids between *A. fistulosum* and *A. chinense* were obtained through ovary culture and pollen storage (Nomura *et al.*, 1994) and with *A. galanthum* (Yamashita *et al.*, 2000). Close taxonomic

Table 2. Important characteristics of accessions of various *Allium* species studied (based on IBPGR Descriptors)

Species**	Early seedling vigour	Leaf colour	Leaf shape	Leaf length (cm)	Leaf girth thickness* (mm)	Leaf habit	Leaf wax	Flower colour	Nature of umbel	Size of Flower to Head	No. of Flower to/ Umbel	Inflorescence height (cm)	Plant height (cm)	Effective tillers/ plant	Bulb colour	Bulb shape	Pungency	100-seed weight (g)
<i>A. schoenoprasum</i>	Vigorous-very vigorous	Dark green	Fistular	18.17 (15.3-20.6)	3.04 (2.7-4.6)	Semi erect	Waxy	Purple	Semi-compact	Small-medium	29.9 (17.0-65.0)	18.1 (13.0-20.9)	22.92 (20.3-25.6)	5.13 (3.3-6.7)	Light purple	Elongated-ovoid	Medium High	0.54 (0.44-0.74)
<i>A. fistulosum</i>	Very vigorous	Dark green	Fistular	22.77 (18.3-30.3)	13.63 (12.0-15.5)	Erect	Waxy	White	Semi-compact	Large	132 (121-141)	25.77 (17.3-39.4)	34.07 (25.6-44.0)	3.2 (2.0-6.0)	Light whitish purple	Elongated	High	1.86 (1.76-2.02)
<i>A. tuberosum</i>	Vigorous	Green	Flat	22.57	2.94	Erect-semi erect	Non-waxy	White	Loose	Medium	37	47.67	57.63	4.03	Light purplish brown	Elongated	High	1.03
<i>A. carolinianum</i>	Poor	Light green-Green	Flat	13.16 (10.7-17.6)	1.10 (0.87-1.28)	Erect	Waxy (less intensity)	Purple	Compact	Medium	25 (21-31)	26.2 (21.7-29.6)	29.54 (24.0-36.3)	1.17 (1.0-1.6)	Brown	Ovoid	High	1.54 (1.21-1.70)
<i>A. auriculatum</i>	Poor	Green	Flat	24.70	1.97	Erect	Non waxy	Purple	Compact	Small-medium	30	20.65	29.66	1.95	Brown	Elongated	Medium	0.59
<i>A. griffithianum</i>	Poor	Dark green	Flat/half rounded	24.12 (19.2-27.8)	2.03 (1.8-2.5)	Erect	Waxy	Light purple	Compact	Medium	18 (15-21)	31.48 (19.8-38.0)	35.08 (20.3-44.3)	1.78 (1.0-4.6)	Light red	Elongated	Medium-high	0.60 (0.5-1.0)
<i>A. przewalskianum</i>	Vigorous	Light green	Fistular	26.63 (28.6-24.5)	2.00 (1.84-2.31)	Semi-erect	Non waxy	Light purple	Compact	Medium	38 (34-42)	37.03 (30.2-40.0)	38.67 (31.2-43.5)	3.53 (2.6-5.0)	Reddish brown	Ovoid-elongated	Medium-high	0.53
<i>A. consanguineum</i>	Vigorous	Dark green	Flat	30.23 (27.5-34.7)	2.58 (2.50-2.66)	Erect	Non waxy	Pale yellow	Compact	Small-medium	98 (76-111)	40.02 (37.5-43.7)	53.22 (50.2-58.3)	1.10 (1.0-1.2)	Brown	Oblong	Medium	1.68 (0.70-2.83)
<i>A. ampeloprasum</i>	Vigorous	Light green	Flat	41.32	2.30	Erect	Non waxy	Purple	Compact	Large	66	63.5	116	Nil	Greenish white	Globose	High	---
<i>A. sativum</i>	Vigorous-very vigorous	Light green	Flat	36.83 (32.6-40.1)	1.63 (0.96-2.41)	Erect	Non waxy	Pale-purple	Compact	Small	54.42 (26-72)	45.54 (42.1-50.6)	65.10 (52.5-71.6)	Nil	White-purplish white	Globose	High	---

* Thickness in case of flat leaves, ** Range noticed only for those species having at least 4 accessions, ^{a,b} In case of *A. sativum*, instead of flowers, bulbills were taken into account

affinity between *A. sativum* var. *ophioscorodon* and garlic's wild progenitor *A. longicuspis* was reported by Al-Zahim *et al.* (1997).

Biochemical analysis of quality-components, antioxidants, flavonols etc. in these *Allium* species and detailed characterization and evaluation for novel traits like disease resistance, cold hardiness and pungency level along with their crossability with cultivated species is the need of hour.

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Plant Germplasm Registration Notice*

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1. WR 95 (INGR 08070; IC563970) Wheat
(*Triticum aestivum*)

Thick culm, high grain no./spike possesses *apd1* gene for apical lethality, moderately resistance to yellow rust.

Bhanwar Singh, SMS Tomar, Vinod, Rajendra Singh,
M Sivasamy, Anil
Division of Genetics, IARI, New Delhi

2. HKI-288-2 (INGR 08071; IC563956) Maize
(*Zea mays*)

Late maturing, disease resistant female parent for single cross hybrid, dark green leaves and yellow grain.

3. HKI-1126 (INGR 08072; IC563958) Maize
(*Zea mays*)

Late maturing, bold seeded, resistant to MLB, seed parent with economic seed production, dark green broad leaves, purple tassel, good general combiner.

4. HKI-1040-4 (INGR 08073; IC563959) Maize
(*Zea mays*)

Medium maturing, dark green leaves, purple tassel and dark orange grain, good tassel trait, resistant to MLB and rust, good for early maturing, single cross hybrid.

5. HKI-1015 WG-8 (INGR 08074; IC 563961) Maize (*Zea mays*)

Less leafy, dark green leaves, orange and flint grain color, medium maturing, good general combining ability.

6. HKI-1347-4LT (1+2+3) (INGR 08075; IC563964) Maize (*Zea mays*)

Dark green leaves, shining white grain, resistant to rust and late maturing, white seeded productive inbred line.

7. HKI-164D-4(0) (INGR 08076; IC563965) Maize
(*Zea mays*)

Dark green leaves, resistant to rust and MLB, good general combiner (QPM), late maturing, with high tryptophan (0.86%).

8. HKI-164-7-6 (INGR 08077; IC563966) Maize
(*Zea mays*)

Dark green leaves, semi-dent grains, QPM, late maturing, good general combiner and high tryptophan content (0.94%).

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju,
Rishi Pal, Dharm Pal Singh
CCS, HAU, Regional Research Station, Uchani, Karnal

9. VQL5 (INGR 08078; IC563999) Maize
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High tryptophan contents (0.82%) which is 110.0% higher over V25.

10. VQL17 (INGR 08079; IC64000) Maize
(*Zea mays*)

High tryptophan contents (0.72%) which is 71.5% higher over original parent V341. VQL17 is extra early female parent of FQH38.

Vinay Mahajan, R Babu, HS Gupta, Sudha Nair,
PK Agrawal, GS Bisht, S Saha, MC Pant
Crop Improvement Division, VPKAS, Almora, Uttarakhand

11. MS463B (INGR 08080; IC560414) Sorghum
(*Sorghum bicolor*)

Converted male and female parents of dual purpose sorghum hybrid, SPH 1148 with high yield.

12. NR 486R (INGR 08081; IC561243) Sorghum
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S Audilakshmi, C Aruna, RV Vidya Bhushanam,
N Seetharama
NRC for Sorghum, Rajendranagar, Hyderabad, Andhra Pradesh

13. EC-13 (INGR 08082; IC345715) Sorghum
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Shoot fly resistant and high grain yielding.

M Elangovan, PG Padmaja, Prabhakar
NRC for Sorghum, Rajendranagar, Hyderabad, Andhra Pradesh

* Communicated by Drs. Anjali Kak and Kalyani Srinivasan (Member Secretary, PGRC), Germplasm Conservation Division, NBPGR

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3. HKI-1126 (INGR 08072; IC563958) Maize
(*Zea mays*)

Late maturing, bold seeded, resistant to MLB, seed parent with economic seed production, dark green broad leaves, purple tassel, good general combiner.

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(*Zea mays*)

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4. HKI-1040-4 (INGR 08073; IC563959) Maize
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6. HKI-1347-4LT (1+2+3) (INGR 08075; IC563964) Maize (*Zea mays*)

Dark green leaves, shining white grain, resistant to rust and late maturing, white seeded productive inbred line.

7. HKI-164D-4(0) (INGR 08076; IC563965) Maize
(*Zea mays*)

Dark green leaves, resistant to rust and MLB, good general combiner (QPM), late maturing, with high tryptophan (0.86%).

8. HKI-164-7-6 (INGR 08077; IC563966) Maize
(*Zea mays*)

Dark green leaves, semi-dent grains, QPM, late maturing, good general combiner and high tryptophan content (0.94%).

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Rishi Pal, Dharm Pal Singh
CCS, HAU, Regional Research Station, Uchani, Karnal

9. VQL5 (INGR 08078; IC563999) Maize
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High tryptophan contents (0.82%) which is 110.0% higher over V25.

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High tryptophan contents (0.72%) which is 71.5% higher over original parent V341. VQL17 is extra early female parent of FQH38.

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Crop Improvement Division, VPKAS, Almora, Uttarakhand

11. MS463B (INGR 08080; IC560414) Sorghum
(*Sorghum bicolor*)

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N Seetharama
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13. EC-13 (INGR 08082; IC345715) Sorghum
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Shoot fly resistant and high grain yielding.

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2. HKI-288-2 (INGR 08071; IC563956) Maize
(*Zea mays*)

Late maturing, disease resistant female parent for single cross hybrid, dark green leaves and yellow grain.

3. HKI-1126 (INGR 08072; IC563958) Maize
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Late maturing, bold seeded, resistant to MLB, seed parent with economic seed production, dark green broad leaves, purple tassel, good general combiner.

4. HKI-1040-4 (INGR 08073; IC563959) Maize
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Medium maturing, dark green leaves, purple tassel and dark orange grain, good tassel trait, resistant to MLB and rust, good for early maturing, single cross hybrid.

5. HKI-1015 WG-8 (INGR 08074; IC 563961) Maize (*Zea mays*)

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11. MS463B (INGR 08080; IC560414) Sorghum
(*Sorghum bicolor*)

Converted male and female parents of dual purpose sorghum hybrid, SPH 1148 with high yield.

12. NR 486R (INGR 08081; IC561243) Sorghum
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Converted male and female parents of dual purpose sorghum hybrid, SPH 1148 with high yield.

S Audilakshmi, C Aruna, RV Vidya Bhushanam,
N Seetharama
NRC for Sorghum, Rajendranagar, Hyderabad, Andhra Pradesh

13. EC-13 (INGR 08082; IC345715) Sorghum
(*Sorghum bicolor*)

Shoot fly resistant and high grain yielding.

M Elangovan, PG Padmaja, Prabhakar
NRC for Sorghum, Rajendranagar, Hyderabad, Andhra Pradesh

* Communicated by Drs. Anjali Kak and Kalyani Srinivasan (Member Secretary, PGRC), Germplasm Conservation Division, NBPGR

Plant Germplasm Registration Notice*

The Germplasm Registration Committee of ICAR in its eighteenth meeting held on 9 July 2008 approved the registration of following 48 germplasm lines/genetic stocks of the 94 proposals received.

1. WR 95 (INGR 08070; IC563970) Wheat
(*Triticum aestivum*)

Thick culm, high grain no./spike possesses *apd1* gene for apical lethality, moderately resistance to yellow rust.

Bhanwar Singh, SMS Tomar, Vinod, Rajendra Singh,
M Sivasamy, Anil
Division of Genetics, IARI, New Delhi

2. HKI-288-2 (INGR 08071; IC563956) Maize
(*Zea mays*)

Late maturing, disease resistant female parent for single cross hybrid, dark green leaves and yellow grain.

3. HKI-1126 (INGR 08072; IC563958) Maize
(*Zea mays*)

Late maturing, bold seeded, resistant to MLB, seed parent with economic seed production, dark green broad leaves, purple tassel, good general combiner.

4. HKI-1040-4 (INGR 08073; IC563959) Maize
(*Zea mays*)

Medium maturing, dark green leaves, purple tassel and dark orange grain, good tassel trait, resistant to MLB and rust, good for early maturing, single cross hybrid.

5. HKI-1015 WG-8 (INGR 08074; IC 563961) Maize (*Zea mays*)

Less leafy, dark green leaves, orange and flint grain color, medium maturing, good general combining ability.

6. HKI-1347-4LT (1+2+3) (INGR 08075; IC563964) Maize (*Zea mays*)

Dark green leaves, shining white grain, resistant to rust and late maturing, white seeded productive inbred line.

7. HKI-164D-4(0) (INGR 08076; IC563965) Maize
(*Zea mays*)

Dark green leaves, resistant to rust and MLB, good general combiner (QPM), late maturing, with high tryptophan (0.86%).

8. HKI-164-7-6 (INGR 08077; IC563966) Maize
(*Zea mays*)

Dark green leaves, semi-dent grains, QPM, late maturing, good general combiner and high tryptophan content (0.94%).

Sain Dass, Dharam Pal, JC Mehla, Kulbir Singh Dhanju,
Rishi Pal, Dharm Pal Singh
CCS, HAU, Regional Research Station, Uchani, Karnal

9. VQL5 (INGR 08078; IC563999) Maize
(*Zea mays*)

High tryptophan contents (0.82%) which is 110.0% higher over V25.

10. VQL17 (INGR 08079; IC64000) Maize
(*Zea mays*)

High tryptophan contents (0.72%) which is 71.5% higher over original parent V341. VQL17 is extra early female parent of FQH38.

Vinay Mahajan, R Babu, HS Gupta, Sudha Nair,
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14. KM-5501 (INGR 08083; IC202803) Cowpea
(*Vigna unguiculata*)

Bold seeded.

Saroj Sardana, NK Gautam, Sangita Yadav, SK Mishra,
SK Sharma
NBPGR, New Delhi

15. KDRS-205 (INGR 08084; IC519745) Cowpea
(*Vigna unguiculata*)

Resistant to *Black eye cowpea mosaic virus*.

Kamala Venkateswaran, RDVJ Prasada Rao,
KS Varaprasad, Someswara Rao Pandravada, N Sivaraj,
Sunil Neelam
NBPGR Reg. Station, Rajendranagar, Hyderabad, Andhra Pradesh

16. RG 72 (INGR 08085; IC274758) Castor (*Ricinus communis*)

Early maturing and drought tolerant.

K Anjani, P Lakshmamamma, M Ramachandram
Directorate of Oilseeds Research, Rajendranagar, Hyderabad,
Andhra Pradesh

17. BAAS-51 (INGR 08086; IC541650) Jatropha
(*Jatropha curcas*)

High oil content (40.6%).

18. SNES-45 (INGR 08087; IC537939) Jatropha
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High oil content (42%).

Sunil Neelam, Babu Abraham, N Sivaraj,
KS Varaprasad, Someswara Rao Pandravada, AS Rajput,
T Suresh Kumar, V Kamala
NBPGR Reg. Station, Rajendranagar, Hyderabad, Andhra Pradesh

19. CINHTi 1 (INGR 08088; IC561248) Cotton
(*Gossypium hirsutum*)

Trypsin inhibitor mediated bollworm tolerant genotype with normal leaf.

20. CINHTi 2 (INGR 08089; IC561249) Cotton
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Trypsin inhibitor mediated bollworm tolerant genotype with okra leaf.

Sandhya Kranthi, Keshav Kranthi, Nitin Zade,
Virendra Vikram Singh, Basavaraj Madavalappa Khadi,
Mansi Kshirsagar
CICR, Shankar Nagar, Nagpur, Maharashtra

21. ABC-5 (INGR 08090; IC563968) Cotton
(*Gossypium hirsutum*)

Interspecific hybrid with five loculed bolls/capsule.

22. CATS-18 (INGR 08091; IC563969) Cotton
(*Gossypium hirsutum*)

Thermo sensitive genetic male sterile (Conversion of sterility to fertility at low temperature i.e below 18-19°C).

BM Khadi, IS Kategari, Vinita Gotmare
CICR, Shankar Nagar, Nagpur, Maharashtra

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Multi-species interspecific hybrid with zero monopodia and long pedicel

24. MSH-345 (INGR 08093; IC563998) Cotton
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Multi-species interspecific hybrid with cleistogamous flowers and big round bolls (5.5g).

Vinita Gotmare, BM Khadi, LA Deshpande,
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25. VC-3117A (INGR 08094; IC565013) Tomato
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Resistant to root knot nematodes (*Meloidogyne javanica*).

26. LO-1761 (INGR 08096; IC565014) Tomato
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Resistant to thrips and mites.

28. SDS-4493 (INGR 08097; IC505489) Chilli
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Resistant to thrips and powdery mildew.

Someswara Rao Pandravada, B Sarath Babu, N Sivaraj,
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22. CATS-18 (INGR 08091; IC563969) Cotton
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Thermo sensitive genetic male sterile (Conversion of sterility to fertility at low temperature i.e below 18-19°C).

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CICR, Shankar Nagar, Nagpur, Maharashtra

23. MSH-SP-91 (INGR 08092; IC563997) Cotton
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Multi-species interspecific hybrid with zero monopodia and long pedicel

24. MSH-345 (INGR 08093; IC563998) Cotton
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Multi-species interspecific hybrid with cleistogamous flowers and big round bolls (5.5g).

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(*Lycopersicon peruvianum*)

Resistant to root knot nematodes (*Meloidogyne javanica*).

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Resistant to thrips and mites.

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NBPGR Reg. Station, Rajendra Nagar, Hyderabad,
Andhra Pradesh

14. KM-5501 (INGR 08083; IC202803) Cowpea
(*Vigna unguiculata*)

Bold seeded.

Saroj Sardana, NK Gautam, Sangita Yadav, SK Mishra,
SK Sharma
NBPGR, New Delhi

15. KDRS-205 (INGR 08084; IC519745) Cowpea
(*Vigna unguiculata*)

Resistant to *Black eye cowpea mosaic virus*.

Kamala Venkateswaran, RDVJ Prasada Rao,
KS Varaprasad, Someswara Rao Pandravada, N Sivaraj,
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16. RG 72 (INGR 08085; IC274758) Castor (*Ricinus communis*)

Early maturing and drought tolerant.

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17. BAAS-51 (INGR 08086; IC541650) Jatropha
(*Jatropha curcas*)

High oil content (40.6%).

18. SNES-45 (INGR 08087; IC537939) Jatropha
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High oil content (42%).

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Trypsin inhibitor mediated bollworm tolerant genotype with normal leaf.

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Bold seeded.

Saroj Sardana, NK Gautam, Sangita Yadav, SK Mishra,
SK Sharma
NBPGR, New Delhi

15. KDRS-205 (INGR 08084; IC519745) Cowpea
(*Vigna unguiculata*)

Resistant to *Black eye cowpea mosaic virus*.

Kamala Venkateswaran, RDVJ Prasada Rao,
KS Varaprasad, Someswara Rao Pandravada, N Sivaraj,
Sunil Neelam
NBPGR Reg. Station, Rajendranagar, Hyderabad, Andhra Pradesh

16. RG 72 (INGR 08085; IC274758) Castor (*Ricinus communis*)

Early maturing and drought tolerant.

K Anjani, P Lakshmamamma, M Ramachandram
Directorate of Oilseeds Research, Rajendranagar, Hyderabad,
Andhra Pradesh

17. BAAS-51 (INGR 08086; IC541650) Jatropha
(*Jatropha curcas*)

High oil content (40.6%).

18. SNES-45 (INGR 08087; IC537939) Jatropha
(*Jatropha curcas*)

High oil content (42%).

Sunil Neelam, Babu Abraham, N Sivaraj,
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T Suresh Kumar, V Kamala
NBPGR Reg. Station, Rajendranagar, Hyderabad, Andhra Pradesh

19. CINHTi 1 (INGR 08088; IC561248) Cotton
(*Gossypium hirsutum*)

Trypsin inhibitor mediated bollworm tolerant genotype with normal leaf.

20. CINHTi 2 (INGR 08089; IC561249) Cotton
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Trypsin inhibitor mediated bollworm tolerant genotype with okra leaf.

Sandhya Kranthi, Keshav Kranthi, Nitin Zade,
Virendra Vikram Singh, Basavaraj Madavalappa Khadi,
Mansi Kshirsagar
CICR, Shankar Nagar, Nagpur, Maharashtra

21. ABC-5 (INGR 08090; IC563968) Cotton
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Interspecific hybrid with five loculed bolls/capsule.

22. CATS-18 (INGR 08091; IC563969) Cotton
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Thermo sensitive genetic male sterile (Conversion of sterility to fertility at low temperature i.e below 18-19°C).

BM Khadi, IS Kategari, Vinita Gotmare
CICR, Shankar Nagar, Nagpur, Maharashtra

23. MSH-SP-91 (INGR 08092; IC563997) Cotton
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Multi-species interspecific hybrid with zero monopodia and long pedicel

24. MSH-345 (INGR 08093; IC563998) Cotton
(*Gossypium hirsutum*)

Multi-species interspecific hybrid with cleistogamous flowers and big round bolls (5.5g).

Vinita Gotmare, BM Khadi, LA Deshpande,
S Vennila, MK Meshram, KB Hebbar, Bntule, Chetali
Bhagat, NR Titarmare
CICR, Shankar Nagar, Nagpur, Maharashtra

25. VC-3117A (INGR 08094; IC565013) Tomato
(*Lycopersicon peruvianum*)

Resistant to root knot nematodes (*Meloidogyne javanica*).

26. LO-1761 (INGR 08096; IC565014) Tomato
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Resistant to thrips and mites.

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Resistant to thrips and powdery mildew.

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29. P/N/SKV-1863 (INGR 08098; IC319045) Kagazi lime (*Citrus aurantifolia*)

Frost tolerant, suitable for cultivation in hills up to 2000 m.

Suresh Kumar Verma, Ratan Ram Arya, Kuldeep Singh Negi, Kamlesh Chandra Muneem, Kaushal Kumar Mishra, DB Parakh, DC Dimri
NBPGR, Regional Station, Bhowali, Nainital, Uttarakhand

30. Coll. No. 5529 of IISR, Calicut (INGR 08099; IC398868) Piper (*Piper thomsonii*)

Trans-sexual species male to bisexual type, piper species occurring in bush form.

31. Coll. No. 5705 of IISR, Calicut (INGR 08100; IC563950) Piper (*Piper nigrum*)

A novel spike variant with 100% proliferating spikes, unique type in bush pepper.

KV Saji, B Sasikumar, K Johnson George, VA Parthasarathy
IISR, Marikunnu, Calicut, Kerala

32. (INGR 08101; IC560415) Ground orchid (*Spathoglottis plicata* Blume)

Milk white flower color green bract in contrast to liliac bract.

Amal Krishna Biswas, Supriya Roy
Department of Biotechnology, University of Kalyani, Nadia, West Bengal

33. IIHRIS-1 (INGR 08102; IC561244) Microcarnation (*Dianthus chinensis* x *D. caryophyllus*)

Interspecific hybrid with potential ornamental value as micro carnation and potted plant for mass bloom effect.

34. IIHRIS-2 (INGR 08103; IC561245) Microcarnation (*Dianthus chinensis* x *D. caryophyllus*)

Inter specific hybrid with mass bloom effect, good spray type.

Tejaswini, MV Dhananjaya, RN Bhat
IIHR, Hessaraghatta, Bangalore

35. Mutant plant (INGR 08104; IC561246) Isabgol (*Plantago ovata*)

Heterostyled stigma protruding out of all the (top to bottom) florets in the spike, peduncle shorter confining in the spike.

S Sriram
AINRP on Medicinal and Aromatic Plants. Anand Agricultural University, Anand (Gujarat)

36. Centella plant type-2 (INGR 08105; IC561247) Bramhi (*Centella asiatica*)

Morphotype with superior yield and quality with high leaf area and high asiaticoside (1.62%).

Satyabrata Maiti, OP Singh, Geetha KA, Narendra Gajbhiye, S Samantaray
NRC for Medicinal and Aromatic Plants, Boriavi, Anand, Gujarat

37. DILL or SOWA (CSSI) (INGR 08106; IC563951) Sowa (*Anethum graveolans*)

Highest tolerance to sodic soils (pH 9.2), maximum seed yield under sodic soil condition.

RK Gautam, AK Nayak, DK Sharma, Ali Qadar, Gurbachan Singh
Central Soil Salinity Research Institute, Karnal, Haryana

38. VJ/99-467 (INGR 08107; IC349746) Greater galangal (*Alpinia galanga*)

High 1, 8-Cineole content (72.49%) in rhizome essential oil.

Archana P Raina, Z Abraham, SK Mishra, Suresh Walia
NBPGR, Pusa, New Delhi

39. Khadara (PD 33) (INGR 08108; IC283026) Paddy (*Oryza sativa*)

Tolerant to complete submergence.

40. Atiranga (RM5/232) (INGR 08109; IC258997) Paddy (*Oryza sativa*)

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Tolerant to vegetative stage drought.

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38. VJ/99-467 (INGR 08107; IC349746) Greater galangal (*Alpinia galanga*)

High 1, 8-Cineole content (72.49%) in rhizome essential oil.

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Tolerant to complete submergence.

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Tolerant to vegetative stage drought.

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Central Rice Research Institute, Cuttack, Orissa

29. P/N/SKV-1863 (INGR 08098; IC319045) Kagazi lime (*Citrus aurantifolia*)

Frost tolerant, suitable for cultivation in hills up to 2000 m.

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Trans-sexual species male to bisexual type, piper species occurring in bush form.

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A novel spike variant with 100% proliferating spikes, unique type in bush pepper.

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32. (INGR 08101; IC560415) Ground orchid (*Spathoglottis plicata* Blume)

Milk white flower color green bract in contrast to liliac bract.

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Interspecific hybrid with potential ornamental value as micro carnation and potted plant for mass bloom effect.

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35. Mutant plant (INGR 08104; IC561246) Isabgol (*Plantago ovata*)

Heterostyled stigma protruding out of all the (top to bottom) florets in the spike, peduncle shorter confining in the spike.

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AINRP on Medicinal and Aromatic Plants. Anand Agricultural University, Anand (Gujarat)

36. Centella plant type-2 (INGR 08105; IC561247) Bramhi (*Centella asiatica*)

Morphotype with superior yield and quality with high leaf area and high asiaticoside (1.62%).

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S Sriram
AINRP on Medicinal and Aromatic Plants. Anand Agricultural University, Anand (Gujarat)

36. Centella plant type-2 (INGR 08105; IC561247) Bramhi (*Centella asiatica*)

Morphotype with superior yield and quality with high leaf area and high asiaticoside (1.62%).

Satyabrata Maiti, OP Singh, Geetha KA, Narendra Gajbhiye, S Samantaray
NRC for Medicinal and Aromatic Plants, Boriavi, Anand, Gujarat

37. DILL or SOWA (CSSI) (INGR 08106; IC563951) Sowa (*Anethum graveolans*)

Highest tolerance to sodic soils (pH 9.2), maximum seed yield under sodic soil condition.

RK Gautam, AK Nayak, DK Sharma, Ali Qadar, Gurbachan Singh
Central Soil Salinity Research Institute, Karnal, Haryana

38. VJ/99-467 (INGR 08107; IC349746) Greater galangal (*Alpinia galanga*)

High 1, 8-Cineole content (72.49%) in rhizome essential oil.

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39. Khadara (PD 33) (INGR 08108; IC283026) Paddy (*Oryza sativa*)

Tolerant to complete submergence.

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Tolerant to complete submergence.

43. Mahulata (PB-294) (INGR 08112; IC256806) Paddy (*Oryza sativa*)

Tolerant to vegetative stage drought.

44. Kusuma (PD 75) (INGR 08113; IC283068) Paddy (*Oryza sativa*)

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Central Rice Research Institute, Cuttack, Orissa

29. P/N/SKV-1863 (INGR 08098; IC319045) Kagazi lime (*Citrus aurantifolia*)

Frost tolerant, suitable for cultivation in hills up to 2000 m.

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Trans-sexual species male to bisexual type, piper species occurring in bush form.

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32. (INGR 08101; IC560415) Ground orchid (*Spathoglottis plicata* Blume)

Milk white flower color green bract in contrast to liliac bract.

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45. DWR 45 (INGR 08114; IC557723) Barley
(*Hordeum vulgare*)

High resistance to stripe rust at seedling as well as adult plant stages.

RPS Verma, B Sarkar, DP Singh
Directorate of Wheat Research, Karnal, Haryana

46. UP 2645 (INGR 08115; IC553255) Wheat
(*Triticum aestivum*)

High resistance to stem, leaf and stripe rust. It has high gluten content and rich in Beta carotene.

47. UP2696 (INGR 08116; IC553257) Wheat
(*Triticum aestivum*)

Source of Glu-1 (10/10) and high protein (13.92%).

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Sohan Pal, TB Singh, KV Singh
GB Pant University of Agriculture & Technology,
Pantnagar, Uttarakhand

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Maize (*Zea mays*)

Resistant to maydis leaf blight.

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CORRIGENDUM

J. Plant Genet. Resour. 21 (2): 113-117 (2008)

Studies on Genetic Variability and Path Analysis for Quality Characters in Rapeseed-Mustard (*Brassica* species)**JS Chauhan, K H Singh, Manju Singh, VPS Bhadauria and A Kumar**

National Research Center on Rapeseed-Mustard, Sewar, Bharatpur-321303, Rajasthan, India

On page 116: Table 3 should read as follows:

Table 3. Path analysis at phenotypic (P) and genotypic (G) level taking erucic acid as dependent variable

(Direct effects in bold)

Characters		Palmitic + stearic acid	Oleic acid	Linoleic acid	Linolenic acid	Eicosenoic acid	Oil content	Protein content	Glucosinolate content
Palmitic stearic acid	P	-0.127	-0.150	0.047	0.080	-0.040	-0.011	-0.011	0.005
	G	-0.364	-0.094	0.004	-0.115	-0.089	-0.083	0.199	-0.005
Oleic acid	P		-0.812	-0.0001	0.247	-0.110	0.004	-0.011	0.027
	G		-0.175	-0.027	-0.336	-0.120	0.019	-0.080	-0.013
Linoleic acid	P			-0.318	0.032	0.070	0.009	-0.001	-0.003
	G			-0.062	-0.240	-0.047	0.015	-0.086	-0.020
Linolenic acid	P				-0.383	0.074	-0.003	0.014	-0.015
	G				0.361	0.074	-0.004	-0.166	0.016
Eicosenoic acid	P					-0.243	0.004	0.0001	0.013
	G					-0.108	-0.019	-0.032	-0.010
Oil content	P						0.101	0.007	0.003
	G						0.150	-0.089	-0.010
Protein content	P							-0.055	0.007
	G							0.279	-0.010
Glucosinolate content									-0.051
									0.018

Residual effects (P) = 0.53 and (G) = 0.35

Referees for Volume 21(1, 2 & 3), 2008

The Editors gratefully acknowledge the help rendered by following referees in reviewing the manuscripts published during 2008.

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ANNOUNCEMENT OF AWARDS

Indian Society of Plant Genetic Resources is pleased to announce Dr HB Singh Award for the biennium 2003-04 and 2005-06, Dr RS Paroda Award for the year 2007-08 and Fellow of ISPGR 2008. Society extends congratulations to the awardees for their contributions and accomplishments in the field of Plant Genetic Resources.

**Dr HB SINGH AWARD
for the biennium 2003-04**

Dr Bhag Mal, Honorary Fellow, Bioversity International, New Delhi

**Dr HB SINGH AWARD
for the biennium 2004-05**

Dr A Seetharam, Former Coordinator, AICRP on Small Millets, Bangalore

**Dr RS PARODA YOUNG SCIENTIST AWARD
for the year 2007-08**

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