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RAPESEED - MUSTARD GENETIC RESOURCES : STATUS AND PRIORITIES

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Rapeseed and mustard comprise a group of 8 cultivated cruciferous oilseed species of tribe Brassiceae. They are the main source of edible oil in Indian diet after groundnut. They play an important role in Indian economy contributing 27 and 25.3 per cent to the total oilseed production and hectarage respectively. *Brassica juncea* is the predominant species and accounts for nearly 80 per cent of the hectarage. Oilseed *Brassica* species represent a rich genetic diversity and are grown in eight agro-ecological zones of the country. However, much of the diversity is concentrated in the Indo-gangatic plains and sub-mountane Himalayas. Since the genetic resources play an important role in breeding programme, their conservation and systematic evaluation merit foremost priority. This paper highlights an state-of-the-art in the rapeseed mustard genetic resource activities in the country. Systematic, planned and coordinated efforts of NBPGR, AICRP-RM (presently NRCRM) and other research institutes have resulted into the acquisition/collection/assemblage of 17,439 accessions of cultivated, wild and allied species of these crops. However, these also include duplicate or even quadruplicate samples. Working collections are being maintained and evaluated for major economic attributes and stresses at the various research stations. Collections made have provided a broad germplasm base the breeding programme. Among the *B. juncea* crop, RC 781 (multiple diseases AB+WR+DM tolerant), YRT 3 (white rust tolerant), T 6342 (aphid tolerant), RW 175 (frost tolerant) and RS 781 (drought and frost tolerant) genes were identified. Among the exotic collections, Midas, Westar and Tower of *B. napus*; Candle, Span and Torch varieties of *B. rapa* have been found promising and used in the breeding programme. A list of useful accessions with desirable agro-morphological and quality traits and tolerance to biotic and abiotic stresses has also been presented for future utilisation. The paper also discusses the future thrust areas for augmenting the ongoing efforts and making the programme more effective.

Key words : Rapeseed - mustard, genetic resources, *Brassica*

Rapeseed-mustard comprises a group of seven cultivated cruciferous oilseed species of *Brassica* (tribe Brassiceae) and its related genus *Eruca*. Rapeseed in the Indian context consists of gobhi sarson (*Brassica napus* L.), the three ecotypes of *B. rapa* L. (syn. *B. campestris* L.) viz., toria, brown sarson (*lotni* and *tora* types) and yellow sarson and taramira (*Eruca sativa* Mill.), while the mustard group includes Indian mustard (*B. juncea* [L.] Czern. & Coss.), black mustard (*B. nigra* Koch), wild mustard (*B. tournefortii*), Ethiopian mustard or karan rai (*B. carinata* Braun.) and white mustard (*B. alba* Rab. [syn. *Sinapis alba*]). These are rabi crops accounting for 27 per cent of the total oilseed production from an hectarage of 25.3 per cent. They are the chief source of edible oil and foreign exchange earners. India's share in the world oil meal export stands at 32.7 per cent during 1995-96 (Mehta, 1998). India earned a sizeable amount of foreign exchange equivalent to Rs. 456 crore from April 1997 to February, 1998 by exporting 1.14 million tonnes of oil meal. (Anonymous, 1998).

Brassica is considered to be of Old World origin. India presents rich diversity of oilseed Brassicas. *Brassica rapa* vars. toria and brown sarson, *B. juncea* and *Eruca vesicaria*, considered to be of Indian gene centre (Arora, 1988), are distributed in eight agro-ecological zones of the country (Table 1). Much of the diversity is concentrated in the Indo-gangetic plains and sub-mountane Himalayas. The oilseed Brassicae are widely grown in the northern plains in the states of Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Gujarat, West Bengal, Assam, Bihar, Punjab, Himachal Pradesh and Jammu and Kashmir. Of these, Rajasthan, Uttar Pradesh, Haryana and Madhya Pradesh together account for 77 per cent of the total hectarage of rapeseed-mustard in India.

Table 1. Oilseed *Brassicas* in different agro-ecological regions of India

S.No.	Region	State
1.	Humid Eastern Himalayan Region	Arunachal Pradesh,Manipur,Meghalaya,Mizoram,Nagaland,Sikkim,Tripura
2.	Humid Bengal - Assam Region	West Bengal,Assam
3.	Sub-humid to humid Eastern and South Eastern uplands	Orissa,Eastern Madhya Pradesh,Andhra Pradesh
4.	Humid to semi-arid Western Ghats and Plateau	Karnataka,Tamil Nadu
5.	Semi-arid Lava Plateau and central uplands	Maharashtra,rest of Madhya Pradesh
6.	Arid Western plains	Gujarat,Rajasthan,Haryana
7.	Sub-humid Sutlej Ganga alluvial plains	Bihar,Uttar Pradesh,Punjab
8.	Humid Western Himalayan Region	Part of Uttar Pradesh,Himachal Pradesh,Jammu and Kashmir

Brassica juncea, the dominant species grown, is followed by *B. rapa* var. *toria*, brown sarson, yellow sarson and *E. sativa*. Since the last three decades, *B. napus* and *B. carinata* are under cultivation with varying success in pockets particularly areas having longer winter spell.

I. EXPLORATION AND COLLECTION

Crop specific explorations organized by the National Bureau of Plant Genetic Resources (NBPGR), formerly Plant Introduction Division, Indian Agricultural Research Institute, New Delhi, since mid sixties collected rich genetic diversity in oilseed Brassicas. Sporadic efforts were also made during 1970s to collect the germplasm under multi-crop explorations. However, in 1980s, under joint programme of the NBPGR and the All-India Coordinated Research Project on Oilseeds (AICRPO), several *Brassica* explorations were undertaken in drier parts of Rajasthan, Gujarat, Haryana, Bundelkhand region of Uttar Pradesh, parts of Bihar plateau, West Bengal, Orissa, hilly areas of Jammu, Kashmir valley, Himachal Pradesh, Uttar Pradesh and the north-eastern Himalayas. The plant exploration undertaken from 1966 to 1986 resulted in collection of 1,903 accessions of different species, types and races of Brassicae (Kumar, 1987). The intensification of efforts during 1986-1996 resulted in acquisition and collection of 3,658 accessions of exotic, cultivated, wild and allied species of Brassica (NBPGR, 1995, 1996, 1997; Singh, 1997). The popular types of mustard collected included 'jatai rai', 'desi rai' and 'maghi rai' from boardering areas of Bangladesh. Dwarf and early types of yellow sarson with pendulous pods were also collected from the same area. Whereas, tall, robust, multilocular types were collected from eastern Uttar Pradesh. The important species of oilseed Brassicae collected included *B. juncea*, *B. rapa* vars. toria, brown sarson and yellow sarson, *E. sativa, E. vesicaria* and *B. nigra*. Besides, a number of semi-wild and wild species such as *B. tournefortii*, *Sisymybrium officinale, Erysimum hieracifolium* and *Nasturtium montanum* were also collected (Kumar, 1987). Diversity of *B. toumefortii* (locally known as 'todia' or 'dholi sarson') and *B. nigra* was collected from drier parts of Haryana and Rajasthan (NBPGR, 1995, 1996, 1997; Singh 1997).

Indeed, *Brassica* species are among the most polymorphic of the crop species surveyed. Even within species there is tremendous variation in form. In general, two distinct morphological types of *B. juncea* were observed during collection, the oleiferous types were prevalent in the sub-continent and the leafy types were observed in hills of North-eastern-states and other hilly regions of the country. Considerable intra-varietal diversity in mustard was observed. Two morphologically distinct types of *B. rapa* L. var. brown sarson, namely *lotni* and *tora* types were also collected. The lotni is spreading type with profuse branching and has high degree of self-incompatibility, while the tora type is mostly compact, shorter in height with self-compatible mating system. The tora brown sarson has evolved from the lotni types, primarily because of the preference of the farmers for bold-seeded, uniformly maturing and tall growing plants in the mixed cropping systems. In the long process of human selection, the self-incompatibility mechanism has been lost. *B. rapa* L. var. yellow sarson was prevalent in eastern Uttar Pradesh, Bihar and West Bengal region. Probably evolved from tora brown sarson as a consequence of macro-mutation for the seed colour, the yellow sarson was morphologically more closer to tora type in its early vegetative phase with deep green divided leaves and slightly indented margins; the plants become more waxy at flowering and maturity, and the siliquae were trilocular (sometimes bivalved). *B. rapa* L. var. *toria* was found prevalent in plains of Assam, Garo hills of Meghalaya, Tripura, penninsular tract of Orissa, tarai region of Uttar Pradesh, along the foot hills of Himalayas. In northern and central region of the country, it is widely cultivated as a catch crop. The only visible difference between lotni brown sarson and toria is the days taken to crop maturity, toria usually matures in 90-110 days, while lotni brown sarson types mature in 125-145 days. *B. nigra* was found in limited scale in areas extending from north to south of the country. Morphologically, two distinct types, differing mostly in plant height and maturity were observed during collection - the northern types were quite tall while the southern types were dwarf. Eruca sativa, a related species of *Brassica*, believed to be a native of southern Europe and North Africa, is grown in the drier parts of north west India comprising the states of Punjab, Haryana, Uttar Pradesh and Rajasthan. It is highly cross-pollinated because of the presence of the homomorphic sporophytic self-incompatibility mechanism. The leaves are broad, juicy and divided-flowers are light yellow and slightly broader than cultivated brassicas and siliquae are club-shaped and closely appressed to fruiting branches (Kumar, 1988).

With the establishment of Germplasm Management (GM Unit) Research Centre in the ICAR-Project Coordinating Unit (Rapeseed Mustard) of the CCS-HAU (formerly HAU), Hisar in 1981, the genetic resource activities of oilseed Brassicae got impetus. The Germplasm Management (Rapeseed-Mustard) Unit had the crop specific objectives of assembly, collection, conservation, characterization, evaluation, cataloguing, documentation and distribution of germplasm for utilization of rapeseed-mustard crops. The National Research Centre on Rapeseed- Mustard established in 1993, is the national repository and takes care of the responsibilities of former Germplasm Management Unit, Hisar. At present, it has a collection of

4548 accessions (Table 2). Further, 6710 accessions of oilseeds Brassicas are available at cooperating centres of AICRP on Rapeseed - Mustard and other research institutes (Table 3).

Table 2. Current status of germplasm at National Research Centre on Rapeseed - Mustard, Bharatpur

Species	Accessions
B. juncea	3381
B. rapa var. *toria*	396
B. rapa var. *brown sarson*	225
B. rapa var. *yellow sarson*	164
Eruca sativa	271
Exotic lines	111
Total	4548

napus, B. carinata, B. nigra, Sinapis alba and *E. sativa* and *Crambe* species from 16 countries (Kumar, 1988). A total of 59 exotic accessions of oilseed *Brassica* species namely, *B. juncea, B. rapa, B. napus*, were obtained from Sweden, U.K. Canada, USA and China (Anonymous, 1993). Apart from these, wild types belonging to sub-tribe Brassicinae were also introduced. Three hundred sixty three accessions of exotic and wild relatives of *Brassica* were subsequently acquired by the NBPGR from 1995 to 1997 (NBPGR, 1995, 1996, 1997). At present the NBPGR has an impressive collection of 2,063 accessions of rapeseed-mustard from over 23 countries (Singh, 1997). The wild or weedy species are good sources for resistance to diseases and pests as well as tolerance to harsh environments (Harlan, 1984).

Table 3. Status of working germplasm collections at various centres in India

Centre	Available germplasm resoures							Total
	Mustard	Toria	Yellow sarson	Brown sarson	Gobhi sarson	Taramira	Karan rai	
Kangra	-	222	-	-	-	-	-	222
Ludhiana	392	-	16	29	126	-	-	563
Hisar	950	-	-	-	-			950
Bawal	-	-	103	62	16	-		327
Navgaon	667	-	-	-	-	-	-	667
Kanpur	1465	238	158	59	-	-	-	1920
Pantnagar	300	150	80	-	32	-	100	662
Faizabad	395	45	38	3	9	32	5	498
Gwalior	100	-	-	-	-			100
Morena	-	250	-	-	-	-	-	250
Jobner	-	-	-	-	-	350		350
Bhubaneswar	149	5	22	17	25	-	-	213
Total	4418	930	417	170	329	353	105	6710

II. INTRODUCTION FROM EXOTIC SOURCES

Broad-based plant germplasm resources are imperative for sound and successful crop improvement programmes. During the period 1981-87, the GM Unit (Rapeseed-Mustard) acquired 269 accessions of *B. juncea, B. rapa, B.*

At the National Research Centre on Plant Biotechnology (NRCPB), IARI Campus, New Delhi, efforts are underway to utilize these wild genetic resources to develop cytoplasmic male sterile lines and to improve the level of disease resistance (Singh, 1997).

MAINTENANCE OF GERMPLASM

Maintenance of genetic stock is an important activity. Rejuvenation and multiplication of the seeds depend upon the mode of pollination. Oilseed Brassicas have a wide range of mating systems ranging from total cross-pollination due to genetic self-incompatibility to predominant self-pollination. Consequently, the techniques employed for the maintenance of genotypes having these two different mating systems are different. *Brassica juncea*, *B. napus* and *B. carinata* have high self-pollination (85-95%) because of self-compatibility, low sucrose content in their nectaries (5-12%) and introse anther arrangement (Rai, 1996). In self-pollinated Brassicas, maintenance is easy and good selfed seeds can be obtained by enclosing inflorescences in bags. For maintaining the germplasm of self-pollinating species, genotypes are grown in augmented design in paired rows of 4.5 to 5 metre row length with 45cm row to row spacing and 90cm pair to pair distance. In order to maintain in pure form, individual accessions are bagged prior to initiation of flowering (Kumar, 1988).

Toria, *lotni* brown sarson and taramira are highly cross-pollinated because of the presence of sporophytic self-incompatibility mechanism, entomophily, very high sucrose content (40-61%) in their nectaries to attract honeybees, and the extrose anther arrangement (Rai, 1996). These crops require special attention for maintenance. Individual genotypes are grown in the field in a similar fashion as indicated for the self-pollinating Brassicas. They are maintained by sibmating. Pollen from representative plants of the same accession is used for pollinating at least 10 plants and female parents bagged prior to flowering. For maintaining genotypes of an individual plant of an outcrossed self-incompatible types, bud-pollination is the best way, through bud-pollination, young buds can be fertilized by compatible as well as by incompatible pollinations. At population level, insect proof cages can effectively be utilized for the maintenance. Pollination is achieved by keeping honeybee colonies (Kumar, 1988). It is better to harvest only central-rows for seed purposes. Another method for maintenance of *Brassica* germplasm is by growing it at an appropriate isolation distance, which varies for different species. An isolation distance of 400 metre has been found to give an adequate isolation in the cross-pollinated B.rapa var. brown sarson for the maintenance of breeder's seeds (Kumar and Singh, 1978). Currently, a total of 16,777 accessions available are being maintained at the NBPGR, NRCRM, NRCPB and various AICRP-RM cooperating centres. These collections are, however, duplicates or even quadruplicates.

IV. CONSERVATION OF GERMPLASM

The NBPGR, New Delhi has been assigned the mandate for long term conservation of germplasm (base collections) and also of coordinating conservation activities at the national level. The facilities for *ex situ* seed storage for both long term and medium term exist. All the accessions are first subjected to test for germination and moisture content. The samples are dried to 6-8 per cent moisture content and sealed hermetically in laminated aluminium foil packets, to store in the separate modules at $-20^{o}C$ for long term and at $4^{o}C$ for medium term (active collections), respectively (Singh, 1997). The IBPGR (1981) has recommended that sample size for long term storage should have a minimum of 12,000 seeds per accession, which correspond to 50 g seeds of *Brassica* species. Gomez Campo (1972) has described a procedure for medium term storage (active collections) whereby small seed samples are stored in an individual glass vial with blue silica gel inside and stored under low temperature ($-50^{o}C$). Presently, over 4,580 accessions of oilseed Brassicae have been conserved in the National Gene Bank (Singh, 1997). The periodic regeneration of the seed accessions is necessary to maintain optimal seed viability over the long term as well as replenish the seed stock.

V. EVALUATION, CHARACTERIZATION AND CATALOGUING

The precise evaluation of genetic resources and dissemination of findings is imperative for their utilization in the crop breeding programme. If evaluated systematically, the genetic resources of a crop plays a pivotal role in breeding programme by continuously providing new genes to evolve better varieties with high level of tolerance to major biotic and abiotic stresses, high crop yield and quality.

Agro-morphological characters

The best evaluation is one that relates the traits measured to plant breeder's need. The NBPGR has prepared a descriptor for characterising and evaluating Indian mustard germplasm on the basis of 49 traits that include agro morphology, seed oil and seed meal quality and reaction to diseases and insect pests (Mahajan *et al.*, 2000). Presently, a total of over 16,777 accessions of Brassica germplasm are being maintained, evaluated for different agromorphological characters and are used at various centres, under different agro climatic conditions in the country. At the Hisar and NRCRM, Bharatpur; Navgaon and Pantnagar cooperating centres of AICRP-RM, a total number of 15,799 accessions of rapeseed mustard were characterized from 1982 to 1996 (Anonymous, 1993; AICRP-RM 1994, 1995, 1996).

Analysis of grouping pattern of about 2,800 accessions of mustard evaluated at GM Unit, Hisar for agro-morphological characters and oil content (Anonymous, 1993) revealed that majority of the accessions (67.03%) matured between 140-150 days-only 2 accessions took less than 110 days to mature. The days to maturity (Fig. la) varied from 131 to 140 days for about 477 accessions. The primary branches ranged from 2.1 to 10.0 but 2,567 accessions (91%) had only 6.0 primary branches per plant (Fig. 1b). The secondary branches per plant ranged from 3.1 to 42.0.Two thousand one hundred and seventy two accessions (76.94%) exhibited variation from 8.1-18.0 (Fig. lc) and 550 accessions had more than 18 secondary branches per plant. The number of siliquae on main shoot is an important yield contributing character and also had high heritabilty. Thus variation in the character is of paramount significance. It varied widely but nearly 72 per cent accessions had only 45 siliquae on main shoot. Only 16 accessions had more than 65 siliquae on main shoot (Fig. 1d). The siliquae length did not show much variation-2,712 accessions had siliqua length 4.5 cm, (Fig. le). Majority of the accessions (95.2%) had 15 seeds per siliqua; only 2 accessions showed very high number of seeds per siliqua (Fig. 1f). The distribution of accessions for seed yield was fairly uniform (Fig. lg). Three hundred twenty three accessions had more than 14.5 g of seed yield per plant (Fig. 1g). The 1000-seed weight ranged from 2.1 to 4 g in 76.5% of the accessions, however, 24 accessions (0.9%) also showed high seed weight (6.0 g) (Fig. 1h).

Oil content in mustard accessions ranged from 30.6 to 44.6 per cent. But 92 per cent of these accessions had 40.5 per cent oil-only 198 had more than 40.5 per cent oil content. (Fig. 1i). Of the 144 accessions of *Brassica* : *B. carinata* (12), *B. napus* (10), *B. rapa* var. *toria* (4), *yellow sarson* (53), *brown sarson* (65), the majority were having excellent oil content (43%). Yellow sarson accessions exhibited as high as 34 seeds per siliqua. In general wide variation was observed in the pattern of inflorescence, siliquae arrangement, siliqua length and root system in the rapeseed mustard germplasm (Fig. 2a,b,c,d).

At NBPGR, over 2,940 accessions of different oilseed Brassicas have been evaluated for 15 morpho-agronomic descriptors *B. juncea* (1,550),

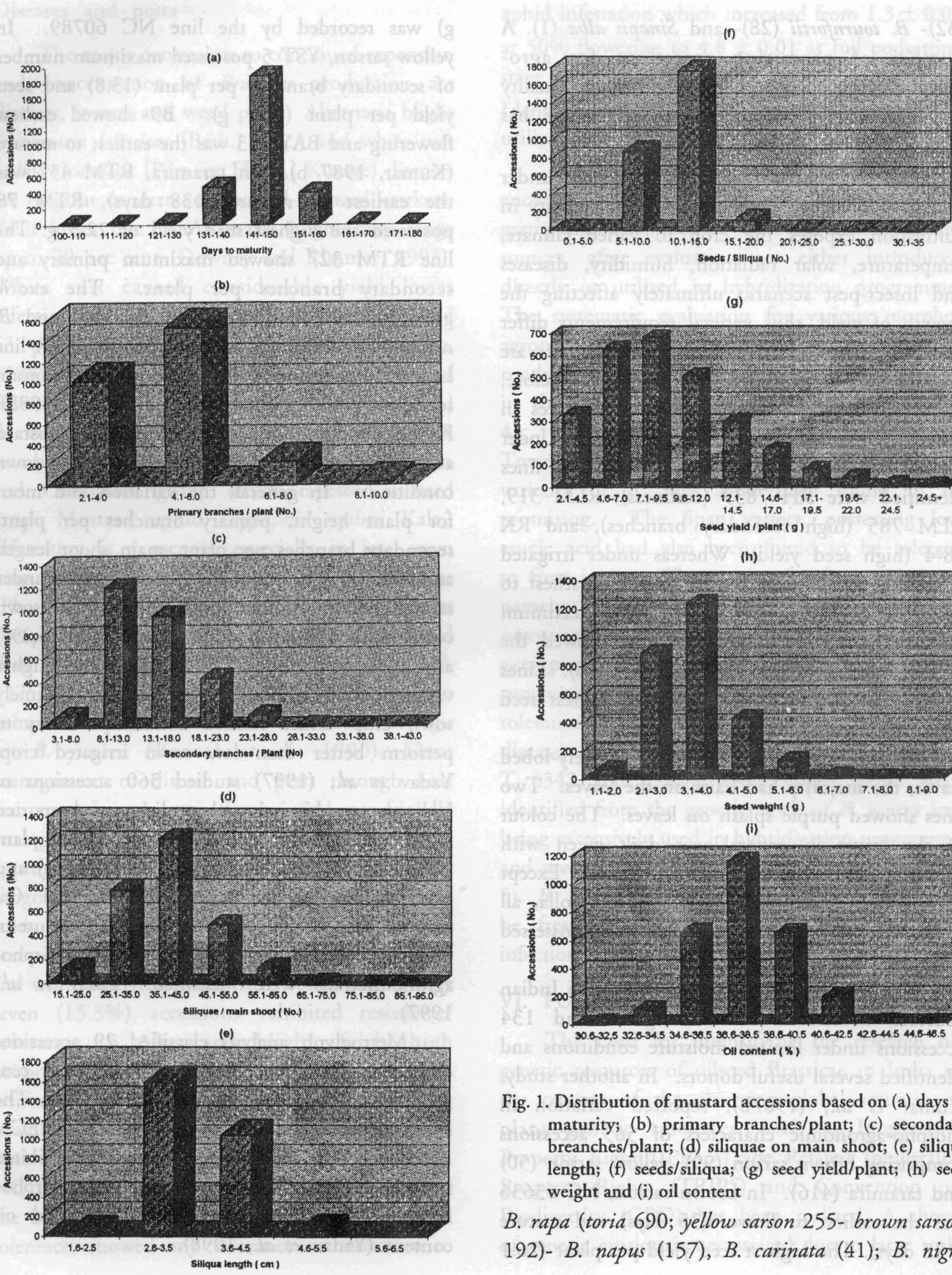

Fig. 1. Distribution of mustard accessions based on (a) days to maturity; (b) primary branches/plant; (c) secondary breanches/plant; (d) siliquae on main shoot; (e) siliqua length; (f) seeds/siliqua; (g) seed yield/plant; (h) seed weight and (i) oil content

B. rapa (*toria* 690; *yellow sarson* 255- *brown sarson* 192)- *B. napus* (157), *B. carinata* (41); *B. nigra*

(32)- *B. tournfortii* (28)- and *Sinapis alba* (1). A number of promising accessions for agro-morphological characters, oil quantity and quality and tolerance to abiotic and biotic stresses has been identified (Singh, 1997).

Oilseed Brassicas are being cultivated under diverse agroclimatic conditions. This diversity in cultivation exposes the crop to varied climate, temperature, solar radiation, humidity, diseases and insect-pest scenario ultimately affecting the growth of yield, thus varietal requirements differ widely. Hence the donors for various traits are relevant only in a specific agro-climate. Therefore, there is a need to evaluate genetic resources in different agro-climatic/specific conditions. Under rainfed conditions, a number of promising lines identified were RH 7839 (earliness), RLM 319, RLM 785 (high secondary branches), and RK 78-4 (high seed yield). Whereas under irrigated condition, B 137 and B 169 were the earliest to mature (121 days); CSR 164 recorded maximum primary branches (20.5)- CSR 498 showed the highest number of secondary branches (46). Lines B 199, B 380, RC 1277 gave the highest seed yield (Kumar, 1988).

Mustard accessions showed lyrately-lobed leaves; the majority had hairs on the leaves. Two lines showed purple splash on leaves. The colour of the leaves in general was dark green with purple splash on the internode and siliqua. Except of one line which had green yellow corolla, all lines had yellow corolla and 53 lines possessed appresed siliquae (Kumar, 1988).

Kumar *et al.*, (1987a) evaluated 1,035 Indian mustard accessions under irrigated and 134 accessions under limited moisture conditions and identified several useful donors. In another study, Kumar *et al.*, (1987b), reported variation in morpho-agronomic characters of 565 accessions comprising brown sarson (99), yellow sarson (50) and taramira (416). In brown sarson, NC 63636 was the earliest to flower (35 days) and mature (122 days). The highest seed yield per plant (26.1 g) was recorded by the line NC 60789. In yellow sarson, YST 5 possessed maximum number of secondary branches per plant (13.8) and seed yield per plant (20.1 g). B9 showed earliest flowering and BAYS 53 was the earliest to mature (Kumar, 1987 b). In taramira, RTM 437 was the earliest to mature (138 days), RTM 78 possessed the highest seed yield of 22.3 g. The line RTM 327 showed maximum primary and secondary branches per plant. The exotic germpiasm lines of *B. juncea*, *B. napus* and *B. carinata* were very tall and late maturing. A line Lini (*B. napus*) with long pods and maximum seeds per pod was also identified (Kumar, 1988). Kumar *et al.*, (1997) evaluated 75 mustard accesions under rainfed and irrigated late sown conditions. In general, the variation and mean for plant height, primary branches per plant, secondary branches per plant, main shoot length and siliquae per main shoot was greater under rainfed conditions than that of under late sown conditions. However, siliqua length (CV 16.2%) and seeds per siliqua (CV 19.2%) had higher variation under late sown irrigated crop. Timely sown crop under rainfed conditions seems to perform better than late sown irrigated crop. Yadav *et al.*, (1997) studied 360 accessions of Indian mustard in irrigated conditions and reported high variability for secondary branches per plant (CV 32.3%), 1000-seed weight (CV 24.5%) and primary branches per plant (CV 20.8 %). Oil content showed the least variation. Several useful donorsforhighoilcontent (41%) andothermorpho-agronomictraits were identified. (Yadav *et al.*, 1997).

Metroglyph analysis classified 29 accessions of gobhi sarson in 4 clusters with 34.5 per cent (10) of the accessions grouped in cluster 1. The cummulative index score ranged from 10 (NECN 15) to 19 (NECN 8). The accessions exhibited substantial variability for different agromorphological traits except days to maturity and oil content (Yadav *et al.*, 1998).

Diseases and pests

The major constraints to continued expansion and concentration of *Brassicas* production are diseases, insects and weed pests. Alternaria blight (*Alternaria brassicae* [Berk.] Sacc.) and white rust (*Albugo candida* [Pers. ex Hook.] Kuntze) diseases are of great concern to rapeseed-mustard workers. Yield losses due to Altemaria blight may range up to 70 per cent (Downey and Rimmer, 1993). White rust caused considerable yield losses infecting leaf and staghead upto 27 per cent and 63 per cent, respectively (Saharan and Lakra, 1988); Downy mildew (*Peronospora parasitica*) and Sclerotinia stem rot (*Sclerotinia scierotiorum* [Lib.] de Bary) are assuming serious proportion. A number of insects belonging to the Lepidoptera and Coleoptera group attack rapeseed-mustard crop. Mustard aphid (*Lypaphis erysimi* Kalt.) infestation is a menace especially in late sown crop causing a heavy toll upto 76 per cent (Phadke, 1980). Varieties of *B. juncea* possess comparativly better tolerance to mustard aphid than the varieties of *B. rapa* (Rai and Sehgal, 1975). However, *B. carinata* selections have shown comparatively better tolerance than either *B. rapa* or *B. juncea* (Bansal *et al.*, 1990). Since management of disease and pests through host resistance is an cost effective and eco-friendly strategy, therefore, there is a need to search for appropriate donors for utilization in the breeding programme to develop resistant varieties. In a study at NRCRM (Kumar *et al*:, 1997), 242 accessions were screened for Alternaria blight (leaf and white rust (leaf under field conditions. Thirty seven (15.3%) accessions exhibited resistance/ tolerance to Alternaria blight, fairly high proportion (71%) of the accessions showed resistance/ tolerance to white rust. The promising strains showing resistance/tolerance to both diseases were IB 1571, IB 1639, NC 60448, NC 60456, NC 60467, CSR 741 and CSR 820. None of the 242 accessions evaluated for aphid infestation tolerance, showed any tolerance or resistance to aphid infestation which increased from 1.3 ± 0.01 at 50% flowering to 4.8 ± 0.01 at full podsetting stage (Kumar *et al.*, 1997).

Identification of resource genes and their utilization

The utilization aspect of genetic resources encompasses the whole of plant breeding. The germplasm assembled or collected from different sources, after evaluation are either introduced directly or utilized in hybridization programme. The systematic evaluation for various morpho-agronomic, quality traits, biotic and abiotic stresess, resulted in the identification of donors for use in the varietal improvement programme (Table 4). Amongst the exotic collections, Midas and Tower of *B. napus*, Candle, Span and Torch varieties of *B. rapa* have been found to be promising. The Span variety, possessing low erucic acid had also been found to be tolerant to frost injury. The sources for frost resistance, namely, RW 175 and DBS 1 identified in *B. juncea* and *B. rapa*, respectively, from the available germplasm are being used in hybridization programme. Likewise, the sources for resistance/ tolerance to Altemaria blight and white rust diseases, RC 781 and YRT 3 and aphid resistance, T 6342 and Cream white flower glossy stem identified from the genetic stock of *B. juncea* and being extensively used in hybridization programme and several varieties/strains were developed (Table 5). *B. carinata* by and large has been found to be free from white rust and downy mildew infection.

VI. FUTURE THRUST AREAS

The need for intensifying the research on genetic resources of oilseed Brassicae in India in the context of the changing global scenario of plant genetic resources, such as Intellectual Property Right (IPR), Trade Related Intellectual Property Rights (TRIPS) and Convention on Biodiversity (CBD) has been realized. A threat of genetic erosion is necessiated due to large scale

Table 4. Promising donors identified for different agro-morphological and quality traits

Stress/Condition	Germplasm lines/Genotypes/Varieties
Biotic Stress	
White Rust	*B. juncea* : RC 781, PYSR 8,PYSR 13, PR 10 *B. rapa* var. yellow sarson - PYS 16 *B. rapa* var. toria : PT 77, Bhabhari
Alternaria blight	RC 781, KRV-tall, SR 142-2, PHR 1, Jatai sarson
White rust	Downy mildew and Alternaria blight
Orobanche	*B. juncea*: Durgamani
Mustard aphid	*B. rapa* - IB 787, Chamba 1, 2 *B. juncea*: T6342, B 85 (Glossary), PR 52 B. 85 (white flower) *B. napus* : GSL 1, Karab,Gulivar, Pi 171538 *B. hirta* : Pi 751516
Abiotic Stress	
Drought	RH 781, RH 785, RH 819, RH 7361, RH 7513, Vardan, Durgamani, Pusa Barani, *B. toumefortii*
Frost	*B. rapa* : Bele, Candle, Span, FR 80 *B. juncea* : RH 781, RW 32-2, PR 52, PR 2030, RH 781, RH 851, DIRA 343,NDR 8604,CS 52
Quality traits	
High oil	*B. juncea*: PR 36, EC126743-1, EC126743, Donskaja *B. rapa* : KT101, TK 8503, PT5, PT25, PT 48
Low erucic acid	*B. juncea* : Zem 1, Zem 2, EC 287711 *B. rapa* : Tobin, Candle
Low glucosinolate	*B. juncea* : RC 247, RC 270, RS 79, RS 81, EC 287711 *B. rapa* : Tobin, Bele, Torch
Yellow seed coat	TM 2, TM4, TM 27, TM 21, YRT 1, RIK 1-1, Domo, UU 22
Other desirable agronomic attributes	
Earliness	IB 1755, IB 1886, Seeta, BR 40, BR 46
Non shattering	RH 30, RIK 8, P 26-31, PR 10, Pusa Bold, Rajat
Bold seeds	RH 30, Pusa Bold, R 74-3, Pusa 1001, NDR 8501
Intercropping	PR 43, RH 30, RH 781, RH785, Laha 101, Vardan, Sanjucta Asech

cultivation of improved varieties replacing the traditional land races, weedy and wild races of the crop. For instance, in India *B. toumefortii*, a close relative of *B. rapa* and very common in northern India is getting extinct (Singh, 1997). Taking all the aspects in totality, the following priority areas of research are identified.

Table 5. Improved germplasm of rapeseed-mustard tolerant/resistant to biotic and abiotic stresses and other situations

Stress/Condition	Varieties/Strains developed
Biotic stress	
Aphid tolerant	*B. juncea* : RH 7846, RH 7847, RH 9006, RH 9020, RWAR 842, CSR 1017B. rapa : Chamba 1, Chamba 2
Alternaria blight tolerant (moderate)	Saurabh (RH 8113), RH 8814
Abiotic stress	
Salt tolerant	Narendra Rai (NDR 8501), CS 52, CSR 50
Frost tolerant	*B..juncea* : RH 781, RH 7361, RW 351, RC 199, *B. rapa* var. brown sarson -. Candle, Bele, Span, KBS 1
Drought tolerant	RH 781, RH 785, RH 7361, RH 7513, CSR 212, CSR 814, CSR 975
Herbicide (Atrazine) resistant (For chemical weed control)	GSL 2
Other conditions	
Late sown condition	RH 7859 (North-West Zone), Pusa Bold (Central Zone), RLM 619 (Eastern Zone)
Non- traditional areas	Rajat, Pusa Jaikisan (Maharashtra), Seeta (TN and AP)
Shattering resistant	*B. juncea* : RH 30, Rajat (PCR 7), RLC 1021, Pusa Bold, Rohini
Yellow seed coat	YRT 4, TM 9, TM 11, DIRA 313, RH 8689
Long siliqua	RH 7859, RH 7860, RH 8816A, RH 8816

- A time bound programme of plant exploration and germplasm collection should be chalked out laying emphasison borderareas of Bihar - West Bengal facing Nepal and Bihar - West Bengal Assam facing Bangladesh, Jammu - Kashmir and Uttar Pradesh hills, Karnataka - Andhra Pradesh, Orissa and North eastern states.

- Characterization, evaluation and documentation especially for biotic and abiotic stresses and oil and seed meal quality should be taken up. For efficient and speedy evaluation and characterization of genetic resources, a network should be created. For effective screening for biotic and abiotic stresses, appropriate 'hot-spots' should be identified rather than carrying out evaluation and running a risk of escape and/or sub-optimal environment.
- Utilization of modern analytical techniques and bio-technological tools to eliminate duplicates and triplicates.
- Synthesis of germplasm complexes in allogamous species.
- Development of low cost system for maintenance of allogamous species.
- Determination of optimum seed sample in case of auto-and allogamous oilseed Brassicae for medium and long term storage conditions.
- Diversity analysis utilizing conventional and modern techniques.
- A national register assigning a common accession number to all the available genetic resources of rapeseed-mustard should be prepared.

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AGRO-BIODIVERSITY OF BAY ISLANDS

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The Andaman and Nicobar Islands even though possess an apparently uniform tropical humid warm climate, shows considerable variation in the species diversity and vegetation pattern. The occurance of over 2500 indigenous and 500 non-indigenous angiospermic species in these Islands makes it unique to Indian flora. In addition to cultivated species (plantation, fruit and vegetable crops, cereals and pulses. Orchids and medicinal plants etc.), wild relatives of crop plants having agricultural, medicinal and industrial value have an impressive array of diversity. Among these significant species found are : *Pandanus* sps., *Garcinia cowa, Mangifera andamanica, Musa balbisiana* var. *andamanica, Anona glabra, Baccuaria ramiflora,* etc in fruits: *Alternathera sessile, Amaranthus viridis, Vigna marina, Acrosticum aureum* in vegetables: *Oryza inandamanica,* the wild relative of rice: *Areca triandra, Myristica andamanica, Zingiber odoreferum, Piper betle* in plantation and spice crops: *Cymbidium oloifolium, Eria andamanica, Vanilla andamanica* in orchids and *Adena penengiana, Aerva lanata, Ardisia solanacea, Cordia grandis, Cassia alata, Euphorbia hirta* in medicinal plants. As main food source, numerous wild plants like *Colocasia esculenta, Dioscorea glabra, Nypa fruiticans, Calamus sps., Ipomoea aquatica, Tacca leontopetaloids* are directly consumed by many tribals of Andaman and Nicobar Islands.

Key words : Andaman and Nicobar Islands, agri-diversity, wild relatives, tribal food

Out of about 17,000 vascular plant species recorded, India has as many as 5000 endemic species and a significant feature of the Indian flora is the confluence of flora of the surrounding countries like Malayasia, Tibet, China, Japan, Europe and also from distinctly separated continents like America, Africa and Australia. India has 12 biographic zones of which the Andaman-Nicobar zone is one whose flora is unique to India because of tropical humid climate and insular nature of the territory (Rodger and Panwar, 1988). The presence of over 2500 indigenous and 500 non-indigenous angiospermic species within a land area of 8290^2km is significant feature of the Andaman and Nicobar Islands, making them a cynosure not only for plant taxonomists but also for conservationists. The rare and the distinct flora, which evolves through millions of years due to insular nature of the territory, physical isolation between the islands and also from the neighbouring continental landmasses, is unique to India. These two group of Islands, separated by 10° channel even though possess an apparently uniform tropical humid and warm climate, shows considerable variation in the species diversity and vegetation patterns. Though related to mainland (India) flora, the flora of Andaman group shows much closer affinity with the Burmese flora while that of Nicobar have affinity towards the Sundra biographical zone. The Andaman group of Islands are inhabited by the tribes of Negrito stock viz., Jarawas, Sentineles, great Andamanese and the

Onges, on the other hand: Nicobar group of Islands are inhabited by tribals of Mangoloid origin, viz., The Nicobarese and Shompeans. The wide variety of plants in the Island ecosystem has supported human existence and contributed to their wellbeing. The interaction between the tribals and people living in the natural system have helped in maintaining the richness of the societies, communities and genetic materials in both productive systems and wild lands of island tropical environment. The insular nature of territory, physical isolation between the islands and also from the neighbouring mainland through millions of years, has resulted in the revolution of rare and distinct flora, which trhough related to the mainland Indian flora, shows much closer affinity with the Burmese, Malayasian and Indonesian flora. The rich tropical and natural, evergreen vegetation of Andaman and Nicobar Islands can be broadly classified as :

(i) Evergreen forests

These forests represent the climax vegetation with a close compact community of diverse tropical plants. The canopy is closed and consists of three sotreys. The soil is composed of clayey loam with micaceous sandstones below. The vegetation is mainly composed of tall trees laden with linans and other epiphytes. *Dipterocarpus griffithii, Hopea odorata, Plachonia andamanica* occur in the upper storey. The other storey consists of smaller trees like *Baccaurea sapida, Myristica* sps., *Pometia pinnata*. Shrubs like *Cleorodendrum viscosum, Leea indica* etc. and common climbers include *Calamus longisetus, Daemonorops manii*. Epiphytic ferns like *Dendrobium aphyllum* and *D. secundum* are the epiphytic orchids commonly seen.

(ii) Deciduous forests

Such forests occur in undulating ground on hills where the soil is comparatively dry. *Pterocarpus dabergoids* is associated with *Termenalia procera, T. manii* etc. The second storey consists of small trees like *Lannea coromandelica, Sageraea elliptica*. The third storey is represented by *Grewia disperma, Cordia grandis* etc.

(ii) Grasslands

Several disturbed, deforested and denuded hillocks exhibit grasslands with *Imperata cylindrica* and *Saacharum spontaneum* as dominant species. Grasses like *Heteropogan contortus, Chrysopogan aciculatus* and *Eragrostic* sps. are found associated with sedges and ferns. The herbs and undershrubs include *Uvaria lagopodioides, Desmodium heterocarpon* etc.

Hydrophytic vegetation

The scarcity of natural stagnant pools and lakes results in poor fresh water flora in these Islands. *Ipomoea aquatica, Lemma purpusilla, Najas indica, Hydrilla verticillata* are some times seen. Notable fresh water marshy plants are *Blyxa roxburghii, Polygonum barbatum, Hydrophila erecta* (Rao, 1996).

The people of Andaman and Nicobar group of islands have been growing and/or collecting large number of plants or their products from wild habitats for consumption. Consumption of such a large array of plants have been the basis of good stamina and sound health from them since immemorial. This combined with high agro-ecological diversity and population of diverse culture and food habits has made these islands a very rich resource of horticultural (fruits, vegetables, spices, orchids etc), pulses and cereals (cultivated food grains) and medicinal plants.

The diversity of useful vascular plant resources in these islands may conventionally be grouped as :

1. Wild and cultivated fruits
2. Wild and cultivated vegetables
3. Wild and cultivated plantations and spices
4. Cultivated food crops
5. Oilseed crops
6. Wild and exotic orchids
7. Aromatic and Medicinal plants

1. Cultivated and wild fruits

The diverse agro-ecological conditions of tropical and humid climate of these Islands are highly suitable for growing tropical sub tropical fruits.

The cultivated fruits constitute an impressive range and include banana (*Musa paradisiaca*), Papaya (*Carica papaya*), pineapple (*Ananas comosus* L.), mango (*Mangifera indica*), custard apple (*Anona squamosa*), soursop (*Anona muricata*), bullock heart (*Anona reticulata*), passion fruit (*Passiflora edulis*), sapota (*Achras zapota* L.), acid lime (*Citrus aurantifolia* Swingle), jackfruit (*Artocarpus heterophyllus*), sweet orange (*Citrus sinensis*), avocado (*Persea americana*), carambola (*Averrhoa carambola*), bilimbi (*Averrhoa bilimbi*) durian (*Durio zibethinus* Mill), mangosteen (*Garcinia mangostana*), lemon (*Citrus lemon*), bael (*Aegle marmelos*), rambutan (*Nephelium lapaceum* L.), west Indian Cherry (*Malpighia glabra*), guava (*Psidium guajava* L.), pomegranate (*Punica granatum* L.), ber (*Zizyphus mauritiana*), aonla (*Phyllanthus emblica*), cashewnut (*Anacardium occidentale*), jamun (*Eugenia jambolana*) (Singh *et al.*, 1994, 1996, 1997 and 1997).

Besides, a large number of fruits are collected and harvested from the wild habitats or forests. Some of these, which need mention include screwpine (*Pandanus tectorius*), kewra (*P. andamanansium*), Nicobar Bread fruit (*P. lerum*), caw phall (*Garcinia cowa*), alligator's apple (*Anona glabra* L.), khatta phal (*Baccuarea ramiflora* Lour), lakoocha (*Artocarpus gomizianus*), gular (*Ficus hispida*), modhuphal (*Salacia chinensis*), wild banana (*Musa balbisiana* var. *andamanica*), wild jamun (*Syzygium claviflorum*), amra (*Spondias pinnata*), wild jamun (*S. jambolana*), lasoda (*Cordia oblique*), dhumiphal (*Nypha fruiticans*), wild passion fruit (*Passiflora foetida*), wild mangoes (*Mangifera andamanica, M. camptosperma* and *M. griffithi*), gnetum (*Gnetum gnemon*), wild lemon (*Atalantia monophylla*), wild amra (*Dracantomelum dao*), wild jackfruit or taung - Peinne (*Artocarpus chaplasha*), ambarella (*Spondias cythera*) (Sreekumar *et al.*, 1986; Vasudeva Rao, 1986; Sreekumar *et al.*, 1996; Singh *et al.*; 1998).

2. Cultivated and wild vegetables

People of Andaman and Nicobar group of islands including local inhabitants and tribals, grow and even collect naturally growing plants or plant products which are eaten or cooked as vegetables. These may be grouped as:

The cultivated vegetable group constitutes bhindi (*Ablmoschus esculentus* (L) Moench.), tomato (*Lycopersicon esculentum* Mill.), chilli (*Capsicum annuum* L.), brinjal (*Solanum melongena* L.), bottle gourd (*Lagenaria siceraria* (Mol) Standl.), pumpkin (*Cucurbita moschata* Poir.), khira or cucumber (*Cucumis sativus* L,), bitter gourd (*Momordica charantia* L.), snake gourd (*Trichosanthes anguina* L.), amaranths (*Amaranthus* sps.), watermelon (*Citrullus lanatus*), lablab (*Lablab purpureus*), radish (*Raphanus sativus*), cowpea (*Vigna unguiculata* (L) Walp.), ridge gourd (*Luffa acutangula* Roxb.), parval or pointedgourd (*Trichosanthes dioica*), tapioca (*Manihot esculenta* Crantz), elephant foot yam (*Amorphophallus campanulatus* Blume), frenchbean (*Phaseolus vulgaris* L.), cabbage (*Brassica oleracea* var. *capitata*), cauliflower (*B. oleracea* var. *botrytis*), knolkhol (*B. caulorapa*), kundru (*Coccinia indica*), palak (*Beta vulgaris* var. *bengalensis*), basella or Poi (*Basella alba*), chinese cabbage (*B. pekinensis*), curry leaf (*Murrya koenigii* L), dhania pathi (*Eryngium foetida* Bieb.), sweet potato (*Ipomoea batarus* (L) Lam.). (Singh *et al.*, 1996; 1996, Shridhar and Sharma 1991).

There are numerous uncultivated vegetables but a few which are consumed as cooked are: madras bhaji (*Alternanthera sessile* L.), kaitali chulai (*Amaranthus spinosa* L.), wild marsa bhaji (*A. viridis* L.), bilaiti kathal (*Artocarpius incissus* L.), kairwal or purple Bauhinia (*Bauhinia variegata* L.), khoja (*Callicarpa arborea* Roxb.), maripatti (*Caryota mittis* Lour.), amaltas or bunder laudi

(*Cassia fistula*), kasondi (*Cassia occidentalis* L.), quail grass (*Celosia argentea* L.), khari phal (*Ardisia solanacea* Roxb.), mitha bhaji (*Champereia griffithiana* Planch.), ghuiyan or arvi (*Colocasia esculenta* Schott.), nali bhaji (*Ipomoea aquatica* Forsk.), podina (*Mentha arvensis*), dhudi kalmi (*Ipomoea alba* L.), kukur jhwa (*Leea indica* Merr.), dalbhaji (*Portulaca capleracea*), star gooseberry (*Saurops androgyms* Merr.), basna (*Sesbania grandiflora*), chowli or sea shore pea (*Vigna marina* Merr.), makoi (*Solanum nigrum*), sensitive pea (*Smithia sensitiva*), drumstick (*Moringa oleifera* Lamk.), khokli or Indian Acalypha (*Acalypha indica*), elephant earn fern or khadibauji (*Acrosticum aureum*), ramdatan (*Smilax zylnica* L.). bara sem (*Canavalia cathartica*) (Sreekumar *et al.*, 1986, Shridhar and Sharma, 1991).

3. Cultivated and wild food crops (cereals)

These constitute the main food items of the populace. It comprised variety of grains such as (i) cereals (ii) pulses (iii) millets.

The cereals are mainly grown in two crop seasons, i.e., rainy season (June to Oct.) and dry season (Nov. to May). The main cereals grown are rice (*Oryza sativa* L.) and maize (*Zea mays* L.). An endemic and wild relative of rice (*Oryza andamanica*) existing in forests of Andaman is under capitative research for the improvement and plant breeding programme. (Ellis, 1987; Ram and Ansari, 1991). The millets and small millets include mandava (*Eleusine coracana* Goertn.), jowar (*Sorghum vulgare* Pers.). In these islands, pulses and legumes are major source of proteins. These are urd, blackgram or mah (*Vigna mungo*), mungo or greengram (*Vigna radiata*), french bean or rajmah (*Phaseolus vulgaris*), horsegram (*Macrotyloma uniflorum* L.), cowpea (*Vigna unguiculata*), ricebean (*Vigna umbellata*), moth (*Vigna acontifolia* Jacq.), arhar/redgram (*Cajamus cajan*) (Gangwar *et al.*, 1990).

Tribal food

Since the tribals of Andaman and Nicobar Islands (Jarawas, Nicobarese, Andamanese, Onges, and Shompeans) are not cultivating pulses and cereals in the field, there are numerous wild food plants used by them. The important plants having more significance in their daily food are:

Bulbs of *Dioscorea glabra*, tubers of *Colocasia esculenta* and *Tacca leontopetaloids*, fruits of *Morinda citrifolia, Nypa fruiticans, Syzygium samaragense, Anona squamosa, Pandanus lerum, Artocarpus incisa, A. integrifolia, baccaurea sapida, Champereia griffithiana, manikara litoralis, Pommetia pinnata, Salacia chinensis, Semicarpus kurzii, Ardisia solanacea, Calamus* spp., *Citrus* spp., *Terminalia catappa, T. manii* and stems of *Flagellaria indica, Celosia argentea, Ipomoea aquatica, Acacua sinuata, Acalypha indica, Alternenthera sessile, Amaranthus spinosa, Areca triandra, Bauhinia purpuea, Blechnum orientale* L., *Callicarpa arborea, Cassia fistula* and *Celosia argentea* etc.

4. Oilseed crops

The farmers of Andaman and Nicobar generally use vegetable oil in various culinary preparations. These include ground nut (*Arachis hypogaea*), sesamum/til or mitha tel (*Sesamum indicum*), sarson (*Brassica campestris*), sunflower (*Helianthus annuus*), coconut (*Cocos nucifera*), oil palm (*Elaeis guineensis* Jacq.) and castor (*Ricinus communis*).

5. Plantation and spice crops

The diverse and typical tropical and humid climate of these islands are highly suitable for growing many plantation and spice crops. The cultivated plantation crops include an imperessive range of high returning crops like coconut (*Cocos nucifera*), arecanut (*Areca catechu*), cashewnut (*Anacardium occidentale* L.), oilpalm (*Elaeis guineensis* Jacq.) while cultivated spices include black pepper (*Piper nigrum* L.), cinnamon (*Cinnamonum zeylanicum*), nutmeg (*Myristica fragrans*), tejpatta/bay leaf (*Cinnamomum verum*), ginger (*Zingiber officinale*), clove (*Eugenia caryophallata*), coriander (*Coriandum sativum*), turmeric (*Curcuma domestica*). Besides these cultivated species of plantation and spice crops, quite a number of wild relatives of these crops also exist in these islands. Some of these included: wild arecanut (*Areca triandra*), wild nutmeg (*Myristica andamanica, M. glabra, M. glaucescens, M. nicobarica*), *Vanilla andamanica,* collections of wild betle vine (*Piper betle*), wild ginger (*Zingiber odoreferum, Z. spectabile, Z. squarrosum, Z. zerumbet*) (Ellis, 1998; Singh *et al.*, 1998).

6. Wild and exotic orchids

Orchidaceae is one of the largest families of the flowering plants in the islands; nearly 110 orchids are naturalized here. These islands are rich in the stock of orchids available in the wild species; many a wild species, due to their beauty and other blossom characters, stand out conscpicuously as competitors with best hybrids. The native orchids having horticultural and commercial value are : *Cymbidium aloifolium*, SW, *Bulbophyllum lepedium* (BL) J.J. Sm, *Dendrobium secundum* (BL) Lindl., *Denodrobium formosum* Roxb., *Eria andamanica* Hook F., (Tooth brush orchid *Geodorum densiflorum* (Lam.), Schltr., *Malleola andamanica* Balakr. and Bharg., *Philodota imbricata* Lindl., *Rhynchostylis retusa* Bl., *Vanilla andamanica* Rofle. (Rao and Srivastav, 1996).

The introduction of exotic orchids in these islands is very recent. However, Cattleya wine festival, *Dendrobium* hybrids, *Vanda* Miss Joaquim, *Aranda* Peter Wart, *Vanda* Jhon Clubb, *Arachnis* Maggie- oei, *Epidendrum* (Holly cross), *Arundina graminiflora* etc have been successfully introduced in CARI, Port Blair (Sharma *et al.*, 1997).

7. Cultivated and wild aromatic and medicinal plants

Large scale ad true cultivation of aromatic and medicinal plants in these islands is not being done. However, due to suitability of climatic conditions and population of diverse culture and tradition, few of the crops of aromatic and medicinal use are being cultivated on very small scale and to kitchen garden level. The important ones are citronella (*Cymbopogon winterianus* Jowitt.), coriander (*Coriandum sativum* L.), *Dioscorea* spp., jasmine (*Jasminum grandiflorum*), vetiver (*Vetiveria zizanoides* L.), lemon grass (*Cymbopogon flexuosus* Sted Wats), periwinkle (*Catharanthus roseus* L.), sarpagandha (*Rauvolfia serpentine* Benth. Ex. Kurz.), tuberose (*Polianthus tuberosa*), podina (*Mentha viridis*), dhania (*Eryngium foetida*), betle vine (*Piper betel*), tulsi (*Ocimum sanctum, O. basilicum*), champak (*Michelia champaka*), vanilla (*Vanilla fragran*), rose (*Rosa chinensis*), palmarosa (*Cymbopogon martini* var. motia), tejpatta (*Cinnamomum verum*), Euclyptus (*E. citriodora*)

Now-a-days ethnomedicinal botany has been attracting researchers of various desciplines all over the world. It is the inter-desciplinary approach of ethnobotany which deals not only with the plants, used for medicinal purposes but also with socio-economic attributes of particular plant. Rural and tribal people of these islands use plants not only as herb but also in different modes of life for their socio-economic benefits. The rural and tribal people consume a large number of plant species for cure of various diseases and disorders. These plant species having medicinal value are : *Adenia penengiana, Adenostemma lavenia, Aerva lanata, Ageratum conyzoids, Alstonia macrophylla, Alstonia kurzii, Ardisia solanacea, A. oxyphylla, Aristolochia tagala, Blumea balsamifera, Caesalpinia* sp., *Callicarpa longifola, Calophyllum inophyllum, Cassia alata, C. occidentale, Catharanthus roseus, Celosia argentea, Claoxylon indicum, Clerodendron inerma, C. viscosum, C. paniculatum, Cordia grandis, Costus speciosus, Crateva religiosa, Cycas rumphii, Desmodium umbellatum, Dischedia major, Dracaena angustifolia, Eclipta alba, Eria bractescence, Euphoria atoto, E. hirta, Garcinia nervosa, Globa marantia, Glycosmis arborea, Hydyotis biflora, Hibiscus tiliaceus, Gloriosa superba* and *Cassia alata*

(Awasthi and John, 1987; Dagar, 1989; Yoganarasimhan *et al.*, 1983; Anonymous, 1994).

Conservation

The insular species are generally characterised by a small gene pool, reduced interspecific competition, inbreeding and small population size by virtue of which they are more vulnerable to extinction due to habitat destruction. Bay islands being no exception to this, conservation of rare and threatened endemic species as well as exotic and introduced species has become inevitable for ensuring the preservation of species diversity. With the increasing population beyond carrying capacity and recent developmental activities in inhabited islands, several economically important species needs first hand attention for proper handling and timely conservation.

The island ecosystem is one of the fragile system in the world, with unique functions and roles in the context of biodiversity. The wide variety of palnts in island ecosystem has supported human existance and contributed to our well being. The interactions between the island people, tribals and natural system have helped in maintaining richness of the species, communities and genetic materials in both production system and wild landof island environment. However, the rich bio diversity of these islands is being impoverished disastrously along with the over all degradation of island environment due to human actions in last few decades. This fundamental natural wealth is disappearing and the process must be slowed and haltered without delay. Conservation of biodiversity calls for both global attention and promot action at the regional level. Many indigenous societies ahve formulated and established their own traditional conservation methods, including the protection of plants. Apart from other activities CARI has been actively involved in collection, conservation and multiplication of this rich natural wealth having food, fruit, vegetable, spice and medicinal values. Various *in situ* and *in vitro* programmes under various institutional and external funding projects like NATP, ICAR Cess fund, DBT programmes for conservation of bio diversity of islands are being carried out for the last few years.

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INTERRELATIONSHIPS AND PATH-COEFFICIENT ANALYSIS IN MAIZE (*Zea mays* L)

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Ten maize inbreds and their 45 single-cross hybrid combinations (total 55 genotypes) along with a standard check were grown in a randomized complete block design with three replications in two locations. The phenotypic and genotypic coefficients of correlation were computed for grain yield and its component traits viz., 1000-grain weight, kernel rows per ear, kernels per row, ear length, ear circumference, days to maturity, plant height, ear height and biological yield. Grain yield showed positive association with 1000-grain weight, kernels per row, ear length, ear circumference, plant height and ear height at the phenotypic level. Path coefficient analysis indicated that plant height, ear circumference and kernels per row were the main characters through which the indirect contribution of most of the traits was positive and high.

Key words: Maize, correlation, path analysis

Knowledge of interrelationships serves two main purposes from the breeder's point of view. Firstly, these are highly useful in selecting for characters, which are not easily observed or genotypic values of which are modified by the environmental effects. There is ample evidence to show that selection directly for yield in plants is not easy. Thus, any morphological character that is associated with yield or which makes a significant contribution to yielding ability would be useful in the improvement of yield. Secondly, inter-relationships between characters make available to the breeders sources of information as to the nature, extent and direction of selection pressure among characters.

MATERIALS AND METHODS

Ten maize inbred parents were crossed in a diallel mating system excluding reciprocals. These ten parents and their 45 hybrid combinations (total 55 genotypes) along with a standard check were grown in a randomized complete block design with three replications at Regional Research Station, Bajaura and Himachal Pradesh Krishi Vishvavidyalaya, Palampur each, representing Mid-Hill Zone of H.P. Each plot consisted of four rows, each row 5 m in length and row-to-row and plant-to-plant spacings of 75 and 20 cm, respectively. Data were recorded on ten randomly chosen competitive plants for grain yield and its components (viz., 1000-grain weight, kernel rows per ear, kernels per row, ear length, ear circumference, days to maturity, plant height, ear height and biological yield). The data over two locations were pooled and the phenotypic and genotypic coefficients of correlation were computed as suggested by Al-Jibouri *et al.*, (1958) and the path coefficient analysis of various traits was done following Dewey and Lu (1959).

RESULTS AND DISCUSSION

A perusal of Table 1 reveals that genotypic coefficients, in general, were higher than the corresponding phenotypic ones, indicating the inherent association among various traits studied. Grain yield showed positive and significant association with 1000-grain weight, kernels per row, ear length, ear circumference, plant height, ear height and biological yield at the phenotypic level. Grain yield was found to be positively correlated with plant height, ear height, ear length, kernels per row (Sathyanarayana, . 1995), kernel rows per ear and ear circumference (Gyanendra *et al.*, 1993). Among other component traits, besides grain yield, 1000-grain weight had positive and significant correlation with kernels per row, ear length, ear circumference, plant height and ear height, whereas negative with days to maturity. Kernels per row had positive and significant correlation with ear length, ear circumference, plant height, ear height and biological yield. Ear length and ear circumference each had positive and significant association with plant height and ear height. Plant height with days to maturity and ear height had also positive correlation. Similar results on correlation coefficients for ear height with plant height (Hemalatha, 1986) and plant height with ear length (Krishnan and Natarajan, 1995) have been observed. Grain yield is an ultimate product of interaction among the characters under the influence of environment. It is quite likely that the contribution of a

Table 1. Phenotypic(P) and genotypic(G) correlation coefficients among different characters pooled over two environments

Characters		GWT	KRE	KER	ELT	ECF	DTM	PHT	EHT	BLY
GYD	P	0.70**	0.10	0.77**	0.67**	0.45**	-0.08	0.52**	0.33*	0.51**
	G	0.78**	1.02**	0.92**	0.76**	0.52**	-0.07	0.64**	0.48**	0.51**
GWT	P		0.03	0.46**	0.52**	0.26*	-0.42**	0.35**	0.27*	0.27
	G		0.52**	0.05**	0.58**	0.30**	-0.49**	0.39**	0.38**	0.31*
KRE	P			-0.07	0.09	0.02	0.06	-0.12	0.07	0.11
	G			-0.54	0.98**	0.03	0.57**	-0.21**	1.33**	1.10**
KER	P				0.70**	0.46**	0.20	0.50**	0.44**	0.61**
	G				0.80**	0.60**	0.29*	0.67**	0.66**	0.77**
ELT	P					-0.05	0.02	0.55**	0.34*	0.37**
	G					-0.09	0.03	0.69**	0.47**	0.42**
ECF	P						0.19	0.43**	0.35**	0.52**
	G						0.29*	0.56**	0.49**	0.62**
DTM	P							0.35*	0.15	0.42**
	G							0.47**	0.32*	0.61**
PHT	P								0.52**	0.42**
	G								0.92**	0.55**
EHT	P									0.24
	G									0.33**

**Significant at 5 and I per cent levels, respectively.
GYD = grain yield, GWT = 1000-grain weight, KRE = kernel rows per ear, KER = kernels per row, ELT = ear length, ECF ear circumference, DTM = days to maturity, PHT = plant height, EHT = ear height and BLY = biological yield.

Table 2. Phenotypic(P) and genotypic(G) path coefficient analysis for different characters pooled over two environments.

Characters		GWT	KRE	KER	ELT	ECF	DTM	PHT	EHT	BLY
GWT	P	0.32	0.01	0.18	-0.16	0.10	-0.06	0.22	-0.01	0.08
	G	-0.80	0.07	-0.50	0.29	0.17	0.61	0.27	-0.09	0.40
KRE	P	0.01	0.38	-0.03	-0.03	0.01	0.01	-0.07	-0.01	0.03
	G	-0.42	0.13	0.50	0.49	0.02	-0.70	-0.83	-0.30	1.43
KER	P	0.15	-0.03	0.39	-0.22	0.18	0.03	0.32	-0.01	0.17
	G	-0.43	-0.07	-0.93	0.40	0.35	0.35	0.46	-0.15	1.01
ELT	P	0.17	0.04	0.27	-0.31	-0.02	0.02	0.35	-0.01	0.10
	G	-0.47	0.13	-0.75	0.50	-0.05	-0.03	0.47	-0.12	0.54
ECF	P	0.08	0.01	0.18	0.02	0.39	0.03	0.27	-0.01	0.15
	G	-0.24	0.01	-0.56	-0.01	0.59	-0.36	0.38	-0.11	0.80
DTM	P	-0.13	0.02	0.08	0.01	0.08	0.14	0.22	-0.01	0.12
	G	0.40	0.07	-0.27	0.01	0.17	-1.24	0.32	-0.07	0.79
PHT	P	0.11	-0.04	0.19	-0.17	0.17	0.05	0.63	-0.02	0.12
	G	-0.31	-0.16	-0.63	0.34	0.33	-0.58	0.69	-0.21	0.72
EHT	P	0.09	0.03	0.17	-0.10	0.14	0.02	0.32	-0.03	0.07
	G	-0.31	0.17	-0.62	0.24	0.29	-0.40	0.63	-0.23	0.43
BLY	P	0.08	0.04	0.24	-0.11	0.20	0.06	0.26	-0.08	0.28
	G	-0.24	0.14	-0.72	0.21	0.37	-0.75	0.38	-0.07	1.30
Corr. with yield	P	0.70**	0.10	0.77**	0.67**	0.45**	-0.08	0.52**	0.33**	0.51**
	G	0.78**	1.02**	0.92**	0.76**	0.52**	-0.07	0.64**	0.48**	0.51**

Significant at 5 and 1 per cent levels, respectively.
GYD = grain yield, GWT = 1000-grain weight, KRE = kernel rows per ear, KER kernels per row, ELT ear length, ECF = ear circumference, DTM = days to maturity, PHT = plant height, EHT = ear height and BLY = biological yield.
Residual P = 0.006; and G = 0.052

component showing highly significant association with grain yield may get diluted through the interaction with other component. Further, the information on relative contribution of direct and indirect effects of components on grain yield helps in giving appropriate weightage for the purpose of selection. Therefore, for efficient indirect selection, it is important to know the causal factors for the observed association between two characters with the help of estimates of direct and indirect effects through path-coefficient analysis.

At the phenotypic level, plant height had the maximum direct positive effect followed by ear circumference, kernels per row, kernel rows per ear, 1000-grain weight and biological yield. Plant height, ear circumference and kernels per row were the main characters through which the indirect contribution of most of the traits was positive and high and, therefore these traits can be found rewarding for increasing grain yield. Direct positive contribution of kernels per row and kernel rows per ear has been reported by Gyanendra *et al.*, (1993), whereas for plant height, kernels per row and 1000-grain weight by Debnath and Khan (1991). Indirect effects of various traits such as ear length via biological yield, 1000-grain weight via biological yield (Prasad,

1987) and biological yield through plant height (Donald and Hamblin, 1976) have been reported.

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GENETIC DIVERSITY FOR SEED YIELD IN A LARGE COLLECTION OF CLUSTERBEAN (*Cyamopsis tetragonoloba* (L) Taub.)

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Two hundred thirty.one Yermplasm lines of clusterbean (*Cyamopsis tetragonoloba*) were evaluated alone with three checks for seed yield and its components in augmented design. Pods per plant exhibited highest variability and contribution to divergence. This trait was also significantly and positively correlated with seed yield which indicates its importance as selection criteria. Following non-hierarchical Euclidean analysis, all the 234 genotypes were grouped into 12 clusters with variable number of genotypes. The highest genetic divergence was observed between cluster V and IX, whereas cluster III and VIII were closest one. On the basis of genetic divergence and mean performance eight diverse and superior genotypes, being exceptionally good for one or more traits and reasonable for others in comparison to checks, were selected and these genotypes may be useful in multiple crossing or diallel selective mating system to recover transgressive segregants.

Key words: *Cyamopsis tetragonoloba,* clusterbean, genetic diversity, seed yield

Clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.), commonly known as guar, is one of the most important kharif legumes grown for green fodder, vegetables, green manuring and seed purpose. Now-a-days it has been emerged as an industrial crop due to importance of its seed as a source of industrial gum, guar meal for animal, nutritional protein to meet human dietary and other uses (Joshi and Arora, 1993). A limited number of varieties have been released in this crop that is also keeping the importance of its fodder value in mind. Thus, breeding a high seed yielding genotype is need of the hour. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop to exploit transgressive segregation has been emphasized (Murty and Arunachalam, 1966 and Bhatt, 1970). But information on genetic diversity in clusterbean, particularly for attributes of seed yield is lacking and hence, the present experiment was aimed at assessment of its genetic diversity for seed yield and its components.

MATERIALS AND METHODS

The experimental materials comprising two hundred thirty-one genotypes collected from different parts of Rajasthan and three checks (Bundel Guar 1, Bundel Guar 2, HG 75) were evaluated in augmented design with 11 blocks in kharif, 1999 at Research Farm, Western Regional Research Station (IGFRI), Avikanagar, Rajasthan. Each block contained 21 different test genotypes (germplasm) and the three checks. Each genotype was sown in a two-row plot of 3 in long with row to row and plant to plant spacing of 30 cm and 15 cm, respectively. After every 10th germplasm line the checks were sown in each block. Recommended agronomic practices were followed to raise a good crop. The data on seed yield and its components were recorded on 10 plants for each genotype and their mean values were subjected to statistical analysis.

Adjusted mean value for all the characters of 231 test genotypes and the estimates of different mean squares were obtained following Federer (1956) and Peterson (1985) and used for subsequent analysis. The mean, range, phenotypic coefficient of variation (%) (PCV), genotypic coefficient of variation (%) (GCV), heritabilty (%) and correlation coefficient were estimated as per standard statistical procedures (Panse and Sukhatme, 1954). The non-hierarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973) was conducted to group the genotypes into different clusters and to estimate the intra- and inter-cluster distances.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes indicating the scope of selection for high (seed) yielding genotypes. Considerable range was observed for all the characters (Table 1). Pods per plant showed the highest GCV and PCV followed by clusters per plant, whereas seeds per pod showed the lowest ones. Accordingly, pods per plant exhibited highest heritability. Again, pods per plant showed significant, positive correlation with seed yield per plant (Table 2). However, clusters per plant, seeds per plant and 100 seed weight also had significant, positive association with seed yield. Pods per plant and clusters per plant were significantly and positively correlated. Thus, pods per plant should be given importance during selection for high seed yield.

Table 1. Estimate of different genetic parameters for attributes of seed yield in clusterbean

Character	Range	Mean	PCV (%)	GCV (%)	Heritabilty (%)
Clusters/plant	5.30-54.40	25.46	60.29	45.64	57.32
Pods/plant	9.40-156.20	66.38	67.18	53.44	63.28
Seeds/pod	5.30-10.90	8.38	14.82	10.41	49.38
Pod length (cm)	4.20-9.10	5.54	20.18	13.96	47.89
100-seed wt (g)	2.13-4.65	3.27	35.11	20.65	34.72
Seed yield/plant (g)	1.26-64.32	16.22	57.26	32.02	31.28

Table 2. Correlation coefficients among seed yield and its components in clusterbean

Character	Pods/ plant	Seeds/ pod	Pod length	100-seed wt	Seed yield/ plant
Clusters/plant	0.51**	0.19	- 0.01	0.06	0.52**
Pods/plant		0.21	0.11	0.1	0.63**
Seeds/pod			0.33*	-0.17	0.33*
Pod length				0.12	0.12
I 00-seed wt					0.43**

*, **: Significant at 5% & 1% level of significance

Based on non-hierarchical Euclidean cluster analysis, the 234 genotypes were grouped into 12 clusters with variable number of genotype (Table 3) revealing the presence of considerable amount of genetic diversity in the material. Cluster III had the maximum number of 49 genotypes followed by cluster VIII with 27 genotypes. These two clusters accounted for sufficient (76) genotypes reflecting narrow genetic diversity. The similarity in base material from which these have been evolved might be the cause of genetic uniformity. The members of cluster V and IX exhibited maximum divergence indicating greatest diversity between genotypes belonging to these two clusters followed by VI and VII, whereas cluster III and VIII were closest one with minimum genetic distance (Table 4). The average intra-cluster distance in cluster V was maximum suggesting that the genotypes in this cluster were relatively more diverse among themselves, whereas closeness among the genotypes in cluster XII was indicated. However, in all cases, the inter-cluster distances were greater than the intra-cluster distances implying the degree of genetic diversity present among the genotype between clusters.

Cluster mean also indicated substantial variation among different cluster as well as superiority of different cluster for different

Table 3. Grouping of clusterbean genotypes into 12 clusters

Cluster No.	No. of Genotypes	Genotypes
I	24	AVKG 9, 19, 20, 24, 26, 30, 40, 60, 68, 78, 101, 126, 138
II	6	AVKG 2, 15, 33, 80, 117, 202
III	49	AVKG 1, 5, 10, 18.21, 25, 27, 29, 34,37, 38, 44, 46, 54, 55, 61, 62, 69, 75, 89, 97, 113, 114, 116, 118, 119, 121, 124, 132, 159, 167, 168, 171, 173, 179, 190, 191, 194, 197, 198, 199, 208, 212, 217, 221, 2221, 225, 2271, 229
IV	21	Bundel Giiar 1,AVKG 7, 11, 17, 28, 41, 45, 53, 70, 86, 87, 93, 98, 110, 115, 125, 131, 143, 149, 166, 193
V	26	AVKG 12, 23, 32, 56, 63, 74, 81, 94, 104, 105, 123, 130, 142, 156, 160, 163, 180, 183, 186, 189, 195, 196, 209, 211, 223, 228
VI	8	AVKG 71, 83, 91, 99, 137, 141, 148, 224
VII	18	AVKG 4, 13, 16, 35, 36, 51, 66, 82, 129, 133, 134, 140, 154, 177, 187, 216, 219, 226
VIII	27	Bundel Guar 2, AVKG 8, 31, 47, 52, 57, 64, 72, 77, 84, 95, 100, 103, 106, 107, 111, 112, 127, 144, 157, 165, 169, 181, 192, 204, 206, 218
IX	13	AVKG 6, 39, 48, 67, 88, 90, 122, 135, 147, 151, 174, 188, 213
X	22	HG 75, AVKG 14, 42, 43, 58, 65, 73, 85, 92, 108, 109, 120, 139, 146, 153, 161, 176, 182, 200, 205, 207, 230
XI	6	AVKG 49, 76, 128, 152, 162, 215
XII	14	AVKG 3, 22, 50, 59, 79, 96, 102, 136, 150, 155, 175, 184, 201, 220

Table 4. Estimates of intra- (diagonal value) and inter-cluster distances of 12 clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	2	4.75	8.56	6.84	5.14	7.58	5.85	8.56	6.84	11.84	13.75	8.51
II		4.25	9.62	8.62	4.91	7.14	5.25	8.78	13.66	11.46	15.64	7.98
III			2.21	9.48	8.07	7.86	4.80	4.32	11.32	9.63	6.25	11.22
IV				6.27	8.85	5.88	7.12	13.16	14.12	12.36	6.85	8.87
V					9.92	17.25	21.65	12.39	39.87	15.62	13.34	16.95
VI						6.92	24.12	7.89	20.06	11.42	10.68	22.34
VII							5.25	6.75	23.66	13.25	12.60	17.12
VIII								2.16	13.25	11.25	9.30	6.25
IX									6.23	9.66	11.25	20.12
X										2.98	4.96	5.25
XI											2.66	4.66
XII												1.01

characters (Table 5). Cluster V showed the highest mean for both clusters per per and pods per plant, whereas cluster IX, XII, VII and VI had the maximum seeds per pod, pod length, 100-seed weight and seed yield per plant, respectively. The differential contribution to total divergence was observed in different seed attributes (Table 5). The germplasm lines were divergent (for seed attribute) mainly on the basis of pods per plant and clusters per plant as these two traits contributed largely to divergence as compared to other traits.

The data on inter-cluster distance and performance of the genotypes was used to select genetically diverse and agronomically superior genotype among 231 genotypes. The genotypes, exceptionally good in respect of one or more character and at least comparable in respect to

Table 5. Cluster mean and contribution to total divergence of different attributes of seed yield

Character	Cluster mean												Contribution to total divergence (%)
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	
Clusters/plant	24.69	19.26	30.16	25.12	34.56	22.19	29.66	20.12	28.76	26.33	20.46	24.20	27.64
Pods/plant	60.18	70.26	71.22	65.66	74.83	71.33	61.23	63.19	65.21	62.49	71.94	59.02	40.44
Seeds/plant	8.32	8.93	9.42	8.44	8.01	7.86	8.22	8.06	8.97	8.06	8.11	8.71	6.78
Pod length (cm)	5.61	5.26	5.05	5.64	4.96	6.04	5.61	5.13	5.04	5.71	6.01	6.42	7.94
100-seed wt(g)	3.06	3.01	3.61	3.22	2.98	3.51	3.72	3.26	3.41	3,06	3.33	3.50	5.10
Seed yield/plant(g)	10.56	18.22	20.17	17.59	16.19	24.32	17.27	18.29	12.78	14.36	11.64	14.01	12.10

Table 6. Diverse and superior genotype with desirable characters selected from different clusters

Sl. No.	Genotype	Cluster No.	Dsireable characters
1	AVKG 63	V	Clusters/plant,Pods/plant,Seed yield/plant
2	AVKG 189	V	Pods/plant,100-seed wt
3	AVKG 137	VI	100-seed wt,Seed yield/plant
4	AVKG 51	VII	Pods/plant,100-seed wt,Seed yield/plant
5	AVKG 187	VII	Pods/plant,100-seed wt,Seed yield/plant
6	AVKG 39	IX	Seeds/pod,100-seed wt
7	AVKG 122	IX	Seeds/pod,Seed yield/plant
8	AVKG 201	XII	Pods/plant,Pod-length

others to the checks, were deemed desirable. On this basis, eight genetically diversed and superior genotypes were selected (Table 6). They belonged to different five clusters. Intermating of divergent (groups would lead to greater opportunity for crossing over which releases latent variability by breaking linkage (Thoday, 1960) and progenies derived from diverse cross are expected to show broad spectrum of genetic variability, providing a greater scope for isolating trangressive segregates in the advanced generation. So, these genotypes may be used in a multiple crossing programme or in diallel selective mating system to recover transgressants. Furthermore, the trait, pods per plant may be used as a selection criteria in segregating generations as it showed the highest GCV heritability (%), contribution to the total divergence as well as significant, positive correlation with seed yield/plant.

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RANGE OF VARIABILITY FOR ECONOMIC CHARACTERS IN COTTON GERMPLASM (*G. hirsutum* L)

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Three hundred germplasm lines of *Gossypium hirsutum* L. were evaluated during 1996-97 and 1997-98 crop seasons. An assessment of range of variability present in respect of various economic characters has been made. Promising germplasm lines with high yield (55 gm and above per plant), mean boll weight (4.00 gm and above), boll number per plant, monopods, sympods, ginning out turn (35.0% and above) and mean halo length (26 mm and above) have been listed. Fifteen germplasm lines combining moderate to high yields with other economic characters have been identified which may be included in the hybridization programme of crop improvement. Two germplasm lines namely, MEX 121 and 51.041 (V 1508) have outyielded for almost all the characters studied.

The contribution of germplasm of *Gossypium hirsutum* L. in the genetic improvement of cotton has been significant. The programme of varietal improvement is specifically Oriented towards evolving better yielding varieties/hybrids in the various quality groups to meet the demands of the textile industry (Srinivasan *et al.*, 1977). In this programme, multiple selection criteria for economic attributes, contributing to yield like boll number per plant, boll weight etc. have been utilised. Increasing emphasis is being laid in recent years on the choice of divergent parents in hybridization programmes to get superior hybrids and segregates for selection. Over 8000 genetic stocks pooled from different sources in the world have to be evaluated at Central Institute for Cotton Research, Nagpur and its regional stations, Sirsa and Coimbatore. In order to evaluate them systemically, initially 300 lines were taken for irrigated field evalaution at Sirsa.

MATERIALS AND METHODS

Three hundred germplasm lines of *G. hirsutum* L. were raised in 1996-97 and 97-98 seasons at a spacing of 67.5 x 30 cm and all standard agronomic and plant protection measures for irrigated conditions were adopted. One plant was retained per hill. From the 10 representative plants grown for each germplasm line, five plants were randomly selected and data were recorded on single plant basis for economic characters like seed cotton yield per plant, boll number, monopods, sympods, boll weight, Ginning out turn (G.O.T.) and mean halo length. The mean for each line and for the characters was calculated and ranges recorded. In the present investigation, an assessment of variability in the genetic stocks in respect of the above mentioned characters was made and outyielding germplasm lines were identified.

RESULTS AND DISCUSSION

The range of variability available in the genetic stocks for various economic characters studied is given in Table 1. It is seen that considerable amount of variability exists in all the characters studied and offers scope for selection and utilization in the further hybridization programme. The utility of each character is discussed below.

Table 1. Range of variability of different characters in *Gossypium hirsutum* L. germplasm

S. No.	Characters	Range (1996-97)	Range (1997-98)
1.	Seed cotton yield/plant (g)	2.3 - 100.4	0.5 - 50.0
2.	Boll weight (g)	3.0 - 4.5	3.2 - 4.0
3.	Number of bolls/plant	1.5 - 24.0	-1.2 - 23.6
4.	Number of monopods/plant	0.2 - 6.5	0.2 - 9.0
5.	Number of sympods/plant	0.8 - 14.3	2.0 - 18.2
6.	Ginning out turn (%)	20.0 - 36.0	14.5 - 37.0
7.	Mean halo length (mm)	12.0 - 29.4	15.0 - 31.5

a) Yield of seed cotton (Kapas)

Yield of seed cotton is a major factor which governs the cash return per hectare. The general yield level in 1996-97 and 1997-98 was moderate Hence, accessions which yielded above 55 gm were listed (Table 2). Twenty four germplasm lines recorded more than 55 gm per plant yield and among these eight lines viz. SA-70, SA-76, SA-125, SA-369, SA-629, SA-839, SA-1052 and SA-1053 have yielded more than 80 g per plant yield. Srinivasan *et al.* (1977) reported germplasm lines have given the yield more than 40g per plant.

b) Mean boll weight

Big boll size is recognized as one of the characters which directly contributes to increased production of seed cotton per unit area. In the present investigation, the variability for means boll weight was not so wide but it was of moderate value. Three lines namely SA-159, SA298 and SA-429 have shown the boll weight more than 4.0g and other 10 lines had boll weight of about 4.0 g. Similar results have also been reported by Singh (1985) for boll weight and other characters in *Gossypium hirsutum*.

c) Mean bolls per plant

Bolls per plant along with high boll weight is reckoned as the best combination of characters for higher yields in cotton. They have direct effect on kapas yield. The mean bolls per plant ranged from 1.5 to 24.0. during 1996-97 and 1.2 to 2'3.6 during 1997-98 respectively. However, two lines (SA-83l and SA-1053) having high yield mainly due to more number of bolls per plant were observed.

d) Monopodia

Many number of monopodia per plant is not a desired character. However, one or few monopodia is desirable with a large number of sympodia. The range observed for this character during 1996-97 is 0.2 to 6.5. and 0.2 to 9.0 1997-98, respectively.

e) Sympodia

Large number of sympodia per plant is a desirable character as it directly contributes to higher kapas yield provided the boll weight and the boll numbers are high. Accessions with over seven sympodia are listed. The range falls 0.8 to 14.3 and 2.0 to 18.2 for *kharif* 1996 and 1997 respectively. The accessions which excelled for almost all the traits also had more number of sympods per plant. The importance of fruit bearing branches has also been reported by Seth and Singh (1984).

f) Ginning out turn (G.O.T.)

Ginning out turn is the ratio of weight of lint to that of kapas (seed cotton) expressed as percentage. Genetic stocks which have recorded more than 35 per cent G.O.T. have been listed in Table 2. It is observed that the germplasm lines do not have much variability for ginning out turn. However, few lines (SA-1088 and SA-1104) had more than 6 per cent ginning out turn which could be utilized in the breeding programme. Higher ginning out turn upto 49.2 per cent has however, been reported in *G. herbaceum* (Singh, 1984).

Table 2. List of selected genetic stocks with their important characters of *Gossypiuni hirsutuni* L.

SA No.Name of genetic stock	Yield (g)	Boll weight (g)	Number of bolls	No. of monopods	No. of sympods	Ginning out turn (%)	Mean halo length (mm)
a) Yield of seed cotton (55 gm/plant & above)							
SA-67 Mcnamarna clean,high lint	58.6	3.80	17.2	4.2	7.8	34.0	19.8
SA-70 Batson Cluster	83.3	3.70	17.0	5.6	3.6	34.0	19.8
SA-73 H.A. 1	60.0	3.70	13.8	2.6	4.8	34.0	24.1
SA-76 H.A. 4	88.0	3.12	13.0	2.0	10.0	31.5	19.1
SA-99 Decidious Original	65.2	3.00	14.2	4.0	8.4	32.5	22.0
SA-125 Brown 3-6-15 1	82.0	3.47	21.0	2.0	10.0	30.0	18.3
SA-130 Chaco	78.0	3.30	13.0	5.0	10.0	32.0	19.3
SA-159 Tipo chaco UA4-4	61.0	4.08	9.2	1.4	7.2	26.0	18.5
SA-186 Felistana UA-7-18	60.0	3.42	9.0	5.5	7.5	35.2	12.4
SA-188 UA 7-20	57.5	3.70	18.0	3.0	10.0	28.0	20.2
SA-369 D and PL 10-1	84.3	4.0	7.5	2.4	7.8	28.0	21.3
SA-380 Stoneville xHop 1-12-1-2-1	64.0	3.70	16.6	4.0	7.2	30.0	20.8
SA-516 Mebane,walson	66.0	3.60	14.5	4.0	8.0	31.2	20.1
SA-591 Sealand whiteflower	60.8	3.00	12.0	2.8	9.6	31.0	26.3
SA-629 CB 2555	81.0	4.00	18.0	1.5	10.5	31.0	21.0
SA-688 Smooth Boll 1	65.0	3.60	17.0	4.6	7.6	31.0	23.0
SA-744 Frego Cluster	78.2	3.90	14.2	2.2	11.0	30.0	23.0
SA-831 Mex. 121	84.0	3.40	20.4	4.2	10.0	33.5	28.0
SA-1052 51.041 (V 1508)	91.0	3.60	11.8	4.7	11.7	33.9	28.0
SA-1053 108F	100.4	3.70	18.6	2.8	11.2	32.6	22.0
SA-1058 Delfos 8274	57.6	3.10	15.7	2.3	12.6	34.4	20.8
SA-1072 Bobshaw high linter	64.0	3.60	13.5	3.6	9.2	34.6	24.7
SA-1080 942	71.7	3.40	16.5	3.0	11.2	30.0	21.2
SA-1088 CB 3106 A	74.0	3.65	12.5	2.5	4.5	36.0	17.0
b) Lines with mean halo length (26mm & above)							
SA-391 Missdel 6 PL. 1	22.5	3.50	6.5	2.5	5.2	34.6	27.8
SA-470 Miller	20.6	3.10	9.3	2.0	9.3	30.7	26.2
SA-56 Acala (Mex.) bud abort.	8.0	3.40	4.4	1.2	7.8	30.5	28.7
SA-588 Sealand 1	33.2	3.40	6.0	1.2	7.6	32.0	29.4
SA-631 CB 2540	21.6	30.0	8.0	1.0	6.0	28.5	31.6
SA-743 Frego upland Cr. Dw. Meade	51.3	3.70	14.4	2.2	9.8	36.0	29.0
SA-831 Mex. 121	84.0	3.40	20.4	4.2	10.0	33.5	28.0
SA-1052 51.041(VI508)	91.0	3.60	11.8	4.7	11.7	33.9	28.0
SA-1084 182	36.6	3.70	6.0	1:0	6.0	35.0	26.1
c) Lines with boll weight (4.0 & above)							
SA-7 Original winesap	20.0	4.00	16.2	6.5	7.8	30.2	19.5
SA-9 Intense red okra cl	6.7	4.00	12.2	2.2	7.8	30.5	19.0
SA-151 U 4	bulk W7	UA8-4	12.0	4.00	10.0	1.0	4.0
SA-159 Tipo chaco ua 4-4	61.0	4.10	9.2	1.4	7.2	26.0	18.0

Table 2. (Contd.)

SA No.Name of genetic stock	Yield (g)	Boll weight (g)	Number of bolls	No. of Monopods	No. of sympods	Ginning out turn (%)	Mean halo length (mm)
SA-298 Wannmakers wonder wilt	18.5	4.50	5.0	3.0	6.0	33.0	20.4
SA-336 Coker 33-12	26.6	4.00	11.8	2.2	8.8	31.0	19.8
SA-351 Rowden 40-5-3-1-2	22.0	4.00	9.2	0.7	3.3	29.8	20.1
SA-369 D and PL 10-1	84.2	4.00	7.5	2.4	7.8	28.0	25.0
SA-429 Columbia	9.0	4.50	4.0	0.1	5.0	29.5	23.0
SA-509 Locket 140-46	2.0	4.00	2.0	0.1	3.0	31.5	17.4
SA-515 Northern star	5.0	4.00	3.0	0.1	0.1	30.7	20.1
SA-573 CB 2480	43.3	4.00	7.6	0.8	7.8	34.0	20.4
SA-629 CB 2555	81.0	4.00	18.0	1.5	10.5	,31.0	21.0
d) Lines with ginning out turn (35.0 % and above)							
SA-346 Station C 42	44.3	3.50	10.4	3.5	9.0	35.0	24.1
SA-1063 DPL 5317-42-56-65	46.0	3.30	9.0	3.6	9.2	35.5	24.7
SA-1073 Bobshaw hybrid 82	41.0	3.5	14.0	1.3	6.3	35.0	19.6
SA-1084 182	36.6	3.70	6.0	1.0	6.0	35.0	26.1
SA-1088 CB 3106 A	74.0	3.65	12.5	2.5	4.5	36.0	17.0
SA-1089 CB 3106 B	23.0	3.70	7.5	0.6	4.0	35.7	24.0
SA-1103 Acala 5	36.7	3.40	8.5	1.7	5.7	35.0	21.3
SA-1104 D 2 smooth mutant	36.0	3.30	12.3	1.3	6.3	36.7	22.5
e) Lines with boll number (20.0 and above)							
SA-86 Brown Egyptian	50.0	3.35	23.0	2.5	11.5	31.0	24.7
SA-125 Brown 3-6-15-1	82.0	3.47	21.0	2.0	10.0	0.0	18.3
SA-182 UA-7-6	38.0	3.47	21.0	2.0	12.0	31.7	21.2
SA-210 Laffery brown lint	11.5	3.14	20.5	3.5	6.5	30.7	21.2
SA-818 MEX. 74	50.0	3.56	20.5	2.7	10.7	34.0	25.2
SA-831 MEX. 121	84.0	3.40	20.4	4.2	10.0	33.5	28.0
f) Lines with sympods (12.0 and above)							
SA-182 UA-7-6	38.0	3.10	23.0	2.0	12.0	1.7	21.2
SA-592 Sealand 883	33.3	3.75	14.0	2.0	14.0	31.0	24.2
SA-965 Plains	51.0	3.60	15.0	5.0	12.0	33.0	23.2
SA-1058 Delfos 8274	57.6	3.10	15.7	2.3	12.6	34.4	20.8

g) Mean halo length

The most important among the fibre properties from the economic point of view is staple length. Most of the genetic stocks fall under the range 22 to 28 mm. The range being 12.0 to 29.4 and 15.0 to 1.5 for 1996-97 and 1997-98 seasons, respectively. Lines with 26.0 mm and above mean halo length were identified. Only one line had mean halo length more than 30.0 min. The lines with longer staple length may be included in the crop improvement programme for enhancing the staple length of varieties and hybrids. May *et al.*, (1996) reported that ten Pee Dee germplasm lines of upland cotton had high yield potential, variable maturity and excellent fibre and spinning properties.

The success of breeding programme largely depends on the amount of variability present in the germplasm stock. An assessment of range of variability for economic characters in *G. hirsutum* L. was made and promising germplasm lines with good economic characters have been identified, which may be utilised in the breeding programme for the development or improvement of productive commercial varieties and hybrids or may be of use for building up a wide genetic base in practical breeding programmes.

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GENETIC VARIABILITY, CORRELATION COEFFICIENT AND PATH ANALYSIS FOR QUANTITATIVE CHARACTERS UNDER RAINFED ECOSYSTEM IN THE NATIVE LANDRACES OF RICE

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A study to find out the genetic parameters, correlation coefficients among yield and yield components, direct and indirect effects of yield components on the yield in the native landraces of rice under Rainfed ecosystem was carried out. 124 rice landraces collected from Bolangir district of Orissa were transplanted in two replications and the data was recorded on ten competitive plants in each accession. The estimates for PCV were higher than GCV for all the traits indicating the effect of environment on the manifestation of traits. The flag leaf width showed the highest estimate followed by panicle length, number of primary branches/panicle, yield/plant and number of effective tillers/plant. From the study of PCV and GCV, the flag leaf width, panicle length, number of primary branches/panicle, yield/plant and number of effective tillers/plant were found to be the important characters. Both the heritability and genetic advance were found high for the number of grains/panicle, number of primary branches/panicle and 1000-grain weight, which indicated the governance by additive gene action. The panicle length, 1000-grain weight, harvest index, biological yield, flag leaf length and its width had high heritability but low genetic advance suggesting that these traits had greater influence of the non-additive gene action with a big role of non-genetic factors in their expression. Moderate heritability estimates associated with moderate genetic advance for some traits suggested that additive and non-additive gene effects were equally important in the inheritance of these characters. The coheritability estimates were highest between harvest index and 1000-grain (48.71) followed by yield/plant and number of grains/panicle (44.71), flag leaf length and plant height (43.15), and number of grains/panicle and panicle length (41.72). A negative coheritability was found between biological yield and harvest index (–39.41), 1000-grain weight and number of grains/panicles (–33.31), 50% flowering and panicle length (–2.74) and 50% flowering and number of primary branches/panicle (–2.94). The yield/plant had positive association with plant height, number of effective tillers, panicle length, primary branches/panicle, number of grains/panicle and 1000-grain weight, harvest index, biological yield, flag leaf length and its width and days to 50% flowering. The path coefficient analysis at phenotypic level revealed that 1000-grain weight had the maximum direct effect on the grain yield followed by number of primary branches, harvest index, number of effective tillers and flag leaf length. Plant height though showed the positive correlation with grain yield but had negative direct effect and contributed indirectly through harvest index. At the genotypic level, panicle length had maximum direct effect on the grain yield followed by number of grain/panicle, 1000-grain weight, harvest index and flag leaf width.

Key words : Rice, genetic variability, path analysis, correlation coefficient

Grain yield in rice is a complex character and greatly influenced by the agroclimatic conditions. The knowledge of associations between yield and yield components under the rainfed ecosystem may be beneficial and helpful to enhance the grain yield. The significant associations of grain yield with 1000-grain weight and tiller number per plant have been reported (Subramanian and Rathinam, 1984; Sharma and Choubey, 1985; Dhanraj and Jagdish, 1987 and Jangle *et al.*, 1987). The correlation between grain yield and total biomass (Rana, 1986 and Mehetre *et al.*, 1994) and grain yield and harvest index (Subramanian and Rathinam, 1984 and Roy and Kar, 1992) have been reported. The grain yield has been reported to be influenced by high direct effects of total tillers and days to flowering (Amrithadevarathinam, 1983), number of panicles per plants, number of filled grains per panicle and 1000-grain weight (Yang, 1986), number of filled grains per panicle and plant height (Reuben and Katali, 1989), productive tillers, panicle length and flowering duration (Ibrahim *et al.*, 1990) and plant height and tiller number (Kumar, 1992).

Very little systematic information regarding the genetic variability and correlation among the yielding contributing traits in the native landraces of rice germplasm under rainfed ecosystem is available. The present study was therefore, planned to estimate genetic parameters, correlation coefficients among the different yield attributes at the phenotypic as well as genotypic levels, coheritability and nature and extent of direct and indirect effects of the yield components on the yield under rainfed ecosystem in the native landraces of rice germplasm.

MATERIALS AND METHODS

One hundred twenty four native rice land races were collected from Bolangir district of Orissa during 1988. 25-day of old seedlings were transplanted in a randomized block design with two replications. Each plot consisted of two rows of 5 meters length with a spacing of 30 × 20 cms. One row gap was left between two plots. In each genotype, 10 plants were taken randomly to record the observations on days to 50% flowering, plant height, number of tillers, number of effective tillers, panicle length, primary branches per panicle, number of grains per panicle, 1000-grain weight, yield per plant, harvest index, biological yield, flag leaf length and its width. The analysis of variance was carried out on the mean values of each character. The phenotypic, genotypic coefficient of variability, heritability in broad sense, genetic advance at 5% selection intensity were computed as suggested by Johanson *et al.* (1955). The phenotypic and genotypic correlations were calculated as per methods of Al-Jobouri *et al.* (1958). Coheritability was calculated using the formula suggested by Nei (1960). The path analysis was carried out as per method of Dewey and Lu (1959).

RESULTS AND DISCUSSION

A wide range of variability was observed for all the characters. The range for days to 50% flowering (79-129), plant height (77-186 cm), number of tillers (4-15), number of effective tillers (3-13), panicle length (13-32 cm) primary branches per panicle (7-17), number of grains per panicle (50-469), 1000-grain weight (12-29 gm), yield per plant (5-20 gm), Harvest index (0.21-0.40), biological yield (15-60 gm), flag leaf length (26-63 cm) and flag leaf width (1.23-2.46) was observed. The range, mean, standard error of mean and critical difference at 5% level of significance are given in the Table 1. Analysis of variance revealed that the differences among the landraces (genotypes) were highly significant. The phenotypic and genotypic variances were also calculated and it was found that phenotypic variances were higher than genotypic variances for all the characters. It indicated the effect of environment in the expression of traits. Similarly phenotypic coefficient of variation (PCV) estimates

Table 1. Range and mean of the various quantitative characters in the native land races of rice germplasm.

Characters	Range	Mean	Sem	CD (5%)
Days to 50% flowering	79-129	115	1.89	5.30
Plant height (cm.)	77-186	130	2.82	7.92
No. of tillers/plant	04-15	8	0.89	2.49
No. of effective tillers/plant	03-13	7	0.70	1.96
Panicle length (cm.)	13-32	20	0.52	1.45
No. of primary branches/panicle	06-17	9	0.63	1.76
No. of grains/panicle	50-469	150	4.35	12.18
1000-grain weight (gm)	12-29	23	1.01	2.82
Yield/plant (gm)	05-20	12	1.09	3.05
Harvest index	0.21-0.40	0.31	0.08	0.07
Biological yield (gm)	14-60	30	0.88	2.29
Flag leaf length (cm)	26-63	41	2.14	5.99
Flag leaf width (cm)	1.23-2.46	1.52	0.09	0.25

were found higher than genotypic coefficient of variation (GCV) estimates indicating again the effect of environment on the manifestation of these traits. However the differences between PCV and GCV were not very high. The flag leaf width showed the highest estimate followed by panicle length, number of primary branches per panicle, yield per plant and number of effective tillers. Thus these traits further offered scope for genetic improvement. Rest of the characters showed the moderate GCV. From the study of PCV and GCV, the flag leaf width, panicle length, number of primary branches per panicle, yield per plant and number of effective tillers emerged to be the most important characters. These findings are not in conformity with the previous findings of Ramalingam *et al.* (1994) who reported that grain yield, and number of grains/panicle had high GCV.

The heritability estimate h^2 ranged from 70.25 (flag leaf length) to 95.84 (number of grains per panicle). The genetic advance ranged from 2.21 (flag leaf width) to 61.52 (primary branches/panicle). The number of grains per panicle, primary branches per panicle, number of effective tillers and days to 50% flowering ahad high genetic advance (> 35) as well as heritability (> 75) (Table 2). It suggested that these attributes were controlled predominantly by additive gene action. Hence genetic improvement through selection for these traits may be effective. The panicle length, 1000-grain weight, harvest index, biological yield, flag leaf length and its width had high heritability but low genetic advance suggesting that these traits had greater influence of the non-additive gene action with a big role of non-genetic factors in their expression. Moderate heritability estimates associated with moderate genetic advance suggested that additive and non-additive gene effects were equally important in the inheritance of the characters. Chauhan (1996) reported that grain yield per plant, spikelets per panicle, grain weight, biological yield and harvest index had high expected genetic advance associated with high heritability. Low to moderate heritability values for grain yield were reported by Ananda Kumar (1992), Roy and Kar (1992) and Chauhan *et al.* (1993).

Coheritability

Coheritability value of the character combination suggests that the increase/decrease in one of the characters of a particular combination will lead to an corresponding increase/decrease in its coheritable character. The yield per plant had high coheritability with number of grain per panicle (44.71), days to 50% flowering (37.94), biological yield (36.24), 1000-grain weight (35.74), flag leaf width (35.61), harvest index (34.14) and flag leaf length (31.24) in the positive direction. The coheritability estimate was the highest between harvest index and 1000-grain (48.71) followed by between yield per plant and number of grains per panicle (44.71), between flag leaf length and

Table 2. Genetic parameters for yield and its attributes in the native landraces of rice germplasm

Characters	σ^2 ph	σ_g^2	PCV	GCV	h2	GA
Days to 50% flowering	464.80	353.00	18.74	16.32	75.9	39.0
Plant height (cm)	459.20	373.00	16.84	14.85	61.3	17.0
No. of tillers/plant	9.79	7.06	39.11	33.21	72.2	37.0
No. of effective tillers/plant	9.17	7.40	43.26	38.86	80.7	35.0
Panicle length (cm.)	94.25	84.80	48.54	46.04	90.0	3.6
Primary branches/panicle	18.94	14.40	48.35	42.22	76.3	62.0
No. of grains/panicle	372.90	357.00	12.87	12.60	95.8	57.0
1000-grain weight (gm)	69.27	61.20	36.18	34.01	88.4	43.0
Yield/plant (gm)	29.29	23.00	45.10	39.94	78.5	31.0
Harvest index	110.20	90.90	34.40	29.79	75.0	3.6
Biological yield (gm)	74.74	52.90	28.81	24.25	70.8	3.8
Flag leaf length (cm)	94.25	66.20	23.67	19.84	70.3	5.8
Flag leaf width (cm)	0.90	0.67	62.41	53.85	74.7	2.2

plant height (43.15) and between number of grain per panicle and panicle length (41.72). A negative coheritability was found between biological yield and harvest index (–39.41), 1000-grain weight and number of grains/panicles (–33.31), 50% flowering and panicle length (–2.74) and 50% flowering and number of primary branches/panicle (–2.94). Rest of the character combinations showed from very low to moderate coheritability (Table 3). It was interesting to note that panicle length, number of effective tillers, 1000-grain weight and number of grains per panicle was positively coheritable with yield per plant which also had high expected genetic advance coupled with high heritability in broad sense. Thus selection for these traits may be effective for yield the improvement.

Simple correlation coefficients

Both the phenotypic and genotypic correlation coefficients were calculated and found that in general the magnitude of phenotypic correlations were higher than the genotypic correlations. Phenotypic expression of correlations was enhanced mostly under the influence of

Table 3. Coheritability values in per cent for different combinations of characters in the indigenous local cultivars

Characters	No. of tillers	No. of effective tillers	Panicle length	Primary Branches	No. of grains per panicle	1000 grain wt.	Yield per plant	Harvest index	Biological yield	Flag leaf length	Flag leaf width	Days to 50% flowering
Plant height	1.90	1.81	29.34	3.95	21.42	2.15	3.42	33.14	36.29	35.12	43.15	1.10
Number of tillers/plant		4.24	1.42	0.67	0.67	4.24	6.25	4.81	31.21	3.74	6.74	2.90
Number of effective tillers/plant			3.42	6.24	3.94	6.24	36.14	24.34	25.74	3.47	5.81	3.29
Panicle length				35.94	41.72	2.14	36.74	31.24	36.94	1.24	3.79	–2.74
Primary branches/panicle					38.74	11.24	31.91	29.64	26.59	3.42	5.71	–2.94
No. of grain/panicle						33.31	44.71	31.74	29.74	3.24	7.61	2.31
1000 grain weight							35.74	48.71	36.75	31.24	26.74	37.14
yield/plant								34.14	36.24	31.24	35.61	37.94
Harvest index									–39.41	25.74	31.41	38.75
Biological yield										25.74	21.74	36.74
Flag leaf length											25.74	24.24
Flag leaf width												1.25

Table 4. Estimate of genotypic and phenotypic correlation coefficients between different pairs of characters in the indigenous rice cultivars

Characters	No. of tillers/ plant	No. of effective tillers	Panicle length	Primary bran- ches	No. of grains/ panicle	1000 grain weight	Yield per plant	Harvest index	Biolo- gical yield	Flag leaf length	Flag leaf width	50% flowe- ring
Plant height	0.008	0.064	0.185*	0.025	0.194*	0.023	0.200*	0.184*	0.341	0.183*	0.189*	0.021
	0.065	0.054	0.194	0.014	0.183	0.011	0.184	0.173	0.284	0.164	0.182	0.018
No. of tillers		0.112	0.092	0.102	0.084	0.097	0.069	0.029	0.150	0.094	0.113	0.126
		0.094	0.091	0.096	0.061	0.009	0.074	0.084	0.156	0.063	0.126	0.134
No. of effective tillers			0.140	0.129	0.124	0.136	0.199*	0.189*	0.201*	0.111	0.121	0.134
			0.134	0.111	0.131	0.124	0.178	0.190	0.194	0.101	0.125	0.121
Panicle length				0.341**	0.384**	0.096	0.192*	0.294**	0.304**	0.009	0.151	–0.160
				0.284	0.290	0.111	0.189	0.299	0.311	0.084	0.158	–0.152
Primary branches					0.401**	0.151	0.211*	0.274**	0.261**	0.141	0.161	–0.161
					0.394	0.142	0.194	0.294	0.272	0.129	0.159	–0.164
No. of grain/panicle						–0.421*	0.461**	0.274**	0.271**	0.134	0.141	0.136
						–0.392	0.394	0.281	0.262	0.131	0.139	0.129
1000 grain wt.							0.344**	0.481**	0.394**	0.241**	0.381**	0.261**
							0.341	0.460	0.381	0.250	0.305	0.258
Yield/plant (gm)								0.401**	0.393**	0.392**	0.409**	0.414**
								0.400	0.398	0.396	0.397	0.384
Harvest index									–0.409*	0.297**	0.281**	0.301**
									–0.419	0.301	0.290	0.321
Biological yield										0.411**	0.390**	0.311**
										0.401	0.387	0.301
Flag leaf length											0.309**	0.443**
											0.311	0.394
												0.151
Flag leaf width												0.142

environment. But in some cases the genotypic correlations were higher than the phenotypic correlations coefficients which were in the same direction either plus or minus. It indicated the elimination of environmental effects and a fairly strong inherent association. The yield per plant had positive association with plant height, number of effective tillers, panicle length, primary branches per panicle, number of grains per panicle and 1000-grain weight, harvest index, biological yield, flag leaf length and its width and days to 50% flowering. Days to 50% flowering showed negative correlations with panicle length and primary branches per panicle. A highly significant negative correlation was recorded between 1000-grain weight and number of grains/panicle. Biological yield also showed a strong and significant negative correlation with harvest index (Table 4). Thus selection for high number of grains per panicle, 1000-grain weight, number of primary branches per panicle will improve the harvest index as a result enhancement of yield. The positive association of grain yield with biological yield and harvest index was observed (Roy and Kar, 1992 and Chauhan *et al.*, 1993). A significant positive correlation of number of grain yield per panicle with grains per panicle, panicle length, and primary branches was reported by Sharma and Dubey

Table 5. Path coefficient analysis among the quantitative characters of native rice landraces

Characters	Days to 50% flowering	Plant height (cm)	No. effective tillers	Panicle length (cm)	Primary branches	No. of grains/ panicle	1000-grain wt.	Harvest index	Biological yield	Flag leaf length	Flag leaf width	Correlation with yield/ plant
Days to 50% flowering	*0.040*	0.004	0.012	0.031	0.073	0.061	0.051	0.014	0.054	0.034	0.030	0.414
Plant height (cm)	0.012	*–0.101*	0.001	0.08	–0.033	0.042	0.031	0.062	0.021	0.081	0.004	0.200
No. of effective tillers	–0.015	–0.002	*0.121*	–0.001	0.004	0.024	0.011	0.102	–0.042	–0.001	–0.002	0.199
Panicle length (cm)	–0.002	0.023	–0.003	*0.084*	0.101	0.094	–0.079	0.054	–0.071	–0.004	–0.005	0.192
Primary branches	0.003	–0.041	–0.042	0.071	*0.131*	0.061	0.072	0.042	–0.031	–0.034	–0.021	0.211
No. of grain/panicle	–0.039	–0.018	0.074	0.043	0.058	*0.124*	0.201	0.082	–0.043	–0.010	–0.012	0.461
1000 grain weight (gm)	–0.042	–0.053	0.008	0.031	0.042	0.102	*0.172*	0.134	0.030	–0.040	–0.045	0.344
Harvest index	0.019	0.023	0.021	0.011	0.021	0.053	0.151	*0.131*	–0.071	0.031	0.011	0.401
Biological yield	0.011	0.161	0.054	0.043	0.022	0.054	0.103	–0.084	*0.074*	–0.040	–0.004	0.393
Flag leaf length	–0.013	–0.006	0.016	–0.002	0.047	0.010	0.012	0.034	0.084	*0.111*	0.104	0.397
Flag leaf width	–0.085	–0.037	0.022	0.041	0.034	0.041	0.117	0.032	0.092	0.051	*0.101*	0.409

Residual effect = 0.028

Table 6. Genotypic path coefficient analysis among the quantitative characters of native rice landraces under rainfed ecosystem

Characters	Days to 50% flowering	Plant height	No. of effective tillers	Panicle length	Primary branches	No. of grain panicle	1000 grain wt.	Harvest index	Biological yield	Flag leaf length	Flag leaf width	Correlation with yield/ plant
Days to 50% flowering	*0.027*	0.091	0.054	0.062	0.014	0.011	0.082	0.021	0.014	0.005	0.003	0.384
Plant height	0.021	*0.012*	0.001	0.080	0.011	0.009	0.022	0.015	0.032	–0.020	–0.008	0.184
No. of effective tillers	–0.054	–0.021	*0.109*	0.022	0.044	0.008	0.032	0.017	–0.034	0.034	0.021	0.178
Panicle length	–0.004	0.011	–0.064	*0.134*	0.060	0.120	–0.024	0.054	–0.064	–0.020	–0.011	0.189
Primary branches	–0.074	0.012	–0.053	0.124	*0.074*	0.084	0.043	–0.037	0.012	0.034	–0.025	0.194
No. of grain/panicle	0.009	–0.044	–0.059	0.119	0.064	*0.124*	0.071	0.094	–0.040	0.036	0.020	0.394
1000 grain weight	0.012	0.063	–0.041	–0.052	–0.073	0.038	*0.121*	0.024	0.134	0.064	0.051	0.341
Harvest index	–0.043	–0.059	0.061	0.031	0.049	0.111	0.152	*0.121*	–0.043	0.008	0.012	0.400
Biological yield	0.034	0.064	0.032	0.034	0.021	0.076	0.094	–0.061	*0.084*	0.034	–0.014	0.398
Flag leaf length	–0.024	0.025	0.044	0.104	0.021	–0.040	0.029	0.031	0.045	*0.102*	0.054	0.396
Flag leaf width	0.012	0.024	0.031	0.011	0.024	0.030	0.051	0.048	0.034	0.019	*0.113*	0.397

Residual effect = 0.027

(1997). Chauhan (1996) found positive association of yield with spikelets number per panicle, biological yield and harvest index. The grain yield per plant showed significant positive correlation with number of grains per panicle at both the phenotypic as well as genotypic levels but with 1000-grain weight, panicle length and flag leaf length at genotypic level only (Reddy *et al.*, 1997).

Path correlation coefficient

The path coefficient analysis carried out at both the phenotypic as well as genotypic level (Table 5 & 6). At the phenotypic level, 1000-grain weight had the maximum direct effect on the grain yield followed by number of primary branches, harvest index, number of effective tillers and flag leaf length. Plant height, though showed the positive correlation with grain yield but had negative direct effect and contributed indirectly through harvest index. The path coefficient analysis at genotypic level revealed that panicle length had maximum direct effect on the grain yield followed by number of grains per panicle, 1000-grain weight, harvest index and flag leaf width. Path analysis revealed that panicle length, no. of grains per panicle, 1000-grain weight and flag leaf width are the major contributor towards grain yield. Sharma and Dubey (1997) found that longer panicle coupled with more grains, primary branches and secondary branches per panicle are important for yield improvement.

Present investigation revealed that panicle length, number of effective tillers, 1000-grain weight and number of grains per panicle was positively coheritable with yield per plant which also had high expected genetic advance coupled with high heritability in broad sense. Thus selection for these traits may be effective for yield the improvement.

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SCREENING GENOTYPES BASED ON STABILITY OF PANICLE CHARACTERS IN PEARL MILLET

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Pearl millet genotypes did not show stability for grain yield. However, they were stable for some panicle characters. Correlation of grain yield with panicle number and panicle width was positively significant. The entry MH 544 not only showed stability of performance for panicle number and panicle width but also recorded the highest grain yield. Identification of genotypes based on stability of panicle characters rather than grain yield stability might be more useful for crop improvement in pearl millet.

Key words : Pearl millet, screening, stability, panicle characters

The interplay between genotype and environment resulting in a phenotype is known as genotype × environment interaction. Presence of G × E interaction not only reduces the correlation between genotype and phenotype but also retards the progress that a breeder can make in his breeding programme. Selection based on environmental fluctuations becomes ineffective. Further more, selection for stable yield attributes rather than yield or yield contributing characters alone is effective. The present study was made to understand G × E interactions and identifying stable genotypes based on stability of panicle characters in pearlmillet.

MATERIALS AND METHODS

Nine genotypes of pearlmillet were grown during three *kharif* seasons of 1992, 1993 and 1994 at Agricultural Research Station, Anantapur in rainfed alfisols. The genotypes were planted in randomised block design with three replications. Row-to-row spacing of 50 cm and plant-to-plant spacing of 10 cm was adopted. Crop was fertilized with N, P_2O_5 and K_2O @ 40:20:O kg ha^{-1} respectively. Nitrogen was applied in two equal splits; one as basal and the other at 30 DAS. Observations on plot basis on threshing percentage, panicle number, panicle weight, test weight and grain yield, and on ten randomly chosen plants on panicle length and panicle width were recorded. G × E interaction and phenotypic stability analysis (Eberhart and Russell, 1966) for all the characters and correlation (Singh and Chaudhary, 1985) of all the traits with grain yield were worked out.

RESULTS AND DISCUSSION

Mean performance and environmental indices indicated that kharif season of 1994 was highly favourable for expression of panicle number, panicle weight, panicle length, panicle width and grain yield. Whereas performance of genotypes for threshing percentage and test weight was better during kharif seasons of 1992 and 1993 respectively. Mean squares due to genotypes and environments for all the characters were significant (Table 1), indicating the presence of variation among genotypes and environments. Predominent effect of varying environments was observed as

Table 1. Pooled analysis of variance (M.S.S) for different characters in pearlmillet

Source of variation	DF	Grain yield	Panicle No.	Panicle weight	Test weight	Panicle width	Threshing %
Genotype	8	26.3374**	0.1668**	66.4626**	3.3669**	0.3664++	22.5729++
Env + (G × E)	18	30.9810**	0.6001**	63.8790**	3.8099**	0.2046++	23.6520++
E (linear)	1	244.5700**	7.3583**	613.5630**	26.8598**	3.3210++	32.9230++
G × E (linear)	8	28.6578**	0.3164**	42.8465**	1.5168**	0.0424**	31.8348++
Pooled deviation	9	9.3127**	0.1014**	21.4990**	3.2870**	0.0026	15.3444
Pooled error	54	2.0342	0.0420	4.5886	0.3790	0.1001	7.3495

**Significant at 1% level against pooled deviation
++significant at 1% level against pooled error

indicated by high differences in environmental indices and significant mean square due to environment (linear).

Genotype × environment interaction for panicle length when tested against pooled error was non-significant. It suggested that the genotypes did not exhibit variable response to varying environments for this character, G × E interactions were found to be significant for all the other characters, indicating considerable interaction of the genotypes with the environments in the expression of these characters. Pooled deviation when tested against pooled error was significant for panicle number, panicle weight, test weight, panicle width and grain yield. Therefore, mean sum of squares due to other sources of variation for these characters were tested against pooled deviation. As pooled deviation was non-significant for threshing percentage, the other sources of variation were tested against pooled error. Significant values of pooled deviation for panicle number, panicle weight, panicle width, test weight and grain yield indicated the importance of non-linear component. For threshing percentage, the G × E (linear) was highly significant only when tested against pooled error and not against pooled deviation, indicating a lesser contribution of linear regression and also difficulty in predicting the performance.

The linear and the non-linear components of G × E interaction were important in building up the total G × E interaction (Perkins and Jinks, 1968). As the magnitude of linear component was higher than the non-linear component, prediction of genotypes across the environments was possible for panicle number, panicle weight, panicle width and grain yield. However, the prediction become difficult in case of test weight as the magnitude of non-linear component was higher.

No strong relationship between mean performance and stability existed for grain yield and panicle weight. Genotypes with mean performance above the average performance were not stable for these characters. Vijendra Das (1990) opined that stability of green fodder in forage pearlmillet could be fixed only to some extent. Data from table 2 revealed that among the genotypes, MH 544 for panicle number and panicle width, HHB 60 for test weight, and ICMH 88088 and ICTP 8203 for threshing percentage were highly stable. A good environment would be favourable for the expression of ICMH 88088 for panicle number, ICTP 8203 for test weight and panicle width, and HHB 67 for threshing percentage whereas, HHB 60 for panicle number, and HHB 67 for test weight were responsive to poor environments.

Therefore, it would be more desirable to select genotypes for stability of panicle characters

Table 2. Estimates of stability parameters

Genotype	Grain yield (Kg ha^{-1})			Panicle No.(L ha^{-1})			Panicle weight (Kg ha^{-1})			Test weight (g)			Panicle width (cm)			Threshing percentage		
	Mean	bi	S^2 di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2 di	Mean	bi	S^2di	Mean	bi	S^2di
MH 544	2532	1.6043	14.2679*	3.49	0.9657	–0.0348	3906	1.1801	19.5176*	11.01	0.8365	8.4259*	2.38	1.0070	–0.0095	64.4	–2.5756*	–1.3152
MH 509	2486	2.2756	16.7364*	3.07	1.2228	0.0844*	3740	1.8987	35.2025*	8.70	1.4121	2.8890*	2.09	0.9607	–0.0060	66.2	0.6548	9.1568
ICMH 88088	2439	2.1703	3.0060*	3.23	1.6701+	–0.0201	3621	1.9775	8.5633*	9.91	0.9656+	–0.3787	2.13	1.2097+	–0.0070	67.4	0.6179	–5.1160
HHB 60	2264	0.2585	3.9992*	3.63	0.2920+	–0.0295	3442	0.5941	27.6623*	10.64	1.4174	0.2122	1.73	0.8928	0.0013	66.4	3.8688+	–7.3475
RAJ 171	2092	0.9146	18.4055*	2.96	0.6900	0.0162	3286	0.9179	9.8461*	10.29	–0.0835	11.5781*	2.04	1.1385+	–0.0097	63.7	63.7	3.2207
ICTP 8203	2040	1.2438	12.3468*	2.94	2.1624+	0.0956*	3004	1.5877	26.2522*	11.75	1.2905+	–0.3711	2.65	1.2378+	–0.0100	68.9	4.2301	4.1755
HHB 68	1898	–0.3683+	–1.3591	3.12	0.3164+	–0.0253*	2657	–0.0316+	–4.4549	9.12	1.0051	2.0927*	1.96	1.0815	–0.0082	71.6	1.4889	53.5063*
HHB 67	1837	–0.5449+	–1.9162	3.16	0.5864	0.4421*	2711	–0.2760+	0.4570	10.45	-0.0226+	–0.0976	1.46	0.1704+	–0.0100	67.9	2.9405+	–7.3407
ICMH 88735	1738	1.4460	0.0201	3.04	1.0942	0.0064	2776	1.1516	29.0847*	8.67	2.1789	1.8217*	2.28	1.3016+	–0.0078	62.8	–4.1353+	–0.4810
Mean	2147	3.18	3238	10.06	66.6													

+Significantly deviated from unity at 5% level
*Significant at 5% level

rather than selecting for yield stability alone (Singh and Bakshi, 1984). Among the panicle characters studied, panicle number (0.5513^{**}) and panicle width (0.2361^{*}) were strongly associated with grain yield. Performance of genotypes for these characters was also observed to be predictable. Genetic mechanism controlling the expression of stability of grain yield might be different from that of the panicle characters. Apart from stability for panicle width and panicle number, MH 544 exhibited grain yield superiority over rest of the genotypes. Hence, it can be selected as a stable genotype for low rainfall alfisols.

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QUALITY CHARACTERISTICS OF SOME SCENTED RICE

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Some scented rice genotypes were evaluated for their quality characteristics. The study revealed that Milagrosa, Gopalbhog, Begami 2-8, Gourab and Type-3 are good donors for good kernel length with some other desired quality characteristics. It is possible to produce long slender scented rice with desired quality characteristics by hybridization or by pyrimiding of genes from the above varieties.

Key words : Scented rice, cooking characters, quality characters

Scented rice has a premium value in international market but they are very poor yielders. They are praised in the market due to their quality characteristics. The present investigation was undertaken to identify the varieties with good quality, long, slender and good elongation after cooking for export purpose. So to sustain export potential of scented rice, care should be taken to produce exclusive rice varieties that would be broadly conform to consumers quality demand of major importing units.

MATERIALS AND METHODS

Twenty scented rice varieties collected from different parts of India were evaluated at Central Rice Research Institute, Cuttack for their quality characteristics. Thirty days old seedlings were transplanted in a randomised block design with 3 replications. Recommended package of practices were followed to raise normal cross. The quality characters were analysed for hulling, milling, head rice recovery percentage as described by Ghosh *etal.* (1971), kernel length and breadth measured by dial micrometer and L/B ratio was calculated. For alkali spreading value method of Little *et al.* (1958), water uptake and volume expansion (Beachell and Stansel, 1963), cooked kernel length was recorded using a graph paper and elongation ratio by the method adopted by Azeez and Shafi (1966) and for amylose by Juliano (1971) methods were followed.

Export quality scented rice mainly depends upon head rice recovery and grain shape and size. The hulling and milling percentage depends upon endosperm characteristics (Govindaswamy and Ghosh, 1969). The variability in grain filling influence the head rice recovery because the starch which are packed in endosperm may loose or tight which affects head rice recovery. Among the different varieties (Table 1) Basanbhog, Kalajira, Katrani and Gopalbhog have head rice recovery more than 60 per cent and BAM-3, IET 8579, Dubraj, Milagrosa, Bankura, Chinisakkar, Hansraj, Gourab, Type-3, Gopalbhog, Begami-2-8 and Rajbhog are long slender kernels having length > 6mm and L/B ratio > 3.

RESULTS AND DISCUSSION

With regards to alkali spreading value, the extent of swelling or digestion of rice kernel in a given alkali solution indicates the spreading after cooking. The alkali spreading value is also affected

Table 1. Quality characters in scented rice

	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel length/ breadth ratio	Alkali sprea-ding value	Water uptake	Cooked kernel length (mm)	Elonga-tion ratio	Volume expan-sion	Amylose content	Grain yield/ plant(g)
BAM-3	60.60	55.25	35.70	6.60	4.06	2.50	260.00	11.10	1.68	3.82	23.47	4.02
Basnabhog	73.00	67.20	61.05	4.51	2.82	3.25	170.00	8.50	1.88	4.07	18.24	8.23
IET-8579	71.90	64.25	47.10	6.41	4.16	4.50	320.00	10.70	1.67	3.75	18.44	7.72
Kalajira	75.90	71.45	65.15	4.50	2.62	2.75	197.50	7.50	1.66	3.75	21.26	5.20
Katrani	74.25	69.20	61.10	5.82	3.57	3.25	195.00	8.70	1.50	3.82	21.23	7.44
Dubraj	72.25	66.25	53.36	6.18	3.89	4.25	225.00	10.50	1.70	4.29	23.30	7.76
Milagrosa	63.25	58.30	44.45	7.27	4.65	4.00	205.00	10.70	1.47	3.94	21.53	3.33
Kalimochi	70.60	63.96	52.90	5.91	3.64	3.75	245.00	9.70	1.64	3.76	21.23	7.15
Muskubhi	72.15	65.75	55.00	5.59	2.99	2.75	232.50	8.40	1.50	4.43	19.38	7.79
Tulsibhog	80.65	75.40	69.10	5.89	3.89	4.00	205.00	8.50	1.44	4.02	24.29	10.70
Seetasail	77.15	71.60	54.00	5.97	3.89	3.75	220.00	9.10	1.52	4.07	25.33	12.35
Bankura	70.40	65.25	58.80	6.47	3.85	3.00	270.00	9.10	1.40	3.69	20.06	5.90
Chinisakkar	69.25	63.25	48.60	7.53	4.66	3.50	197.50	11.10	1.48	3.94	23.06	5.72
Gopalbhog	80.75	75.36	63.65	6.65	3.88	4.25	255.00	10.45	1.57	2.95	20.26	7.78
Begani-2-8	75.05	68.80	55.10	7.12	4.26	3.50	242.50	12.30	1.73	4.23	19.40	6.59
Hansraj	73.05	67.95	56.05	7.70	4.71	2.50	145.00	9.30	1.21	3.86	23.80	4.45
Gourab	67.00	59.80	46.95	7.29	4.59	4.25	282.50	11.70	1.61	3.38	17.28	9.00
Type-3	61.00	56.10	43.65	8.09	4.98	2.75	300.00	13.35	1.65	3.78	20.28	5.14
Rajbhog	70.65	65.00	53.15	6.35	4.08	2.50	245.00	10.50	1.65	4.14	19.55	5.00
Laxmibilash	75.55	69.85	59.65	5.09	3.07	3.00	190.00	7.45	1.47	3.66	22.79	4.00

by the ratio of amylose and amylopectine. If the kernel splits more, means the rice will be waxy after cooking and if it splits little, the rice will be non-waxy. The people of Japan and Vietnam prefer waxy rice whereas others prefer non-waxy rice. In the present study the value ranged from 2-4, which are low to medium. The intermediate value 4-5 are (IET 8579, Dubraj, Gopalbhog and Gaurab) preferred as good quality rice because the kernel become soft during eating and these varieties may be used as good donors for this character.

For water uptake BAM-3, IET 8579, Bankura, Gopalbhog, Gaurab, Type-3 and for volume expansion all the varieties except Gopalbhog are excellent. The elongation ratio ranged from 1.4 to 2.0 which indicates their good linear expansion after cooking. The endosperm of kernel is composed of starch, which is a fraction of amylose and amylopectine. The amylose content of non-waxy rice ranged from 8-37 per cent of total starch whereas glutaneous or waxy rice have practically no amylose (Webb and Starmar, 1972). The amylose content of twenty varieties ranged from 17-24 per cent. Milarosa, Kalimochi, Bankura, Gopalbhog, Begami 2-8, Type-3, Rajbhog, and Laxmibilash are good for amylose content.

The results of present investigation revealed that Milagrosa, Gopalbhog, Begami 2-8, Gourab and Type 3 having most of the key traits for quality which are preferred by the consumers in

Table 2. Best donors for different quality characters

1.	Hulling (%)	Kalajira, Tulasibhog, Seetasail, Gopalbhog, Laxmibilash
2.	Milling (%)	Kalajira, Katrani, Tulasibhog, Seetasail, Gopalbhog, Laxmibilash
3.	Head rice recovery (%)	Basnabhog, Kalajira, Katrani, Gopalbhog, Laxmibilash
4.	Kernel length	Milagrosa, Chnisakkar, Begami 2-8, Hansaraj, Gourab, Type-3
5	Kernel length/breadth ratio	Milagrosa, Chinisakkar, Hansaraj, Gourab, Type-3
6	Alkali spreading value	IET-8579, Dubaraj, Milagrosa, Tulasimanjari, Gopalbhog, Gourab
7	Water uptake	BAM-3, IET 8579, Bankura, Gourab, Type-3
8	Cooked kernel length	BAM-3, IET 8579, Milagrosa, Chinisakar, Begami2-8, Gourab, Type-3
9	Elongation ratio	BAM-3, Basnabhog, Dubraj, Begami 2-8, IET 8579
10	Volume expansion	Basanbhog, Dubaraj, Muskbudhi, Seetasail, Begami 2-8, Rajbhog
11	Amylose content	Milagrosa, Kalimochi, Bankura, Begami 2-8, Type-3, Rajbhog

India and abroad. Gene manipulation followed by multiple selection criteria will help in quick realization of better selections for export purpose. The above five varieties may be utilized as donors in the hybridization programme in the improvement of scented rice.

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AGRI-DIVERSITY EROSION IN THE NORTH-WEST INDIAN HIMALAYAS — SOME CASE STUDIES

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There is a worldwide concern over the loss of diversity of plant genetic resources. In the past, hills were considered as natural harbour of biodiversity in general and agri-bidoversity in particular mainly due to their inaccessibility and less population pressure. But now the plant genetic resources even in these nature's treasures are being eroded at much faster rate largely due to habitat destruction/ alteration, over exploitation, urbanisation and increased population pressure. While conducting surveys in different parts if hills it was observed that two types of genetic erosion have occurred firstly is within the diversity of crop i.e. the substitution of a diverse set of genetically variable landraces by few genetically uniform modern varieties and secondly between crops i.e. the substitution of un-used/ under-utilised crops (amaranth, buckwheat, chenopod, small millets and barley by high valued cash crops like green pea, hops, potato and apple). Other associated factors such as changed food habits, depletion in the diversity of agricultural related animals have also been found responsible to narrowing the agricultural horizon. Several landraces, which were there in the farmer's field in 1977-78, were found totally eroded in the year 1997-98.

Key words: Agri-biodiversity, genetic erosion, Himalayas,

The species named *Homo sapiens* facing no major threat of extinction is changing almost all the ecosystems by adopting all modem developmental techniques, unethical and unscientific life style of consumerism. Consequently, the traditional and ages old floral and faunal diversity is no longer found in the accessible habitats. Obviously in doing so, the quality of life on the earth has been simply overlooked. It has resulted in living a poor quality of life, though we might have achieved the tantalising and debatable easy life style in the name of "Development in civilisation". In this context, the present study was undertaken to assess the present status of agro-biodiversity and its depletion over the years in different parts of N-W Indian Himalayas.

MATERIALS AND METHODS

The study was undertaken by conducting surveys in Kangra, Mandi, Shimla, Kullu and Kinnaur districts of Himachal Pradesh in the year 1997 and 98. The base year to calculate the per cent rate of depletion was kept as 1977 and 78. The rate of depletion was calculated over a span of 20 years. Twenty villages were selected from each district and 50 families in each village were randomly taken for collecting the data. The data were recorded as per the questionnaire prepared. A few important question asked from the interviewee were - i) name and age of the farmer; ii) name and number of the landraces grown in the base year (1977-78) and in the year of study (1997-98); iii) name of the crops grown/consumed; iv) number of approximate days in a week for which a particular food crop is consumed; v) number and type of cattle rare and vi) if there is any change i.e. increase or decrease in diversity and reason thereof. While interviewing the people, it was considered that interviewee should have age not less than fifty years. Notes on socio-cultural value of landraces were also taken.

RESULTS AND DISCUSSION

The hills are very rich both in crops and cattle diversity. The landraces of cereals such as wheat, rice, maize and barley and local breeds of cattle have been a part of the hill agriculture systems and contributing to the sustainable livelihood of hill people. But with the advent of modem agriculture, traditional agriculture has almost extinct not only in the high intensive cropping areas but in the remote areas like Kinnaur and Lahaul & Spiti districts. Case studies conducted in the region support this view very strongly and it was found that present status of agro-biodiversity is not very encouraging even in traditional areas. A major shift has taken place in the number of crops being grown, breeds of cattle rare and the food habits of the people. The studies undertaken to assess the actual scenario of agri-biodiversity and changes over the years have been discussed below:

Landraces status in paddy and wheat: The introduction of high yielding varieties has caused and big shift in the cropping patterns involving wheat and paddy resulting into almost complete wipe-off of landraces that have been once grown over vast areas. With the result, landraces which were either highly competitive or have some special attributes were left in cultivation. During the surveys, data were recorded on the number, name of landraces, their cultivation and consumption status and other associated significance.

Paddy: Paddy forms a staple component of the diet of hill people and consumed as a part of daily diet. In this region, paddy is mostly grown as upland in Kangra, Kullu, Chamba, Mandi and Solan. The data collected on number and name of paddy landraces showed that prominent landraces grown in the year 1977-1978 were; *Madholu, Rodu, Rehdi, Cheena, Japani dhan, Rattu, Chhota parmal, Rodu, Jawas, Rangadi, Kaulpatash , Safed Fulpatsh, Lal Dhan, Ramjawain, Lal dhan, Kala dhan, Jhini, Pulpatasha, Ladheri, Bowru, Katheri, Tapta, Kodri, Sukul, Rangri, Jaldara, Jartai, Jawas, Matalu, Bowru, Jiri, Reesa, Vkhil, Jattoo, Jaldara Sukhdawas, Jhinjhini, Jaulia, Bathal, Begumi, Naknda, Achhain, Tiu, Dinu and Lal naknda, Ratuwa, Sunduru, Motadhan, Kolo, Mangoi* and *Jarati.* On the other hand landraces found under cultivation presently are: *Cheena, Japani dhan, Ramjawain, Lal dhan, Kala dhan, Jhini, Pulpatasha, Katheri, Rohdu, Jiri, Reesa, Jattôo, Rattu, Chhota parmal, Rodu, Jawas, Rangadi, Kaulpatash, Safed Fulpatsh, Lal Dhan, Jaldara, Begumi, Naknda* and *Lal naknda*. From the data collected, it was derived that the landraces, which are still in cultivation, are only mainly because of their special attributes such as aroma, long grain, medicinal properties, fast cooking, appearance etc. The overall depletion of landraces over the 20 years (1977-78 to 1997-98) was found to be 50-60%. This revealed that half or more landraces that were grown 20 years ago have now totally extinct. It was also observed that the depletion rate was much faster in the last decade than that of previous decade.

Wheat: It is also an equally important crop of the hills and grown right from the plains to the Trans-Himalayas. Generally, the spring wheat is grown in this region but winter wheat is also grown in some parts of Trans-Himalayan region such as Lahaul & Spiti, Kinnaur and Pangi areas. However, due to non-availability of superior varieties of winter wheat, the farmers in these areas were very reluctant to continue its cultivation. By growing winter wheat, farmers harvest two crops, which is not possible when they grow spring wheat as the previous one is sown in October/November before snowfall and harvested in May/June and after that another crop of buckwheat can be easily taken. The land races grown during 1977-78 as told by the farmers were; *Shruin, Tarmori, Chiti kanak, Kankoo, Darmori, Misri, Lal puri, Brad kanak, Mandalu, Kasieun, Ralieun, Bhangru, Daru, Daron, Paluwa, Rundan, Latar, Kiawali, Trimudi, Safed Dharmori, Kali Dharmori, Keshwali farm, Bangla kalyan, Kanak, Keshwali Kanak, Linda farm, Lal Kanak, Gameun, Gasheun, Mundra Marodu, Lal kanak* and *Chawera.* The landraces, which were in cultivation under present conditions are; *Chiti kanak, Kankoo, Darmori, Brad kanak, Kasieun, Safed Dharmori, Kali Dharmori, Keshwali farm, Bangla kalyan, Kanak, Keshwali Kanak, Linda farm, Lal Kanak, Gameun, Gasheun, Mundra, Ralieun, Rundan, Latar, Kianwali, Trimudi* and *Chawera.* It was also noticed that most of landraces are being maintained by a handful of elderly people who have developed special affection to some of the varieties due to their special attributes. The new generation of farmers was not found very encouraging in maintaining these old landraces as they consider them poor yielders and wastage of resources. The data on per cent depletion of landraces in wheat showed that about 40-60% of the land races depending upon the area have been totally extinct over 20 years.

Erosion in the crops diversity grown/consumed: In the past, many parts of this region were highly inaccessible and people had to sustain on the local crop genetic resources. With the changed agricultural scenario and developmental network, almost every village has better access to get every thing which they need if not round the year then at least for 8-10 months. Thus, an easy style of consumerism has been adopted by the people who used at one time used to grow/consume a variety of crops and now confining to a few crops. This has led to genetic erosion of not only landraces but also of many traditional crops and ultimately a very broad dietary horizon has become very narrow. In this investigation, information was collected on number and names of crops grown/ consumed in the year 1977 & 78 and 1997 & 98. The crops, which were used to consume and are being consumed given below:

a) Crops diversity grown/consumed in 1977 and 78

Maize, wheat, rice, finger millet, barnyard millet, proso-millet, amaranth, buckwheat, chenopod, barley, pea, *Lathyrus,* lentil, horsegram, urd, moong, beans, soybean, cowpea, chickpea, faba bean, garlic, onion, radish, turnip, potato, mustard, linseed, taramira, sesame, sugarcane, cotton, *Colocasia,* cucurbits, okra, tomato, suran (zimikand), chilli, brinjal and various naturally occurring plant species such as *Trichosanthes, cumeriana* (jangli chachinda), *Bauhinia variegata* (kachnar), *Ficus palmata* (fig, bruneee), *Momordica balsamina* (ban kakora), *Nastartium officnale* (water cress, Choonuli, chuchha), *Utrica dioca* (bichhu buti), *Nelumbo nucifera* (kamal kakri), *Diplazium polypodiodes* (lingru), *Rheum moorcroftiana* (Himalayan rhubarb, Chukri), *Cordia dictoma* (lasoora), *Selinum wallichianum* (Thoa, celery), *Portulaca oleracea* (purslain) *Asparagus* spp., *Basella alba, Cichorium* spp., *Ipomea aquatica, Artocarpus lakoocha* (bread fruit, daihun), *Arisaema* spp. (chamus), *Moringa oleifera* (horse radish), *Sagittaria* spp., *Allium* spp., *Bambusa* spp., *Chenpodium album* (bathua), *Lactuca* spp., *Spilanthes* spp., *Tragopogon* spp., *Citrullus colocynthis, Sechium edule* (Chow-chow, Lanku), *Perilla* spp., *Melilotus macrorhiza, Moghania vestita, Malva* spp., *Phytolacea acinosa* (jalga), *Cassia tora* and *C. occidentalis* (aelu) *Dioscorea sagittata* (Tardi), *Aloe vera* (Kuwar), *Opuntia* spp., *Agave americans, Boerhavia diffusa, Polygonum alpinum, Alocasia* spp., *Marsilea quadrifolia, Crambe cordifolia* and *Typha angustata* (jangli alu).

b) Crops diversity grown/consumed in 1997-98

Maize, wheat, rice, amaranth, barley, pea, lathyrus, lentil, beans, cowpea, horsegram, faba bean, garlic, onion, radish, turnip, potato, mustard, linseed, taramira, sesame, *Colocasia*, cucurbits, okra, tomato, chilli, brinjal and various naturally occurring plant species such as *Bauhinia variegata* (kachnar), *Ficus palmata* (fig, bruneee), *Diplazium polypodiodes* (lingru), *Rheum moorcroftiana* (Himalayan rhubarb), *Cordia dictoma* (lasoora), *Cichorium* spp., *Artocarpus lakoocha* (bread fruit, daihun), *Arisaema* spp. (chamus), *Chenpodium album* (bathua), *Sechium edule* (Chow-chow, Lanku), *Perilla frutesence, Melilotus macrorhiza, Rheum moorcroftiana* (Himalayan rhubarb, Chukri), *Phytolaca acinosa* (jalga), *Polygonum alpinum, Alocasia* spp. and *Typha angustata* (jangli alu).

The comparison of number of crops that people used to consume 20 years ago and now revealed that a sizeable number of crops have been eroded from the present cropping scenario. It is further mentioned that some crops that were consumed are still occurring naturally but due to changed food habits they remain neglected. The rate of depletion of the diversity comes around 53 per cent and it is still increasing at much faster rate. The rate at which we are dropping the crops from our cultivation and consumption, it appeared that day is not far when we will be consuming only a handful of crops viz. wheat and rice that too in the form of fast foods. This study clearly stated the basic fundamental of biodiversity that no biodiversity can be saved unless it is put in greater and wider sustainable use. Maximum sustainable utilisation of these valuable plant genetic resources is only possible if they are attached some value or economic gain either directly or indirectly. Therefore, our conservation and utilisation strategies must include a wide range of tools and techniques for their safeguard.

Change in the food habits: It is a well-known fact that when we don't put anything into use it looses its existence or bound to extinct. The same thing has happened with the agricultural biodiversity i.e., all the age-old varieties; crops and technologies, which were not in use since long, have been dropped from our system and got extinct. The people when interviewed say that when they are not consuming a particular crop or a variety then why that should be maintained and consider this as a futile practice. While interacting with a group of young boys and girls in Raksham and Sangla areas of Kinnaur district, I found that they don't take any of the traditional crops such as amaranth, buckwheat, chenopod and smaller millets in their daily diet, whereas their elders are still fond of such foods. They also showed reluctance in growing all such crops. Moreover, they don't want to deprive themselves from the economic benefits that they earn from cash crops. The data given in the Table 1 and interviews revealed a major shift from traditional foods to common foods viz., wheat and rice in both Kangra and Kinnaur district. It can also be concluded that even in Kinnaur where millets and pseuocereals were the staple food have been replaced by the recently introduced maize wheat and rice. In most of the areas, farmers are growing amaranth and buckwheat and selling in the shops as a part of barter system i.e. in turn they are getting equal amount of rice. It was therefore realised during the investigation that changing food habits is also one of the factors responsible for depletion of agri-diversity. The changes in the food habits of the people are given in Table 1.

Erosion in agriculture based cattle diversity: Cattle are also one of the most important components of agricultural diversity in the hills. Due to difficult terrain, the mechanisation of agriculture is difficult and the cattle, carry out most of the agricultural operation. Data on the number of cattle rare by a family in the year

Table 1. Consumption of different food crops by a family for number of days (average) per year

Food crops	Kangra		% ±	Kinnaur		% ±
	77-78	97-98		77-78	97-98	
Rice	205	350	+ 70	144	304	+111
Wheat	121	290	+ 140	258	103	+ 103
Maize	145	75	-48	21	85	+ 304,
Millets	30	10	-66	164	38	- 76
Amaranth	26	20	-46	246	160	- 35
Buckwheat	21	05	-76	320	201	- 37
Chenopod	18	04	-77	102	17	- 83
Traditional vegetables	142	65	-54	301	118	- 34
Pulses (own produce)	241	112	-53	276	98	- 64

1977-78 and 1997-98 were recorded. The emerging picture is again not very encouraging and depletion has occurred in number of cattle being rared. The replacement has occurred mainly for cows and buffaloes by the improved breed such as jersey and farmers who used to rare cows and buffaloes and even goats for milk are now satisfy with one cow or one buffalo. Similarly due to mechanisation of agriculture even in sub-mountainous areas and protection of forests, a drastic reduction has taken place in the number of bullocks and goat and sheep, respectively. The data in this regard is given in Table 2.

Major reasons for the depletion of agro-biodiversity: Several reason were emerged form the data collected through surveys and case studies. The important are:

1. Better access to the modem means of livelihood e.g. better transport facilities, communication facilities, availability of better technologies etc.

2. Lack of awareness and inadequate technical understanding of agro-biodiversity.

3. Shift in agriculture i.e. from traditional crops to cash crop. Farmers don't want to deprive themselves from the lucrative benefits they receive from high value cash crops.

4. Absence of economic valuation of agro-biodiversity - how much can it contribute to the economy of the community, nation, global community and on what terms?

5. Migration from rural to urban areas. Majority of the rural people has shifted form villages to cities in search of jobs, better education facilities and prospects for their children.

6. Agriculture considered as low social status profession as compared to other professions. In the hills any young chap would prefer to join as daily wages employee rather than to opt agriculture as occupation.

7. Agriculture occupation considered as highly risk oriented i.e. most of the agriculture holdings are small, and entirely rain-fed, thereby subjected to natural calamities.

8. Commercialisation of agriculture has led to the cultivation of only high valued crops and in the process many traditional crops and varieties have been ignored.

Table 2. Traditional cattle diversity rared by the people and depletion over the years

Cattle population	Buffaloes		Bullocks (pair)		Cow		Sheep		Goats	
	K	S	K	S	K	S	K	S	K	S
1977-78	46	50	42	46	56	72	116	25	218	30
1997-98	29	28	19	34	41	48	64	10	78	18
% Depletion	36	40	54	26	26	33	45	60	64	40

K - Kangra district; S - Shimla district

9. Shrinking of the dietary base of the people. Among cereals, only rice and wheat are being consumed by majority of the people and all the traditional crops even maize has been dropped from the normal diet. Majority of the young generation farmers does not relish traditional foods e.g. amaranth, buckwheat, chenopod, other coarse cereals etc. and also does not want to waste time in the adoption of traditional technologies as better substitutes are available.

10. Disintegration of joint families into nucleus families has resulted in the fragmentation of land holdings and reduction of working hands in the family, thereby some portion of land in the villages is left as barren and uncultivated. It is worth mentioning that in each village at least 4-5 families have left their land uncultivated and 15-20 families have given their land on lease basis to landless families.

11. Protection of community forests has caused fodder scarcity and thus leading to erosion in cattle population. The people used to keep a few goat and sheep herds in the village, which were entirely dependent on community forests. After the protection of village forests by the forest department, people had no other alternative but to sell out their animals. Many rural people were of the opinion that it has affected their socio-economic status as they were not able to fetch their basic needs viz., fuel, small timber and fodder from the forests and now had to opt for LPG, Kerosene and other costly means of living.

12. The menaces of wild animals in most of villages have also forced the people to sell out their domestic animals. Increasing incidences of attacking human beings by the wild animals had develop a negative sense in the people's mind and they are not ready to accept such challenges.

Future thrust for saving agro-biodiversity

1. Survey and collection of left over agro-biodiversity without further delay.

2. Thorough evaluation of already collected agro-biodiversity to make it worth using.

3. Both *in situ* and *ex situ* conservation of agro-biodiversity in various forms such as natural habitats, seed gene banks, *in vitro* gene banks, cryo-banks, field gene banks, botanical and herbal gardens etc. should be promoted and facilities in this regard should be strengthened.

4. Commercialisation of agriculture in order to derive maximum returns from the limited land resources has faded the ideas of *in situ* conservation at farmers' field. In order to conserve the age old landraces, crops and traditional technologies in their natural habitats, there is a need to develop a strategy or a kind of compensation mechanism where farmers should not be deprived from the economic benefits and simultaneously our efforts to allow the biodiversity to evolve continually to the changing environments should not be stopped.

5. Value addition to the agro-biodiversity. It can not be saved unless it is used and while in use, it can continue to evolve and be appreciated enough to be saved. The ultimate users and protectors of biodiversity i.e. farmers should be educated as it provides enormous direct economic benefits in the form of food, forage, timber, medicine (many pharmaceuticals are derived from plants), rural health care systems and industrial raw material, and has the potential for generating many more. It also provides an array of essential service to humanity like keeping air clean, modifying climate extremes, degrading wastes, recycling nutrients, creating soils, controlling diseases and scientific research etc.

6. Those plant species, which have not brought under cultivation yet, but are of very high value e.g. many medicinal plants should be promoted to cultivate in private lands. These plants are being extracted at a much faster rate from than ever before from their natural habitats.

7. Germplasm centres for the species that

are endangered or threatened should be developed in different regions/ zones i.e. save the most beleaguered species and ecosystem first.

8. In order to conserve landraces, efforts may be concentrated on people's participation for "on farm conservation", concept, on the basis of crop diversity occurring in a particular area.

9. Accelerated research and support on the fragmentation of biodiversity and ecological process, community restoration and rehabilitation of degraded lands and proper monitoring of biodiversity is needed.

10. Integration of biodiversity conservation programs into cultural diversity before it is irretrievably lost.

11. Enhance traditional systems of resource use rather than replacing them

12. Integration of various departments such as agriculture, forestry, irrigation, ground water development board, village industries etc. in drawing up village level programs interpreting conservation and sustainable use of biodiversity.

13. Keeping in view the pace of depletion of traditional technologies, knowledge and crops it is of utmost importance to document them as 'leads' for gene and drug prospecting

14. Enhancement in professional competence and HRD of those who are directly or indirectly involved in the promotion and conservation of biodivesity.

15. The need of agro-biodiversity in never ending, therefore, conservation/ management efforts will have to continue for better posterity.

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PATH ANALYSIS OF METRIC TRAITS IN *Acacia catechu* Willd.

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Correlation and path-coefficient analysis was conducted on eight characters of *Acacia catechu* Willd. seedlings for higher shoot dry weight. Phenotypic correlation of shoot dry weight was positive and significant with all other component characters. The genotypic correlation coefficients were positive, significant and greater in magnitude than the phenotypic correlations. Path-coefficient analysis revealed that shoot fresh weight, root dry weight, number of leaves and leaf area comprehend direct effect on shoot dry weight. Therefore, these traits should be given greater importance while formulating selection indices for better establishment of seedling growth in the plantation areas.

Key words: *Acacia catechu*, correlation, path analysis and shoot dry weight

Biomass yield of a tree species is a complex and composite biological function, the expression of which is associated with a number of component characters. The component characters are quite often inter-related which affects their direct relationship with biomass yield, thereby, making the correlation coefficients less effective for selection. So much so. when more variables are included in the correlation studies, the indirect association becomes more complex and it becomes imperative to separate them out. In such a situation, path coefficient analysis helps to determine the direct and indirect contribution of various associated traits towards the trait of interest.

Correlation and path analysis have been used in forest tree species by workers like Rathinam *et al.* (1982) in *Eucalytptus tereticornis*; Chandrasekharan *et al.* (1985) in *Leucaena lecocephala*; Kumar and Gurumurthy (1996) in *Casuarina equisetifolia* and Khosla *et al.* (1985) in *Pinus roxburghaii*. In order to initiate any selection programme, the present studv was undertaken to study the relationship among shoot dry weight and its component traits through path-coefficient analysis.

MATERIALS AND METHODS

The experimental material consisted of seedlings raised from 40 different locations representing diverse geographic regions in a Randomised Complete Block Design with three replication (Table. 1). Five seedlings per replication were selected at random after one and a half year growth in the nursery. The data were recorded on nine quantitative characters viz; seedling height, collar diameter, inter nodal length, number of leaves, leaf area, shoot fresh and dry weight, root fresh and dry weight. The genotypic and phenotypic correlation coefficients between all pairs of characters were calculated as per the procedure suggested by Searle (1969). Path-coefficient analysis was carried out as per Dewey and Lu (1959).

RESULTS AND DISCUSSION

The estimates of genotypic and phenotypic correlation coefficients between all pairs of eight characters are presented in Table 2. The genotypic correlations were in general higher than the phenotypic correlations. All pair of character combinations were significantly correlated with each other at genotypic as well as phenotypic level. This showed that increase in seedling height resulted in considerable increase in the collar diameter, inter nodal length, number of leaves, leaf area, shoot fresh, root fresh and root dry weight, thus, leading to strong inherent association with higher shoot dry weight. Therefore, special emphasis needs to be given to these traits at the time of selection in the nursery. There was no negative association observed among these traits which may lead to the genetic slippage. These findings are in line with that of Srivastava (1995) among morphological and biomass traits of *Bauhinia variegata* seedlings and Chauhan and Verma (1993) in *Acacia catechu*.

The path-coefficient analysis in Table 3 depicts the direct and indirect effects of seedling height, collar diameter, inter nodal length, number of leaves, leaf area, shoot fresh weight, root fresh and dry weight. From the perusal of Table 3, it is apparent that seedling height which gave significant and positive correlation with shoot dry weight which was primarily due to the positive indirect effects via number of leaves, leaf area, shoot fresh weight and root dry weight. The indirect effects via collar diameter, inter nodal length and root fresh weight were negative.

Collar diameter revealed negligible direct effect on dry shoot weight (–0.0192). The indirect effects through seedling height, inter nodal length and root fresh weight were negative and non-significant to counter balance the high positive effects via shoot fresh weight, root dry weight, number of leaves and leaf area, thereby, resulting in a strong genotypic correlation coefficient. Inter nodal length exhibited small negative direct effect (–0.0362) but the cumulative effect obtained from the indirect positive effect through number of leaves, leaf area, shoot fresh weight and root dry weight compensated the indirect negative effects through seedling height, collar diameter and root fresh weight resulting a highly significant positive correlation.

Number of leaves showed significantly positive association with shoot dry weight (0.1689) which resulted from the direct positive correlation of this trait and indirect positive contribution through leaf area, shoot fresh weight and root dry weight. Association of leaf area and shoot dry weight was positive and highly significant (0.1294). Path analysis revealed that leaf area gave direct positive effect on the resultant trait. The indirect effects via number of leaves, shoot fresh weight and root dry weights were positive and other effects were negative.

The direct effect of shoot fresh weight was maximum and positive (0.9519). The indirect effect via seedling height, collar diameter, inter nodal length and root fresh weight was very small but negative, while number of leaves, leaf area and root dry weight depicted positive indirect effect. The highest positive and significant genotypic correlation was mainly due to the direct positive effect of shoot fresh weight.

The genotypic correlation of root fresh weight with shoot dry weight was positive and highly significant. However, the direct effect was negative (-0.4270) but it was contributed by the positive indirect effects via number of leaves, leaf area, shoot fresh weight and root dry weight. The association of root dry weight with shoot dry weight was positive and highly significant due to its direct effects (0.4477) and indirect positive effects through number of leaves, leaf area, and shoot fresh weight. These positive effects counter balanced the indirect negative effects resulting highly significant correlation coefficients. The residual effect was found very low which indicated that majority of the traits contributing to shoot dry weight were included in the present study.

The above observation clearly depicted that seedling height, collar diameter, and inter nodal length contributed very less but with negative direct effect on shoot dry weight which may be attributed to the very young age of the seedlings

Table 1. Geographical locationa nd habitat data of various seed sources under study

Source No.	Name of seed source	District	State/ Country	Latitude	Longitude	Altitude (cm)	Rainfall (cm)
1	Arki	Solan	HP	31° 09' N	76° 57' E	1260	120.1
2	Awadevi	Hamirpur	HP	31° 40' N	76° 39' E	996	131.0
3	Badrama	Sambalpur	Orissa	21° 09' N	83° 10' E	300	160.1
4	Badsar	Hamirpur	HP	31° 32' N	76° 28' E	717	145.3
5	Bagar	Solan	HP	30° 51' N	76° 15' E	1190	139.6
6	Balera	Solan	HP	31° 08' N	76° 54' E	1100	141.3
7	Bhanjal	Una	HP	31° 46' N	76° 07' E	730	100.8
8	Bharighat	Solan	HP	31° 15' M	76° 50' E	1150	124.4
9.	Bharmour	Chamba	HP	31° 54' N	76° 39' E	1100	110.6
10	Bhota	Hamirpur	HP	31° 37' N	76° 33' E	900	144.8
11	Bilaspur Sadar	Bilaspur	HP	31° 19' N	76° 48' E	825	131.5
12	Dalautpur chowk	Una	HP	31° 49' N	75° 57' E	650	108.6
13	Dharja	Solan	HP	30° 48' N	76° 13' E	1124	142.1
14	Dhameta	Kangra	HP	31° 50' N	75° 55' E	700	121.3
15	Kothi	Solan	HP	30° 58' N	77° 03' E	1100	139.2
16	Gagret	Una	HP	31° 40'N	76° 05' E	500	110.4
17	Gandhal	Sirmour	HP	30° 48' N	70° 15' E	1009	121.4
18	Ghumarwin	Bilaspur	HP	31° 25' N	76° 45' E	1050	122.9
19	Gadchiroli	Gadchiroli	Maharashtra	20° 03' N	80° 01' E	250	160.0
20	Jabalpur	Jabalpur	MP	23° 05' N	79° 58 ' E	400	140.5
21	Kalah	Jammu	J & K	32° 35' N	74° 40' E	621	92.3
22.	Khadpanjawar	Una	HP	31° 32' N	76° 09' E	512	112.8
23	Kharah	Jammu	J & K	33° 10' N	74° 12' E	950	89.5
24	Kheri	Sirmour	HP	30° 50' N	77° 08' E	1106	121.6
25	Kothipura	Bilaspur	HP	31° 17' N	76° 47' E	1076	107.2
26	Kotlabarog	Sirmour	HP	30° 50' N	77° 14' E	1101	122.7
27	Kwangdhar	Sirmour	HP	30° 51' N	76° 19' E	1253	132.5
28	Manlogkala	Solan	HP	30° 56' N	77° 04' E	1200	138.1
29	Naglahar	Kangra	HP	31° 37' N	76° 41' E	750	121.2
30	Nainatikkar	Sirmour	HP	30° 48' N	77° 07' E	1100	124.7
31	Nakroh	Una	HP	31° 46' N	76° 02' E	702	112.2
32	Narag	Sirmour	HP	30° 49' N	77° 11' E	1150	121.9
33	Oel	Una	HP	31° 38' N	76° 05' E	500	117.6
34	Pasha river	Bara	Nepal	27° 18' N	86° 03' E	280	200.0
35	Rewa	Rewa	MP	24° 32' N	81° 11' E	300	116.8
36	Salohberi	Una	HP	31° 53' N	75° 55' E	600	102.9
37	Sithu	Solan	HP	31° 10' N	76° 54' E	1090	123.5
38	Swarghat	Bilaspur	HP	31° 14' N	76° 42' E	850	121.6
39	Talwara	Una	HP	31° 51' N	75° 49' E	622	109.2
40	Taunidevi	Hamirpur	HP	31° 42' N	76° 36' E	1024	131.5

Table 2. Phenotypic and genotypic correlation coefficients among different morphological and biomass traits of *Acacia catechu* under nursery condition

Traits		Seedling height	Collar diameter	Inter-nodal length	No. of leaves	Leaf area	Fresh shoot weight	Fresh root weight	Dry shoot weight
Collar diameter	P	0.8873							
	G	0.8997							
Intenodal length	P	0.8163	0.8148						
	G	0.8083	0.8158						
No. of leaves	P	0.8596	0.8901	0.8001					
	G	0.8901	0.9184	0.8253					
Leaf area	P	0.7702	0.6942	0.6419	0.6130				
	G	0.8406	0.7368	0.6771	0.6357				
Fresh shoot weight	P	0.7955	0.6745	0.8775	0.5269				
	G	0.8456	0.8884	0.9149	0.5778				
Fresh root weight	P	0.7624	0.7839	0.6680	0.7914	0.5746	0.8674		
	G	0.7978	0.8056	0.6901	0.8152	0.6249	0.8675		
Dry shoot weight	P	0.8005	0.8739	0.7191	0.9091	0.5593	0.9754	0.8403	
	G	0.8437	0.9060	0.7500	0.9381	0.6056	0.9781	0.8412	
Dry root weight	P	0.7645	0.8163	0.7579	0.8299	0.5919	0.8242	0.9276	0.8651
	G	0.7979	0.8353	0.7824	0.8515	0.6359	0.8287	0.9297	0.8693

All the Phenotypic correlations are significant at 5% level of significance

Table 3. Direct and indirect effects of nursery traits on dry shoot weight of Acacia catechu

Traits	Seedling height	Collar diameter	Inter-nodal length	No. of leaves	Leaf area	Fresh shoot weight	Fresh root weight	Dry root weight	GC with dry shoot weight
Seedling height	-0.1902	-0.0173	-0.0293	0.1504	0.1085	0.8050	-0.3406	0.3572	0.8437
Collar diameter	-0.1711	-0.0192	-0.0295	0.1551	0.0951	0.8457	-0.3440	0.3739	0.9060
Interiaodal length	-0.1537	-0.0157	-0.0362	0.1394	0.0874	0.6732	-0.2947	0.3503	0.7500
No. of leaves	-0.1693	-0.0176.	-0.0299	0.1689	0.0821	0.8708	-0.3481	0.3811	0.9381
Leaf area	-0.1599	-0.0142	-0.0246	0.1074	0.1294	0.5501	-0.2668	0.2847	0.6058
Fresh shoot weight	-0.1608	-0.0171	-0.0256	0.1545	0.0746	0.9519	-0.3704	0.3710	0.9781
Fresh root weight	-0.1517	-0.0155	-0.0250	0.1377	0.0807	0.8258	-0.4270	0.4162	0.8412
Dry root weight	-0.1518	-0.0160	-0.0283	0.1438	0.0821	0.7888	-0.3970	0.4477	0.8693

Residual effect = 0.0073; Bold faces values are direct effects

and may change with their establishment in the plantation area. These results are in conformity with Khosla *et al.*, (1985) in *Pinus roxburghii* seedlings and with Kumar and Gurumurthy (1996) in *Casuarina equisetifolia*.

The present study suggested that traits viz; number of leaves, leaf area, shoot fresh weight and root dry weight not only depicted high and positive direct effects but also revealed positive indirect effects with other associated traits. Therefore, these traits may be given greater emphasis while designing selection indices for biomass improvement programme in this forest tree species.

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GENETIC RESOURCES AND CONSERVATION OF LEGUMES IN NBRI BOTANIC GARDEN

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NBRI Botanic Garden is the third largest and one of the oldest Botanic Gardens in India. This holds an exquisite germplasm collection of 7000 taxa representing 210 families. The genetic diversity of legumes in India is quite rich (179 genera and 1152 species) and distributed to all biogeographic zones. Considering the economic, medicinal and industrial importance, there is a world-wide attention on legumes for its genetic resources in order to screen the potential and underexploited species as a source of food. Moreover, scientific studies being carried out on different aspects viz. identification, nomenclature, preparation of check-list, conservation and its sustainable utilisation. This paper deals with the genetic resources of legumes in the NBRI Botanic Garden and their horto-botanical importance besides *ex-situ* conservation measures.

Key words : Germplasm, conservation, legumes

Botanic Garden of NBRI was established in 1800 A.D. in the heart of the city Lucknow, (Uttar Pradesh). This is the third largest and one of the oldest Botanic Gardens of India. This holds an exquisite collection of 7000 taxa comprising trees, shrubs, creepers/climbers besides herbaceous plant. The genetic diversity of plants has been displayed in the Arboretum, Shrubbery borders, Plant Houses and various other sections under *ex-situ* conservation programme. Being one of the oldest Gardens, it has well grown specimen trees which are important and interesting from botanical and aesthetic point of view. Moreover, every year germplasm collection of diversified groups of plants is enriched through seed exchange programme with the 400 leading Botanical gardens of the world specially those located in the iso-climatic zones. Thus, this Botanic Garden serves as an excellent centre for conservation of plant genetic diversity representing 210 plant families. The important ones are- Bignoneaceae, Leguminosae (Fabaceae), Lythraceae, Moraceae, Myrtaceae which have large number of representatives. The majority of plant wealth belongs to the family Leguminosae comprising trees, shrubs, creeper and climbers, besides herbaceous plants. Thus, it is pertinent to have an account of the genetic resource of the legumes in the Botanic garden and their horto-botanical importance besides conservation measures.

MATERIALS AND METHODS

Botanical importance - The family Leguminosae (Fabaceae) is the third largest family after the (Compositae), Asteraceae and Orchidaceae. It consists of about 600-650 genera and 12,000-18,000 species distributed all over the world (Everett, 1980; Wiersema *et al.*, 1990; Polhill and Raven, 1981). The species are prevalent in temperate, tropics, sub-tropics, high land, savannas, deserts, low lands and even in the aquatic form. The family includes trees, shrubs, climbers/creepers, herbs and aquatic plants of diverse nature which are important for economic, food, forage, medicinal, industrial and ornamental purpose (Anonymous, 1979; Bailey, 1963; Bailey and Bailey, 1940; Lock, 1989). Botanically also, this family exhibits a great variations in growth habit and flower characters. Fabaceae (or Leguminosae) is divided into three sub-family viz. Caesalpinioideae, Mimosoideae and Faboideae (or Papilionoideae). Caesalpinioideae includes about 2,800 species, mainly tropical forest trees and savannas distributed in Asia, Africa and South America. About, 12,000 species which are mostly herbs and distributed world wide come under the sub-order Papilionoideae. On the contrary, Mimosoideae consist of 2,800 species of conspicuous shrubs and trees of Africa, Australia and South America (Anonymous, 1979).

Horticultural significance - The horticultural importance of this family is noteworthy. It includes genera like *Acacia, Albizia, Bauhinia, Caesalpinia, Calliandra, Cassia, Delonix, Erythrina* etc. which bear conspicuous colourful flowers and have high ornamental value. Many of the trees are excellent for avenue plantation while shrubs are equally popular as garden plants. Most of the trees and shrubs of the Leguminosae are well suited in the tropical and sub-tropical conditions. Their free flowering habit, wide adaptability to different agro-climatic conditions and easy multiplication have made them popular in the tropical and sub-tropical gardens. Aside, their exquisite flowers in a wide range of colours and form are added attraction for selecting them in landscaping.

Economic, medicinal and industrial importance - A large number of species of the genus Leguminosae has economic, medicinal and industrial importance. The seeds are rich in protein and starch and are eaten all over the world. These are excellent source of food as peas and beans and have tremendous agricultural importance next to Poaceae. But the diversity and number of species in cultivation all over the world are much greater for Leguminosae (Wiersema *et al.*, 1990). There are more than 50 minor tropical legumes, in addition to the major species in cultivation, which needs scientific attention for their study and exploitation (Anonymous, 1975). The seeds of tamarind which are the good source of pectin are valued for manufacturing jam and jelly (Bor and Raizada, 1954). Acacias are also economically important as they are good source of tannin, gum and timber. Moreover, some of the species are very successful in afforestation and reclamation of wasteland by their ability of fixing nitrogen. *Acacia catachu* is an important drug and an essential constituent of 'Pan' (Betel leaf). Some of the species of Caesalpineas (*C. crista*) have medicinal importance as tonic and antipyretic. *Cassia absus* is also used for ophthalmic and skin treatment. Species of *Indigofera* produces blue colour and used for dyeing purpose since time immemorial (Wlth India, 1985).

RESULTS AND DISCUSSION

World scenario - There is world-wide attention for the study of genetic resources and diversity of legumes in order to screen the potential species which are still unexploited or under-exploited as a source of food and their economic use. As a result, International Legume Database Information Service (ILDIS) has been set up in United Kingdom with regional centres engaged in preparing check list of legumes of different countries of the world. In France also, there is an international group looking after the sub-family Mimosoideae. United States Department of Agriculture (USDA) has also developed database as the Germplasm Resource Information Network through Agricultural Research Service's Plant Germplasm System. More than 6,600 legumes have been catalogued in the Technical Bulletin No. 1777. It coordinates national efforts to collect and conservation of legumes (Wiersema *et al.*, 1990).

Therefore, Legumes as a crop are very

important world-wide. Scientific studies are focusing different aspects of their identification, nomenclature, conservation, economic importance and as a source of food.

Germplasm collections at NBRI Botanic Garden - The genetic resource of legumes in India is quite rich. About 1150 taxa under 167 genera have been listed by Husain and Kapoor, 1990 which represents 7 per cent of the world's legume collection. According to a recent report, legume diversity in India is represented by 1152 species belonging to 179 genera distributed in all biogeographic zones. Out of the total legume flora, Papilionoidae constitute ca· 71 per cent while Caesalpinoideae and Mimosoideae 14.6 per cent and 14.4 per cent, respectively (Rao, 1998). A good number of species are native to India while some are introduced and well acclimatized. The germplasm collection of legumes in the NBRI Botanic Garden is quite significant. Out of the total 500 species of trees in our Botanic Garden, 20 per cent comes from the family Leguminosae. These are mainly located in the arboretum, along the circular road and by side of lawns. A few of them are well grown and very old specimen trees of botanical significance viz., *Albizzia procera, Colvelia recemosa, Delonix regia, Parkia biglandulosa, Peltophorum ferrugineum, Prosopis juliflora, Tamanindus indica* etc. Out of the total 51 genera and 170 species existing in the Botanic Garden, the genus *Acacia* is having maximum number of species (26 nos.) followed by *Erythrina* - 18 species, *Cassia* - 16 species and *Bauhinia* - 15 species. The other notable genera which have less number of representation are : *Brownia, Butea, Caesalpinea, Dalbergia, Desmodium, Millettia, peltophorum, Saraca* etc.

The details of the germplasm collections are furnished here under according to sub-family besides grouping on the basis of growth habit.

CAESALPINIACEAE

Trees : *Bauhinia blakeana* Dunn, *B. hookeri* F. Muell., *B. monandra* Kurz, *B. purpurea* L., *B. roxburghiana* Voigt, *B. variabilis* Hort. ex Gentil, *B. variegata* L., *Brownea ariza* Benth., *Caesalpinia cacalcao* Humb. & Bonpl., *C. coriaria* (Jacq.) Willd., *C. pannosa* Brandegee, *Cassia excelsa* Schrad., *C. fistula* L., *C. grandis* L.f., *C. javanica* l., *C. marginata* Roxb., *C. nodosa* Buch. - Ham. ex Roxb., *C. renigera* Wallich ex Benth., *C. roxburghii* DC., *C. siamea* Lamk., *Colophospermum mopane* (J. Kirk ex Benth.) J. Leon., *Colvillea racemosa* Bojer, Delonix elata (L.) Gamble, *D. regia* (Bojer) Raf., *Gleditsia ferox* Desf., *G. sinensis* Lam., *G. tricanthos* L., *Hardwickia binata* Roxb., *Parkinsonia aculeata* L., *Peltophorum ferrugineum* Benth., *Saraca asoca* (Roxb.) De Wilde, *S declinata* (Jack) Miq. (32 species).

Shrubs : *Bauhinia acuminata* L., *B. galpinii* N.E. Br., *B. glauca* Wallich, *B. tomentosa* L., *Caesalpinia elata* Sw., *C. pulcherrima* (L) Sw., *C. mexicana* A. Gray., *Calliandra brevipes* Benth., *C. confusa* T. Sprague & Riley., *C. emarginata* Benth., *C haematocephala* Hassk., *C. portoricensis* (Jacq. Benth.), *C. tweedii* Benth., *Cassia alata* L., *C. australis* Sims., *C. didymobotrya* Fresen, *C. hirsuta* L., *C. laevigata* Willd., *C. surattensis* burm. f., *Gleditsia bispinosa*. (20 species).

Climbers

Bauhinia vahlii Wight & Arn., *Caesalpinia bonduc* (L.) Roxb. (2 species)

FABACEAE

Trees : *Bolusanthus speciosus* (Bolus) Harms, *Butea monosperma* (Lamb.) Taub., *Castanospermum australe* A. Cunn. ex Frappier, *Dalbergia lanceolaria* L.f., *D. latifolia* Roxb., *D. melanoxylon* Guill. & Perr., *D. sissoo* Roxb., *Derris indica* (Lamk.) Bennet, *Erythrina indica* Lam., *E. lithosperma* Blume ex Miq., *E. princeps* A. Dietr., *E. resuparcellii* Srivastava, *E. suberosa* Roxb., *E. subumbrans* (Hassk.) Merr., *E. variegata* L. var. alba, *E. variegata* L. var. orientalis (L.) Merr., *E. variegata* var. picta (L.) Baker, *E. velutina* Willd., *E.*

vespertilio Benth., *Gliricidia maculata* (H.B. & K) Steud., *G. sepium* (Jacq.) Kunth ex Walp., *Millettia tetraptera* Kurz, *M. thonningii* Baker, *M. ovalifolia* Kurz, *Pterocarpus indicus* Willd., *P. marsupium* Roxb., *Tamarindus indica* L (27 species).

Shrubs

Desmenthus sp., *Desmodium cephalotes* Wallich, *D. canedense* DC., *D. diffusum* DC., *D. gangeticum* DC., *D. gyrans* DC., *D. pulchellum* Benth., *Erythrina blakei, E. resupinata* Roxb., *Indigofera suffruticosa* Mill., *Moghania macrophylla* Blume, *M. strobilifera* jaume St. Hil., *Petaladium barbrioides* Nees, *Sophora japonica* L., *S. secundiflora* (Ort.) Lag. ex DC., *S. tomentosa* L., *Uraria macrostachya* Wallich. (17 species).

Climbers

Abrus precatorius L., *A. precatorius* L. var. albus Hort., (Lamb.) Taub., *Butea superba* Roxb., *Clitoria ternatea* L., *Derris scanden* bength., *Lathyrus odoratum* L., *Milletia extensa* Benth., *Wisteria sinensis* Sims (8 species).

MIMOSACEAE

Trees

Acacia auriculaeformis A. Cunn. ex Benth., *A. brachystachya* Benth., *A. brachystachya* Benth., *A. burkittii* F. Muell. ex Benth., *A. catechu* (L.f.) Willd., *A. coriacea* DC., *A. erubescens* Welw. ex Oliver, *A. farnesiana* (L.) Willd., *A. galpinii* Davy, *A. gerrardii* Benth., *A. karroo* Hayne, *A. lenticularis* Buch. - Ham. ex Benth., *A. modesta* Wallich, *A. monoliformis* A. Cunn. ex Benth., *A. nilotica* (L.) Del. ssp. *indica* (Benth.) Brenan, *A. nilotica* (L.) Del. ssp. *cupressiformis* (Stewart) Ali & Farid, *A polycantha* Willd., *A. polycantha* Willd. ssp. *polycantha, A. salicina* Lindl., *A. siamia* Lamk., *A sieberana* DC., *A. welwitschii* Oliver, *Adenanthera pavonina* L., *Albizia amara* Boine, *A. lebbek* (L.) Willd., *A. lucidior* (Steud.) Nielsen, *A. petersiana* Oliver, *A. procera* (Roxb.) Benth., *A. richardiana* (Wallich ex Voigt) King and Prain, *Haemotoxylon campechianum* L., *Leucaena glauca* L., *L. leucocephala* Lam., *Parkia biglandulosa* Wight & Arn., *P. pendunculata* (Roxb.) Macbr., *Pithecellobium dulce* (Roxb.) Benth., *Prosopis cineraria* (L.) Druce, *P. juliflora* (Sw.) DC., *Samanea saman* (Jacq.) Merr. (37 species).

Shrubs

Acacia farnesiana Willd., *Mimosa pudica* L., *Pithecellobium unguiscati* Mart. (3 species).

II. ANNUAL HERBS

Fabaceae

Alysicarpus monolifer (L.) DC., *Clianthus dampieri* Cunn. ex Lindley, *Lathyrus odoratus* L., *Lupinus hartwegii* Lindl., *Melilotus indica* All., *Rhynchosia sericea* Span. (6 species).

Endangered species : *Sophora mollis* Royle

Rare species : *Erythrina resupinata* Roxb.

III. NEW INTRODUCTIONS

CAESALPINIACEAE

Bauhinia grandiflora Juss., *B. rufescens* Lam., *B. saigonensis* Pierc. ex Gagnepain, *Calliandra surinamensis* Benth., *Caesalpinia gilliesii* Wallich ex Hook, *C. velutina* Brotton & Rose, *Cassia corymbosa* Ortega (7 species).

MIMOSACEAE

Acacia elata A. Cunn. ex Benth. *A. concianna* (Willd.) DC, *A. rothii* Bailey, *A. senegal* (L.) Willd., *Proposis chilensis* Molina (Stcontz) (5 species)

FABACEAE

Erythrina americana Miller, *E. herbacea* L., *E. lysistemon* Hutch., *E. sandwicensis* Degener (4 species).

CONCLUSION

***Ex-situ* conservation measures** : *Ex-situ* conservation is defined as the maintenance of organism out side or away from their natural habitat such as in the Botanic Gardens, in the field gene banks or by storage in the form of seeds, pollens, vegetative propagules, tissue or cell culture (Anonymous, 1989). The objective is to simulate the habitat requirements for the conservation of diversified groups of plants to serve as the plant genetic resources for posterity.

Therefore, the efforts are underway for the effective conservation of the legumes in our Botanic Garden by paying regular attention with regard to their cultural requirements. The population of rare and endangered species are being monitored and efforts are underway to increase their population through multiplication. Propagation is the best way to increase the number of population and also helps in the better conservation because a limited number of population is always at risk of disappearance. The greatest advantage of the Legumes is their seed bearing character and thereby offer a unique potential for their future preservation. By exploiting this, seeds of these plant species are being collected for preservation in Seed Bank as well as seed exchange programme. Aside, some of the shrubs are being multiplied vegetatively also. Exchange of surplus planting material (live plants/seeds) is another noble way which enhance the possibility of survival of the genetic resources since it drastically reduces the chance of catastrophic loss of genetic diversity.

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GENETIC ANALYSIS FOR YIELD AND ITS COMPONENT IN HIMALAYAN CHENOPOD

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A set of 53 genetically diverse genotypes of *Chenopodium album* L. originating from different agro-ecological areas of Himalayas and 3 exotic introductions of *C. quinoa* from South America was tested and analysed for genetic variability, correlation and path coefficient analysis. A wide range of variation was observed for all the traits. Phenotypic coefficient of variation and genotypic coefficient of variations were highest for inforescence length, number of leaves on main shoot, number of branches/plant and plant height. Heritability and genetic advance (in broad sense) were high for plant height, number of leaves on main shoot and days to mature. Grain yield showed positive association with inflorescence length, days to flower, number of branches per plant and leaf length. Inflorescence length had highest and positive direct effect on grain yield followed by days to flower and number of branches per plant. On the basis all the variability and productivity parameters studied, inflorescence length, days to flower and number of branches/plant were observed to be the most potential traits for genetic improvement of Himalayan chenopod. Since late flowering and maturity beyond certain limit are not desirable, greater emphasis is given to inflorescence length and number of branches/plant while making selection or formulating component breeding programme for the genetic improvement of chenopod.

Key words : *Chenopodium*, quinoa, phenotypic/genotypic coefficient of variation, heritability, genetic advance, correlation

Yield being the most important and complex quantitative character, is governed by many physiological processes. The outcome of the phenotypic selection does not give expected genetic advance mainly due to the presence of genotype × environment interaction, non-allelic interactions and undesirable association between the component characters. In order to identify yield component for defining an ideal plant type, the knowledge of cause and effect relationship of these components on yield, heritability and genetic gain are of great importance to the plant breeders. In chenopod, the literature available on such aspects is very limited on Himalayan chenopod (Joshi, 1991 and Partap, 1987), therefore, an attempt was made to know the nature and magnitude of genetic variability, correlation among yield and its components and their direct and indirect effects.

MATERIALS AND METHODS

Fifth-three genotypes of *Chenopodium album* L. originating from different agro-ecological regions of the Himalayas including 3 exotic introductions of *C. quinoa* from Andean region were grown in the rainy seasons of 1993 and 1994 in an augmented incomplete block design (Federer, 1956). The seeds were drilled in rows 50 cm apart first followed by thinning and plant to plant distance was kept 20 cm within rows. Five competitive plants of each accession were selected at random. Data were recorded on 10 characters *viz.* plant height (cm), number of branches, number of leaves on main shoot, inflorescence length (cm), leaf length (cm), days to flower, days to mature, 1000-grain weight (g) and yield per plant (g). The average value of 5 plants for each character were used in the statistical analysis. Genotypic and phenotypic coefficient of variation, heritability and genetic advance were calculated according to Johnson *et al.* (1955) and correlation and path analysis were worked out as per the method described by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance revealed a wide range of variability and significant differences among all the genotypes for all the characters studied (Table 1). Coefficient of variation both phenotypic (pcv) and genotypic (gcv) was highest for inflorescence length (Table 2), number of leaves on main shoot and number of branches/plant. In general the differences between the magnitudes of pcv and gcv were very less, indicating little influence of environment for all the traits. Heritability was very high (93 to 99%) for all the traits, indicating the effectiveness of simple selection methods in segregating populations. Genetic advance was high for plant height followed by number of leaves on main shoot, days to mature, number of branches and days to flower. High heritability coupled with high genetic advance was observed for plant height, number of leaves on main shoot, days to mature, number of branches and days to flower indicating the influence of additive genetic variance for these traits. Beru and Mukherjee (1987) also observed variability within wild populations of chenopod while identifying genetic resources for use in improving the cultivated hexaploid used as leaf vegetable and diploid (2n = 18) cytotypes. Variation in leaf character was high, one cytotype tended to produce larger plants. Variation was low for protein content of seeds but high for saponin content. Chromosome size and behaviour were generally similar in both cytotypes.

Correlation analysis revealed that grain yield was positively and significantly associated with inflorescence length, number of branches/plant, days to flower, plant height and leaf length. In order to have a clear picture of interrelationship with grain yield of various characters direct and indirect effects at phenotypic and genotypic levels were worked out using path analysis parameter. Considering the direct effects at genotypic level of each character on grain yield, inflorescence length had highest and positive direct effect (0.55) followed by days to flower (0.45) and number of branches per plant (0.28). Days to flower had highest indirect effect on yield via 1000-grain weight. Thus longer vegetative as well as reproductive period may be more conducive for

Table 1. Estimates of various parameters of variability

Characters		Range	Mean	GCV	PCV	Heritability	Genetic advance
1.	Plant height (cm)	77.0-232.5	123.9	30.80	31.00	99.0	78.4
2.	No. of branches	18.5-65.5	35.1	34.50	35.46	94.4	24.2
3.	No. of leaves on main shoot	21.0-92.0	40.0	44.70	45.43	96.8	36.2
4.	Inflorescence length (cm)	4.4-30.3	16.5	48.78	49.93	95.4	16.2
5.	Leaf length (cm)	3.8-8.4	5.7	26.66	27.24	95.7	3.1
6.	Leaf width (cm)	2.7-6.8	4.6	23.72	24.60	93.0	2.2
7.	days to flower	33.5-66.5	54.7	20.18	20.57	96.2	22.3
8.	Days to mature	54.5-149.5	117.0	15.07	15.25	97.6	35.9
9.	1000 grain weight (g)	0.5-1.7 0.8	23.17	23.50	97.2	0.4	
10.	Grain yield/plant (g)	4.1-11.5	7.5	21.78	22.29	95.5	3.3

Table 2. Phenotypic (P) and genotypic (G) correlations in chenopod

Traits		Plant Height	Branches/ plant	Leaves/ main shoot	Inflores-cence length	Leaf length	Leaf width	Days to flower	Days to mature	1000 grain weight	Grain yield
		1	2	3	4	5	6	7	8	9	10
1.	P	1.000	–0.005	–0.414**	0.201	–0.313*	–0.253	0.275	0.160	–0.147	0.369**
	G	1.000	–0.007	–0.399**	0.198	–0.311*	–0.242	0.271	0.157	–0.146	0.259
2.	P		1.000	0.774**	0.265	0.575**	0.336*	–0.621**	–0.429**	0.114	0.480**
	G		1.000	0.739**	0.252	0.567**	0.317*	–0.589**	–0.417**	0.107	0.451**
3.	P			1.000	0.210	0.619**	0.640**	–0.427**	–0.299*	–0.027	0.059
	G			1.000	0.206	0.589**	0.612**	–0.411**	–0.296	–0.024	0.062
4.	P				1.000	0.143	–0.064	–0.0564	–0.046	0.047	0.648**
	G				1.000	0.132	–0.041	–0.056	–0.048	0.045	0.623**
5.	P					1.000	0.314*	–0.713**	–0.545**	0.214	0.365**
	G					1.000	0.304*	–0.684**	–0.524**	0.208	0.348*
6.	P						1.000	–0.118	–0.080	–0.204	–0.228
	G						1.000	–0.105	–0.069	–0.189	–0.211
7.	P							1.000	0.813**	–0.238	0.477**
	G							1.000	0.791*	–0.235	0.434**
8.	P								1.000	–0.225	0.049
	G								1.000	–0.213	0.042
9.	P									1.000	0.251
	G									1.000	0.247
10.	P										1.000
	G										1.000

more leaves and bold grain size. Similarly Risi and Galwey (1989) investigated significant correlation between stem diameter, inflorescence length, inflorescence diameter, number of leaf protrusion and saponin content of quinoa.

The present investigation can be concluded that inflorescence length, days to flower and number of branches/plant showed significant positive correlation and also maximum positive direct effect on grain yield which should be given attention while making selection or formulating component breeding programme for genetic improvement of chenopod. Since late flowering and maturity beyond certain limit are not desirable hence inflorescence length and number of branches/plant be given due consideration while making selections.

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Table 3. Direct and indirect effects (direct effects in the main diagonal bold figures)

Traits		Plant height	Branches/ plant	Leaves/ main shoot	Inflore-scence length	Leaf length	Leaf width	Days to flower	Days to mature	1000 grain weight	Correlation with yield
		1	2	3	4	5	6	7	8	9	10
1.	P	**0.057**	–0.001	**0.020**	0.111	–0.070	0.055	0.124	–0.013	–0.014	0.369
	G	**0.085**	–0.001	–0.005	**0.108**	–0.037	0.054	0.074	–0.003	–0.016	0.259
2.	P	**0.000**	0.286	–0.074	**0.146**	0.129	–0.073	–0.281	0.035	0.011	0.480
	G	–0.001	0.163	0.017	0.137	0.068	–0.080	–0.162	0.007	0.012	0.450
3.	P	–0.012	**0.222**	–0.095	**0.116**	0.139	–0.136	–0.113	0.005	–0.003	0.059
	G	–0.018	**0.120**	**0.070**	0.112	0.071	–0.136	–0.113	0.005	–0.003	0.062
4.	P	**0.012**	0.076	–0.020	0.551	**0.032**	0.014	–0.025	0.004	0.004	0.648
	G	**0.017**	0.041	0.005	0.545	0.016	0.009	–0.015	0.001	0.005	0.623
5.	P	–0.018	**0.165**	–0.059	–0.079	0.125	–0.068	–0.323	**0.045**	0.020	0.365
	G	–0.027	**0.092**	0.014	0.072	**0.120**	–0.067	–0.188	0.009	0.023	0.348
6.	P	–0.014	**0.096**	–0.061	–0.036	0.071	–0.217	–0.053	**0.007**	–0.020	–0.228
	G	–0.021	**0.052**	0.014	–0.022	0.037	**–0.222**	–0.029	0.001	–0.021	–0.211
7.	P	**0.016**	–0.178	0.041	–0.030	–0.160	0.026	0.456	–0.067	–0.023	0.471
	G	**0.023**	–0.096	–0.009	–0.30	–0.082	0.023	0.274	–0.013	–0.026	0.434
8.	P	**0.009**	–0.123	0.029	–0.025	–0.123	0.017	0.368	–0.83	–0.022	0.049
	G	**0.013**	–0.068	–0.007	–0.026	–0.063	0.015	0.217	**–0.016**	–0.024	0.042
9.	P	–0.008	**0.033**	0.003	0.026	0.048	0.044	–0.108	0.019	0.096	0.251
	G	–0.012	**0.017**	–0.001	0.025	0.025	0.042	–0.065	0.004	0.112	0.247

Residual (G) 0.1720; (P) 0.1232

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PATHOGENIC FUNGI INTERCEPTED IN GERMPLASM INTRODUCED DURING 1995-99

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During 1995-99, over 2,67,000 imported germplasm in the form of true seeds and vegetative propagules of various agri-horticultural crops were examined for quarantine clearance. A number of destructive pathogens which are not known to occur in India namely, (*Peronospora manshurica* and *Uromyces betae*; having large number/more virulent races (*Puccinia carthami, Tilletia foetida, Drechslera maydis, D. oryzae, D. sorokiniana* and *Ustilago tritici*); and those having a wide host rage (*Botrytis cinerea, Colletotrichum gloeosporioides, Fusarium solani* and *Drechslera sorokiniana*) were intercepted. The significance of interceptions is discussed from quarantine viewpoint.

Key words : Quarantine, germplasm, pathogenic fungi

Though international exchange of planting material of agri-horticultural crops and their wild relatives provides a wide genetic diversity; there is an inherent risk of introducing dangerous exotic pathogens. The National Bureau of Plant Genetic Resources intercepted a number of destructive fungi, some of which are new to India. They include *Peronospora manshurica* (Naum.) Syd. (Mukewar *et al.*, 1980), *Uromyces betae* Kickx (Agarwal *et al.*, 1984) and *Fusarium nivale* (Fr.) Ces. (Dev *et al.*, 1989). In this paper pathogenic fungi intercepted in introduced planting material during 1995-99 are reported and the economic significance of certain important pathogens is discussed from quarantine viewpoint.

MATERIALS AND METHODS

During 1995-99, a total of 2,67,218 samples in the form of true seed and vegetative propagules of a wide variety of agri-horticultural crops and their wild relatives were received for quarantine clearance. Out of this, 11,480 accessions comprising chemically treated samples of wheat (8010); barley (2270) and triticale (1200) were sown in post-entry quaratine nursery (PEQN). Ramaining 2,55,738 samples were subjected to laboratory tests such as examination under stereo-binocular microscope for the detection of fungal fructifications as well as symptoms such as discolouration, deformation and malformation etc. and blotter test. Unhealthy-looking seeds were placed on moist blotters in plastic Petri plates, the number of seeds tested varied according to the size of the sample. The plates were incubated for seven days at 20 + 1°C under alternating cycles of 12 h. light and darkness. Observations on associated fungi were recorded on the eighth day under stereo-binocular microscope. Microscopic slides were also prepared whenever required.

RESULTS AND DISCUSSION

A large number of fungi of quarantine significance were detected during dry seed examination, washing test and blotter test. As a result of these laboratory tests, 1129 samples were found infected with 44 fungal species (Table 1). Most of the fungi intercepted during examination are known to be seed-borne and seed transmitted in various crops (Richardson, 1990). Some of the fungi of high quarantine significance included *Peronospora manshurica* (downy mildew of soybean), *Puccinia carthami* (rust of safflower), *Puccinia helianthi* (rust of sunflower), *Uromyces betae* and *Phoma betae* (rust and black leg of sugarbeet, respectively), *Phomopsis sojae* (seedling blight on *Lucaena leucocephala* and soybean), *Alternaria brassicae* and *A. brassicicola* (leaf spots and seedling blight of *Brassica* spp.), *Botrytis allii* (grey mold on *Allium cepa*), *Drechslera maydis* and *Ustilago maydis* (blight and smut on maize) and *Tilletia foetida* (hill bunt of wheat) etc.

Peronospora manshurica, the downy mildew fungus of soybean which is of wide geographical distribution, has so far not been reported to occur in the country. In India, this fungus was intercepted for the first time in this laboratory on soybean seeds introduced from USA (Mukewar *et al.*, 1980) and subsequently from 16 other countries (Agarwal and Singh, 1998). The oospores of *P. manshurica* are reported to retain viability upto eight years (Pathak *et al.*, 1978) and a large number of physiological races are known to be present (Marcinkowska, 1987 and Li *et al.*, 1992). During this period out of 1357 introduced soybean samples, *P. manshurica* was intercepted on 213 samples (Brazil-7, N. Korea-12, Russia-3, Taiwan-6 and USA-185). Almost 15 per cent of the introduced soybean germplasm was found infected with this pathogen of great quarantine significance.

Uromyces betae, the rust of sugarbeet was intercepted in this laboratory for the first time in the washing test of seeds introduced from USA and Italy (Agarwal *et al.*, 1984). This pathogen is not known to occur in India. The seed-borne inoculum is reported to have caused epidemics (Emdal and Foldo, 1979). The rust spores were detected in three samples from Germany. The contaminated samples were salvaged by washing with cone. sulphuric acid followed by washing in running water (Ram Nath *et al.*, 1986).

Teleutospores of *Puccinia helianthi* (sunflower rust) were detected in 66 samples of sunflower from Australia, USA and Yugoslavia; and teleutospores of *P. carthami* (safflower rust) were detected on the seed surface of 454 safflower samples from China and USA. Spores of *P. carthami* are reported to retain viability upto eighteen months (Calvert and Thomas, 1954). All the samples were salvaged by subjecting to ethyl alcohol wash (Agarwal *et al.*, 1990b).

Fungi like *Drechslera sorokiniana, Macrophomina phaseolina, Botrytis cinerea, Colletotrichum gloeosporioides* and *Fusarium solani* that are known to have a wide host range were intercepted on seeds of various crops. A large number or more virulent races are also known to exist in *Tilletia foetida, Phoma betae, Puccinia carthami, Ascochyta rabiei, Cercospora sojina, Drechslera sorokiniana, D. teres, D. maydis, D. oryzae* and *Ustilago tritici.* Introduction of pathogenic races or pathotypes to the region, where local cultivars are resistant to endemic races of the same species, may have serious consequences (Neergaard, 1977). Therefore, these interceptions on a variety of crops from various countries are of quarantine significance.

Seeds showing discoloration, deformation, malformation and fungal fructifications were removed under stereo-binocular microscope followed by seed dressing with required pesticides. Seed samples infected with *Alternaria brassicae, A brassicicola, A. ricini, A. dauci, Phoma lingam* and *P. betae* were subjected to hot water treatment at 50°C for 20 minutes. Prophylactic hot-water treatment at 52-55 C for 30 minutes was given to 54,440 samples of paddy against seed-borne pests and pathogens. During the grow-out test

Table 1. Pathogenic fungi intercepted in introduced germplasm material during 1995-99

Pathogen	Crop	Source/Country
Alternaria brassicae (Berk) Sacc.	*Brassica* spp.	Belgium,Canada,UK,USA
Alternaria brassicicola (Schw.) Wilts	*Brassica* spp	Canada, North Korea,Taiwan,UK,USA
Alternaria dauci (Kuhn) Groves & Skolko	*Daucus carota*	Mauritius
Alternaria raphani Groves & Skolko	*Brassica* spp	Canada
Alternaria ricini (Yoshii) Hansford	*Ricinus communis*	USA
Alternaria sesami Mohanty & Behera (Kawamura)	*Sesamum* spp	USA
Ascochyta rabiei (Pass.) Labr.	*Cicer arietinum*	Australia
*Ascochyta*sp.	*Lens culinaris*	Syria
Balansia sp.	*Cenchrus ciliaris*	Ethiopia
Botrytis allii Munn.	*Allium cepa*	UK
Botrytis cinerea Pers. ex Pers.	*Avena sativa*	UK
Cephalosporium spp.	*Corchorus* spp.	Pakistan
	Leucaena leucocephala	UK
Ceroscpora corchori Sawada	*Coriandrum* spp.	Bangladesh
Cercospora sojina Hara	*Glycine max*	USA
Colletotrichum acutatum Simmonds	*Coriandrum* spp.	Bangladesh
Colletotrichum dematium (Pers. ex Fr.) Grove	*Glycine max*	USA
	Demonthus spp.	Ethiopia
Colletotrichum gloeosporioides (Penz.) Sacc.	*Glycine max*	USA
	Leucaena leucocephala	UK
	Linum spp.	USA
Drechslera avenae (Eidam) Scharif	*Avena sativa*	UK
Drechslera maydis (Nisik) Subram. & Jain	*Zea mays*	Thailand
Drechslera oryzae (Breda de Hann) Subram. & Jain	*Oryza sativa*	Philippines
Drechslera sorghicola (Lef. & Shre.) Richardson & Fraser	*Sorghum* spp.	USA,Zimbabwe
Dreschlera sorokiniana (Sacc.) Subram & Jain	*Avena sativa*	Russia
	Cenchrus spp.	UK
	Hordeum spp.	Denmark
	Lycopersicon spp	Spain,Taiwan
	Triticum spp.	Mangolia,Mexico
Drechslera teres (Sacc.) Shoemaker	Rye grass	UK
Fusarium poae (Peck) Wollenw	*Avena sativa*	UK
Fusarium solani (Mart.) Sacc.	*Acacia* spp.	Australia
	Beta vulgaris	Germany,Iran
	Brassica spp.	Taiwan,UK
	Capsicum annuum	Italy
	Carthamus tinctorius	USA
	Cucurbita pepo	Mauritius
	Jasmine spp.	UK
	Lens culinaris	Syria
	Leucaena leucocephala	UK
	Oryza sativa	UK

Table 1. (Contd.)

	Pennisetum spp	Zimbabwe
	Solanum tuberosum	Mauritius
	Vigna radiata	Thailand
Fusarium sp.	*Cucumis* spp.	USA
Gleosporium sp.	*Leucaena leucocephala*	UK
Macrophomina phaseolina (Tassi) Goid.	*Glycine max*	Brazil,Taiwan,USA
	Leucaena leucocephala	UK
Macrophomina sp.	*Cicer* spp.	Syria
	Citrullus lunatus	USA
Periconia sp.	*Leucaena leucocephala*	UK
Peronospora manshurica (Naum.) Syd.	*Glycine max*	Brazil,N. Korea,Russia,Taiwan,USA
Pestalotia sp.	*Vitis vinifera* (cuttings)	Brazil
Phoma betae Frank	*Beta vulgaris*	Germany,Iran
Phoma lingam (Tode ex Fr.) Desm.	*Brassica* spp.	Canada
Phoma spp.	*Lycopersicon* spp.	Taiwan
	Sorghum spp.	Zimbabwe
Phomopsis sojae Lehman	*Leucaena leucocephala*	UK
	Glycine max	USA
Phomopsis sp.	*Vigna radiata*	Thailand
Puccinia carthami Corda	*Carthamus tinctorius*	China,USA
Puccinia helianthi Schw.	*Heliantrhus annuus*	Australia,USA,Yugoslavia
Rhizoctonia solani Kuhn	*Cucurbita pepo*	Mauritius
	Glucine max	USA
	Leucaena leucocephala	UK
	Solanum tuberosum	Mauritius
Tilletia foetida (Wallr.) Liro	*Triticum* spp.	Mangolia
Uromyces betae Kickx	*Beta vulgaris*	Germany
Ustilgo maydis (DC) Corda	*Zea mays*	Thailand
Verticillium spp.	*Beta vulgaris*	Iran
	Leucaena leucocephala	UK

of chemically treated seeds in PEQN, loose smut (*Ustilago sagetum* var. *tritici*) was detected in 50 lines (wheat 36 and barley 14); while covered smut (*Ustilago sagetum* var. *hordei*) was found in two lines of barley. The appearance of disease in the chemically treated seeds indicates that blanket seed-treatment would not eliminate the risk of introducing exotic pathogens or their new races into the importing country.

Interception of as many as 44 fungal species in the laboratory and 2 in the PEQN infecting 1181 samples representing a wide variety of crops is of high quarantine significance. This also includes pathogenic fungi, which are not yet reported in the country. About 82 per cent of the infected germplasm were salvaged using various techniques. Thus the role of quarantine in safer exchange of plant genetic resources is of paramount importance.

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GENETIC DIVERSITY OF LEAF RUST RESISTANCE IN INDIAN WHEATS

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Investigations were conducted on 58 Indian wheats for assessing the extent of genetic diversity for leaf rust resistnace. Seedling studies of these wheats had indicated that the genetic basis of resistnace was due to 9 *Lr* genes while the adult plant resistance studies showed as many as 18 distinct groups. Seedling testings of these genotypes displayed the maximum preponderance of *Lr*26, *Lr*34, *Lr*13 and *Lr*23 genes and all of them have become susceptible to the newly evolved pathotypes of leaf rust barring *Lr*34. Therefore there was an urgent necessity to mobilize the highly effective resistance genes *Lr*9, *Lr*19, *Lr*24 and *Lr*28 in breeding programmes. *Lr*34, partial adult plant resistance gene which is invariably associated with durable resistance, confers a high degree of adult plant resistance in combination with other seedling resistance genes in these studies. Therefore a data base of adult plant resistance sources must be characterised in terms of the number and the nature of resistance genes to breed for durable resistance.

Key words: Wheat, genetic diversity, leaf rust resistance

Leaf rust of wheat (*Triticum aestivum* L.) caused by *Puccinia recondita* Roberge ex Desmaz. f. sp. *tritici* Eriks. and E. Henn. is the most cosmopolitan and the regularly occurring of the three rusts found on wheat (Samborski, 1985) and the wheat cultivars that are susceptible to leaf rust regularly suffer yield reduction of 5-15 per cent or greater. Genetic resistance is the most economical and preferred method of reducing yield losses due to leaf rust which invariably was based on specific resistance genes. However, resistance to leaf rust in common wheat was short lived possibly because it was based on single resistance genes (Samborski, 1985). The genetic basis of most durable resistance to leaf rust has been the combination of resistance genes (Roelfs, 1988). Gene combinations exploit the gene interactions usually between, (1) the seedling resistance genes and (2) the interactions of seedling resistance genes with adult plant resistance genes, resulting in higher resistance than that conferred by individual genes (Samborski and Dyck, 1982). The present investigation was undertaken in a collection of Indian wheats possessing different combinations of resistance genes (identified in seedling stage), during 1993-94 rabi season to assess the extent of genetic variation for the adult plant resistance.

MATERIALS AND METHODS

The materials for the present investigation comprised collection of Indian wheats which were under testing in the final year of All India Coordinated Wheat Improvement Programme (AICWIP) and the respective checks of the mega environments as defined by AICWIP where wheat is cultivated. Seedling postulation of resistance genes was done at the Rust Laboratory, Directorate of Wheat Research, Flowerdale, Shimla. Seedling studies of such wheat genotypes detect the seedling genes, however, the adult plant resistance genes remain undetected. In order to identify such resistance sources, these wheats were tested under field conditions in the isolated nurseries with leaf rust pathotypes chosen for virulence on one or more of the seedling resistance genes.

Each nursery was bordered on all sides with susceptible spreaders and test entries were planted in 1m long row spaced 30 cm apart. Artificial plant epiphytotics were initiated by inoculating the plants with a selected pathotype of leaf rust using hypodermic syringe. The avirulence and virulence formulae of leaf rust pathotypes in respect of resistance genes are as follows:

Table 1. Avirulence/virulence formulae of three leaf rust pathotypes

S. No.	Race/ Variant	Avirulence/virulence
1.	77-2	*PLr26*/p*Lr*1, *Lr*2, *Lr*3, *Lr*10, *Lr*11, *Lr*12, *lr*13, *Lr*15, *Lr*16, *Lr*17, *Lr*20, *Lr*21, *Lr*23, *Lr*27+*Lr*31, *Lr*30
2.	77-5	P*Lr*21/p*Lr*1, *Lr*2, *Lr*3, *Lr*10, *Lr*11, *Lr*12, *Lr*13, *Lr*15, *Lr*16, *Lr*17, *Lr*20, *Lr*23, *Lr*26, *Lr*27+*Lr31*, *Lr*30
3.	104-2	P*Lr*2a, *Lr*3, *Lr*15, *Lr*20, *Lr*27+*Lr*31/p*Lr*1, *Lr*10, *Lr*11, *Lr*12, *Lr*13, *Lr*16, *Lr*17, *Lr*21, *Lr*23, *Lr*26, *Lr*30

[a]Common avirulence : *Lr*9, *Lr*18,*Lr*19, *Lr*24,*Lr*25,*Lr*28,*Lr*29

Data on disease severity and response of adult plants were recorded according to oegering (1959) and the maximum incidence of disease infection is reported as the terminal disease severity.

RESULTS AND DISCUSSION

Genetic constitution of wheat genotypes in respect of an array of named resistance genes based on seedling testing in glass house is presented in Table 1. The seeding resistance of wheat genotype was based on the following 9 Lr genes: *Lr*1, *Lr*3, *Lr*10, *Lr*13, *Lr*14a, *Lr*23, *Lr*24, *Lr*26 and *Lr*34 wherein *Lr*26 appeared to be the most preponderant (28 times) followed by *Lr*34 (20 times), *Lr*13 (18 times) and *Lr*23 (17 times). The genes were present either singly or in two or three gene combinations (Table 2).

Table 2. Genetic constitution of wheat genotypes in respect of named leaf rust (*Lr*) genes

Lr genes	Genotypes
One gene	
Lr 3+	Vl616
Lr 13 +	Ska,Lok1,K9305,K9329,K9362,K9367, HUW452,HUW453,K3027
*Lr*14a +	Sujata,HUW234
*Lr*24 +	HW2004,HP1776,DL788-2
*Lr*26 +	VL719,UL751,PBW383,PBW396,Wh601,Raj 3856,HD2667
Lr 34 +	C306,HP1731
Two gene combinations	
Lr 10 + *Lr* 13	K9351,K9361,K8962
*Lr*10 + *Lr*23	HD2380,K9334
*Lr*13 + *Lr* 34	UP2338,PBW299,PBW343,PBW373,HS361,HS277
*Lr*23 + *Lr*34	HS295,PBW175,GW173
*Lr*3 + *Lr* 26	Vl755,DT46
*Lr*3 + *Lr* 26	K9321
*Lr*23 + *Lr* 26	HUW206,K8804,HUW318,GW190,MACS2496,DL1014-2
Three gene combinations	
*Lr*l + *Lr*10 + *Lr* 13	HS364
*Lr*l + *Lr*26 + *Lr*34	HS240,HPW42
*Lr*10 + *Lr* 13 + *Lr* 34	HD2329
*Lr*23 + *Lr* 26 + *Lr* 34 +	HS317,VL739,Wh542

The genotypes viz., HW2004, HP1776 and DL788-2 gave a very high level of resistance to all the three races of leaf rust employed in this study at the adult plant stage obviously due to the highly effective seedling leaf rust resistance gene *Lr*24 (Table 3).

Very high levels of resistance were recorded in K9362, HUW452 and K8027, carrying *Lr*13. Obviously, some adult plant resistance components interacted with seedling resistance (APR). Other seedling resistance genes *Lr*23, *Lr*26 and *Lr*34 interacted with APR components to confer high level of resistance (Table 3). Two gene comminations of *Lr*13 + *Lr* 34, *Lr*23 + *Lr* 34 and *Lr* 26 + *Lr* 34 as postulated in NIAW34, MS295 and UP2338 respectively display high order of resistance. The interactive role of Lr34 in conferring high resistance levels is now well documented (Dyck and Samiborski, 1982; German and Kolmer, 1992; Sawhney, 1992). Three gene combination of *Lr*1 + *Lr*26 + *Lr*34 and *Lr*23 + *Lr* 26 + *Lr*34 observed in HPW42, HS317 and WH542 also fall in this category (Table 3).

Table 3. Adult plant resistance response patterns of 58 wheat genotypes with different degrees of resistance to selected leaf rust pathotypes

Response Patterns	Lr genes	Genotypes	Interaction phenotypes to leaf rust pathotypes		
	Gene		77-2	77-5	104-2
1. LLL	*Lr*24	HW2004	TR	TR	TR
One gene combination					
		HP1776	TR	TR	TR
		DL788-2	TR	TR	TR
	*Lr*13	K9362	5MR	10S	TR
		HUW452	TR	TR	TR
		K8027	10MS	5MS	TR
	*Lr*23 +	HI1418	10MR	TMR	TR
		K93223	10MR	TR	TR
	LR 26 +	Raj3856	TR	TMR	5MR
	Lr 34 +	HP1731	TR	10MR	TR
	Lr 10 + *Lr* 13 +	K9351	5R	TR	TR
Two gene combinations	*Lr*10 + *Lr* 23 +	K9334	TR	TR	TR
	*Lr*13 + *Lr* 34 +	NIAW34	TR	TMS	TR
	*Lr*26 + *Lr*34 +	UP2338	TMR	10MR	TMR
	*Lr*23 + *Lr*24 + HS295	TR	10 MR	TR	
	*Lr*1 + *Lr* 26 + *Lr* 34	HPW 42	TMR	5MS	5MR
Three gene combinations	*Lr*23 + *Lr*26 + *Lr*34	HS317	TR	10R	TMR
		Wh542	TMR	10S	TMR

H : High M : Medium L : Low

Table 4. Adult plant response patterns of wheat genotypes with different degrees of resistance to selected leaf rust pathotypes

Response Patterns	Genotypes	Interaction phenotypes to leaf rust pathotypes		
		77-2	77-5	104-2
1. MMM	Sujata	30S	40S	40S
	HD2380	20S	30S	20S
2. HHH	Sonalika	70S (H)	60S(H)	40S(H)
3. HHM	Lok1	60S(H)	80S(H)	20S(H)
	HUW234	90S(H)	80S(H)	20MS(H)
	WH147	90S(H)	90S(H)	30S(H)
4. HHL	J8962	50S(H)	60S(H)	TR(L)
	HD2329	80S(H)	50S(H)	5MR(L)
5. HLL	GW173	50S(H)	10MR(L)	5MR(L)
6. HML	PBW175	60X(H)	40X(M)	5MR(L)
7. MHM	C306	40S(M)	50S(H)	30S(M)
8. MHL	PBW382	40S(M)	70S(H)	TR(L)
9. MMH	GW190	20S(M)	20MR(M)	80S(H)
10. MML	K9329	20MR(M)	30MS(M)	TR(L)
	K9367	20MS(M)	20M(M)	TR(L)
	K9330	40MS(M)	20MS(M)	TR(L)
	K9361	20S(M)	20MS(M)	TR(L)
	HD2189	30MS(M)	20MS(M)	TMR(L)
11. MLH	K9305	20MR(M)	5MR(L)	50S(H)
12. MLL	HUW453	30S(M)	TR(L)	TR(L)
	HD2501	20MR(M)	5MR(L)	TR(L)
13. LHL	PBR343	TR(L)	50S(H)	5S(L)
	PBW373	TR(L)	50S(H)	5R(L)
14. LMH	HUW206	10S(L)	20MR(M)	80S(H)
	HUW318	10MS(L)	40MS(M)	70S(H)
15. LMM	Dt46	TR(L)	20S(M)	305(M)
16. LML	PBW299	TMR(L)	20S(M)	TMR(L)
	HS361	TS(L)	40MR(M)	TR(L)
	HS277	TR(L)	20S(M)	5MR(L)
	HS363	5R(L)	20MR(M)	TMR(L)
	HS240	TS(L)	305(M)	10MR(L)
17. LLH	K8804	TR(L)	10MR(L)	60MS(H)
	MACS2496	5MS(L)	10MR(L)	70MS(H)
	DL1014-2	5MS(L)	10MR(L)	70S(H)
	VL738	TS(L)	10MR(L)	50MSS(H)
	VL719	10S(L)	5S(L)	70S(H)
	VL751	5MS(L)	10MR(L)	50S(H)

Besides this group, the adult plant response patterns of wheat genotypes to individual races of leaf rust could be classified in 17 distinct groups (Table 4) suggesting the different genes were involved. Of the 19 groups, wheat in some group were susceptible, their APR being race specific. In similar studies of adult plant resistance Sawhney (1992) also detected race specific APR.

Studies indicated that while the seedling testing of resistance genes could detect only 9 *Lr* genes in Indian wheat, there was substantial variation for adult plant resistance genes for as many as 19 diverse groups were detected through APR tests. Besides, the diversification of seedling resistance genes other than the most preponderant genes floating in Indian wheat (*Lr*26, *Lr*23, *Lrd*13 and *Lr* 10) must be resorted to, mobilizing the highly effective alien genes like *Lr*9, *Lr*19, and *Lr*24. It calls for launching of an aggressive national breeding effect to mobilise such genes. This can prove to be an effective strategy to checkmate the possible buildup of leaf rust epidemic of wheat in near future. The results reveal that :

1. The genetic basis of leaf rust resistance based on adult plant resistance studies is not so narrow as revealed by seedling resistance studies.

2. Adult plant resistance gene *Lr*34 is associated with enhanced resistance to different leaf rust pathotypes in association with different seedling leaf rust resistance genes.

3. Highly effective, alien, seedling resistance genes viz. *Lr*9, *Lr*19 and *Lr* 24 should be mobilised in future breeding programmes.

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EVALUATION OF DIVERSE INBRED LINES FOR SEED SET UNDER AUTOGAMY, GEITONOGAMY, AND OPEN POLLINATION IN SUNFLOWER (*Helianthus annuus* L.)

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Seventy seven diverse sunflower inbred lines, four hybrids and one open pollinated variety (Morden) were evaluated for autogamy, geitonogamy and open pollination based on six characters viz., head diameter, no. of filled seeds per head, no. of unfilled seeds per head, test weight, oil per cent and yield per plant under three treatments namely complete bagging (SP), bagging with hand pollination (HP) and open pollination (OP). The mean per cent of seed set was observed to be higher under open pollination (80.8%) followed by bagging with hand pollination (58.35%) and complete bagging (50.37%). Under HP, SP, hybrids recorded higher per cent of seed set (62.50%, 59.06%) followed by inbred lines (58.58%, 50.47%) and Morden variety (40.25%, 28.11%). Among the inbred lines GPI 1949, GPI 1499, ARM-239 and ARM-240 recorded higher rate of seed set under complete bagging and were on par with yields of HP and OP. These promising inbred lines having high self compatibility should be used in sunflower breeding programme.

Key words : Sunflower, seed set, autogamy, geitonogamy

Poor seed set is one of the important factor limiting productivity in sunflower. The problem of seed setting arises due to pollination problems of insects and the insect activity is seriously impeded by adverse weather conditions. Under such conditions seed setting is lower. This problem is more severe particularly in self incompatible sunflower varieties (Birch *et al.*, 1984). Although this crop is cross-pollinated due to the presence of sporophytic incompatibility, increased seed set per cent in bagged capitulums of sunflower has been reported in hybrids, open pollinated varieties and inbred lines to varying extent (Fick, 1978; Shivaraj *et al.*, 1987; Swamy Gowda and Giriraj, 1989). Thus breeding hybrids and open pollinated varieties for higher autogamy is one of the solution to alleviate the problem of poor seed set. Keeping in view with the earlier research reports, 82 sunflower genotypes (including diverse inbreds, four hybrids and one open pollinated variety) were evaluated to estimate the extent of seed set per cent under 3 different conditions viz., complete bagging, hand pollination with bagging and open pollination and also the estimation of autogamy and geitonogamy per cent.

MATERIALS AND METHODS

The material comprising 82 genotypes (77 diverse inbreds, four hybrids and one open pollinated variety-Morden) were sown in two rows of 5 m length with 60 × 30 cm spacing in randomised block design (R.B.D) with 2 replications at College Farm, College of Agriculture, Rajendranagar, Hyderabad during *rabi*, 1997. All the recommended package of practices were taken to raise a good crop. Out of 16 plants in each genotype, 10 plants were bagged after the appearance of first ray floret in the capitulum. In these bagged plants, 5 plants were left undisturbed till harvest to estimate the autogamy per cent and remaining 5 bagged plants were hand sibbed daily till the fertilization is completed to estimate the geitonogamy per cent. The rest of 5 random plants were allowed for open pollination.

Per cent seed setting

The seed set was calculated in the three treatments by the following formulae

$$\text{Seed set \%} = \frac{\text{Number of filled seeds under OP}}{\text{Total no. of seeds under OP}} \times 100$$

Seed set under autogamous condition =

$$\frac{\text{No. of filled seeds under SP}}{\text{Total no. of seeds under SP}} \times 100$$

$$\text{Autogamy \%} = \frac{\text{\% seed set under SP}}{\text{\% seed set under OP}} \times 100$$

Seed set under geitonogamous condition =

$$\frac{\text{No. of filled seeds under HP}}{\text{Total no. of seeds under HP}} \times 100$$

$$\text{Geitonogamy \%} = \frac{\text{\% seed set under HP}}{\text{\% seed set under OP}} \times 100$$

RESULTS AND DISCUSSION

The mean per cent seed set (Table 1) recorded was maximum under OP (80.8%) followed by HP (58.35%) and SP (50.37%). Hybrids gave higher per cent of seed set under HP (62.5%) and complete bagging (54.06%) followed by inbreds (58.58%, 50.47%, respectively) and open pollinated variety (40.25% and 28.1%, respectively). Similar results were observed by Fick (1983), Petrov and Siskov (1985); Burlov and Krotko (1986), Swamy Gowda and Giriraj (1989) and Doddamani *et al.* (1997).

In open pollination, the per cent seed set ranged from 68.11 per cent (GPI 1937) to 90.75 per cen t (KBSH-1). Among the inbred lines

Table 1. Percent seed set, Autogamy, Geitonogamy in sunflower under different conditions

S. No.	Genotype	Seed set percent OP	HP	SP	Autogamy percent	Geitonogamy percent
I. Inbreds						
1	DRM 82	82.60	52.50	48.90	59.20	63.50
2	DRM 69	82.30	52.40	48.96	59.48	63.66
3	DRM 7	83.20	50.94	48.35	59.11	61.22
4	DRM 77	78.25	46.60	40.66	51.96	59.55
5	DRM 6	83.03	63.13	49.17	59.21	76.03
6	DRM 91	74.05	48.8	45.17	60.99	65.90
7	DRM 3	82.48	52.18	46.20	56.01	63.26
8	DRM 85	84.21	52.46	45.29	53.78	62.29
9	DRM 11	78.16	46.93	41.96	63.69	60.04
10	DRM 84	86.26	41.58	50.44	58.48	48.20
11	DRM 1	80.66	52.73	32.72	40.56	65.37
12	DRM 83	81.80	55.76	53.67	65.61	68.16
13	DRM 89	88.55	52.32	47.48	53.61	59.08
14	DRM 81	77.37	54.89	39.60	47.00	70.94
15	DRM 88	82.97	44.17	38.96	46.95	53.23
16	DRM 78	84.47	58.17	34.77	41.16	68.86
17	DRM 86	81.50	47.50	36.07	44.25	58.28
18	DRM 93	74.74	49.95	39.77	52.76	66.83
19	DRM 59	78.40	47.98	52.52	66.98	61.19
20	DRM 63	77.18	39.26	38.28	49.59	50.86
21	DRM 68	86.38	64.21	34.18	39.56	74.33
22	DRM 12	80.72	61.75	42.75	52.96	76.49
23	DRM 60	81.30	54.01	46.28	56.92	66.43
24	DRM 15	79.05	49.14	49.24	62.28	62.16
25	DRM 4	80.60	48.81	49.15	60.98	60.55
26	DRM 5	79.01	45.86	40.36	51.08	58.04
27	DRM 11	81.09	60.97	49.84	61.46	75.18
28	DRM 2	81.89	47.86	42.11	51.42	58.44
29	GPI 545	84.29	56.09	45.38	53.83	66.54
30	GPI 529	81.57	73.62	68.90	84.46	90.25
31	GPI 1949	80.57	78.26	76.80	95.32	97.13
32	GPI 1288	82.45	57.88	55.42	67.21	69.83
33	GPI 1519	82.50	66.32	53.18	62.19	77.56
34	GPI 1499	79.00	77.66	77.06	97.54	98.30
35	GPI 255	87.84	45.87	35.28	40.16	52.21
36	GPI 594	73.53	44.44	32.91	44.75	60.43
37	GPI 2324	84.27	49.35	47.31	56.14	58.56
38	GPI 19.37	68.11	58.78	52.53	77.12	86.30
39	GPI 3001	76.53	63.06	49.53	64.71	82.39
40	GPI 1669	69.48	66.95	64.81	93.27	96.35
41	ARM 245	89.33	51.90	50.77	56.83	64.81

42	ARM 238	86.24	59.84	46.22	53.59	69.38
43	ARM 247	86.07	59.22	50.53	58.70	68.80
44	ARM 248	76.50	59.50	47.13	61.60	78.30
45	ARM 242	80.40	71.90	69.34	86.24	89.42
46	ARM 241	80.59	70.08	54.37	67.46	86.95
47	ARM 244	80.84	62.70	57.72	71.40	77.56
48	ARM 249	69.65	49.75	47.42	68.08	71.42
49	ARM 239	87.19	78.94	79.00	90.60	90.53
50	ARM 246	69.54	50.46	49.27	70.85	72.56
51	ARM 250	80.87	64.33	47.86	59.18	79.54
52	ARM 240	85.86	83.33	79.45	92.53	97.05
53	X15NB-5	69.24	47.45	38.03	52.97	73.86
54	X15NB-2	73.54	48.27	40.55	53.82	64.06
55	R-17	84.17	75.56	44.43	52.78	89.97
56	R-856	87.78	71.95	44.81	51.04	81.96
57	R-272-I	79.27	63.05	58.67	74.01	79.53
58	R-272-II	77.15	53.18	48.46	62.81	68.93
59	R-298	75.48	59.41	48.73	64.56	78.70
60	R-265	85.31	59.82	47.06	55.16	70.12
61	6D-1	84.09	69.44	51.44	61.17	82.57
62	RHA-859	70.42	56.30	43.13	61.24	79.94
63	RHA-271	85.09	46.60	32.85	38.60	54.76
64	234-B	79.99	59.27	48.62	60.78	74.09
65	P-356-R	72.96	62.27	56.45	77.37	85.34
66	IV55NB-13	84.99	51.23	48.58	57.15	60.27
67	LIB02M-14	77.01	57.36	48.12	62.48	74.48
68	LIB02M-1	79.01	68.47	57.11	72.28	86.65
69	LIB02M-6	74.88	65.03	60.29	80.51	86.84
70	LIB02M-3	79.86	55.83	50.29	66.71	71.14
71	VNDNB-7	85.43	64.22	48.76	60.37	73.46
72	VNDNB-2	87.81	70.16	65.57	74.72	79.06
73	VNDNB-10	82.67	63.57	59.04	71.73	78.05
74	88-2	82.31	77.71	70.55	85.71	94.41
75	88-4	83.86	73.60	62.92	78.25	85.38
76	88-9	80.76	68.82	59.32	73.45	85.21
77	88-8	80.12	73.22	69.89	87.23	91.38
	Mean	**80.46**	**58.58**	**50.47**	**60.68**	**70.86**
II. Hybrids						
78	APSH-11	84.27	57.77	46.66	60.36	70.55
79	KBSH-1	90.75	65.28	59.67	65.75	71.93
80	MSFH-17	89.84	63.48	55.16	61.39	70.65
81	Jwalamukhi	86.24	63.49	54.75	64.38	73.62
	Mean	**87.77**	**62.50**	**54.06**	**61.99**	**72.18**
III. Open pollinated variety						
82	Morden	79.52	40.25	28.11	35.95	50.73
	Overall mean	**80.80**	**58.35**	**50.37**	**62.29**	**72.50**
	C.D.S.E.	4.73	4.56	8.92	4.92	5.36

OP: Open Pollination; HP : Hand Pollination + Bagging; SP : Complete Bagging

ARM-245 recorded maximum seed set per cent (89.33). The mean per cent seed set was higher in hybrids (87.77%) than inbreds (80.46%).

Under bagging with hand pollination, the seed set per cent ranged from 39.26 (DRM 63) to 83.33 per cent (ARM-240), among the hybrids KBSH-1 recorded the highest seed set per cent (65.28) and Morden recorded 40.25 per cent. Under complete bagging, ARM-240 recorded maximum seed set (79.48%), however, minimum was in Morden (28.1%). Among the hybrids, KBSH-1 recorded the highest seed set per cent (59.67%), while in inbred lines GPI-594 minimum seed set per cent (32.91%) was recorded. Among the inbred lines, GPI-1949, GPI-1499, ARM-239 and ARM-240 recorded good seed set under SP and were on par with the yields of HP and OP These inbred lines with high self compatibility may be used in sunflower breeding programme.

The mean values of autogamy ranged from 39.95 (Morden) to 97.54 per cent (GPI-1499), while in inbred lines, the minimum autogamy per cent was recorded in DRM-68 (39.56). In hybrids, KBSH-1 recorded the highest autogamy per cent (65.75%). The mean value of geitonogamy ranged from 48.20 per cent (DRM-84) to 98.30 per cent (GPI-1499). In hybrids, Jwalamukhi recorded the maximum geitonogamy per cent (73.62%), while in Morden, it was 50.73 per cent. In general, hybrids recorded maximum autogamy and geitonogamy per cent than inbred lines and open pollinated variety Morden. These findings are in confirmity with the earlier results of Leclercq (1980) and Swamy Gowda and Giriraj (1989). Among the inbred lines, GPI-1499 exhibited maximum autogamy and geitonogamy per cent followed by GPI 1669 and ARM-240.

For the development of population, highly self compatible lines with uniform plant height, head diameter, high seed yield and high oil content should be utilized. This may further enable us for accumulate self compatible genes in the population and for the development of superior parental lines. Further this helps to derive high autogamous hybrids for stabilising sunflower productivity in- farmers fields.

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GENETIC VARIABILITY AND CORRELATION STUDIES IN WHEAT (*Triticum aestivum* L)*

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Thirty wheat cultivars were evaluated during rabi seasion of 1998-99 under agro-climatic conditions of western Uttar Pradesh (India). Among the characters studied plant height, number of tillers plant^{-1}, ear length, 1000 grain weight and yield plant^{-1} exhibited higher values of variability. Flag leaf area showed moderate heritability value (65.6%) for better sink development. Grain yield was positively correlated with 1000-grain weight and harvest index. Numbers of grain ear^{-1} were found to be negatively correlated with 1000-grain weight, harvest index, and flag leaf area. While it was positively correlated with seed and straw yield, suggesting significant effect of number of grains ear^{-1} on grain yield of wheat.

Key words: Wheat, genetic variability, correlation

Wheat being a promising cereal crop possess second ranks after rice in India. The wheat production was substantially increased with the introduction of dwarf Mexican varieties from 1967 onwards but the production reported to be decreased after 1996-97. Hence, it needs immediate attention for grain yield improvement. Genetic improvement of economic character like yield through selection depends largely on the amount of genetic variability present in the population, heritability and genetic advance under selection. However, direct selection for a complex character like yield is not very effective. Therefore, knowledge of correlation among the characters and their direct and indirect effects on the complex character is required to construct suitable selection indices. The present investigation was therefore, carried out to estimate the amount of genetic variability, heritability and genetic advance for yield and its components, correlation among these characters and their analysis with seed yield in wheat cultivars.

MATERIALS AND METHODS

The experiment was laid out at the experimental farm of the Janta Vedic Post Graduate College, Baraut, Uttar Pradesh, during *rabi* season of 1998-99 to evaluate thirty cultivars of wheat. These cultivars were tested in randomized block design with three replications. Each treatment consisted of six lines with a row length of 4 meters. The distance between rows was 22.5 cm and within row 2.5 cm, the crop was fertilized by 100 kg N, 40 kg P2O5 and 40 kg K/ha. At harvest growth and yield data were recorded and was subjected to further analysis for correlation and other variances as per standard procedure.

RESULTS AND DISCUSSION

Estimates of variability, heritability and genetic advance for yield and its component characters are presented in Table 1. Among the characters studied, plant height, length of ear, number of grains per ear, 1000 grain weight and seed yield exhibited wide range of variability.

*Part of MSc (Ag) Thesis of the first author

Phenotypic and genotypic coefficient of variations for number of tillers per plant, number of ears per plant, plant height, 1000 grain weight and flag leaf area were higher as compared to other characters, namely germination count, ear length, number of spikelets per ear and harvest index. For straw yield, numbers of grains per ear and grain yield per m^2, the coefficient phenotypic and genotypic variance were high suggesting effectiveness of phenotypic and genotypic selection. Paroda and Joshi (1970) reported that number of ears per plant, grains per ear and grain weight were the major yield component.

Higher heritability of 82.5 per cent was recorded for harvest index, followed by plant height (78.7%), number of spikelets per ear (73.9%) and 1000 grain weight (72.6%), the characters like flag leaf area, grain yield, ear length, number of grains per ear and grain yield had heritability of medium range 55.9 to 65.6 per cent. This indicates the pre-dominance of additive gene action and thus selection for these characters would be effective. However, characters viz., tillers per plant, ears per plant and germination count showed low heritability of the expression. These traits are mainly governed by several environmental and agronomic factors like soil fertility, moisture and temperature. Major change in trend was found in case of harvest index, where the heritability was higher i.e., 82.5 per cent, while genetic advance was only 4.26 per cent. High heritability coupled with low genetic advance for harvest index suggested that high heritability is due to favourable environment influence rather then genotypic effects (Singh *et al.*, 1997). In case of straw and grain yield, the heritability was of medium order but genetic advance for these traits was 74.01 and 48.05 respectively. Highly significant positive correlation of germination count was found with harvest index and grain yield but strongly and negatively correlated with tiller number, ears per plant and ear length. However, 1000 grain weight, flag leaf area and straw yield were negatively correlated with low magnitude, while positive correlation was observed with grain yield and harvest index. Tillers per plants were positively correlated with number of ears per plant, ear length and straw yield. It was negatively correlated with plant height, number of grains per ear, 1000 grain weight, harvest index, flag leaf area and grain yield. Plant height was positively correlated with

Table 1. Estimates of variability, heritability and genetic advance for seed yield and its components in wheat

Character	Range	Mean SE	CV%	GCV	PCV	h2b	GA
Germination per meter	31.00-40.00	37.66±2.03	6.61	4.56	8.03	32.3	2.01
Tillers per plant	1.74-3.03	2.32±0.20	10.57	9.58	14.26	45.1	0.31
Ears per plant	1.55-2.56	2.00±0.20	12.22	10.68	16.23	45.3	0.29
Plant height (cm)	54.80-80.77	71.72±2.81	4.80	9.24	10.41	78.7	12.11
Length of ear (cm)	9.60-12.93	11.51±0.42	4.52	5.71	7.28	61.5	1.06
No. of spikelets per ear	15.27-20.70	17.92±0.61	4.21	7.08	8.24	73.9	2.25
No. of grains per ear	41.47-62.47	53.19±3.12	7.20	8.84	11.41	60.1	7.51
1000 grain weight (g)	26.17-46.47	33.34±2.07	7.59	12.36	14.51	72.6	7.23
Harvest index (%)	33.40-43.80	40.73±0.86	2.57	5.59	6.15	82.5	4.26
Flag leaf area (cm)	20.40-33.27	26.50±2.03	9.39	12.98	16.02	65.6	5.74
Grain yield (gm^{-2})	333.33-468.00	412.09±19.04	5.66	7.20	9.16	61.8	48.05
Straw yield (gm^{-2})	487.33-693.33	600.48±34.82	7.10	8.00	10.70	55.9	74.01

ear length, number of spikelets, number of grains per ear, 1000 grain weight, flag leaf area, grain yield and straw yield, but negatively correlated with harvest index, there by suggesting that improvement of any of these characters may simultaneously improve the other except harvest index. 1000 grain weight was positively correlated with harvest index, flag leaf area, grain yield significantly and was positive with straw yield. Harvest index was significantly and positively correlated with grain yield and positively correlated with low magnitude flag leaf area, but negatively correlated with straw yield. Flag leaf area was positively correlated with higher magnitude in both grain and straw yield and similarly grain yield also positively correlated with straw yield.

The phenotypic correlation with germination count was negatively correlated with number of tillers, ears per plant, length of ear, 1000 grain weight and straw yield. (Table 2). However, for rest of the characters i.e., number of spikelets per ear, number of grains per ear, harvest index, flag leaf area and grain yield was positive with low magnitude. Tillers per plant was positively and significantly correlated with number of ears per plant. The positive correlation was also with length of ear, number of spikelets per ear and straw yield was favourable. Number of ears per plant was negatively correlated with plant height, number of spikelets per ear, number of grains per ear, 1000 grain weight, harvest index, flag leaf area and grain yield. Plant height was positively correlated with most of characters.

Table 2. Genotypic (G) and Phenotypic (P) correlation coefficient of seed yield and its components in wheat

Character		Tillers/ plant	Ears/ palnt	Plant height (cm)	Length of ear (cm)	No.of spikelets/ear	No.of grains/ ear	1000 grain weight (g)	Harvest index (%)	Flag leaf area (cm^2)	Grain yield/ (gm^{-2})	Straw yield (gm^{-2})
Germination/metre	G	-0.563**	-.0658**	0.014	-0.319	0.086	0.030	-0.0212	0.149	-0.078	0.181	-0.012
	P	-0.269	-.0354	0.000	-0.084	0.068	0.034	-0.073	0.080	0.060	0.074	-0.045
Tillers/plant	G		0.698**	-0.188	0.157	0.044	-0.324	-0.317	-0.415*	-0.218	-0.406*	0.133
	P		0.677**	-0.120	0.119	0.032	-0.086	-0.195	-0.256	-0.158	-0.200	0.091
Ears/plant	G			-0.350.	-0.038	-0.248	-0.669**	-0.155	-0.334	-0.006	-0.345	0.073
	P			-0.219	0.075	-0.145	-0.291	-0.137	-0.261	-0.084	-0.137	0.176
Plant height (cm)	G				0.615**	0.313	0.349	0.326	-0.308	0.312	0.342	0.624**
	P				0.456*	0.290	0.225	0.246	-0.292	0.198	0.274	0.514**
Length of ear (cm)	G					0.261	0.238	0.145	-0.372*	0.245	0.150	0.575**
	P					0.358	0.301	0.062	-0.320	0.218	0.192	0.426*
No.of spikelets/ear	G						0.839**	-0.426*	-0.695**	-0.218	-0.317	0.506**
	P						0.664**	-0.315	-0.541**	-0.137	-0.139	0.352
No.of grains/ear	G							-0.404*	-0.370*	-0.271	-0.315	0.134
	P							-0.338	-0.277	-0.165	-0.107	0.150
1000 grain weight (g)	G								0.442*	0.524**	0.699**	0.101
	P								0.383*	0.346	0.446*	0.020
Harvest index (%)	G									0.140	0.494**	-0.680**
	P									0.074	0.377*	-0613**
Flag leaf area (cm^2)	G										0.526**	0.315
	P										0.344	0.198
Grain yield (gm^{-2})	G											0.337
	P											0.449*

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

Similarly ear length was positively correlated with rest of the characters except harvest index. Its association with number of spikelets, number of grains per ear, flag leaf area, both grain and straw yield were most important. 1000 grain weight was positively correlated with harvest index, flag leaf area, grain yield, their correlations were significant. However, low positive correlation of 1000 grain weight with straw yield was also important as this character can help in grain yield without hampering straw yield. These results are in agreement with those of (Singh *et al.*, 1979).

Germination count was negatively correlated with tillers per plant, number of ears per plant, plant height, grain and straw yield. But positively correlated with ear length, number of spikelets per ear, number of grains per ear, 1000 grain weight, harvest index and flag leaf area though most of these correlations were of very low magnitude (non significant) except with flag leaf area. Number of tillers per plant were significantly and positively correlated with number of ears per but positive correlation was found with length of ear, number of spikelets, number of grains per ear, flag leaf area, grain and straw yield. Their negative correlations were found with plant height, 1000 grain weight and harvest index.

Plant height was positively correlated with ear length, number of spikelets per ear, grain and straw yield, but had negative association with number of grains per ear, 1000 grain weight, harvest index and flag leaf area. Harvest index was strongly and negatively correlated with straw yield and flag leaf area, but positively correlated with grain yield further suggested the limitation of increasing straw yield without reduction in harvest index. Flag leaf area was positively correlated with grain and straw yield. Grain yield had strong positive correlation with straw yield at environmental level.

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GENETIC VARIABILITY IN GENEPOOL OF BUTTERFLY PEA (*Clitoria ternatea*) FOR FORAGE ATTRIBUTES

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Ninety two genotypes of Butterfly pea (*Clitoria ternatea*) collected from different parts of the country were evaluated. A wide range of variation in various characteristics for different genotypes in germplasm collections were observed. The maximum variation (CV 35%) was recorded in green fodder yield per plant followed by number of leaves per plant (CV 31%) and leaf stem ratio (CV 27%). Genotype ILCT 281 from Uttar Pradesh and ILCT 276 from Rajasthan had the lowest total index score value after the meteroglyph analysis. Genotypes ILCT 261, ILCT 213 and ILCT 221 were found to have the maximum total index score value and thus the aggressive growth habit. Results indicated that materials from the different regions were randomly represented in all TIV grades of plant growth types.

Key words: *Clitoria ternatea*, genetic variability, forage attributes

Availability of nutritious fodder from arable areas is vital to increase animal productivity in the country. The major source of cattle feed is through pasture crops and native grasslands besides other sources. The native grasslands are in a highly degraded state providing low biomass of poor nutritional quality, and are dominated by different grass species namely *Sehima nervosum, Dichanthium annulatum, Cenchrus* spp., *Heteropogon contortus, Phragmites* spp., *Saccharum* spp., *Themeda* spp., and *Iseilema* spp. etc. (Dabhadgaon and Shankarnarayan, 1973). The cheapest way to improve forage quality world over has through increasing the occurrence of productive forage legumes in the native grasslands. Grass-legume pastures are known to improve forage quality and soil status in terms of organic carbon, available nitrogen and phosphorus.

Among the indigenous legumes, *Clitoria ternatea* commonly known as Butterfly pea or aparajita is a productive forage legume that has shown wide range of adaptability and persistence in arid to warm humid areas of the country (Singh and Singh, 1988; Singh and Gupta, 1991). *Clitoria* is endowed with excellent forage productivity and quality, as its crude protein content varies from 13-25 per cent on dry matter basis and has more than 70 per cent digestibility (Upadhyay and Pachauri, 1983). Wide genetic diversity in different regional accessions of *Clitoria* has been observed in Indian material (Singh and Singh, 1988). Keeping in view the immense importance of germplasm collections and its proper evaluation and categorization, the present investigation was framed to study the genetic diversity and also to classify the material and identify the desirable types among a sizeable collection of *Clitotia ternatea* genotypes made from different parts of the country.

MATERIALS AND METHODS

Ninety-two genotypes of butterfly pea were collected from different agroclimatic situations of tropical and warm humid regions of India. The material was grown at Central Research Farm of National Research Centre for Agro-Forestry, Jhansi. The research farm is situated at 25°-27' North, 78°-35' East, 271 m above the sea level and falls in semi arid plateau of Bundelkhand having mean annual rainfall 890 mm. The soil is neutral in reaction, poor in nitrogen and organic content but rich in potassium. The experiment was laid out in randomized block design in sandy loam soils. The seeds of all the germplasm lines were sown in 3m long row spaced at 50 cm and 10-15 cm distance between plant to plant respectively. Each plot had three lines and was replicated thrice. The experiment was maintained under rainfed conditions for three consecutive years.

The observations on various morphological, growth and fodder yielding attributes were recorded at 50% flowering stage on three randomly selected plants from each plot. These were cut at 10 cm above the ground level for recording data on fodder yielding attributes. For the classification and cataloguing of germplasm, score index method was followed as proposed by Anderson (1957). Each parameter was divided into three scoring groups: 1. Low II. Medium III. High. These groups were denoted by numerical values 0, 1 and 2 respectively. For score index, various characters viz., days to flowering, plant height (cm), branch number, secondary branch number, branch length (cm), number of leaves per plant green fodder yield per plant (g), dry matter yield per plant (g), leaf stem ratio (dry matter) and crude protein content were considered. Score for each character ranged from 0-2 and accordingly maximum score by any genotype could be 20. The entire germplasm was thus grouped and classified.

RESULTS AND DISCUSSION

A wide range of variation observed in characters in germplasm collection (Table 1). Among all the characters studied, maximum variation (CV 35%) was observed in green fodder yield per plant followed by number of leaves per plant (CV 31%), leaf stern ratio (CV 27%) and minimum in branch number per plant (CV 140/o) and days to flowering (CV 15%) (Table 1).

Table 1. Mean, range and coefficient of variation, values of different morphological and fodder yielding attributes in 92 genotypes of *C. ternatea*

Characters		Range	Mean	CV%
1.	Days to flowers	39.5-49.6	44.55±1.18	15.05
2.	Plant height (cm)	53.2-94.9	73.88±3.15	20.72
3.	Branch numbers	8.0-17.9	12.86±0.93	14.00
4.	Number of secondary branches	10.0-24.8	17.40±1.30	18.00
5.	Branch length	54.1-95.1	73.68±3.45	20.86
6.	Leaf numbers	90.4-183.5	136.80±5.36	31.00
7.	Green fodder yield	39.3-97.7	68.00±2.16	35.00
8.	Dry matter yield (g)	11.01-26.66	17.96±1.35	24.06
9.	Leaf-stem ratio (dry matter)	0.64-1.24	0.93±0.92	27.04
10.	Crude protein content %	20.13-26.99	23.56±0.56	17.54

The genetic diversity is the basic input required for any crop improvement programme. It offers scope for direct selection of elite material as a new cultivar or helps in identifying specific traits for use in breeding programme. On the basis of index score method (Anderson, 1957). the entire genepool was classified into 15 groups. The values of total index score in the different group ranged between 1-15 (Table 2). The materials from different regions were distributed in different groups with specific index score values (Table 3). The values of total index score of respective groups were further classified into four major groups and their index score values are : group I : 0-4, group II : 5-8, group III : 9-12, and group IV : 13-15. Depending upon the magnitude of the expression of all the traits the respective group indicate; (I) low vigour expression (II) medium vigour expression, (III) medium high vigour expression and (IV) very high vigour expression.

Among all the genotypes ILCT 281 from Uttar Pradesh and ILCT 276 from Rajasthan had the lowest total index score value [TIV (Table 2)]. The medium vigour expression group had the maximum number of accessions (45). Medium high vigour expression group comprising

Table 2. Grouping of *C. ternatea* genepool in respected of their score values and name of accessions

Groups	Score value	Name of accessions
I	01	ILCT.281
II	02	ILCT.276
III	03	ILCT.218, 259 and 266
IV	04	ILCT.256, 263, 274, 280 and 291
V	05	I LCT.230, 240, 267, 275, 287, 293 and 294
VI	06	ILCT. 210, 226, 233, 237, 242, 253, 255, 282, 284 and 285
VII	07	ILCT.209, 211, 217, 225, 229, 231, 232, 234, 238, 250, 252, 257, 268, 286
VIII	08	ILCT.223, 245, 251, 258, 260, 264, 270, 273, 279, 283, 288, 296, 297 and 300
IX	09	ILCT.220, 235, 236, 265, 277 and 290
X	10	ILCT.227, 241, 246, 254, 262, 271 and 292
XI	11	ILCT.214, 216, 224, 239, 244 and 299
XII	12	ILCT.212, 219 and 243
XIII	13	ILCT.215, 222, 228, 247, 248, 278, 289, 295 and 298
XIV	14	ILCT.249, 269 and 272
XV	15	ILCT.213, 221 and 261

22 genotypes was characterised by medium expression of most and high expression of some of the characters. The accessions of very high vigour expression group were most productive forage yielders as most of the characters showed maximum expression. Out of 15 genotypes in the group, accessions ILCT 261, ILCT 213 and ILCT 221 were the most aggressive plant growth types. Results also indicated that materials from different regions were randomly represented in all TIV grades of plant growth types (Tables 2 and 3).

Table 3. Grouping of *C. ternatea* genepool in respect of their score value, number of accession and source of origin

Groups	Score value	No. of accessions	Source and number of accessions
I	1	1	UP (I)*
II	2	1	Raj (1)
III	3	3	UP (1), Raj (1) and Dlh (1)
IV	4	5	UP (2), Raj (2) and Guj (1)
V	5	7	UP (1), Raj (3),MST (1), NT (1); Guj (1)
VI	6	10	Raj (3), MP (4), Dlh (1), Guj (1), VM (1)
VII	7	14	Raj (6), NT (3), Dih (3), Guj (1), WB (1)
VIII	8	14	UP (5), Raj (5), NV (1), MS (2), Bhr (1)
IX	9	6	UP (3), Dlh (1); Guj (2)
X	10	7	UP (2), Raj (4); Guj (1)
XI	11	6	UP (3), Dlh (2); TN (1)
XII	12	3	UP (1); Dlh (2)
XIII	13	9	UP (2), Raj (3), Dlh (2), MS (1); Bhr (1)
XIV	14	3	Raj (2); Dlh (1)
XV	15	3	Dlh (2); TN (1)

Number of accession, given in parenthsis
UP: Uttar Pradesh; Raj: Rajasthan; Dlh : Delhi State; MP: Madhya Pradesh; MS: Mahrashtra; Guj: Gujarat; WB: West Bengal; TN: Tamil Nadu; Bhr: Bihar

Studies also emphasized the existence of considerable genetic diversity within the major geographical areas of *Clitoria ternatea* distribution. Presence of diverse growth forms in the material from same region may as well indicate the different plant types may have differential adaptation to varying range of soil, climatic conditions prevailing within the broad expense of *Clitoria* distribution. Trend, which has emerged in the present study, may potentially be utilised for selecting the desirable types among the collections as per need.

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SELECTION OF PERSIAN WALNUT (*Juglans regia* L.) VARIETIES IN SHIMLA DISTRICT OF HIMACHAL PRADESH

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Population of Persian walnuts (*Juglans regia* L.) in north-eastern part of India represents important genetic resources consisting large number of seedling trees. Improved varieties of walnut were also introduced in the state in early seventies from USA and erstwhile USSR. Recent attempt has been made to survey seedling trees in important walnut growing localities of Shimla district of Himachal Pradesh. For comparative purpose nut, samples were collected only from 27 types having good nut characters and best yield performance to select most promising strains/varieties. These were compared with already selected Indian and other exotic walnut varieties. On the basis of nut and kernel characteristics and shelling quality, three strains viz No. 10, 22 and 23 have been selected and on the basis of their sources respectively named as K.S. Bagh, Nand and Partap walnuts with nut wt of 11.7g, 17.1 and 24.4g and kernel contents of 62.2, 49.7 and 47.1 per cent respectively. These have smooth light amber coloured nuts with excellent shelling quality and light yellow delicious kernel.

Key words : Walnut, nut, kernel, shelling quality, exotic, indigenous

Walnut (*Juglans regia* L.) is grown in all over the temperate region of India where climate and soil conditions are more or less favourable. Almost entire plantations are of seedling origin and a large number of these occur in Jammu and Kashmir from where nearly 1,194 tonnes of kernels and 58 tonnes of shell walnuts worth Rs. 12.50 crores were reported to be exported each year (Anon, 1989). However, this production does not conform to the well defined commercial standards due to traditional practice of raising the trees through seeds. Himachal Pradesh is the next largest producer with nearly 2,474 tonnes dry fruits each year (Anon, 1996). Large number of seedlings in these temperate areas are found growing in forests alongwith oak trees and a few with quality nuts are grown by orchardists on their farm. Some varietal orchards have been planted on government farms and research stations, but suitable varieties are lacking which could be used for regular orchards.

In view of the vast diversity in walnut seedling trees, selections were made within them and standard germplasm with desirable attributes were developed. Some attention has already been given on this aspect in Jammu and Kashmir (Queshi and Dalal, 1985, Bhat *et al.*, 1992). The present study deals with seedling selections in prominant localities of Shimla district in comparison to already selected strains within country and elsewhere.

MATERIALS AND METHODS

Survey of four important localities of Shimla district namely Chirgaon, Jubbal, Kotkhai and Theog, was carried out during mid September 1994-95 when walnuts are generally ready for harvest in these areas. The fruits of indegenous varieties were collected from Horticultural

Development Station, Boktu, Kinnaur and that of the exotic varieties from National Bureau of Plant Genetic Resources, Regional Station, Shimla. The data were recorded of a random sample of 10 nuts from each of 35 types drawn after proper drying of nuts. The various parameters were determined as per procedure listed below :

Nut weight : Weight of the inshell nuts; nut size : represents nut length (height), width (suture diameter) and thickness (cheek diameter); nut colour : A -amber, DA-dark amber, LA-light amber shell; nut smoothness : R- rough, S-Smooth and kernel colour and shelling quality : 5 excellent, 4-very good, 3-good, 2-fair and 1-poor.

RESULTS AND DISCUSSION

The importance of nut and kernel characters of walnut has significant role in international market. The data on various characteristics of nut quality is given in Table 1.

Nut weight : Nut weight ranged from 8.2 to 24.4 g. Maximum nut weight was recorded in seedling 23 followed by 7 (21.5g), 19 (19.0g) and 11 (18.0g). All the indigenous and exotic varieties had lower nut weight. Gouzhen and Yang (1990) reported nut weight of 5.8 g with the smallest nuts and 25 to 27 g of the largest sized nuts in China. Nut weight can serve as good parameter for selection provided the shelling percentage norms are fulfilled by higher nut weight types. Minimum standard for nut weight is above 12.0 g. A large number of seedlings confirm this criteria.

Nut size : Nut size especially diameter at suture line is an important character. For commercial grading, a standard nut diameter at suture line not less than 3.13 cm is essential (Serr and Ford, 1956). The size of nuts ranged from 2.68 to 3.94 cm and as much as 16 seedling selections confirmed the standards laid out by these research workers.

Shell thickness : Shell thickness is an important characteristic which determines the crack quality of the nuts. Nuts with shell thickness less than 1.5 mm are considered thin shelled and 1.5 to 2.0 rated as medium shelled. In the present studies, seedling No. 22 seems to be thin shelled and eight seedlings (7, 9, 10, 12, 16, 22, 23 and 24) as medium shell. All others were observed hard shelled which is not a good character from market point of view.

Nut shape : Nuts having round or oval shape are much preferred due to their better filling. Seedling 23, 7, 11 had ovoid to oblong shapes with attractive appearance, whereas seedling 19 has long conic nuts though of good size but with poor filling.

Nut colour and surface : Nut colour and surface of seedling 10, 22, 23 was much attractive with blight coloured nuts having smooth surface. The seedling 7 and 11 which also had larger nuts were amber coloured with rough surface and hence can not be graded promising.

Crack and shelling quality : The nuts with thin shell are considered easily crackable. Minimum shell thickness (1.4) was recorded in seedling 22, followed by 10(1.6), 27(1.5) 23 and 14(1.7). These are comparable in shell thickness with various indigenous and exotic varieties. Shelling quality i.e., case of kernel extraction was superior in seedling 2, 7, 9, 10, 12, 14, 16, 22 and 23. This is an important criterion for selection of walnut for domestic and export use.

Kernel colour and taste : Light coloured kernel is most preferred for domestic as well as export. Seedling 5, 6, 7, 8, 10, 11, 13, 17, 18, 22, 23, 25 and 26 had light kernel, however the taste was only superior in 8, 10, 14, 15, 16, 19, 21, 22, 23. Exotic varieties had inferior taste and kernel colour. Govind was found between in these attributes.

Kernel percentage : Kernel percentage in various

Table 1. Variation in nut characters of different walnut seedlings and cultivars

Seedling no./ cultivar	Nut characteristics									Kernel characteristics		
	Wt. (g)	Ht. (mm)	Width (mm)	Thick-ness (mm)	Shape	Colour	Surface	Shell thick-ness(mm)	Shelling quality (grade)	Colour	Taste (grade)	Kernel (%)
A) Seedling												
1.	13.8	36.2	34.2	31.2	Conical	DA	R	2.8	3	V	3	36.2
2.	8.8	36.8	29.2	29.0	Oblong	DA	S	1.9	5	LY	3	38.6
3.	10.2	37.0	31.4	32.0	Ovoid	A	S	2.0	4	Y	4	30.8
4.	13.2	37.8	33.0	32.1	Oblong	A	S	2.5	3	DY	3	21.2
5.	9.4	37.2	29.6	30.4	Conical	A	S	2.3	4	LY	3	35.7
6.	8.2	30.4	26.8	27.8	Ovoid	A	R	2.4	3	LY	4	29.3
7.	21.5	39.4	35.0	37.3	Ovoid	A	R	2.0	5	LY	3	40.3
8.	14.6	40.8	31.4	32.0	Oblong	A	S	2.2	4	LY	5	32.9
9.	14.5	39.0	33.8	33.0	Oblong	DA	S	2.0	5	Y	4	36.2
10.	12.7	32.2	31.7	34.3	Ovoid	LA	S	1.6	5	LY	5	62.2
11.	18.0	40.3	33.7	36.3	Oblong	A	R	2.4	3	LY	4	33.3
12.	14.0	35.0	32.2	36.3	Ovoid	A	R	2.0	5	V	3	47.1
13.	15.1	41.0	31.8	35.0	Oblong	A	R	2.1	4	LY	4	37.7
14.	11.2	34.0	29.6	31.0	Conical	LA	R	1.7	5	Y	5	50.0
15.	12.2	37.6	30.8	32.4	Oblong	LA	R	2.2	3	V	5	42.6
16.	13.0	38.0	31.5	21.2	Oblong	DA	S	1.9	5	V	5	30.8
17.	11.5	40.5	31.8	32.0	Conical	DA	S	2.0	2	LY	3	26.1
18.	14.3	34.5	31.0	32.3	Ovoid	A	S	2.3	2	LY	5	23.2
19.	19.0	42.8	35.2	36.0	Oblong	A	S	1.9	4	V	5	40.0
20.	11.4	42.0	29.6	31.6	Conical	DA	S	1.8	4	V	2	29.8
21.	12.0	32.4	32.0	35.4	Ovoid	LA	R	2.3	2	V	5	33.3
22.	17.1	41.4	35.2	37.2	Ovoid	LA	S	1.4	5	LY	5	47.1
23.	24.4	49.4	39.4	43.8	Oblong	LA	S	1.7	5	LY	5	49.7
24.	17.0	44.2	33.2	35.6	Oblong	A	R	1.8	4	V	4	35.3
25.	11.5	38.5	30.0	32.2	Conical	A	R	2.4	1	LY	1	30.4
26.	9.3	29.8	29.0	30.8	Ovoid	A	R	2.0	1	LY	2	22.2
27.	10.8	41.8	31.0	31.4	Oblong	A	R	1.5	4	LY	4	29.6
B) Indegenous												
R. K. Selection	16.3	45.0	34.7	33.4	Oblong	LA	S	2.0	5	V	4	41.5
Kashmir Budded	11.3	38.3	30.8	31.0	Conical	LA	S	1.8	5	Y	5	42.2
Govind	9.2	39.2	28.0	29.2	Ovoid	LA	S	1.3	5	LY	4	44.4
C) Exotic Cultivars												
Tutle - 16	9.3	31.0	26.4	29.2	Ovoid	DA	S	2.2	2	V	4	30.9
Psyne	9.0	32.5	30.2	30.0	Oblong	DA	S	1.9	4	V	2	30.9
K × Giant	12.6	47.2	30.6	36.8	Conical	DA	R	1.7	2	V	2	23.6
Hartley	6.8	32.2	28.4	29.9	Conical	A	S	1.4	4	DY	4	29.4
Lake English	6.1	26.0	24.4	26.2	Ovoid	DA	S	1.3	4	V	4	33.3

Legends:Shell Colour:A-amber, DA - dark amber, LA - Light amber; Nut surface - R rough, S - Smooth; Kernel colour : V-violaceus, DY-Dark yellow, Y-yellow, LY:Light yellow; Shelling quality; 5:excellent, 4;very good, 3-good, 2-Fair, 1: Poor; Taste: 5:excellent, 4-very good, 3-good, 2- Fair, 1-poor

selections ranged from 21.2 to 62.2. The highest kernel percentage (62.2%) was obtained in seedling 10, followed by seedling 14 (50.0%) seedling 23 (49.7%) and seedling 12 and 22 (47.1%).

Serr and Ford (1954) suggested that any selection should have above 50 per cent shelling percentage and 50 to 60 per cent is the reasonable goal. In the present study, seedling 10, 14 and 23 fulfill the standard. Abdul and Dalal (1985) reported 30-35 per cent kernel in Kashmir walnuts, whereas Bhat *et al.* (1992) reported high kernel percentage ranging from 54.2 to 63.2 in two indigenously selected and two exotic cultivars. Pieko and Czynczyk, (1990) reported 37.6 to 52.5 per cent kernel in selected varieties in Poland. In Italy, kernel content in 19 cultivars ranged from 40.5 to 53.1 per cent (Radicarti *et al.*, 1990). Chauhan and Sharma (1979) reported as high as 64.3 per cent kernel in a seedling from Kinnaur but the nut size of this selection was small. Highest kernel records of 67.0 per cent was reported from China (Sheng ke, 1990).

In the present survey, the seedling No. 10, 22 and 23 were observed superior in kernel content as compared to various indigenous and exotic varieties studied. On the basis of their source of collection these are named as K. S. Bagh, Nand and Partap selections.

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VARIABILITY ANALYSIS AND CAUSE AND EFFECT RELATIONSHIP IN ASHGOURD [*Benincasa hispida* (Thunb.) Cogn.]

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The study revealed significant variances for all the eight characters studied. High heritability along with high genetic advance were observed for fruit yield per plant while number of fruits per plant and fruit weight showed only high genetic advance. Genotypic correlations were found higher than the phenotypic correlations. Fruit weight and number of fruits per plant exhibited maximum direct effect on fruit yield.

Key words: *Benincasa hispida*, germplasm, variability, correlation, path analysis

Ashgourd is a monotypic genus with only one cultivated species *Benincasa hispida* (Thunb) Cogn. It is known by several names; as wax gourd, winter melon, hairy melon, chinese preserve melon, ash pumpkin, white pumpkin, kooshmanda (in Sanskrit), petha (in Hindi) etc. Ashgourd has unique characteristic and use in confectionary and ayurvedic medicinal preparations (Ramesh *et al.*, 1989 and Satpute, 1989). Surprisingly, this crop has not been much exploited on commercial basis in the past. Although ash gourd is becoming a crop of industrial importance, relatively less attention has been paid towards the varietal improvement of existing strains available in different parts of the country. There is an imperative need to pick up an ideal plant type having maximum desirable traits.

As variation in a character is an interplay of heritable and non heritable components, selection based on merely phenotypic expression is misleading. To begin with a successful breeding programme in a crop, it is necessary to have the knowledge of the interrelationship among the various characters and their dependency on each other. Correlation analysis measures the degree of association among the different component characters but does not imply any cause and effect relation. Path coefficient analysis, on the other hand, splits the correlation coefficient into direct and indirect effects and thus provides a detailed examination of specific factors responsible for correlation and measures their relative importance. Keeping the above points in view, the present investigation was undertaken to find out the genetic parameters of variability and understand the association of various quantitative characters in ashgourd.

MATERIALS AND METHODS

Forty four germplasm of ashgourd collected from various parts of the country were evaluated in a randomized complete block design with three replications at the experimental farm of the Indian Institute of Vegetable Research, Varanasi during *kharif* season of 1998-99 and 1999-2000. Each entry was sown in a plot size of 4m x 5m with plant-to-plant spacing of 80 cm and row-to-row spacing of 5m. The data were recorded on eight quantitative characters, viz., number of fruits per plant, fruit weight, fruit length, fruit diameter, vine length, days to first male flower, days to first female flower and fruit yield. Pooled data for the two years were analyzed statistically using SPAR 1 package developed by the IASRI, New Delhi.

RESULTS AND DISCUSSION

Significant differences were observed among the genotypes for all the characters under study. The estimates of various parameters of genetic variability are presented in Table 1. The phenotypic coefficients of variation (PCV) were higher than the genotypic coefficients of variation (GCV) for all the characters which indicated that the manifestation of these characters was highly influenced by the environment. The GCV was higher (25%) for fruit yield (35.57%) followed by fruit weight (26-06%) which indicated that the genotypes had a wide variation for the two characters (Hamid *et al.*, 1 983) and direct selection may be useful to exploit such variation.

The broad sense heritability (H) estimates were high (80%) only for fruit yield per plant and moderate (50-80%) for number of fruits per plant, fruit weight, fruit length and fruit diameter. The genetic advance expressed as per cent of mean was high (30%) for fruit yield, number of fruits per plant and fruit weight and moderate (20-30%) for fruit length and fruit diameter. Low estimates of heritability (50%) and genetic advance (20%) were observed for vine length, days to first male flower and female flower appearance. Variation in physical characters of ashgourd fruit was also observed by Randhawa *et al.* (1983). From variability analysis, it can be observed that high estimates of GCV, H and genetic advance have been obtained for fruit yield. Yield being a complex character is dependent on a number of components, selection can not be made directly but through contributing characters like fruit weight and number of fruits per plant which have shown high to moderate estimates of various variability parameters.

Table 1. Genetic parameters of variability

Sr. No.	Character	Mean	SE(m)	PCV (%)	GCV (%)	Heritability in broad sense (%)	Genetic advance as % of mean
1.	Number of fruits per plant	1.70	0.16	23.50	16.19	73.0	44.12
2.	Fruit weight (kg)	9.04	1.02	32.54	26.06	68.4	39.71
3.	Fruit length (cm)	28.38	2.05	15.94	9.89	57.9	20.48
4.	Fruit diameter (cm)	23.8	1.28	15.79	12.66	78.7	25.30
5.	Vine length (cm)	8.30	0.91	20.78	8.52	31.5	13.73
6.	Days to first male flower	56.89	3.45	11.95	5.66	14.5	1.59
7.	Days to first female flower	64.20	3.50	9.97	3.22	9.6	1.15
8.	Fruit yield (kg/plant)	15.26	1.38	38.87	35.57	84.2	56.22

The estimates of correlation coefficients at phenotypic and genotypic levels are presented in Table 2. A perusal of correlation coefficients realed that genotypic correlation coefficients were, in general, higher than the corresponding phenotypic ones, indicating the inherent association among the various traits. At the phenotypic level, fruit yield showed positive and significant association with number of fruits per plant, fruit weight, fruit length and fruit diameter, while vine length, days to first male and female flower appearance

Table 2. Phenotypic (P) and genotypic (G) correlation coefficients for eight characters in ashgourd

Character		Fruit weight	Fruit length	Fruit diameter	Vine length	Days to first male flower	Days to first female flower	Fruit yield
Number of fruits/plant	P	–0.128	–0.051	–0.099	–0.135	0.112	–0.012	0.467*
	G	0.299	0.394	0.155	–0.112	0.113	–0.164	0.655
Fruit weight	P		0.395*	0.822*	0.246	–0.212	–0.183	0.798*
	G		0.193	0.957	0.401	–0.477	–0.717	0.908
Fruit length	P			0.019	0.114	0.016	–0.045	0.317*
	G			–0.101	0.094	0.188	–0.203	0.332
Fruit diameter	P				0.169	–0.232	–0.208	0.659*
	G				0.518	–0.598	–0.739	0.816
Vine length	P					–0.251	–0.200	0.104
	G					0.172	0.633	0.240
Days to first male flower	P						0.826*	–0.124
	G						0.912	–0.365
Days to first female flower	P							–0.181
	G							–0.704

P = Phenotypic, G = Genotypic, *Significant at 5% level

Table 3. Estimates of direct and indirect effects at the phenotypic (P) and genotypic (G) levels

Character		Number of fruits per plant	Fruit weight	Fruit length	Fruit diameter	Vine length	Days to first male flower	Days to first female flower	Correlation with fruit yield
Number of fruits/plant	P	0.572	–0.113	0.000	0.001	0.005	0.002	0.000	0.467*
	G	0.439	0.477	–0.045	–0.131	–0.002	–0.043	–0.039	0.656
Fruit weight	P	–0.073	0.883	0.000	–0.005	–0.009	–0.003	0.006	0.799*
	G	0.132	0.953	–0.022	–0.812	0.006	0.184	–0.172	0.909
Fruit length	P	–0.029	0.349	0.000	0.000	–0.004	0.000	0.002	0.317*
	G	0.173	0.308	–0.115	0.086	0.001	–0.072	–0.049	0.407
Fruit diameter	P	–0.057	0.725	0.000	–0.007	–0.006	–0.004	0.007	0.658*
	G	0.068	0.824	0.012	–0.848	0.008	0.230	–0.177	0.817
Vine length	P	–0.077	0.217	0.000	–0.001	–0.037	–0.004	0.007	0.105
	G	–0.049	0.639	–0.011	–0.439	0.015	–0.066	0.152	0.241
Days to first male flower	P	0.064	–0.187	0.000	0.002	0.009	0.016	–0.028	–0.124
	G	0.049	–0.759	–0.022	0.507	0.003	–0.385	0.243	–0.364
Days to first female flower	P	–0.007	–0.162	0.000	0.001	0.007	0.013	–0.034	–0.182
	G	–0.072	–0.141	0.023	0.627	0.010	–0.390	0.240	–0.703

Figures in bold letters denote direct effects and the remaining indirect effects
Phenotypic residual effect = 0.0323
Genotypic residual effect = 0.0212

did not show any significant association with fruit yield. Fruit weight exhibited positive and significant correlation with fruit length and fruit diameter besides fruit yield which meant that by increasing fruit weight and fruit number, fruit yield can be increased. Days taken to first male and female flower appearance were highly correlated with each other but did not show any association with fruit yield.

The results of the phenotypic path coefficient analysis in the form of direct and indirect effects on fruit yield are presented in Table 3. The value of residual effect after deducting the direct and indirect effects was fairly low (0.0323). Fruit weight followed by number of fruits per plant contributed maximum positive direct effect on fruit yield. These characters were having significant and positive correlation with fruit yield and hence can be selected directly for improving yield. Among the other characters, fruit length and fruit diameter also exhibited significant and positive correlation with fruit yield but this correlation was entirely through fruit weight. The association of vine length with fruit yield was positive but its direct effect was negligible and the positive indirect effect was again through fruit weight which meant that increase in vine length may increase the fruit weight and ultimately the fruit yield. Similarly, the remaining two characters, days to first male and female flower were negatively associated with fruit yield but this association was further through fruit weight, meaning thereby that decrease in days taken to first male and female flower appearance may increase the yield via increased fruit weight.

From the estimates of correlation coefficients and direct and indirect effects of the yield contributing characters, it is clear that for bringing out desired improvement towards fruit yield in ash gourd, fruit weight and number of fruits per plant should be used as direct selection parameters.

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Short Communication

SIMILIPAL BIOSPHERE RESERVE: HOME OF CULTIVATED AND WILD *Oryza* SPECIES

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Notes on occurrence and morpho-agronomic traits of major *Oryza* species i.e., *Oryza officinalis, O. granulata, O. rufipogon* and *O. nivara* from Similipal hill ranges of Orissa are reported. Importance of the region for *in-situ* conservation for wild *Oryza* is emphasized in the paper.

Key words: Wild rice, *in-situ* conservation

Similipal Biosphere Reserve in Mayurbhanj district of Orissa is located between 21^{o} 30' to 22^{o} 08' N latitude and 86^{o} 04' to 86^{o} 37' E longitude and covers an area of 2,750 sq.km. The area is characterised by innumerable crests and valleys clad with rich forests, interspersed with countless streams and rivers and contains a confused and broken mountain system ranging from 300 to 1166 metres, thus exhibiting a great degree of topographic variation. The Similipal Biosphere Reserve is the abode of 92 species of orchids and 1,076 species of other plants including 551 species of medicinal plants. Out of which two species of orchids are endemic, eight species endangered, eight species are vulnerable and 34 species are designated as rare plants. The average rainfall of the area is 173 cm with a maximum of 225 cm and minimum of 110 cm. The rainfall is not well distributed, most of it falling during the rainy season. Relative humidity is generally high throughout the year but more in the rainy season. The mean temperature varies from 20^{o} to 28^{o} C. A small population of aboriginal tribes mainly Santhal, Kolha, Bhumij, Bhuiyen, Bathudi, Kharia, Gondo, Mankdias, Pauri-Bhuyan, Mahalis, Sounti and Saharas inhabited in Similipal. There are 4 villages in the core area, 61 villages in the periphery and 1,200 villages in the transitional area.

The main forest types found in the area are: northern tropical moist deciduous forests (type 3 C/C 2 e), northern tropical semi-evergreen forests (type 2B/C3), dry deciduous hill forests (type 5B/C 1c and 3C/C3), high level sal forests (type: 3C/C 2e (I) and grassland and savannah (type 3C/DS-I). Sal is the predominant type in most areas. However, it varies with the edaphic conditions and its associates vary with the type.

Three exploration trips were conducted during 1989, 2000 and 2001. The species were collected and the passport data were recorded at the collection site. The collected germplasm were later grown in the experimental garden of NBPGR Base Centre, Cuttack. Morpho-agronomical characteristics were noted and the diversity between the species was recorded.

Similipal is very rich in rice and its wild relatives. *Oryza sativa*, *O. rufipogon* and *O. granulata* were earlier reported from Similipal (Saxena and Brahman, 1989). *Oryza officinalis* was collected for the first time from Similipal in addition to the collection of all the reported species. The information on distribution of cultivated and wild *Oryza* species along with characteristics are mentioned.

Table 1. Similipal: A habitat rich in cultivated and wild rice species

Botanical name	Genome	Distribution
Oryza rufipogon	AA	Thakurmunda
Oryza nivara	AA	Similipal hill range
Oryza officinalis	CC	Khejri hills
Oryza granulata	Unknown	Meghasani, Nawana, Thakurmunda, Chahala, Dalangi
Oryza sativa	AA	Ulkudar, Gurguria, Khejari
Oryza sativa var. *spontanea*	AA	Similipal hill range

1. *Oryza officinalis* Wall. ex Watt

Oryza officinalis is a perennial, herbaceous and rhizomatous species of wild rice which is highly resistant to BPH and WBPH (Valusamy, 1981) and is reported for the first time in Orissa state. It is collected from Khejari hills of Similipal hill range, which is situated 45 km east side of Jashipur town. The approximate height of this hill is 800 metres from sea level. The plants of *O. officinalis* were grown in thick sal forest on stream banks in marshy land. The distribution of this species was very rare. It is not used for any purpose in the area. The plants of this species were erect, tall (148.5 cms) with 5.4 average number of internodes per plant. Average number of leaves per plant were 5.25 having light green colour. Average length and width of leaves (5th) were 33.45, 1.50 and 1.37 cms respectively. The panicle length varied from 27.5 to 37.5 cms with 50 to 83 grains per panicle. The average length and width of spikelets were 5.2 and 2.5 mm respectively with small awns.

2. *Oryza granulata* Nees et Arn. Ex Watt

It is a perennial herbaceous species of wild rice collected from Dalangi hills of Similipal hill range, which is situated 8 km north side of Bisipur village at about 400-metre height from sea level. The plants of *O. granulata* were grown in thick forest on rocky slopes over red lateritic soil near stream bank. The plants of this species were semi-erect, with medium height (75.05 cms), shade loving, rhizomatous, stem having 2-4 tillers per plant. Leaves were of light green colour and their average length and width were 15.9 and 1.45 cms respectively. Average length and width of flag leaf were 8.35 and 0.76 cms respectively. The panicle length varied from 5.2 to 6.2 cms and panicle had 9-10 grains on the unbranched rachis. Average length and width of spikelets were 5.48 and 2.70 mm respectively. Spikelets were oblong having black colour, while kernel colour was brownish black. The plants of *O. granulata* collected from Jeypore tract were almost the same except that of variation in height (75.05 cms and 55 cms), internode length (8.8 cms) and grains per panicle (9-10 and 10-15) respectively. Tribal people of this area are using the seeds of this species as contraceptive.

3. *Oryza rufipogon*

It is perennial, spreading or floating, adventitious roots and extravaginal branching at higher nodes, panicles lax and well exserted, long awns, slender grains, black husk

4. *Oryza nivara*

It is aAnnual, semi-erect to decumbent, panicle compact until maturity and not well exserted, short anthers panicle with fewer primary and secondary branches, spikiest black bold, oblong and deciduous, awn-thick about 4.0-6.0 cm.

5. *Oryza sativa* var. *spontanea*

These are probably crosses of *O. sativa* and

O. nivara and *O. rufipogon* and *O. sativa*. The panicle and grain characteristics are highly variable. Seed yield is high as compared to *O. nivara* or *O. rufipogon*.

6. *Oryza sativa*

The tribal farmers are cultivating landraces of rice since long for their home consumption. As the area is inaccessible and cut off by high hills and villages are scattered, sometimes landraces are restricted to particular communities, therefore, local types are observed with varying in names and characters. Diversity is exhibited in maturity duration e.g., **earliness**: Jereng, Karanga, Kanchi, Mahulia, **medium**- Kache bhajana, Chingudisukha **late**- Bankasira, Bhajana, Golei, Mughi, **Awned**-Barasal, Sauradhan, **Puffed** - Dhabajanaa are the popular varieties among the tribals. This is suitable for puffing purpose (broadly called as murrhi).

Striking variability in these landraces was recorded in plant height (102.04-174.96 cm), leaf length (36.58-56.42 cm), leaf breadth (0.9-1.36 cm), ear bearing tillers (5.0-9.2), panicle length (23.02-290.32 cm), culm diameter (4.6-9.4 mm), panicle weight (1.3g-3.4g), number of primary branches per panicle (9.4-12.2.), number of secondary branches per panicle (15.0-41.2), total spikelets per panicle (90.2-198.6), kernel length (5.05-6.5 mm), kernel width (2.08-3.0 mm), 100 grain weight 2.16 g (Laghuna) - 2.91 g (Bhajana). The varieties vary from long bold to (20), short bold (5) and medium slender (2) types.

The *Oryza officinalis* once available in plenty near the stream banks (during 1989) are now reduced to countable number of plants. This is because the streams are now drying either due to the diversion of water for irrigation purpose or cleaning of area in the vicinity. Besides, the the grazing by wild animals are also there. Communication facilities have also replaced some traditional cultivars in the peripheral areas e.g., in Lulung and Jashipur areas-a high yielding modern varieties - Lalat landrace has replaced traditional cultivars to a considerable extent.

Forest fire and indiscriminate felling of trees and poaching of wild animals particularly tigers, elephants, and other wild animals are causing serious threat to the biodiversity in the region. Therefore, efforts should be made to create awareness among the tribal inhabitants regarding importance of *in-situ*/on-farm conservation of these valuable resources in the region.

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Short Communication

STUDIES ON THE SMALL MILLETS AND OTHER RELATED WILD SPECIES OF GRASSES FROM SOUTHERN RAJASTHAN

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During the germplasm collection mission of grasses of Rajasthan, 11 small millets and 21 other related wild species of grasses have been identified and collected from southern Rajasthan. Ethnobotanical information about these small millets have revealed that cultivation area of most of these is under shrinkage. These are indespensible for the drought prone area and hence there is an immediate need to conserve these resources as well as other related wild species of grasses of southern Rajasthan.

Key words : Small millets, wild grasses, south Rajasthan

Small millets are grown in situations where there is a risk of famine. In this context, studies on small millets as well as other minor wild cereals are of immense importance in a state like Rajasthan where famines due to drought occur rather frequently. Southern Rajasthan is tribal dominated region of Rajasthan where small millets still constitute the staple food of poor tribals during famines. Other minor wild cereals also played an important role in the diets of native people of southern Rajasthan.

Aravalli hills of southern Rajasthan are extremely rich in its grass wealth. Energy value of certain important grasses of Aravalli hills have been determined by Katewa and Tiagi (1982, 1984 and 1990). Workers like King (1969), Kanodia and Gupta (1968) and Bhandari (1974) have documented famine food plants through personal collection of information from the desert tribalmen, women and old generation people in western Rajasthan. Being the food of the poorest of the poor segment of the society, little attention have been paid on these crops of tribal importance. Therefore, an attempt has been made to identify and collect the germplasm of small millets and other minor wild cereals.

An exploration mission for identification and germplasm collection of grasses of tribal dominated districts of southern Rajasthan was undertaken during September and October, 1999 and it was observed that in certain areas, the tribals still cultivate the small millets and their grains are used as supplementary food during scarcity period. Tribal dominated district of this region comprised a major part of the Aravalli system of mountain. The whole area is highly uneven and arid. The tribal economy is mainly pastoral with agriculture practiced only in a limited way because flat terrains are little to make agricultural fields. Because of limited area for agriculture, the tribals use grains of certain minor wild cereals as supplementary food. Ethnobotanical information about such wild cereals was noted. The exploration was undertaken when seeds were physiologically matured. The

Table 1. Small millets and others wild related species of grasses collected from southerin Rajasthan

S. No.	Botanical Name	IC No.	Local name	Habitat	Ethnobotanical uses
Small millets					
1.	*Brachiaria ramosa*	255263	Salki	Common in and along the margins of cultivated fields	Grains are used as famine food.
2.	*Echinochloa colonum*	255269	Sama	Grow in moist situations	The grains are eaten by the tribals in the famine.
3.	*Echinochloa crus-galli*	255303	Batda	Commonly found in highly moist areas. Also in water logged conditions	Grains famine food
4.	*Echitiochloa frumentacea*	-	Batti	Grow in moist areas	Grains famine food
5.	*Eleusine coracana*	255324	Maal/Madua	Cultivated in the field	Grains are eaten in the scarcity period
6.	*Panicum miliaceum*	255363	Samlie	Cultivated in the field	Grains are eaten in the scarcity period
7.	*Panicum paludosum*	-		Grow in moist situations	Grains scarcity food
8.	*Panicum trypheron*	255244		Grow in moist situations	Grains scarcity food
9.	*Paspalum scrobiculatum*	255325	Kodra	Cultivated in the field	Grains are cooked like rice. Grain flour is used for making bread.
10.	*Setaria glauca*	255302	Kukarva	Cultivated in the field along with other small millets	The grains are powdered and mixed with the flour of maize to make the breads during scarcity of food grains
11.	*Setaria italica*	255362	Kura/Kangni	Cultivated in the field	The grains are powdered and mixed with flour of cultivated cereals to make the bread
Other wild related species of grasses					
12.	*Acrachne racemosa*	55342	Phundalli ghas	Grow in undisturbed areas	Grains are used as famine food
13.	*Apluda mutica*	255248	Bhangtu/Pamta Bhera	Dominant grass in protected forest areas	Grains are used as famine food
14.	*Brachiaria deflexa*		Grow in moist situations	Grains are used as famine food	Grain are used as famine food
15.	*Brachiaria eruciformis*	255336	Chawla grass	Grow in cultivated fields	Grains are used as famine food
16.	*Brachiaria reptans*	255353	Soraya	Grow in moist situations	Grainsa re used as famine food
17.	*Coix lacryma jobi*	255253	Jorgadi/ Garelo	Aquatic grass	Grain of this grass are mixed with the grains of *Zea mays* and are used for making porridge. Seeds are eaten after boiling. It is also considered as a good fodder. The grains are ground to flour for making bread during scarcity of food
18.	*Dactyloctenium aegyptium*	255254	Malicha/makra	Grow in cultivated fields	Grains are used as scarcity food
19.	*Dacttyoctenium aristatum*	255332	Grow on the margins of cultivated fields	Grains are used as scarcity food	Grains are used as scarcity food

Table 1. (Contd.)

20.	*Echinochloa stagnina*	-	-	Grow in moist situations	Grains are used as scarcity food
21.	*Eleusine indica*	255290	Chitki/Malwari	Grow along the margins of cultivated fields	Grains are used as scarcity food
22.	*Eragrostis tremula*	-	Chirri ghas	Drought tolerant grass	Grains are used as scarcity food
23.	*Eriochloa procera*	-	-	Grow in moist and shady places	Grains are used in the famine
24.	*Hackelochloa granularis*	-	Majri Hankli	Grow in grassland fields	Grains are used as famine food
25.	*Ischaemum rugosum*	255249	-	Grow in rice field	Grains are used as famine food
26.	*Panicum sumatranse*	255361	-	Forest grass	Grains are used in the scarcity period by the tribals
27.	*Panicuin psilopodium*	-	Grow in moist situations	Grains are used as scarcity food	
28.	*Paspalidium geminatum*	255331	Kuri	Grow in grassland fields	Grains are used as famine food
29.	*Paspalidium geminatum*	-	Kahli	Aquatic grass	Grains are used as famine food
30.	*Sehima nervosum*	255297	Heren	Grow on hillocks	Grains are used as famine food
31.	*Setaria verticillata*	255306	Jhetudi	Prefers to sow in soil having high organic matter	Grains are used as famine food
32.	*Urochloa panicoides*	255329	Sanwal/Kuri	Grow in cultivated fields	Grains are used as famine food

passport data were recorded at the site of collection. Specimens of each small millet species and wild cereals have been preserved in the Agrostological Herbarium of the Department of Botany, M. L. Sukhadia University, Udaipur.

Small millets and other minor wild cereals collected from the tribal dominated districts of southern Rajasthan are presented in Table 1. The small millets (which are of course cultivated to some extent by the hill tribes on limited terrain) are used as scarcity food by the tribals of the area. Hill tribes store the grains of these millets and other wild cereals in air tight earthern pots for use in distressed conditions. The grains of these millets are eaten either after boiling in water or by making chapatis from the flour of the grains. The grains of these small millets and other wild cereals, being nutritionally superior to rice and wheat provide cheap proteins, minerals and vitamins to the poor tribals where the need for such ingredients is the maximum. Their nutritional superiority over wheat and rice is further confirmed by the ethnobotanical information from the tribals that "One chapati from the grains of these millets is sufficient to quench their hunger for whole day". This fact about their nutritional superiority was further confirmed by taking interviews of many tribals about their nutritional significance from different localities of the region. Some tribals are of the opinion that one chapati of these millets is equivalent to three chapatis of wheat.

Practically devoid of grain storage pest, the small millets have indefinite storage life. The untapped grain yield potential coupled with nutritional superiority makes these small millets potential future food crops particularly in the tribal dominated rainfed area of Rajasthan.

In southern Rajasthan, there are still some unexplored areas and there is an urgent need to retrieve the genetic diversity under natural conditions. This requires significance in Rajasthan state which is faced with chronic drought. Besides cultivated landraces, there is a need to collect related wild species also. This is especially relevant with small millets, where very little of the available vast natural variations have been explored, studied and utilized. Further, there is an immediate need to conserve the genetic resources of small millets, since areas under these crops are gradually depleting in the state of Rajasthan.

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Short Communication

SCREENING OF *Cenchrus ciliaris* AND *Cenchrus setigerus* GENOTYPES FOR FORAGE YIELD

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Twenty genotypes of *Cenchrus ciliaris* and 19 genotypes of *Cenchrus setigerus*, collected through exploratory survey in 1997, were evaluated for forage yield in a field trial during 1998 and 1999. Differences for forage yield were found to be significant in both the species. Forage yield ranged between 0.78 kg to 3.12 kg/line (2.5 meter in length) in *Cenchrus ciliaris* and between 0.89 kg to 2.65 kg/line in *Cenchrus setigerus*. In general, *Cenchrus ciliaris* was found to be more forage yielder than *Cenchrus setigerus*.

Key words : *Cenchrus ciliaris, Cenchrus setigerus*, forage yield, genotypes

The genus *Cenchrus* has two important species viz., *C. ciliaris* and *C. setigerus* suitable for pasture in arid and semi-arid regions. These are drought tolerant, hardy, perennials, nutritive and palatable to all kind of animals. The grasses have very deep as well as very developed extensive root system, therefore, if planted on the soil, will act as very good sand binder. Thus, besides forage production, these grasses can also be planted for sand dune stabilization and erosion control. In India, these grasses are widely distributed in the plains of Rajasthan, Punjab, western Uttar Pradesh, extending to the foot hills of Jammu. These are also found in Madhya Pradesh, Andhra Pradesh, Haryana, Gujarat, Tamil Nadu and Karnataka (Sharma *et al.*, 1999). These grasses are adapted to varying edapho-climatic conditions and can be raised with as low rainfall as 150 mm to as high as 1250 mm per annum. These grasses have very high degree of drought tolerance and can withstand temperature upto 48°C. A wide range of variability in terms of plant type and growth habitat has been observed in these two grasses (Patil and Singh, 1963; 1965; 1969; Pandeya *et al*, 1977; Whyte, 1964; Chakravarti *et al*, 1970; Yadav, 1981; Annon, 1997). Eight chromosome races with 2n = 32, 34, 36, 38, 40, 52, 54, and 56 in *Cenchrus ciliaris*; and three chromosome races in *Cenchrus setigerus* with 2n = 34, 36 and 54 have been reported (Ramaswamy *et al*, 1969). Thus, grasses offer a very wide scope of selective breeding. Because, variety of genotypes varying in morphometric traits and in production potential are expected from the collection of germplasm through exploratory survey of natural habitat. Evaluation of germplasm for high yielding genotypes through field trials is the fundamental step of crop improvement programme. Hence, high yielding genotypes, if identified through field trials, will be able to enhance the forage production. Therefore, keeping the importance and utility of the grasses in view, the present study was carried out with the following objectives:

1. Collection of vigorous genotypes of *Cenchrus ciliaris* and *Cenchrus setigerus* from natural habitat through exploratory survey, and

2. Selection of high yielding genotypes through field trial

During 1997, 20 genotypes of *Cenchrus ciliaris* (listed in Table 1) and 19 genotypes of *C. setigerus* (listed in Table 2) were collected through exploratory survey from the locality of Agricultural Research Station, Keshwana, Jalore. In 1998, collected germplasm were planted in randomised complete block design with three replications. Sowing was done in rows of 2.5 meter length. Row to row distance was maintained as 50 cm. At the time of sowing, a fertilizer dose of 30 kg nitrogen and 30 kg phosphorus per hectare was applied as basal. Experiment was irrigated during establishment period to assure germination of the grasses. During 1999, experiment was maintained as per standard agronomical practices. Green forage yield received in both the years was used for statistical analysis.

Table 1. Green forage yield (kg/line) of *Cenchrus ciliaris* during 1998 and 1999

Genotypes	Green forage yield kg per line		
	1998	1999	Mean
CCT-1	2.23	1.67	1.95
CCT-2	1.73	2.12	1.93
CCT-3	2.23	1.98	2.11
CCT-4	1.07	2.08	1.58
CCT-5	1.58	1.47	1.53
CCT-6	2.25	2.40	2.33
CCT-7	2.58	2.97	2.78
CCT-8	2.85	2.40	2.63
CCT-9	2.92	3.00	2.96
CCT-10	0.43	1.13	0.78
CCT-11	2.63	2.63	2.63
CCT-12	3.05	3.18	3.12
CCT-13	2.00	2.93	2.47
CCT-14	1.48	1.47	1.48
CCT-15	2.08	1.83	1.96
CCT-16	3.08	2.67	2.88
CCT-17	2.05	2.18	2.12
CCT-18	0.85	2.20	1.53
CCT-19	2.58	3.08	2.83
CCT-20	2.20	2.62	2.41
CAZRI-358	1.17	2.13	1.65
Mean	2.05	2.29	2.17
SEm ±	0.26	0.35	
CD ($p = 0.05$)	0.73	0.96	

Table 2. Green forage yield (kg/line) of *Cenchrus setigerus* during 1998 and 1999

Genotypes	Green forage yield kg per line		
	1998	1999	Mean
CST-1	2.62	1.47	2.05
CST-2	2.53	2.38	2.46
CST-3	1.00	0.78	0.89
CST-4	1.50	1.75	1.63
CST-5	1.72	1.97	1.85
CST-6	1.58	1.42	1.50
CST-7	1.50	1.67	1.59
CST-8	1.88	1.83	1.86
CST-9	2.33	1.72	2.03
CST-10	2.38	1.50	1.94
CST-11	3.42	1.87	2.65
CST-12	1.50	1.17	1.34
CST-13	2.50	1.97	2.24
CST-14	2.70	2.00	2.35
CST-15	2.08	2.18	2.13
CST-16	1.42	1.67	1.55
CST-17	1.67	2.08	1.88
CST-18	1.70	1.75	1.73
CST-19	2.08	1.67	1.88
CAZRI-76	2.08	1.25	1.67
Mean	2.01	1.71	1.86
SEm ±	0.22	0.25	
CD ($p = 0.05$)	0.62	0.70	

Differences in green forage yield of the genotypes of *Cenchrus ciliaris* and *C. setigerus* were found to be significant in both the years. In case of *Cenchrus ciliaris*, forage yield ranged between 0.43 kg per line to 3.08 kg per line in first year with the mean of 2.05 kg per line, and between 1.13 kg per line to 3.18 kg per line in second year with the mean of 2.29 kg per line. The yield of check (CZARI-358) was 1.17 kg per line in first year and 2.13 kg per line in second year (Table 1). On the basis of the performance of 1998 and 1999, genotype CCT-12 holds the rank first which is followed by CCT-9, CCT-16 and CCT-19 with the forage yield of 3.12, 2.96, 2.88 and 2.83 kg per line, respectively. In case of *Cenchrus setigerus*, first year's forage yield ranged between 1.0 kg per line to 3.42 kg per line with the mean of 2.01 kg per line. In second year, yield ranged between 0.78 kg per line to 2.38 kg per line with the mean of 1.71 kg per line, whereas, the yield of check (CAZRI-76) was 2.08 kg per line in first year and 1.25 kg per line in second year (Table 2). On the basis of two years data, genotype CST-11 ranked first, which is followed by CST-2, CST-14, and CST-13 with the forage yield of 2.65, 2.46, 2.35 and 2.24 kg per line, respectively.

A persual of yield data of both the species revealed that production potential of *Cenchrus ciliaris* is higher than *Cenchrus setigerus.* Further, to get the higher forage supply in long run, *Cenchrus ciliaris* is better than *Cenchrus setigerus* because in case of *Cenchrus setigerus* forage yield showing a decreasing trend in second year, whereas, *Cenchrus ciliaris* yields higher than the first year. In second year, average forage yield of *Cenchrus ciliaris* was found to be 33.92 per cent higher than *Cenchrus setigerus.* Therefore, in general, the growing of *Cenchrus ciliarus* is more beneficial than *Cenchrus setigerus* in Jalore region.

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OBITUARY

K.P.S. Chandel
(1937-2000)

A devoted plant explorer, distinguished scientist, a Fellow and founder member of the Indian Scoiety of Plant Genetic Resources (ISPGR), Dr. K. P. S. Chandel passed away prematurely on December 13, 2000, while he was on an exploration tour to north-west Himalayas.

Dr. Krishna Pal Singh Chandel was born in a Rajput family in village Ghatampur in the district of Kanpur on 14th April, 1937. He obtained his early education in the village. Due to his keen interest in agriculture, he joined Government Agriculture College, Kanpur (affiliated to Agra University, Agra) and passed his BSc (Ag) and MSc (Ag) degrees from there. He received his PhD in Genetics from PG School, Indian Agricultural Research Institute (IARI), New Delhi in 1975. He also obtained a post graduate degree in Plant Conservation and Utilization from University of Birminghum (UK) in 1980.

He started his career as Botanical Assistant in 1964 in UP Sugarcane Research Institute. In persuit of a professional research career, he joined the erstwhile Plant Introduction Division of IARI (now NBPGR) in 1965 and was posted to work at its regional station at Shimla in the field of plant genetic resources. Later, at the NBPGR Headquarters, from 1976-97, he held various positions such as Assistant Botanist, Senior Scientist, Principal Scientist, Head of Plant Exploration and Collection Division, Joint Director and Director (1995-1997) and thus associated with total gamut of plant genetic resources activities.

The innate desire to give a meaningful direction to the genetic resources conservation of "problem crops", he led the ICAR-DBT funded project 'National Facility for Plant Tissue Culture Repository' as Joint Director, which is now recognized as one of the best in the world. Dr. Chandel contributed a great deal in almost all aspects related to plant genetic resources, particularly in the field of germplasm exploration and *in-vitro* conservation and cryo-preservation. His contributions include collection and build up of large number of germplasm from difficult areas, such as Lahaul Spiti and from north-west Himalayas. Dr. Chandel authored over 200 scientific publications which include research papers in national and international journals, books and monographs. Dr. Chandel travelled far and wide in countries like Europe, UK and USA in connection with PGR related activities. As an excellent scientist, he inspired his colleagues a great deal.

Dr. Chandel was committed to the cause of the ISPGR and contributed significantly. He held the position of General Secretary of the Society for two terms.

He was recipient of several awards. He was Fellow of National Academy of Sciences, India (NASc) and National Academy of Agricultural Sciences (NAAS) and Indian Society of Genetics and Plant Breeding in India. Dr. K.P.S. Chandel, combined a brillient mind with a sensitive heart, will continue to be remembered by PGR community and scores of his friends and colleagues in future.

Recognizing his passion for plant genetic resources, Ministry of Environment and Forest, Government of India awarded him prestigeous Dr. B. P. Pal National Environment Fellowship, a rare distinction for a scientist in agriculture sector. This was a great affirmation for someone, who dedicated his career to collecting and conserving plant genetic resources for today and tomorrow. He was at the job when cruel destiny snatched him at the premature age of 63 years.

Survived by his wife, a son and a daughter, Dr. Chandel's demise is very deeply mourned and condolled by the Indian Society of Plant Genetic Resources with a pray to the Almighty that his departed soul may rest in peace. We convey our sympathies to the bereaved family.

Umesh Srivastava, Ruchira Pandey and Neelam Sharma

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CONTENTS

(*Contd. on inner cover page*)

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