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NBPGR Campus, New Delhi-110 012, India

BIODIVERSITY UTILIZATION AND CONSERVATION IN UNDERUTILIZED PLANTS : INDIAN PERSPECTIVE*

Bhag Mal

National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi – 110 012

With ever increasing population pressure and fast depletion of natural resources, it has become extremely important to diversify the present day agriculture in order to meet various human needs. The underutilized plants which have tremendous potential for commercial exploitation but remained ignored, offer a good scope in this context. The Hindustani gene centre houses 160 cultivated species, out of which 56 species are less known food plants. In the present paper, an attempt has been made to enlist underutilized plants of economic value which could, in future, serve as new crops and supplement agricultural production in India. The results of recent efforts on this group of plants made by the All India Coordinated research Project on Underutilized Crops, the National Bureau of Plant Genetic Resources, New Delhi and other institutions towards germplasm collection, evaluation, documentation and utilization have been enumerated. The status of germplasm conservation and the future strategies have also been discussed.

Agriculture is a resource which renews itself quickly and in abundant measure. It is the world's oldest profession, and also the noblest. It pulled man out of the animal world of killing, grabbing, garnering and devouring and developed in him the humane qualities of exploring, observing, growing and sharing. However, of the 80,000 edible plants explored since the beginning of

* Based on the paper presented at the International Workshop on 'Biodiversity of Traditional and Underutilized Crops' held at Valletta (Malta), 12-15 June, 1991

civilization, man has never made a major use of more than 150 species. Today, less than 30 species meet 90 per cent of world's requirement.

Most experts think that it is dangerous to allow the future of 500 billion people to depend upon the performance of less than 0.4 per cent of the edible plants. We must learn to diversify our food base and try to find out better uses for the much ignored underutilized plants. Many of them are far superior to what our present-day cereals were when our ancestors first sampled them. Underutilized plants are a veritable treasure-house, waiting to be explored, altered and improved upon to suit our needs and tastes. Resilient and adaptive, many of them are tolerant to adverse conditions and can grow on lands that do not support other plants. They do not require a high input technology and can be raised with comparatively lower management costs. Several of them are very nutritious and have often come to the rescue of people in times of crisis.

Agro-ecological regions in India

India is located between 8–38°N and 68–97.5°E and exhibits extreme variation in altitude, from sea level to heights above vegetational limits (3500 m) in the Himalayas. It is also characterised by a wide variety of climate, from the monsoon, tropical in the south to temperate and alpine in the north-western plains. It is floristically rich with more than 50 per cent of its botanical wealth comprising over 15,000 species of higher plants. This makes the Indian region botanically unique and interesting. Based on physiographic, climatic and cultural features, eight agro-ecological regions (Table 1) are recognised in India (Murthy and Pandey, 1978).

Underutilized plants of economic importance

The Hindustani (Indian) gene centre, with 160 cultivated species of economic plants, serves as a reservoir of a large number of useful plant species. The diversity of less known cultivated food plants is confined to 56 species. Further, about 320 species represent the truly wild and weedy counterparts as components of different vegetation types (Arora and Nayar, 1984). Information on plant genetic resources of these less known cultivated food plants and their wild relatives is well documented (Arora and Nayar, 1984;

Table 1 : Agro-ecological regions of India and their characteristics

S.No. Region	Temperature	Rainfall	Soil
1. Humid Western Himalayan Region	Jan. 8° -4°C July 5° -30°C	1500 mm	Forest and Hill, Mountain Meadow Soils
2. Humid Bengal-Assam Basin	Jan. 10° -25°C	2000 mm	Alluvial, Red Sandy, Laterite and Soils
3. Humid Eastern Himalayan Region and Bay Islands	Jan. 11° -24°C	2000 mm	Riverine Alluvial, Red and Laterite Soils
4. Sub-Humid Sutlej Ganga Alluvial Plains	Jan. 6° -23°C July 25° -41°C	1000 to 1500 mm	Riverine Alluvial Soils With saline and alkaline Patches
5. Sub-Humid to Humid Eastern and South Eastern Uplands	Jan. 16° -28°C July 27° -35°C	750 to 1500 mm	Red and Yellow, Red Sandy, Black and Coastal Alluvial Soils
6. Arid Western Plains	Jan. 10° -22°C July 28° -45°C	250 to 750 mm	Alluvial, Sandy Desert and Black soils
7. Semi-Arid Lava Plateaus and Central Highlands	Jan. 13° -29°C July 26° - 42°C	500 to 1000 mm	Predominantly Black Soils, Red Sandy and Red Loamy Soils
8. Humid to Semi-Arid Western Ghats and Karnataka Plateaus	Jan. 20° -29°C July 28° -38°C	750 to 2000 mm	Predominantly Red Sandy Soils, Black Coastal Alluvial and Laterite soils

Arora, 1985). There are also several introduced species which have a great potential to be exploited for various purposes in the country. An account of important underutilized plant species which await exploitation for food, fodder, energy and industrial purposes have been given earlier (Paroda and Bhag Mal, 1989; Bhag Mal, 1990).

In India, there are large areas which suffer with edaphoclimatic extremes of different kinds and the people face problems for their food and other requirements. However, there exist several indigenous plant species which can support life during difficult environments and emergency situations. Information on such plant species has been well documented (Gupta and Kanodia 1968; Bhandari, 1974; Saxena, 1979; Shankarnarayan and Saxena, 1989; Shankar, 1989 and Singh and Gupta 1989). The important plant species which can be successfully grown for food under harsh environmental conditions are listed in Table 2.

Table 2 : Food plants for emergency situations

Situation	Usage	Species
Hot desert	Grain	<i>Setaria verticillata</i> , <i>Haloxylon salicornicum</i> , <i>Citrullus colosynthis</i> , <i>C. lanatus</i> , <i>Echinochloa colonum</i> , <i>E. crus galli</i> , <i>Abutilon indicum</i> , <i>Eleusine compressa</i>
	Leaves, tender shoots	<i>Amaranthus gracillis</i> , <i>A. hybridus</i> , <i>A. spinosus</i> , <i>Chenopodium album</i> , <i>Boerhavia diffusa</i> , <i>Euphorbia cacodifolia</i> , <i>Moringa oleifera</i> , <i>Portulaca oleracea</i> , <i>Aloe barbadense</i>
	Fruits	<i>Grewia tenax</i> , <i>Zizyphus nummularia</i> , <i>Cordia gharaf</i> , <i>Coccinia grandis</i> , <i>Cucumis callosus</i> , <i>Momordica dioica</i> , <i>Salvadora oleoides</i> , <i>S. persica</i>
	Tubers	<i>Cyperus rotundus</i> , <i>C. bulbosus</i> , <i>Asparagus racemosus</i> , <i>Ceropegia bulbosa</i> , <i>Butea monosperma</i> , <i>Portulaca tuberosa</i>
Cold desert	Grain	<i>Fagopyrum esculentum</i> , <i>F. tataricum</i>
	Leaves	<i>Allium leptophyllum</i> , <i>Aconitum heterophyllum</i> , <i>Cicer songarium</i> , <i>Polygonum viviparum</i> , <i>Sedum tibeticum</i> , <i>Scorzonera mollis</i>
Semi-arid region	Leaves	<i>Boerhaavia diffusa</i> , <i>Bryonia lacimosa</i> , <i>Triumfetta rhombifolia</i> , <i>Cocculus hirsutus</i> , <i>Amaranthus viridis</i> , <i>Leptadenia reticulata</i>
Saline areas	Fruit	<i>Salvadora oleoides</i> , <i>S. persica</i>
	Foliage	<i>Salicornia brachiata</i>
	Leaves	<i>Chenopodium album</i> , <i>Portulaca oleracea</i> , <i>Trianthema portulacastrum</i>
Marshy lands/ flood areas	Vegetables	<i>Alternanthera sessilis</i> , <i>Hygrotoryza aristata</i> , <i>Monochoria hastata</i>

Species prioritization

There is an increasing need to broaden the range of plant species for the diversification of Agriculture. A massive untapped potential of species exists for meeting the needs for food, fodder, feed, fibre, energy and industrial products. The prospects of these species to become agricultural crops vastly differ due to several factors. The cost of domesticating and bringing a new species into agriculture, horticulture or forestry is very high and the time required is many years. The change of environmental conditions poses problems and, therefore, an environment similar to the natural one should be selected for initial evaluation to understand the potential of the crop. The new crop has to find a place in the existing or modified cropping system or a place in an area not presently used. It should be sufficiently commercially attractive by

justifying a change. Quality of the produce, marketability, profitability and people's preference are also important considerations. Keeping in view the various factors, a few plants with a good promise for commercial exploitation have been selected for undertaking intensified research efforts under the All India Coordinated Research Project on underutilized plants. These species requiring priority attention are listed in Table 3.

Table 3 : Underutilized plants needing priority attention

Crops/species	Usage	Adaptation/Areas of cultivation
A. First Priority Crops		
Amaranth (<i>Amaranthus</i> spp.)	Grains, leafy vegetable	Northern hills, north and south Indian Plains.
Buckwheat (<i>Fagopyrum</i> spp.)	Grains, leafy vegetable	Temperate Himalayan region, southern India hills
Rice bean (<i>Vigna umbellata</i>)	Pulse, fodder	Hot humid climates, sub-tropical Hilly regions
Winged bean (<i>Psophocarpus tetragonolobus</i>)	Pulse, vegetable, fodder, edible roots	Sub humid tropical parts of north-eastern region, central/ eastern peninsular region
Faba bean (<i>Vicia faba</i>)	Pulse, vegetable, fodder	Eastern, northern and penninsular India.
Tumba (<i>Citrullus colocynthis</i>)	Seed oil for industrial use; pulp of roots used in medicine	Warm arid and sandy tracts of north-west, central and southern India.
Jatropha (<i>Jatropha curcas</i>)	Seed oil used in oil mixtures; making soaps and candles	Marginal lands, gravelly sandy, clayey, eroded lands
Jajoba (<i>Simmondsia chinensis</i>)	Industrial oil, pharmaceuticals, cosmetics	Arid lands and coastal wasteland
B. Second Priority Crops		
Chenopod(<i>Cheno- podium</i> spp.)	Grains, leafy vegetable	Himalayan region
Adzuki bean (<i>Vigna angularis</i>)	Pulse, vegetable	Northern hilly region
Kankora (<i>Momordica dioica</i>)	Vegetable	Central India
Guayule (<i>Parthenium argentatum</i>)	Good source of rubber	Arid lands
Paradise tree (<i>Simarouba glauca</i>)	Edible oil	Central, Eastern India
Cuphea (<i>Cuphea</i> spp.)	Industrial oil	North and north-eastern hills
Subabool (<i>Leucaena leucocephala</i>)	Fodder, fuel wood	Arid and semi-arid regions
Saltbush (<i>Atriplex</i> spp.)	Fodder	Arid situations, salt affected lands

Table 3 Contd.

Crops/species	Usage	Adaptation/Areas of cultivation
Casuarina (<i>Casuarina</i> spp.)	Fuelwood	Coastal wastelands
Bamboo	Cottage, paper industry, fuelwood, vegetable	North-eastern region, western ghats
C. Third Priority Crops		
Bambara groundnut (<i>Vigna subterranea</i>)	Grains rich source of carbohydrate and lysine	Dry arid tracts
Forage groundnut (<i>Arachis glabrata</i>)	Green fodder, silage, leaf meal pellets	Rangelands in humid tropics and sub-tropics
Vegetable wild rice (<i>Zizania caduciflora</i>)	Fodder	Marshy lands, swampy, Waterlogged areas
Euphorbia (<i>Euphorbia</i> spp.)	Source of hydrocarbons	Sandy and rocky soils in arid regions

Present status of research on Underutilized Plants

The research activities on various aspects of different underutilized plants are underway at several Institutions including the State Agricultural Universities, the Research Institutes under the Indian Council of Agricultural Research (ICAR) and the Council of Scientific and Industrial Research (CSIR) as well as the voluntary organisations. The All India Coordinated Research Project on underutilized and underexploited plants with its headquarters at the National Bureau of Plant Genetic Resources (NBPGR) and 25 centres including the cooperating centres in different agro-climatic zones of the country, coordinates the programme. A brief account of germplasm collection, evaluation, utilization and conservation relating to this group of plants is given here.

Germplasm acquisition

The germplasm building efforts are being made consistently through plant explorations for collecting the diversity available in particular crops in different parts of the country. The NBPGR organises periodic crop specific and multi-crop explorations. Sizeable germplasm has been collected in a few selected species mostly through multi-crop explorations. Five crop-specific explorations were conducted during the last decade and over 1000 accessions of amaranth were collected from Himachal Pradesh,

Uttar Pradesh, Gujarat and eastern Maharashtra. However, it is felt that in multi-crop explorations, underutilized plants do not get the required emphasis and, therefore, there is a great need to conduct more crop-specific explorations for these crops to enrich the germplasm assemblage.

Useful germplasm is also introduced from different countries through the National Bureau of Plant Genetic Resources, New Delhi which maintains exchange links with about 70 countries of the world. The information on the source data etc. of the introductions made is regularly published in the Plant Introduction Reporters brought out quarterly. Crop inventories highlighting information on introduced materials have also been published by the NBPGR for different crops namely, winged bean and jojoba.

Table 4 : Germplasm assembled and evaluated in important under-utilized crops

Crop	No. of accessions	Source country
Amaranths	4100	India, Nepal, Malawi, Zambia, Poland, Taiwan, USA
Buckwheat	331	India, USSR
Chenopods	92	India, Poland, USA, Italy, Hungary, USSR
Rice bean	500	Nepal, China, India, Indonesia, Brazil, Nigeria
Winged bean	321	India, Ghana, Papua, New Guinea, Nigeria, Indonesia, Philippines, USA, Thailand, Sri Lanka
Faba bean	700	West Germany, Syria, USA, UK
Adzuki bean	70	Japan, USA, India
Bambara groundnut	192	Nigeria, India, Australia, UK, USA
<i>Leucaena</i>	574	Philippines, Australia, USA, Syria
<i>Casuarina</i>	65	Philippines, Australia, Tanzania
Bamboo	45	India
Guayule	80	USA, Mexico
Jojoba	75	USA, Israel, UK, Mexico
<i>Jatropha</i>	16	India, Brazil
Tumba	190	USA, India
<i>Cuphea</i>	30	USA, Germany
<i>Euphorbia</i>	56	USSR, USA, Philippines

Information on the total germplasm assembled through plant explorations within the country and the introductions from abroad alongwith source countries, is given in Table 4.

Genetic diversity and its utilization

Systematic evaluation and characterisation of indigenous and introduced materials have been done at the Bureau's headquarters, its regional stations and other centres involved in work on underutilized plants. Based on the evaluation carried out and the data recorded on various characters, crop catalogues were prepared for amaranth and winged bean and are in process for other crops. Promising accessions with specific desirable traits have been earmarked for use in the breeding programmes. Native and introduced germplasm variability has been successfully utilized in developing improved varieties through selection in a few selected species. The varieties released or identified for release and other strains identified promising are listed in Table 5.

Table 5 : Promising varieties released/identified in selected underutilized crops

Crop	Variety	Year of release/ identification	Eco- nomic product	yield potential (q/ha)	Areas for which recommended
Grain amaranth	Annapurna	1984	Grain	22.50	North-west hill region
	GA-1	1991	Grain	25.00	Gujarat, Maharashtra
Buckwheat	Himpriya	1991	Grain	15.0	High altitude regions
	VL 7	1991	Grain	10.0	Mid-hills of Uttar Pradesh
Winged bean	AKWB-1	1991	Green pods	105.0	All winged bean growing areas
Rice bean	RBL-1	1986	Grain	15.0	Punjab State
	RBL-6	1991	Grain	18.0	North and North-eastern region
Guayule	Arizona-2	1986	Rubber	13.50	Arid and semi-arid regions
	HG 8	1991	Rubber	15.00	Arid and semi arid regions
Jojoba	EC 33198	1986	Oil	5.00	Arid regions and coastal areas

Information on available genetic diversity and its utilization in respect of a few important crops is briefly enumerated below :

I. FOOD PLANTS

Grain amaranth (*Amaranthus* spp.)

Evaluation of germplasm (2610 accessions) for 40 descriptors at NBPGR Regional Station at Shimla revealed a wide genetic variation for the production traits. Plant height, inflorescence length, 1000 grain weight, protein content and grain yield showed high coefficient of variability, heritability and genetic advance which suggested that these could be effectively used in the improvement programme. Distribution pattern of three main grain species suggested that there was a basic difference in their physiological adaptation. Some accessions of *Amaranthus caudatus* from chauhar valley in Himachal Pradesh had 150 cm long dropping inflorescence (Paroda and Joshi, 1990). Compared to landraces from Himachal Pradesh, those from the Uttar Pradesh hills were taller and higher yielding. Collections from the north eastern hills were less tall, stout and late maturing. Pink seeded types were confined to higher hills. A total of 852 accessions were evaluated at NBPGR Regional Station, Akola and a wide variation was observed for different characters.

Hybridization work carried out at the National Botanical Research Institute, Lucknow revealed that intraspecific crosses between Indian and Mexican accessions of *A. cruentus* succeeded easily in both directions. However, interspecific crosses between *A. cruentus* and *A. hypochondriacus* succeeded only with *A. cruentus* as female parent. Close genetic homology of *A. retroflexus*, a weedy species, with cultivated species opened the possibilities of combining adaptability to cold and dry conditions of *A. retroflexus* with edible seed features of *A. cruentus*.

Based on multi-locational trials, selection IC 42258-1 was identified the best and released as 'Annapurna' for cultivation in the hill region. This variety possesses 15 per cent protein, drought tolerance and wider adaptability and is capable of producing 22.5 q/ha grain yield. Recently, another variety GA1 with long inflorescence, bold grains and high yield potential of 25.0 q/ha has been released for cultivation in Gujarat and Maharashtra states. Two other accessions IC 5564 and an exotic introduction of *A. edulis* from Taiwan were observed to be promising.

Buckwheat (*Fagopyrum* spp.)

Germplasm comprising 408 accession belonging to six species, namely, *F. esculentum*, *F. tataricum*, *F. cymosum*, *F. emarginatum*, *F. himalayanum* and *F. giganticum* were evaluated for 31 descriptors at NBPGR Regional station, Shimla and the information has been catalogued. The germplasm showed a wide range of variation for different agromorphological traits and promising types possessing specific desirable traits particularly early maturity (75-85 days), short height (65-85 cm), bold grains (3.8-5.0 g/100) and high seed yield (15-20g/plant) were identified for further use (Joshi and Paroda, 1991).

Evaluation of 19 accessions for fodder production at K.D. Farm, Srinagar revealed a good degree of variation in plant height (20.8-86.6 cm), number of leaves per plant (122-125) and green fodder yield (65.6-3432 q/ha) (Arora and Engels, 1992).

Concerted selection programmes at NBPGR Regional Station, Shimla and Vivekanand Parvatiya Krishi Anushandhan Shala, Almora and multi-locational testing of promising types under the auspices of All India Coordinated Project on Underutilized crops resulted in the release of variety 'Himpriya' for high altitude regions and VL7 for mid-hills of Uttar Pradesh.

Chenopod (*Chenopodium* spp.)

Eighty four germplasm accessions were evaluated for 12 characters at NBPGR Regional Station, Shimla. There was a wide variability in plant height, flowering and maturity period, leaf size, inflorescence size, seed size and grain yield. An accession NC 58613 was identified as the most promising. Promising types were identified based on multi-locational trials which included BDJ 476, BDJ 480, CH/LKW 10, CH/LKW 49. Tall growing strains of *Chenopodium album*, namely BDJ 171, BDJ 285, and BD 519 from hill region showed excellent growth under water stress situations in the northern plains. This offered a good scope for their exploitation as fodder types during the lean period of summer (May-June). Further studies for their use as fodder are underway.

Evaluation of 9 entries of *C. album* during 1991 revealed a good degree of variation for days to flowering (51-65 days), days to maturity (95-125 days), plant height (71.6-146.3 cm), clusters per

plant (13.5-24.2) and grain yield (5.8-16.0 q/ha). The range of variation in *C. quinova* entries was 58-148 days for flowering 34-297 cm per plant height, 0.58-4.06 cm for stem thickness, 8.3-39.0 for spikes per plant, 19.0-60.1 cm for spike length and 3.16-6.87 q/ha for grain yield (AICRP, 1992).

The analysis conducted at the National Botanical Institute (NBRI), Lucknow revealed that protein and amino acid present in a new species of *Chenopodium* collected from eastern Himalaya was comparable to that of *C. album* and *C. quinova* (M. Pal, personal communication). Analysis of foliage of 10 different species of *Chenopodium* at NBRI, Lucknow exhibited a wide variation for protein (26.0-64.0 g/kg), carotenoid (78.0-190.0 mg/kg), vitamins (0.5-2.4 g/kg), nitrate (2.6-5.0 g/kg) and oxalate (9.0-39.0 g/kg).

Rice bean (*Vigna umbellata*)

Over 500 accessions from north-eastern, central and east peninsular regions as well as introduced from other countries were evaluated at the NBPGR Regional Station, Shimla. The analysis of inter-regional diversity patterns for agro-morphological traits, biochemical constituents and disease and pest screening indicated a rich diversity in Indian germplasm. Cultivated forms are erect/semi-erect. Tendrillous types also occur in its region of distribution in Asia and Southeast Asia. Mainly intermediate forms are found in India. Considerable genetic polymorphism was observed for pod shape, size and colour. Several accessions with black, purple, red, violet, greenish, yellowish or mottled seeds were observed. Biochemical studies revealed its nutritional richness with high protein, calcium, iron and phosphorus along with comparatively high tryptophan and methionine.

Hybridization between an early variety from China, a bold seeded variety from Mysore and a yellow seeded variety from Nepal led to the development of several promising lines combining earliness and high yield. A promising selection C X M₁₂ P₂₋₃ capable of giving upto 25 q/ha grain yield under Shimla conditions holds good promise for cultivation in the hills. Variety RBL-1 has been developed at Punjab Agricultural University, Ludhiana, and has been released for cultivation in Punjab state. Another variety 'RBL6' with grain yield potential of 18 q/ha was released in 1991 for cultivation in north and north-eastern region. Mutation breeding

involving an indeterminate landrace treated with 100 Kr gamma rays resulted in the production of an early, photo insensitive and determinate mutant (Singh and Tomar, 1989).

In multi-locational experiments conducted under the auspices of All India Coordinated Research Project on Underutilized crops, rice bean cultivars showed a grain yield range of 6-15 q/ha at hilly locations and 10-21 q/ha at different locations in the plains (AICRP, 1992). The crop has produced 200-220 q/ha green fodder after 70-80 days and is capable of giving upto 350 q/ha, if harvested after 120-130 days (Chandel *et al.*, 1988).

Winged bean (*Psophocarpus tetragonolobus*)

Rich genetic diversity was observed in the germplasm assembled from various sources and most of the agro-morphological traits exhibited polymorphism. Majority of the accessions were tall, viny and tendrillar which were vigorous in growth and biomass production. The accessions from India had condensed internodes and were less vigorous compared to exotic strains from Indonesia. Some strains flowered in 60 days but majority were late, taking 140 days for flowering. Indonesian types were better in pod and seed characters. The information on different aspects is well documented (Chandel *et al.*, 1984).

Promising strains were tested in multilocal trials and four selections namely, EC 38821, EC 38821B, EC 38955 and IHR-13 a yield level of 105 q/ha for green pods has been released for cultivation as a vegetable type in the winged growing areas in the country. A few introductions viz., Blue course (EC 27884), Blue Fine (EC 28854) both from Ghana, Molk (EC 38855) for Papua New Guinea and EC 116886 and EC 121818 appeared promising in grain yield. Promising early types included EC 121296 from Nigeria and EC 37755A, EC 38823A, EC 38825 and EC 27886A from Papua New Guinea. Mutation breeding programme at the University of Agricultural Sciences, Bangalore resulted in the development of promising mutants with bushy, dwarf, determinate/semi-erect growth habit and early maturity (Shivshankar, 1982; Veeresh, 1986; Savithramma, 1987).

Faba bean (*Vicia faba*)

Evaluation of 607 germplasm accessions at NBPGR, New Delhi revealed wide variability in pod size, seed size and seed colour. Evaluation studies at Haryana Agricultural University, Hisar (Chhabra, 1983) indicated a good degree of variation for flowering time (68-94 days), maturity period (121-188 days), plant height (44.1-100 cm), branches per plant (1-6), internode length (1.4-4.0 cm), clusters per plant (4.0-46.3), pods per plant (4.7-73.6), seeds per pod (2.0-3.0), 100 seed weight (18.3-78.9 g), and seed yield per plant (2.4-49.8 g). Significant differences among genotypes were observed for seed yield, harvest index, 100 seed weight and seed protein both under water-stress (rainfed) and non-stress (irrigated) conditions.

A high yielding selection VH 82-1 possessing indeterminate growth habit, medium bold seeds, high yield potential (25-35 q/ha) and maturity duration of 155-160 days has been identified promising (Akbar *et al.*, 1992). Other promising types include HB 24, HB 123, HB 180 and HB 186.

Adzuki bean (*Vigna angularis*)

Thirty one accession were evaluated at NBPGR Regional station, Shimla and a wide range of variation was observed for plant height (25-49 cm), branches per plant (3-8), clusters per plant (6-10), pods per cluster (3-5), pods per plant (11-30), pod length (6-10 cm), seeds per pod (6-9) and seed yield per plant (9-16 g).

Systematic screening resulted in identification of EC 108080, IC 15256 and EC 120460 giving high seed yields with higher mean values for pods per plant, pod length and seeds per pod. EC 108080, EC 120460 and EC 241041 appeared promising in northeastern hill region, while HPABT, HPAB 9 and HPAB 21 showed better performance in Uttar Pradesh and HPU 51 in Himachal Pradesh. A selection VL Gruns 5 was also observed promising.

Bambara groundnut (*Vigna subterranea*)

Germplasm comprising 30 accessions was evaluated at NBPGR Regional Station and a good degree of variation was observed in pod size, seed size and grain yield. Testing of 12 promising accessions revealed that EC 134511, EC 37527 and EC 27881 were high yielding types.

II. FODDER PLANTS

Forage groundnut (*Arachis glabrata*)

Studies conducted at the Indian Grassland and Fodder Research Institute, Jhansi indicated that this species which surpasses the growth of perennial weeds like *Parthenium*, *Saccharum* and *Desmostachya* is capable of producing upto 950 q/ha green fodder in six cuts, in a year. Another species *Arachis hagenbeckii* showed better yield potential and persistancy. Animal feeding of *A. glabrata* forage indicated the absence of anti-nutritional factors.

Vegetable wild rice (*Zizania caduciflora*)

Trial plantations of this species at the University of Agricultural Sciences, Bangalore indicated its good adaptability yielding 436 q/ha green fodder in four cuts in a year. Exploratory studies conducted at NBPGR, New Delhi revealed its good establishment and very fast growth under water-logged conditions. Further studies need to be conducted to assess the yield potential of this species.

Leucaena (*Leucaena leucocephala*)

Evaluation of 574 germplasm accessions indicated a wide range of variation for several traits. This species has been found to perform well in agro-forestry system. Hybridization involving Hawaiian Salvador and Peru types of *L. leucocephala* and *L. pulverulenta* has been attempted and promising types combining useful characters have been developed. K-8 (EC 124343) from Phillippines and El Salvador (EC 123866) from Australia proved superior for fodder and fuel in Gujarat and Kerala states. Silvi- 4 and K-28 were observed to be the best in above-ground biomass yield. In varietal trials at Urlikar, chan, FG7, FG32, FG24, K-8, EC 150183 and EC 123519 proved superiod.

Salt bush (*Atriplex* spp.)

Nine species, namely, *A. amnicola*, *A. bunburyana*, *A. cinerae*, *A. lentiformis*, *A. paludosa*, *A. undulata*, *A. nummularia*, *A. canescens* and *A. halimus* have established well in arid zones at Jodhpur. Accession EC 129766 of *A. nummularia*, EC 129767 of *A. halimus* and EC 129768 of *A. canescens* showed good performance under extreme arid situations. Fodder yield potential of these species

under saline-alkali soils needs to be determined through well planned experimentation.

***Casuarina* spp.**

Sixty five accessions of different species, viz., *Casuarina equisetifolia*, *C. cunninghumiana* and *C. cristata* have been evaluated at Mattupalayam (Tamil Nadu) for different growth traits. An accession of *C. equisetifolia* from Philippines was observed promising. Accession No. 13223 of *Alcocasuarina corniculata* with higher plant growth and basal diameter was identified promising. This species with short side branches and straight bole is desirable for agro-forestry. The studies conducted at the Central Soil Salinity Research Institute, Karnal revealed that *C. equisetifolia* showed 90-95% survival both in surface planting and channel planting methods under high salinity levels (Tomar and Gupta, 1985).

Bamboo

Germplasm comprising 36 accessions of 30 species belonging to 8 genera, *Arundinacea* (2), *Bambusa* (16), *Cephalostachyum* (3), *Chimonobambusa* (3), *Phyllostachys* (2), *Pseudostachyum* (1), *Dendrocalamus* (8) and *Teinostachyum* (1) were established at Basar (Arunachal Pradesh). The widest diversity was observed in *Bambusa* (12 species and 4 morphotypes) followed by *Dendrocalamus* (6 species and 2 morphotypes). Initial screening of the established clumps indicated three distinct classes, viz., tall, less prolific; medium tall, medium prolific and short, highly prolific which could be put into three utility classes (i) pulping and timber (ii) handicraft making and (iii) live fencing, respectively.

Population behaviour of three species, *Bambusa tulda*, *B. pallida* and *Denodrocalamus hamiltonii* was studied at two locations (240 m and 690 m above msl). The vigour of all the three species was expressed better at the lower altitude. In *B. pallida*, ethral treated variants showed increased vigour and proficiency, while colchicine treatment affected dwarf and bushy appearance. Fifteen mutant selections are being further studied.

III. INDUSTRIAL PLANTS

Guayule (*Parthenium argentatum*)

Eighty accessions introduced from Mexico and the United States were evaluated for growth attributes and a wide range of

variation was observed for plant height, stem thickness, branching and biomass yield. Promising accessions were tested in multi-locational trials and Arizona-2, G-4, HG 8 and HG 9 were identified superior in biomass yield. EC 148913 and HG 9 were observed to be high rubber and resin producers. Based on multilocal trials over the years, HG 8 has been released for commercial exploitation as an additional source of rubber in the arid and semi-arid zones of the country.

Efforts were also made to hybridize guayule with other Parthenium species like *P. incanum*, *P. tomentosum* and *P. stramonium* and the hybrids with *P. tomentosum* and *P. stramonium* showed considerable promise (Patel *et al.*, 1986).

Jojoba (*Simmondsia chinensis*)

Evaluation of germplasm comprising 75 accessions revealed wide range of variation in growth and seed yield attributes. This plant species has been tried at several sites with variable edapho-climatic conditions and has been found successful on arid lands and coastal wastelands. Accession EC33198 from USA has been found promising and recommended for large scale cultivation. Three other accessions, namely, EC 124381, EC 99690 and EC 99691 were also observed promising. Breeding work at the NBPGR Regional station, Jodhpur revealed the possibility of developing early fruiting types. Agro-techniques for raising a good crop have been standardised. Propagation through cuttings has been perfected. Standardization of techniques for micropropagation through tissue culture is in progress at the NBPGR, New Delhi.

Plant height and plant spread were observed to be significantly correlated with seed yield, number of seeds per plant and 100 seed weight. Investigations were also conducted at the central salt and Marine chemicals Research Institute, Bhavnagar on physiological and biochemical characterisation of male and female plants to identify sex at an early stage. Important metabolic constituents i.e. nucleic acids, total proteins and carbohydrates were found accumulated more in female plants than males. Electrophoretic analysis of proteins showed difference in the banding pattern in male and female plants and specific bands were absent in males.

Jatropha curcas

A wide variation in plant height, branching, 100-seed weight and grain yield was observed in 16 accessions collected from

Banaskantha and Mehsana districts of north Gujarat. Good performing genotypes, both in small seeded and large seeded groups, were earmarked. Multi-locational testing revealed the superiority of Dantiwada bold, Patan local and S.K. Nagar local.

Tumba (*Citrullus colocynthis*)

Germplasm comprising 360 accessions were evaluated for seed yield and other characters at Mandore (Rajasthan) and considerably high range of variation was observed for seed yield, 1000 seed weight and seed weight per fruit, the top ranking genotypes being GP 285, GP 116 and GP 294, respectively. Interspecific hybridization was attempted involving different forms of *tumba* (*Citrullus colocynthis* and *Citrullus lanatus*) and the material has been advanced to F₄ and F₅-generations. Crosses were also attempted between GP3 and superior segregants to incorporate bold seeded, thin testa and high seed yield. Mutation breeding programme was also undertaken and the bulk seed harvested from F₃ generation of interspecific cross, *C. colocynthis* x *C. lanatus*, was irradiated with 30 and 50 kr. gamma rays. Single fruits were harvested on the basis phenotypic appearance of desirable traits for further studies.

***Cuphea* spp.**

Germplasm evaluation of 30 accessions belonging to different *Cuphea* species, namely *C. wrightii*, *C. lutea*, *C. painteri*, *C. procumbens* and *C. carthagenensis* revealed a wide variation for different traits. A few promising types were selected for further testing. These high seed yielding accessions were EC 133501, EC 133506, EC 133508, EC 258142 and EC 258150.

***Euphorbia* spp.**

Thirty seven accessions of *Euphorbia caducifolia* were evaluated at Sardar Krushinagar and the genotypes viz., Sabarmati-1, Vijapur, Keva-2 and Jesanpura were observed to be high dry matter producing types. Evaluation of 15 accessions of *E. tirucalli* revealed that Chandisor-1 was the best in growth performance. *E. antisiphilitica* which is a good source of candellila wax was observed to perform well under arid conditions at Jodhpur. Other species which could be exploited for hydrocarbon include *E. lathyrus*, *E. nerifolia*, *E. nivulea* and *E. trigona*.

Germplasm conservation

The National Bureau of Plant Genetic Resources, New Delhi maintains the valuable germplasm of different under-utilized and under-exploited plants at the Headquarters and its Regional Stations located in different agro-climatic zones of the country. Also, a few selected centres of the All India coordinated Research Project on under-utilized Plants have the responsibility for maintenance of germplasm of particular plant species. The germplasm holdings of important under-utilized crops at different centres are given in Table 6. The germplasm is presently being maintained through periodic rejuvenation. However, cold storage facilities are being developed at the crop based Institutes of the Indian council of Agricultural Research as well as the Regional Stations of the Bureau. For long term storage of base collections, five cold storage modules have been commissioned to maintain the germplasm at -20°C . Currently, over 1,40,000 accessions of different crops including the under-utilized plants are maintained in laminated alluminium foil packets in these modules. The construction of the new National Gene Bank building under the Indo-USAID project on Plant Genetic Resources already operative at the NBPGR is underway and with this facility, Bureau's capability for long term storage will increase to 600,000 accessions.

Future strategies

The need for reducing dependence on a few species, man's desire for novelty and new useful compounds, continued interest in increasing crop returns and reducing imports and surplus are some important consideration in the search for new useful crops. Such crops may also be important for new agricultural systems and for expanding the productive area into marginal regions where few known crops are in cultivation. Therefore, careful planning needs to be done towards the choice of proper species, their genetic improvement aimed at developing better varieties, standardization of cultivation practices, popularization and their proper utilization.

Concerted efforts to build-up the germplasm of prioritized species from indigenous and exotic sources need to be made. Crop specific exploration programmes need to be undertaken to collect the available diversity. Adaptability studies will help a great deal in finding out suitable agro-climatic conditions for different species. Standardization of package of practices for their efficient cultivation

Table 6 : Current germplasm holdings of important underutilized plants

Institution	Location	Crops	Accessions
ICAR Institutes			
National Bureau of Plant Genetic Resources	New Delhi	Amaranth	824
		Buckwheat	250
		Faba bean	220
		Guayule	23
NBPGR Regional Stations	Shimla	Amaranth	3133
		Buckwheat	543
		Chenopods	90
		Rice bean	340
		Adzuki bean	38
		Cuphea	30
	Jodhpur	Tumba	190
		Jojoba	33
		Bambara groundnut	50
		<i>Atriplex</i>	11
	Akola	Amaranth	1065
		Winged bean	242
		Faba bean	108
	Shillong	Ricebean	338
		Adzuki bean	48
Indian Grassland & Fodder Research, Institute	Trichur	Winged bean	153
	Jhansi	Leucaena	174
	Basar	Bamboo	36
State Agricultural Universities			
Gujarat Agricultural University	S.K. Nagar	Jatopha	16
		<i>Euphorbia</i>	56
Tamil Nadu Agricultural University	Mattupalayam	<i>Casuarina</i>	65
Rajasthan Agricultural University	Mandor	Tumba	154
Haryana Agricultural University	Hisar	Guayule	20

is also necessary. Well planned plant breeding efforts are also required to develop genetically superior strains for raising the level of productivity. Efforts are also required to be made to examine

the possibility of introduction of new crops into the existing cropping systems/land use systems. This would greatly help in promoting these crops as supplementary crops and not as substitute crops. For crops that produce raw materials for the industry, simultaneous arrangements for setting up required infra-structure for processing the products as well as their marketing need to be made. Many of these species, though economically important yet are less known and hence must be given due attention for their popularisation. Also appropriate research and development efforts are required to be made for their utilisation. The entire genetic diversity built-up is required to be maintained through appropriate long and short term conservation measures.

The All India coordinated Research Projected Unit maintains close linkage with National Bureau of Plant Genetic Resources and its Regional Stations, selected ICAR crop based Institutes, CSIR Institutes, State Agricultural Universities and other Govt. Departments for effective implementation of the programme on underutilized plants. There is an active interaction with other National Coordinated programmes on pulses, oilseeds, forage crops and agro-forestry which also deal with some under-utilized plants in respective groups. Such linkages need to be further strengthened to create an effective national network to undertake multi-disciplinary research efforts on underutilized plants of promise. Linkage also needs to be established with International centre on Underutilized crops, London (U.K.), International Board for Plant Genetic Resources, Rome (Italy) and other related International Organisations to give a boost to the Indian programme on this group of plants.

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OCCURRENCE AND DIVERSITY OF *CICER MICROPHYLLUM* BENTH. IN THE TRANS-HIMALAYAN COLD DESERT OF SPITI AND LAHAUL

K.P.S. Chandel

National Plant Tissue Culture Repository
NBPGR, New Delhi - 110 012

Wild species of genus Cicer are of considerable importance as they possess useful genes for morpho-agronomic attributes, quality traits, adaptation and also confer resistance to biotic/abiotic stresses. C. microphyllum is the only wild species of Cicer that occurs in the cold arid desert of Trans-Himalayan region. Germplasm collections of this species were made in the past and studies showed its usefulness and importance in the chickpea breeding/improvement programme. Ample scope exists for its utilization using biotechnology and molecular biology. A case for establishing a genetic reserve in Lari hills, Spiti Valley has been proposed to conserve biodiversity of this valuable species.

The survey and collection of wild *Cicer* species from their natural habitats has been emphasized to widen the genepool diversity (Vander Maesen, 1973). Paradoxically, due to ignorance or unconscious neglect, such resources have been lost or brought to the brink of extinction without getting an opportunity for detailed investigations. Often live plants become so rare that it is difficult to collect the seeds and live material from natural habitats. However, based on the herbarium specimens and well documented passport data, it is much easier for plant explorers to re-locate material of such wild species and this is true in case of *Cicer microphyllum* Benth. Comprehensive exploration strategy for capturing adequate germplasm diversity in India and adjacent region of Afghanistan has been considered very useful. Adequate genepool resources of the wild *Cicer* species are of immense value to chickpea breeders.

In Indian gene centre, apart from rich genetic diversity in cultivated species (*C. arietinum*), two wild species *C. songaricum* Steph. and *C. microphyllum* Benth. are enumerated in Indian Floras and Botanical accounts. *C. songaricum* Steph., a commonly cultivated species is listed in the Flora of India (Hooker, 1879) and also dealt in Flora of Ladakh, Western Tibet (Stewart, 1916-17). However, it appears that some taxonomic and nomenclatural confusion exists. *C. songaricum* Steph., ex. DC mentioned in the Indian Floras is really *C. microphyllum* Benth., the real *C. songaricum* Steph. is a native of Kazakhstan, Kirghizia and Tadzkistan of the erstwhile Soviet Russia (Vander Maesen, personal communication). According to recent taxonomic treatment. *C. microphyllum* is grouped under section III, *Polycicer* (non-spiny perennials) and is reported to be distributed in Himalaya, East Afghanistan, West Tibet, Pamir mountains (3000-5600 ft.) and generally comes under vegetation during June-August (Vander Maesen, 1972). This species was first collected from Lahaul Valley, opposite Keylong across the river and later from Zanscar Valley of Ladakh Himalaya. Interestingly in an extensive exploration trip undertaken in Spiti region of cold Himalayan desert (Fig. 1), the occurrence of *Cicer microphyllum* was recorded from Pin Valley, Lari hills, Tabo hills, Poh, Getta Tashigang hills and sporadically along the route from Lossar to Khoksar.

Occurrence of *C. microphyllum* Benth.

Lahaul and Spiti region lies in the east of Lahaul and Kullu at the extreme north-eastern portion of Himachal Pradesh between 31° 42'N and 33° and 76°E and 77° 75'E longitude. Trans-Himalayan cold desert lies adjoining Tibet at mean elevation of about 4,485 m above sea level. Spiti region constitutes a typical mountain desert with an annual precipitation of about 177 mm possessing bare rocky mountains from bottom to top except for a few locations. The topography is very rugged. Vegetation cover of the entire Spiti region is very sparse, yet due to dry climate, it is most varied and attractive. The ground vegetation, though usually sparse in Spiti valley yet in Bhar and Tud regions consisting of high altitude alpine regions (Getta hills, Lalung hills, Pin Valley etc.), rich vegetation cover is found. Amazing array of wild species such as *Agropyron*, *Medicago falcata*, *M. minima*, *Linum perenne*, *Bunium persicum*, *Carum bulbocastanum*, *Avena*, *Astragalus*, *Vicia*, *Cymbopogon jwarancusa*,

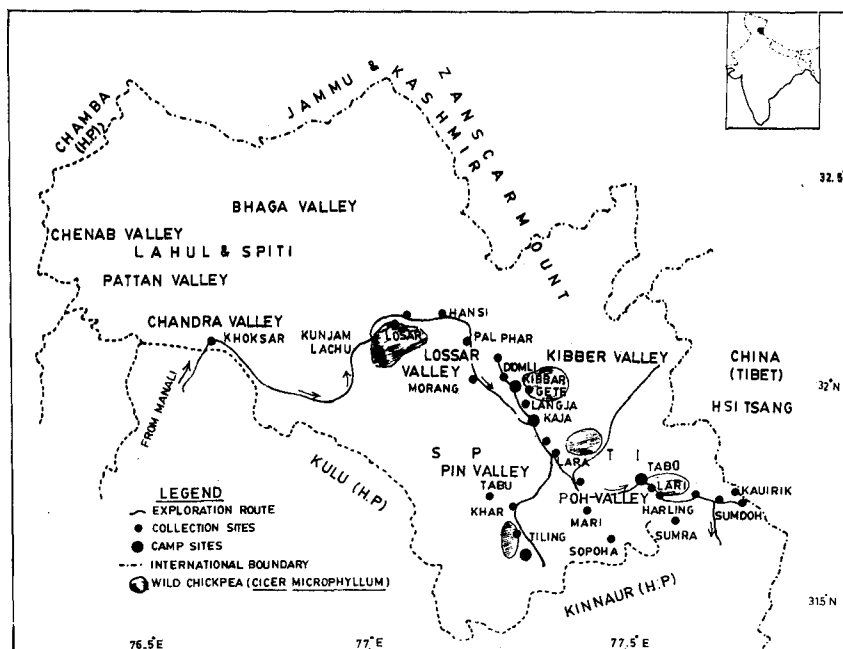


Fig. 1 : Distribution of *Cicer microphyllum* and sites of collection in Spiti Himalayas

Hyssopus officinale, *Fragaria indica* etc. occur in diverse locations. *C. microphyllum* is fairly wide spread in Spiti region in well isolated colonies often showing disjunct distribution. The occurrence of *C. microphyllum* was observed at several sites down the Rohtang pass on way to Kaza. However, in these sites only sporadic occurrence, much sparse and smaller plant populations occur. Interestingly at Lari hills extensive populations occur in the steep mountainous slopes facing westwards. These sites were explored in 1982, 1985 and in 1992 and fairly large population samples were collected. Earlier, this wild species was also located at Chhota Dara, Lossar, Poh, Gettle-Tashigang hills, Lari hills, Tabo hills and from Pin valley opposite Tangti hills. Samples comprised pods, herbarium specimens and photographs. Lari hills slopes are very steep, stony

with loose soil and generally being devoid of surface moisture. In this natural habitat, perennial, luxuriant tufted bushes occur ranging from 0.5-0.8m in diameter; the plant populations are evenly distributed over an area covering almost one km long mountainous range. Plants are found to grow well on a range of well drained soils, usually allowing its thick long perennial tap roots to penetrate deep down the hilly soils to survive on receding moisture after glaciers have melted down. The soil pH generally ranged between 7.0-7.5 and species preferred open hill slopes exposed to intense sunlight. Flowering and fruiting commences early in light dry soils (Lari hills) than a slightly heavy soils (Gette hills) and on slopes exposed to intense solar radiation. At Lari, Tabo and Poh hills, high seed setting was observed, while at Gette hills, although flowering and fruiting appeared to be normal yet most of the pods were either empty or had low seed setting.

In Lahaul-Spiti regions, both high mountainous and valleys receive a heavy snowfall and most of the area remains covered with deep snow several meters until mid April/May, when snow starts melting on hill slopes due to intense solar heat. At this stage, seeds which have remained buried under deep snow under ultra freezing temperature (-20° to -35°C) and have received sufficient freezing treatment, start germinating. Besides, the deep, woody tap roots of the previous stands remain embedded in the rocky slopes. The dormant shoots under deep snow, start sprouting only at the fall of spring. Similar observations were made by vander Maesen (1979). According to him perennial *Cicer* species grow at higher altitudes (900-1800m) in rubble slopes, under dry conditions with reasonable humidity. They are subjected to severe cold in winter and aerial parts die off. The following spring, woody tap roots often penetrating deep into the crevices give rise to new shoots. Normally in Spiti region during this period, days are fairly long, while temperature is low initially. In general, long days induce early flowering and short days delay flowering. During the flowering period (July-August), the average minimum and maximum temperatures are $10-18^{\circ}\text{C}$ and $20-35^{\circ}\text{C}$ respectively depending upon the altitudes, location and sunshine. Under such ecological sites, wild *Cicer* grows well during the dry spring-summer season (May-August) and generally survives on residual moisture. The fruiting was observed to be exceptionally high at several locations, yet ripening was slightly delayed in Pin

valley as well as Gette-Tashigang hills. The details of collections are given Table 1.

Table 1 : Collection of wild *C. microphyllum* in Spiti Himalayas

Collector's number	National collection No.	Place/site of collection	Altitude (m)
C-457	NC 60734	Lari hills	3300-4200
C-520	NC 60735	Gette hills	4350-4500
C-556	NC 60736	Pin Valley (Tangti hills)	3750-4200
C-501	NC 60737	Lossar hills	4050-4200

Taxonomical description

C. microphyllum Benth., unlike the cultivated chickpea (*C. arietinum* L.) is truly wild, perennial species, usually erect or procumbent in habit, often tufted due to excessive grazing by wild blue sheeps. Stem, thin woody, wiry, sub-glabarous about 30-40 cm. in height. Branches, 4-10; leaves, 7.5-9.0 cm. long, alternate, imparipinnate; leaflets, 6.8 × 0.5 cm., in 10-12 pairs growing gradually smaller upward, strongly veined, serrate margins; bracts prominent; inflorescence, axillary raceme, pedicellate; pedicel 5.0-6.0 cm long. Flower, purplish; calyx, green, 5, gamosepalous, persistent; corolla, light blue or purplish, petals, 5, gamopetalous, 1.5-2.0 cm long; stamens 10 (9+1), diadelphous condition; anthers yellow. Pods usually one, occasionally two, 2.5-3.5 cm long, linear, oblong, slightly curved, cuneate, densely pubescent; hairs fine, whitish; seeds, usually 4-6, small, brownish black, mottled and mature during August depending upon the site, slopes and its location. Profuse fruiting occurs in the natural habitats and pod shattering is usually very violent with spiral twisting of pod valves. This process confirms the presence of strong parchment layer, which in naturally occurring wild species, enables the seeds to disperse far apart. Coiling of pod valves helps to retain one or two seeds within the coil that ensures safe seed dispersal beneath the bushes thus allowing potential natural mechanism for survival, perpetuation and evolution.

Genetic diversity

Variations occur for plant type in different agroecological and microniches. Pod size and number of seeds per pod also vary considerably. The pod size range from 2.5 to 3.5 cm, while number of seeds per pod varied from 4-6 (Fig. 2). Inter and intra-population variations also occur presumably due to spatial and temporal differences. Isolation and local environmental factors also contribute significantly. Young unripe seeds of *C. microphyllum* are usually collected by tribal inhabitants for consumption. The lush green foliage, a bit sticky and with mild saltish taste is relished by wild blue sheep as well as domesticated goats and sheep. These animals easily climb the tenaceous alpine slopes for grazing. Plants are also cut at ground level during August-September and are sun-dried as hay for cattle feed. The detailed analytical studies (Chandel *et al.*, 1987) showed that seeds and herbage both are fairly nutritious. In *C. microphyllum*, crude protein varied from 9.27 to 13.30 per cent in forage (Table 2), while it ranged in seeds from 24.1 to 25.6 per cent. The seed protein content of the two accessions analysed were relatively high. N.C. 60734 contained 25.6 per cent crude protein while N.C. 60734 possessed 24.1 per cent (Table 2).

Table 2 : Chemical constituents of *C. microphyllum*

Accession number	Material	Crude protein (%)	Acid detergent fibre (%)	Neutral detergent fibre (%)	<i>In vitro</i> -dry matter digestibility (%)	Calcium (%)	Phosphorus (%)
C-967	Dried	9.27	36.40	47.20	69.79	3.50	0.43
C-1067	leaves	13.30	40.20	54.00	65.44	2.40	0.23

The nutrient status of wild chickpea compares well with that of the cultivated species. The leaves are also rich in protein and carbohydrate and appears to have good potential as forage species in cold desert regions of Himalayas (Chandel, 1992).

Utilization prospects

The wild *Cicer* species can play an important role in the improvement of chickpea. Interspecific hybridization could be of particular importance, which assumes much greater significance today with the emergence of new techniques of biotechnology and

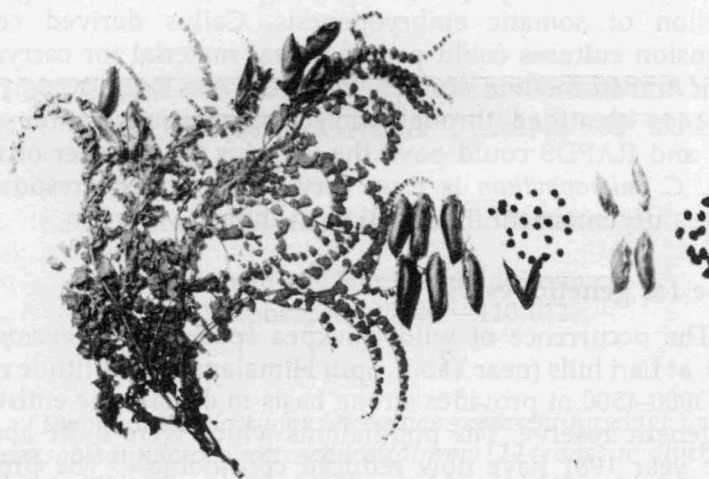


Fig. 2 : Plant type in *Cicer microphyllum*; Pods and seeds separately shown

genetic engineering. Embryo rescue, somaclonal variation, protoplast fusion (somatic hybridization) and recombinant DNA technology can be profitably integrated with conventional chickpea breeding programme. *C. microphyllum* could be of special interest in breeding, as it appears to possess high tolerance to drought and cold (frost). The genes available for long poddedness and high number of seeds per pod, could enhance productivity of chickpea cultivars. The screening for resistance for pod weevil and bruchids could be of interest in chickpea breeding. Vander Maesen (1973) reported that *C. microphyllum* and *C. pinnatifidum* have been used for hybridization in India, Pakistan and Israel. It is also indicated that there is lack of information on disease resistance in most of wild species of *Cicer*. Yet, high degree of drought tolerance and cold hardiness found in *C. microphyllum* could be profitably utilized. Hence, genetic resources of this wild species offer good prospects in chickpea improvement. The seed dormancy developed during the course of long evolutionary history of this wild species require intensive physiological and biochemical investigations to enable its full utilization. Seeds require breaking of dormancy which imposes hard seededness and non germinability. This could be overcome by seed scarification and stratification at low temperature (0-4°C) for atleast 30-60 days. Both partially and fully mature seeds and embryos can be used for *in vitro* studies. The regeneration could

be achieved directly or through organogenesis leading to the induction of somatic embryogenesis. Callus derived cell and suspension cultures could provide ideal material for carrying out genetic transformation studies. Once this has been accomplished, the genes identified through molecular characterization such as RFLP and RAPDS could pave the way for the transfer of nuclear genes. *C. microphyllum* is thus very precious gene resource and requires urgent scientific attention in India.

A case for genetic reserve

The occurrence of wild chickpea species *Cicer microphyllum* Benth. at Lari hills (near Tabo), Spiti Himalaya at an altitude ranging from 3000-4500 m provides strong basis to declare the entire range as a genetic reserve. The populations which were quite abundant in the year 1981 have now reduced considerably. The protective measures are required not only to halt the genetic erosion in the wild occurring populations but also to allow the process of evolution to continue unaltered. Lari hills perhaps provides the unique microniches for this potential wild species likely to be of considerable importance in the future. Thus, it requires adequate measures for its protection. Department of Environment in collaboration with Himachal Pradesh can jointly work out the plan for making Lari hills as the genetic reserve for *C. microphyllum*. This will lead toward successful implementation of biodiversity conservation programme.

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COLLECTING WILD SUNFLOWER GERMPLASM FROM THE CENTRAL GREAT PLAINS OF U.S.A.

S.S. Duhoon, G.J. Seiler¹ and R. Marinkovic²

National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi - 110 012

One hundred forty-four accessions representing eight wild species of sunflower were collected from 124 sites in diverse habitats of the Central Great Plains of United States of America during September, 1991. A wide range of in-situ variability was observed for various morphological and economic characters including stress tolerance. The populations of H. annuus were observed to be highly variable and widely distributed in different habitats in the seven states surveyed. Helianthus pumilus which has low variability and limited distribution, was represented by only one sample in Colorado. Helianthus petiolaris ssp. petiolaris, the only source species of cytoplasmic male sterility was found, widely distributed and along sandy roadsides of highways. Helianthus pauciflorus ssp. subrhomboides, H. nuttallii, H. grosseserratus and H. tuberosus were sparsely distributed in some specific habitats. Other species such as H. hirsutus, H. salicifolius and H. pauciflorus ssp. pauciflorus occur in this area but were not collected due to immature stage of seed growth.

The sunflower (*Helianthus annuus* L.) was first domesticated in the central parts of United States (Sindagi and Virupakashappa, 1986). The Central Great Plains of USA are still the centre of diversification of several wild species of sunflower (Rogers *et al.*, 1982). The wild species are important sources of genes for resistance to various abiotic and biotic stresses including major pests and

1. Research Botanist, USDA-ARS, Northern Crop Science Laboratory, P.O. Box 5677, Fargo, North Dakota, USA-58105

2. Sunflower Breeder, Institute of Field and Vegetable Crops, M. Gorkog 30, 2100 Novi Sad, Yugoslavia

diseases, the main causes of instability in crop production. Some wild species are also donors for other useful characters like dwarfness and male sterility, the essential prerequisites for heterosis breeding which is now emphasized for further increase in productivity. Many wild species are either not available or are under-represented in the National Germplasm System to reasonably match the potential genetic diversity available. Therefore, these valuable raw materials for plant breeders deserved to be collected and conserved before their erosion due to the destruction of habitat by men and animals. Accordingly, a joint exploration, sponsored by INDO-US PGR Project was undertaken by a team consisting of scientists from National Bureau of Plant Genetic Resources, India, United States Department of Agriculture, Agricultural Research Service and Institute of Field and Vegetable Crops, Yugoslavia to increase genetic diversity of the wild sunflower species from 7 states in Central Great Plains of USA. The results of the exploration are reported in this paper.

MATERIALS AND METHODS

The states of Montana, Wyoming, Nebraska, Colorado, Kansas, North and South Dakota, comprising the Central Great Plains of USA, were explored from 4 to 18 September, 1991, covering a distance of about 7400 km. The area explored lies between 38° to 49° North latitude and 94° to 144° West longitude (Fig. 1). The sandy, sandy-loam, clay, clay loam, stony and gravelly soils of black, grey, brownish to yellowish colours were observed in this region. The seed samples of 144 randomly selected populations representing various species were collected from 124 sites in different habitats ranging from dry sand dunes, marshy lands, roadside ditches, cultivated fields, waste/pasture lands, river beds, sandy and stony hills. Depending on the population size, 25 to 65 randomly selected plants were sampled in each population to record *in-situ* variability for plant height, number of branches, branching pattern, number of heads per plant, head size, head-clipper damage and incidence of rust alongwith other distinct morphological characters. One head each was collected to obtain additional seeds from the sampled population for further *ex-situ* studies. Common collector's numbers were assigned to each sample to facilitate easy retrieval and independent assignment of plant introduction (PI) (USA), Exotic Collection (EC) (India) and Introduction (I) (Yugoslavia) numbers for conservation and utilization in respective countries.

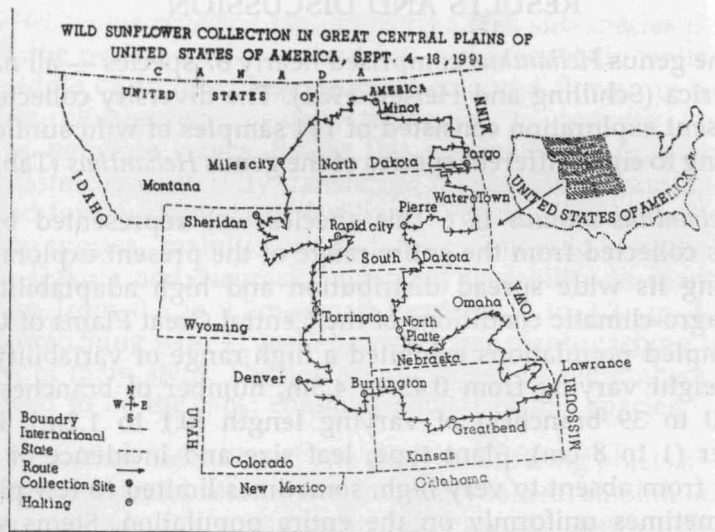


Fig. 1. Route followed and area explored for collection of wild sunflower germplasm.

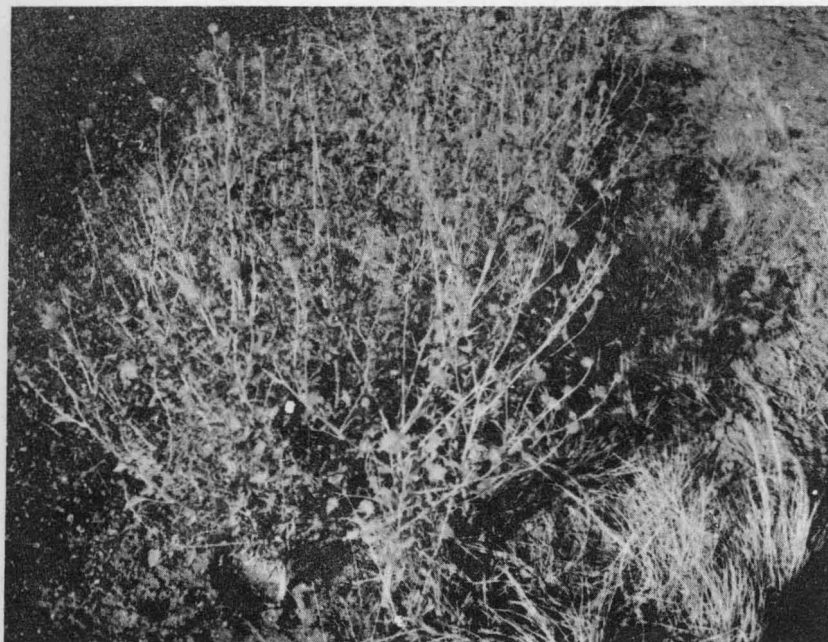


Fig. 2. *Helianthus petiolaris* ssp. *petiolaris* — growing in wild habitat near turtle lake, North Dakota.

RESULTS AND DISCUSSION

The genus *Helianthus* comprised nearly 67 species — all native to America (Schilling and Heiser, 1981). The diversity collected in the present exploration consisted of 144 samples of wild sunflower belonging to eight different species of the genus *Helianthus* (Table 1).

Helianthus annuus L. : This species was represented by 83 samples collected from the entire range of the present exploration, indicating its wide spread distribution and high adaptability to varied agro-climatic conditions of the Central Great Plains of USA. The sampled populations exhibited a high range of variability for plant height varying from 0.45 to 4.5m, number of branches per plant (0 to 39 branches) of varying length (0.1 to 1.2m), head diameter (1 to 8 cm), plant type, leaf size and incidence of rust varying from absent to very high, sometimes limited to few plants and sometimes uniformly on the entire population. Stems were covered with varying densities of bristly hairs. This species was observed to be the most diverse geographically, morphologically and habitat wise.

Table 1 : Diversity in wild species of sunflower from Central Great Plains of USA

Species	Number of collections
<i>Helianthus annuus</i> L.	83
<i>H. petiolaris</i> Nutt. ssp. <i>petiolaris</i>	25
<i>H. maximiliani</i> Schrad.	15
<i>H. pauciflorus</i> Nutt. ssp. <i>subrhomboides</i> (Rydb) Spring & E. Schilling	8
<i>H. nuttallii</i> T. & G. ssp. <i>nuttallii</i>	4
<i>H. nuttallii</i> T. & G. ssp. <i>rydbergii</i> (Britt.) Liong	3
<i>H. grosseserratus</i> Martens	3
<i>H. tuberosus</i> L.	2
<i>H. pumilus</i> Nutt.	1
Total	144

Helianthus petiolaris ssp. *petiolaris* : This sub-species is usually called the prairie sunflower and has a characteristic white spot in the middle of an otherwise purplish coloured flowering head and shining bluish-green ovately triangular to broadly lanceolate shaped petiolate leaves. So far this species is the only source of cytoplasmic male sterility transferred into cultivated sunflower and utilized for developing self fertilized hybrids. Twenty five samples of this species, mainly collected from Colorado, North Dakota, South Dakota and Nebraska exhibited variability in plant height ranging from 0.3 to 1.2m, small heads of 1 to 2.3 cm diameter, basal branching with 11 to 15 branches per plant reaching upto the height of main stem. The soft sandy slopes of the highways were observed to be the most common habitat of this species.

Helianthus maximiliani : The elongate tapering bracts and slight green to grey green, sessile, longitudinally folded, smooth margined leaves covered with soft whitish hairs are the distinct characters of *H. maximiliani*, fifteen samples of this species were collected from North and South Dakota. Two distinct ecotypes were observed. The longitudinally folded leaves forming undulating furrows with occasional occurrence of 1-2 okra-shaped leaves in the middle portion of plant, is the characteristic feature of this ecotype, endemic to North and South Dakota. The other type with leaves forming plain furrows is common in the rest of the distributional range of the species. Populations of *H. maximiliani* exhibited variability for plant height ranging from 0.6 to 1.4m, number of heads from 1 to 25 per plant with disks averaging from 1.5 to 2.5cm in diameter. Leaves were numerous mostly alternate, lanceolate with smooth to sometimes slightly serrated margins. Bracts were narrowly lance-shaped, loose and conspicuously protruding the disk. Generally few to several secondary branches were present on the upper half of the plant, but sometimes primary branches also occur on light green to light red coloured thin stiff stems.

Helianthus pauciflorus ssp. *subrhomboideus* : Eight samples of *H. pauciflorus* ssp. *subrhomboideus* were collected from North and South Dakota. The plants were erect with reduced height varying from 30 to 90cm., bearing 8 to 12 opposite, sessile to petiolate (1cm), lustrous green, rough and tough uprightly-oriented leaves. Bracts were narrowly ovate and 8 to 10mm long. Disk florets were deep red or reddish-purple coloured. Heads per plant varied from 1 to 4. The populations exhibited apparent resistance/tolerance to

drought, head clipper/stem borer and other sucking pests and rust coupled with a very good plant type to facilitate high plant density.

Helianthus nuttallii : Of the reported 3 sub-species of *H. nuttallii*, *H. nuttallii* ssp. *nuttallii* and *H. nuttallii* ssp. *rydbergii* were distributed in the area surveyed and represented by 4 and 3 population samples respectively (Table 1). The populations of *H. nuttallii* ssp. *nuttallii* generally grew in marshy lands, near ponds or lakes in association with cat tails (typha). Plant height varied from 1.3 to 1.5 m with hairless to bristly stem and occasional appressed branches on the upper half; mostly alternate lanceolate leaves with dorsal side moderately to densely covered with bristles; 2 to 25 small heads per plant with disks ranging from 1.5 to 2cm. in diameter. The sub-species *rydbergii* grows in dry to wet soils. The plants varied from 0.6 to 1.6m in height with mostly smooth stem. Leaves are mostly alternate to all opposite, pale green in colour, nearly smooth to slightly serrated margins. Bracts have fine hairs on margins, nearly hairless or with soft hairs on back.

Helianthus grosseserratus: This species may be distinguished from other species by its smooth stem, flat serrated and petiolate leaves with lower surface covered with soft woolly hairs. The tough canopy with its dark green colour, lanceolate shape, medium size, upright orientation and balanced distribution on the stem, appears to be highly desirable for increased photosynthetic efficiency, high plant population and resistance to drought, diseases and particularly sucking pests, an essential features required in modern cultivars. The populations of this species exhibited variability for plant height ranging from 1 to 1.6m, branching mostly absent on the lower two-third of stem but with a few appressed secondary branches commonly on the top portion. The flowering disks averaging 1.5 to 2.5cm, in diameter, and narrowly lanceolate bracts exceeding the disks. The populations collected were free from all the major disease and pests including rust, *Phomopsis*, head clipper and sucking pests.

Helianthus tuberosus : The most common features of the Jerusalem artichoke or artichoke sunflower (*H. tuberosus*) is the production of slender rhizome terminally enlarging into tubers. The tubers are rich in sugars and starches. Though it was commonly distributed in Kansas and Nebraska, only 2 populations were sampled due to its late maturity. The plants varied in height from

1 to 1.7m, stems were bristly to gritty mostly branched above. Leaves were opposite below and alternate above to all opposite, oval to broadly lanceolate, ventral side gritty and dorsal softly pubescent, and serrated to entire margins. Usually several small head with disks measuring about 2 to 4cm, in diameter were present. Both populations sampled were free of diseases and pests especially rust and head clippers.

Helianthus pumilus: This species is found in dry, often rocky soils. Only one sample of this species was located and collected from a small rocky hillock in Colorado. The plants in the population varied from 30 to 40 cm in height and had single to branched rough stem, ovate to lanceolate, opposite, rough and scabrous leaves of ash-green colour with smooth to slightly serrated margins tapering towards petioles of varying length up to 1cm. The plants had very small heads with disks measuring about 1cm. in diameter. The bracts were lance shaped, pointed to sharp tipped, shorter than or equal to disk and slightly to densely covered with white hairs on back and margins. In mixed populations of *H. pumilus* and *H. petiolaris*, fully mature, diseases and pest free plants with intact lustrous foliage were seen under an extremely dry habitat in the *H. pumilus*, whereas the plants of *H. petiolaris* showed symptoms of damages by pest and diseases and drought. This indicated some built-in mechanism of resistance to biotic and abiotic stresses present in *H. pumilus*. Other species such as *H. hirsutus*, *H. salicifolius*, and *H. pauciflorus* ssp. *pauciflorus* were not collected due to their immature stage but were located in an area with high population concentrations near Lawrence, Kansas.

The germplasm, so collected, has been deposited at the USDA-ARS, National Plant Germplasm System, Regional Plant Introduction Station, Ames, Iowa, National Bureau of Plant Genetic Resources, New Delhi, India and Institute of Field and Vegetable crops, Novi Sad, Yugoslavia for evaluation, enhancement and conservation. Since hypothesized origin of wild and cultivated sunflower is from the Central Great Plains, wild populations from this area have potential for increasing genetic variability of cultivated sunflower. The addition of 144 wild population samples to the germplasm collections will greatly increase the available genetic diversity and preserve it for future improvement of cultivated sunflower before its natural habitat is destroyed.

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PHYLOGENY OF VIGNA SPECIES AS INDICATED BY SEED PROTEIN AND ISOZYME ELECTROPHORESIS

Alka Sehgal and K.P.S. Chandel

National Facility for Plant Tissue Culture Repository,
NBPGR, New Delhi - 110 012

The evolutionary relationships between cultivated and wild species of Asiatic Vigna species were investigated through biochemical parameters utilizing isozyme variation patterns of peroxidase, catalase and seed protein polymorphism studied through polyacrylamide gel electrophoresis. The results of above investigations are presented in this paper. The studies provide strong evidence in elucidation of phylogenetic relationships. The results indicated that mung and urid beans are two distinct species and they have independently evolved from wild progenitors V. radiata var. sublobata and V. mungo var. silvestris, respectively, which show remarkable similarities in isozyme profiles particularly in number of bands, position and Rf values. The wild putative forms occurring in natural habitats belonging to V. umbellata, V. aconitifolia and V. trilobata also appear to be quite distinct. They exhibited fewer bands. Close affinity could not be discovered as revealed by protein and isozyme polymorphism.

Seed protein gel electrophoresis techniques have been used to establish the origin of some taxa in plants (Gallez and Gottlieb, 1982) and in animals (Sekiguchi and Sugita, 1980). The electrophoretic analysis involving both seed proteins and isozymes provide useful evidences in the study of phenetic variation at the lowest taxonomic level in terms of intensity of common bands and presence or absence of other bands or their displacement. Isozyme polymorphism has been used for legume and bean systematics where electrophoretic mobility values of formic and glutamic acid dehydrogenases were determined in legume species from different tribes, including beans (Thurman *et al.*, 1967). On the basis of

electrophoretic patterns of seed proteins, the *Phaseolus* species of American and Asiatic origin were clearly differentiated and grouped separately (Derbyshire *et al.*, 1976). The isozyme electrophoretic patterns in bean species studied by Bassiri and Adams (1978 a) showed that most of them were characterized by unique isozyme spectrum. The origin and evolutionary relationships between several predominantly cultivated taxa such as mung bean (*V. radiata* (L.) Wilczek), urid bean (*V. mungo* (L.) Hepper), rice bean (*V. umbellata* (Thunb.) Ohwi and Ohashi), moth bean (*V. aconitifolia* (Jacq.) Marechal) and *V. trilobata* (Ait.) with their closely related wild species particularly *V. radiata* var. *sublobata* (Roxb.) Verdc. and *V. mungo* var. *silvestris* Lukoki, Marechal and Otoul (1980) have remained a subject of intensive research. The present investigations were aimed to have comparative study of isoenzymes particularly peroxidase, catalase and total seed proteins among cultivated Asiatic *Vigna* species and their related wild taxa.

MATERIALS AND METHODS

The germplasm collections of cultivated and wild species of *Vigna*, being maintained by NBPGR and also regenerated from time to time in the field and greenhouse, were used for this study. The wild species and their diverse morphotypic forms were grown in the green house during the rainy season (July-November), 1988 and 1989 and fresh materials were used for present studies. The details of the species, their accessions, source of collection etc. are presented in Table 1.

Electrophoretic studies on seed proteins were conducted on samples of seeds obtained from the 1988/1989 raised crops. Four accessions each in *V. radiata* var. *sublobata*, *V. mungo* var. *silvestris*, *V. umbellata* var. *major* and var. *rumbaiya* and *V. trilobata* were utilised. The typical cultivars of mung, urid, rice bean and moth bean were also included. A complete schematic representation of the protein profiles (banding patterns) have been depicted in Fig. 1. Similarity indices among the protein profiles of *Vigna* genotypes have been calculated and shown in Table 3. Isozyme studies were conducted on the fresh leaves obtained from 5 months old plants. Three other wild species; *V. vexillata*, *V. dalzaliana* and *V. aconitifolia* were included in addition to above mentioned species. The relative mobility of two isoenzymes, peroxidase and catalase is indicated in Table 4.

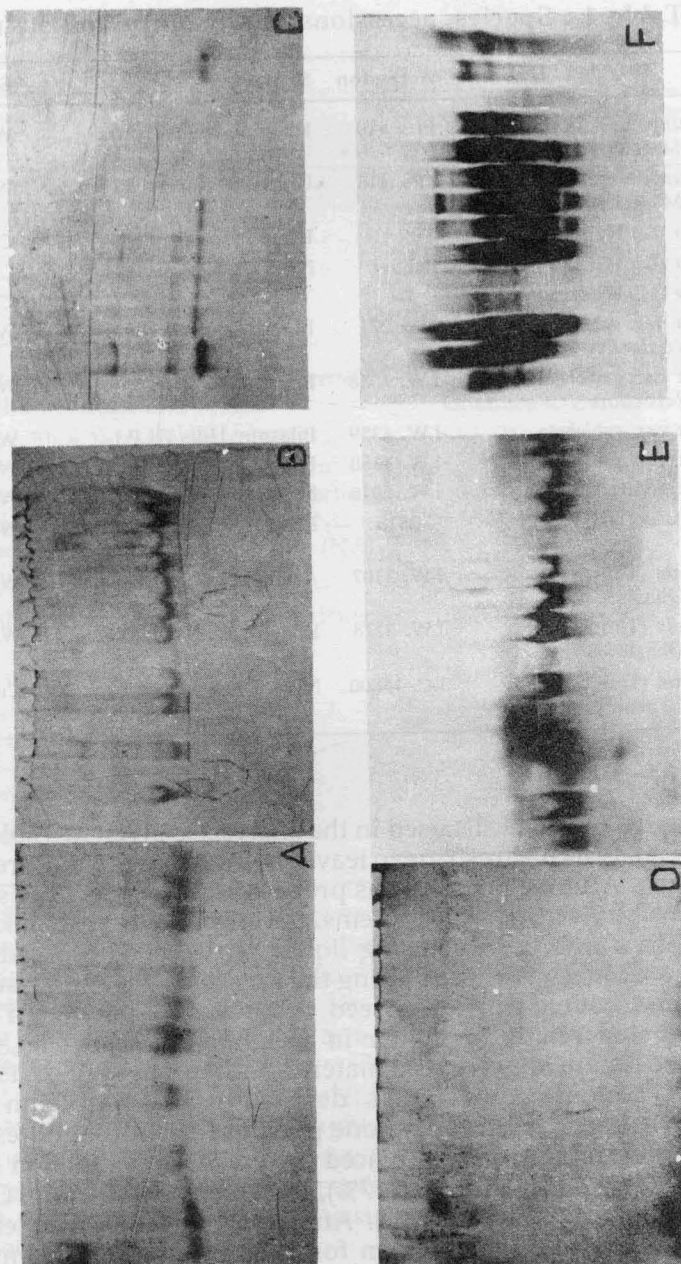


Fig. 1 : Schematic representation of banding patterns in *Vigna* species complex

Table 1 : Species, accessions, their source and status

Species	Accession	Source	Status
<i>Vigna mungo</i> var. <i>silvestris</i> Lukoki, Marechal and Otoul	Pl x 410	Khopoli, Maharashtra	Wild
<i>Vigna mungo</i> var. <i>silvestris</i> Lukoki, Marechal and Otoul	Pl x 416	Chipulin, Karnataka	Wild
<i>V. mungo</i> (L.) Hepper	T ₉	Uttar Pradesh	Cultivated
<i>V. radiata</i> (L.) Wilczek	Pallavi	NBPGR, New Delhi	Cultivated
<i>V. radiata</i> (L.) Wilczek	—	—	Cultivated
<i>V. radiata</i> var. <i>sublobata</i> (Roxb.) Verdcourt	Pl x 271	Bhowali, U.P. Hills	Wild
<i>V. radiata</i> var. <i>sublobata</i> (Roxb.) Verdcourt	I.W. 4358	Bilaspur Hills (H.P.)	Wild
<i>V. radiata</i> var. <i>sublobata</i>	I.W. 4359	Bilaspur Hills (H.P.)	Wild
<i>V. radiata</i> var. <i>sublobata</i>	I.W. 4360	Bilaspur Hills (H.P.)	Wild
<i>V. trilobata</i> (Ait) Jacq.	I.W. 2549	NBPGR, New Delhi	Wild
<i>V. aconitifolia</i> (Jacq.) Marechal	C-2515	Rajendranagar, Hyderabad	Wild
<i>V. umbellata</i> (Thunb.) Ohwi & Ohashi	I.W. 3107	Arbila peak, Meghalaya	Wild
<i>V. umbellata</i> (Thunb.) Ohwi & Ohashi	I.W. 3178	Khasi hills, Meghalaya	Wild
<i>V. umbellata</i> (Thunb.) Ohwi & Ohashi	I.C. 16800	NBPGR, New Delhi	Cultivated

Biochemical methods

The list of chemicals used in the analysis is given in Table 2. For isozyme analysis the fresh green leaves of 5 months old mature plants were taken. Acetone powder was prepared from each of the sample. For electrophoresis of seed proteins, the fresh seeds were taken and crushed to a fine powder using liquid nitrogen. The powder was washed with acetone while putting the extract on the funnel and care was taken to avoid mixing of seed coat with the powder. The fine powder being relatively lighter in weight than seed coat, it was possible to decant only the seed material without the seed coats. Thus, prepared acetone powder was defatted using petroleum ether. Protein was extracted from acetone powder for 10-15 minutes using a prechilled mortar pestle placed in ice. The extraction buffer contained Tris (0.1 M), Sucrose (17%), ascorbic acid (0.1%) and Cystine hydrochloride (0.1%) at pH 7.4. After crushing, the samples were centrifuged at 4°C at 17,000 rpm for 15 min. Protein concentration was determined colorimetrically by the Lowry modification of the Folin method (Lowry *et al.*, 1951) using the supernatant. Vertical migration towards the anode on 7.5 per cent polyacrylamide was then performed using Pharmacia Slab Gel Electrophoresis Apparatus

Table 2 : List of chemicals used, their quality brand name and source

S.No.	Name of Chemical/s	Quality Brand Name (Product/Source)
(1)	Sodium Thiosulfate, Disodium Hydrogen Phosphate, Sodium Citrate and Urea	E MERC, Bombay, India
(2)	Potassium Iodide, Sodium Dihydrogen Phosphate and Acetic Acid	Glaxo, Bombay, India
(3)	Fast Blue RR Salt, Hydrogen Peroxide, Sodium Acetate and Iodine	BDH Laboratory Chemicals, England, U.K.
(4)	Nitro Blue Tetrazolium (NBT), Dithiothresitol (DTT), Phenyl Methyl Sulphonate (PMS), Hypoxanthine, aspartic acid, Pyridoxal Phosphate and Nicotinamide Adenine Dinucleotide (NAD)	SRL, Bombay, India
(5)	Acetone	Qualigens, India
(6)	Trishydroxyl Methyl Aminomethane (TRIS) and Calcium Chloride	Spectrochem, India
(7)	Ethanol	Bengal Chemicals, India
(8)	Fast Blue BB Salt, D.L. Malate, 3- (4,5-Dimethyethiazol-2-yl) -2.5- Diphenyl Tetrazolium Bromide	Sigma Chemicals Co. U.S.A.
(9)	Starch	Indian Drugs and Pharmaceuticals Ltd. India

GE 2/4LS allowing the simultaneous electrophoresis of 14 samples for a gel of 0.4 m thickness. Reservoir buffer contained Tris (0.025 M) and glycine (0.133 M) at pH 8.3 Electrophoresis was performed at 70V for 4-5 hours. The staining for different isozymes was done following the procedures of Vallejos (1983). Proteins were stained using the procedure described by Davis (1964), with 25 per cent methanol and 10 per cent acetic acid (glacial). The gels were examined and photographed while on a light box. The similarity between various protein profiles and isozyme patterns were expressed in the percentage similarity index. The percentage similarity (Whiteney *et al.*, 1968) was computed for the various species/genotypes of the *Vigna* species.

$$\text{Percentage similarity} = \frac{\text{No. of pairs of similar bands}}{\text{No. of different bands} + \text{No. of pairs of similar bands}} \times 100$$

RESULTS AND DISCUSSION

Several cultivated and wild species of *Vigna* and their polymorphic forms studied in the present investigations, produced very characteristic protein profiles. The total number of visible bands varied from 16 to 30. The data in Table 3 indicated the number of bands and relative mobility of two isoenzymes, peroxidase and catalase. Rf values of differential bands among the various genotypes indicated that the fastest migrating band had a Rf value of 0.57. In case of *V. umbellata*, *V. vexillata*, *V. dalzaliana* and other wild *Vigna* species no specific enzymatic activity was exhibited for peroxidase, and catalase enzymes. The variation patterns among the closely related groups were determined on the basis of electrophoretic patterns of both isozyme profiles as well as protein polymorphism.

Table 3 : Similarity indices among the profiles of *Vigna* spp. genotypes

	<i>V. radiata</i> var. sub- lobata PI x 271	<i>V. radiata</i> var. sub- lobata IW4358	<i>V. radiata</i> var. sub- lobata IW4359	<i>V. radiata</i> var. sub- lobata IW4360	<i>V. trilobata</i> IW 2549	<i>V. mungo</i> var. syl- vestris PI x 410	<i>V. mungo</i> var. syl- vestris PI x 416	<i>V. umbe- llata</i> IW 3178
<i>V. radiata</i> PIMS (Pallavi)	55.5	50	51.4	48.5	40	65.6	58.8	34.2
<i>V. mungo</i> T-9 (urid)	47.5	—	—	—	37.2	60	58.3	35.0
<i>V. mungo</i> var. silvestris PI x 410	—	—	—	—	—	—	70.9	—

The results of the biochemical studies showed that considerable similarities exist between the cultivated species mung bean (*V. radiata* (L.) Wilczek) and urd bean (*V. mungo* (L.) Hepperi) and their putative progenitors (*V. radiata* var. *sublobata* (Roxb.). Verdcourt and *V. mungo* (L.) var. *silvestris* Lukoki, Marechal and Otoul, respectively. In *V. radiata* var. *sublobata*, the number of bands varied from 25-29, while *V. radiata* showed the presence of 27 bands. The position of bands and Rf values were also corresponding very well. Similarly, in wild forms of *V. mungo* var. *silvestris*, the number of protein bands were 26-27 which differed very little from cultivated *V. mungo* with the exception of only few additional bands. Other wild forms of *V. umbellata*, *V. aconitifolia* and *V. trilobata* originating from diverse ecological regions/habitats showed the presence of relatively fewer number of bands.

Cultivated rice bean (*V. umbellata*) possessed 16 and 25 bands while wild forms exhibited activity with 18 bands only.

It was also evident from the results that intraspecies variation was very little, while intraspecies similarity was quite high as was evident from the similarity index (S.I.) value of 70.9 in case of *V. mungo* var. *silvestris* (PIX416 and PIX410). When compared with cultivated form (T₉) of urid bean (*V. mungo*), the wild type *V. mungo* var. *silvestris* (PIX410) resembled very much. It may be indicated here that PIX410 has been designated as the holotype specimen of *V. mungo* (L.) var. *silvestris*. (Lukoki, Marechal and Otoul, 1980). This phylogenetic relationship was also clearly established earlier by Chandel (1980) and Chandel *et al.* (1984). Similarly, several accessions of wild *V. radiata* var. *sublobata* (Roxb.) Verdcourt, exhibited close resemblance with mung bean cultivars **Pallavi** supported by similarity index (S.I. value 48.5-55.5%). Among other species, *V. trilobata* possessed some affinity with mung bean and its wild putative progenitor forms.

The data presented in Table 4 indicates the number and relative mobility of two enzymes peroxidase and catalase. In case of peroxidase, the R_f values among the various genotypes showed that slowest migrating band had a value of 0.18, while the fastest migrating band had 0.57. In case of catalase isoenzyme the values of slowest and fastest migrating bands were 0.16 and 0.30, respectively. It was unexpected to find that wild occurring putative forms of *V. umbellata*, *V. vexillata*, *V. dalzaliana* and *V. aconitifolia* exhibited no enzymatic activity at all for the catalase enzyme. The migration rates of different bands of the two enzymes (Table 4; Fig. 2) show that no intraspecies variations appeared. *V. mungo* var. *silvestris*, however, exhibited some similarity with *V. umbellata* for peroxidase enzyme and wild form of *V. aconitifolia* collected from Hyderabad region for peroxidase isoenzyme activity. Interestingly, *V. mungo* var. *silvestris* differed from rice bean (*V. umbellata*) for the catalase enzyme as the latter species did not exhibit any enzymatic activity. All the accessions of *V. trilobata* showed only the presence of one catalase band. While different forms/accessions of *V. trilobata* possessed three enzyme bands of catalase. *V. dalzaliana* resembled *V. trilobata* in having three enzyme bands and the position of each band also corresponded very well. The two bands of peroxidase in case of *V. vexillata* were entirely different from *V. trilobata*, *V. mungo* var. *silvestris*, *V. radiata* var. *sublobata* as well as *V. umbellata* and *V. aconitifolia*.

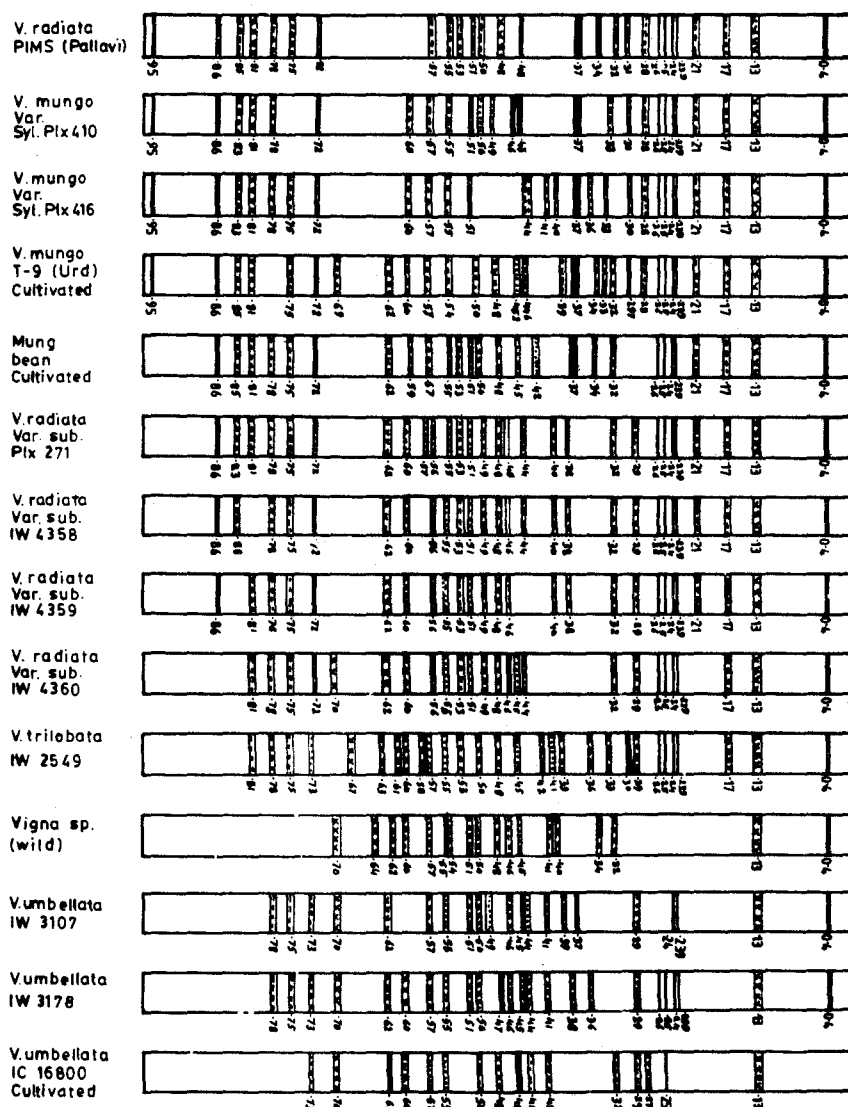


Fig. 2. Isozymes profiles of different accessions in *Vigna* species et al.

Table 4 : Number of peroxidase and catalase Bands and their R_f values determined for different genotypes of *Vigna* species by Slab Gel Electrophoresis using leaves

Genotype	Peroxidase				Catalase			
	No. of bands	Rf values			No. of bands	Rf values		
<i>V. mungo</i> var. <i>silvestris</i>								
" - IW 3385	1	0.57	—	—	1	0.30	—	—
" - IW 3386	1	0.57	—	—	1	0.30	—	—
" - IW 3387	1	0.57	—	—	1	0.30	—	—
" - IW 3388	1	0.57	—	—	1	0.30	—	—
" - IW 3389	1	0.57	—	—	1	0.30	—	—
" - IW 3393	1	0.57	—	—	1	0.30	—	—
" - Pl x 412	1	0.57	—	—	—	—	—	—
" - Pl x 413	1	0.57	—	—	1	0.30	—	—
" - Pl x 416	1	0.57	—	—	1	0.30	—	—
<i>V. radiata</i> var. <i>sublobata</i>								
" - Pl x 271	1	0.57	—	—	2	0.30	0.16	—
" - Pl x 272	1	0.57	—	—	2	0.30	0.16	—
" - Pl x 274	1	0.57	—	—	2	0.30	0.16	—
" - Pl x 278	1	0.57	—	—	2	0.30	0.16	—
" - Pl x 298	1	0.57	—	—	2	0.30	0.16	—
" - IW 4358	1	0.57	—	—	2	0.30	0.16	—
" - IW 4359	2	0.57	—	—	2	0.30	0.16	—
<i>V. vexillata</i>								
" - Pl x 401	2	0.51	0.21	—	—	—	—	—
" - IW 3426	2	0.51	0.21	—	—	—	—	—
" - IW 4347	2	0.51	0.21	—	—	—	—	—
<i>V. dalzaliana</i>								
" - Pl x 397	3	0.57	0.52	0.36	1	0.30	—	—
<i>Vigna</i> spp.								
" - Pl x 278	1	0.57	—	—	—	—	—	—
<i>V. aconitifolia</i>								
" - PLMO 211	—	—	—	—	1	0.30	—	—
" - PLMO 377	—	—	—	—	1	0.30	—	—
" - IC 9080	—	—	—	—	1	0.30	—	—
<i>V. aconitifolia</i> Wild putative (Type progenitor Hyderabad)	1	0.57	—	—	1	0.30	—	—
<i>V. umbellata</i>								
" - IW 3107	1	0.57	—	—	—	—	—	—
" - IW 3173	1	0.57	—	—	—	—	—	—
" - IW 3178	1	0.57	—	—	—	—	—	—
<i>V. trilobata</i>								
" - IW 4350	3	0.57	0.52	0.36	1	0.30	—	—
" - IW 4364	3	0.57	0.52	0.36	1	0.30	—	—
" - IW 4378	3	0.57	0.52	0.36	1	0.30	—	—
" - IW 2214	3	0.57	0.52	0.36	1	0.30	—	—
" - IW 2482	3	0.57	0.52	0.36	1	0.30	—	—
" - IW 4364	3	0.57	0.52	0.36	1	0.30	—	—
" - IC 24830	3	0.57	0.52	0.36	1	0.30	—	—
" - IC 24832	3	0.57	0.52	0.36	1	0.30	—	—
" - Pl x 92	3	0.57	0.52	0.36	1	0.30	—	—
" - Pl x 394	3	0.57	0.52	0.36	1	0.30	—	—
" - Pl x 511	3	0.57	0.52	0.36	1	0.30	—	—

Protein polymorphism in *Vigna* species was studied earlier by Chandel (1980) involving nine cultivated and wild species of *Vigna* of Asiatic origin. Using polyacrylamide gel electrophoresis the evolutionary relationships were conclusively elucidated amply supported by extensive study of comparative morphology, scanning electron microscopy of seed coat cellular and hilum morphology and leaf phenolic chromatography (Chandel *et al.*, 1984). The results analysed employing the numerical taxonomy techniques showed that evidences from all above independent studies, interestingly, arrived to the same conclusions. The results also convincingly identified the wild putative progenitors of mung and urid bean and showed that mung bean and urid bean are quite distinct species and are not closely related as contended by most earlier workers. In fact, these species have evolved independently, in India, from their widely occurring wild putative progenitors namely *V. radiata* (L.) var. *sublobata* (Roxb.) Verdcourt and *V. mungo* (L.) var. *silvestris* Lukoki, Marechal and Otoul, respectively. In the same year, parallel studies were carried out by Marechal's group in Belgium, who used one wild form (PIX410) in common and designated it as *V. mungo* var. *silvestris* Lukoki, Marechal and Otoul indicating similar relationships.

Using chromatography and seed protein electrophoresis in Ethiopian cereal *Eragrostis tef* (Bekele and Lester, 1981) and in *Festuca arundanacea* (Radomska and Lester, 1986) phylogenetic relationships were established. In latter case, morphological and seed protein studies of selected species of *Festuca* were carried out to elucidate the relationships between species of section *Ovineae* and their affinity with other fescue (Radomska and Lester, 1986).

Classical identification of cultivars and more so the germplasm diversity based on standard morphological markers has proved to be inadequate because of wide spectrum of phenotypic variation and their interaction with environment (Mannetji, 1984). In such instances, electrophoretic patterns illustrated through electrophorograms of seed proteins can be used effectively to decipher the similarities and differences between cultivars and genotypes (Bushuk and Zillman, 1978; Cooke 1984; and Hussain *et al.*, 1986).

Electrophoretic banding homology is considered to be a powerful approach in estimating genetic relationships between two or more species (Johnson, 1968; Johnson and Thein, 1970), as well as in the identification and classification of cultivars (Cooke and Draper, 1983). The techniques used in our studies have shown the

potential and usefulness in finding out the close affinities between various cultivated *Vigna* species and their several wild polymorphic forms. Electrophoresis together with other easily executable molecular methods on the proteins have the potential to supplement traditional methods of classification and thus provide strong basis for studying the finer relationships among organism at the species and subspecies level. The present study supports earlier view (Chandel, 1980; Chandel, 1984; Chandel *et al.*, 1984 and Chandel, 1991) with more detailed study on several accessions of *Vigna* and provides evidences in resolving prevalent confusion about species relationships in genus *Vigna*.

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**IN VITRO MICROPROPAGATION OF CARALLUMA
EDULIS (Edgew.) Benth. & Hook. f. — A RARE EDIBLE
PLANT SPECIES OF INDIAN DESERT**

Gurdeep Kaur, T.S. Rathore, S. Rama Rao and N.S. Shekhawat

Plant Biotechnology Laboratory,
Department of Botany, University of Jodhpur
Jodhpur – 342 003

An in vitro micropropagation protocol was developed using shoot segment explant of Caralluma edulis – a very rare and endangered edible plant of the Thar desert. Four to six multiple shoots were initiated from nodal explant on MS medium containing 0.25 mg l⁻¹ IAA (Indole-3-acetic acid) and 2.5 mg l⁻¹ BAP (benzylamino purine). The shoots elongated and multiplied on a medium supplemented with 0.25 mg l⁻¹ IAA + 2.5 mg l⁻¹ BAP and 2.5 mg l⁻¹ GA₃ (Gibberellic acid). In vitro produced shoots rooted on half strength MS medium containing 1.0 mg l⁻¹ IBA (Indolebutyric acid) within three weeks. Plantlets were transplanted to pots and grown to maturity.

Increasing human activities and various types of stresses have caused widespread disturbances in the habitats of plants. This has resulted in the gradual reduction of plant resources and the genepools of valuable plants. There has been increasing concern and emphasis on conservation of germplasm of threatened plants (Harry and Thorpe, 1991). Multiplication and conservation of rare, threatened and endangered taxa can be carried out efficiently through techniques (Arora and Bhojwani, 1989; Bhojwani *et al.*, 1989; Upadhyay *et al.*, 1989; Arumugam and Bhojwani, 1990 and Rathore *et al.*, 1991).

Caralluma edulis (Edgew.) Benth. & Hook. f. (Asclepiadaceae) is a very rare herb of the extremely arid regions of the Thar desert. It is locally known as **Pimpa**. The tender shoots of plants are used as vegetable in Jaisalmer. Natural propagation of this plant is extremely poor under the xeric conditions. There is an urgent need

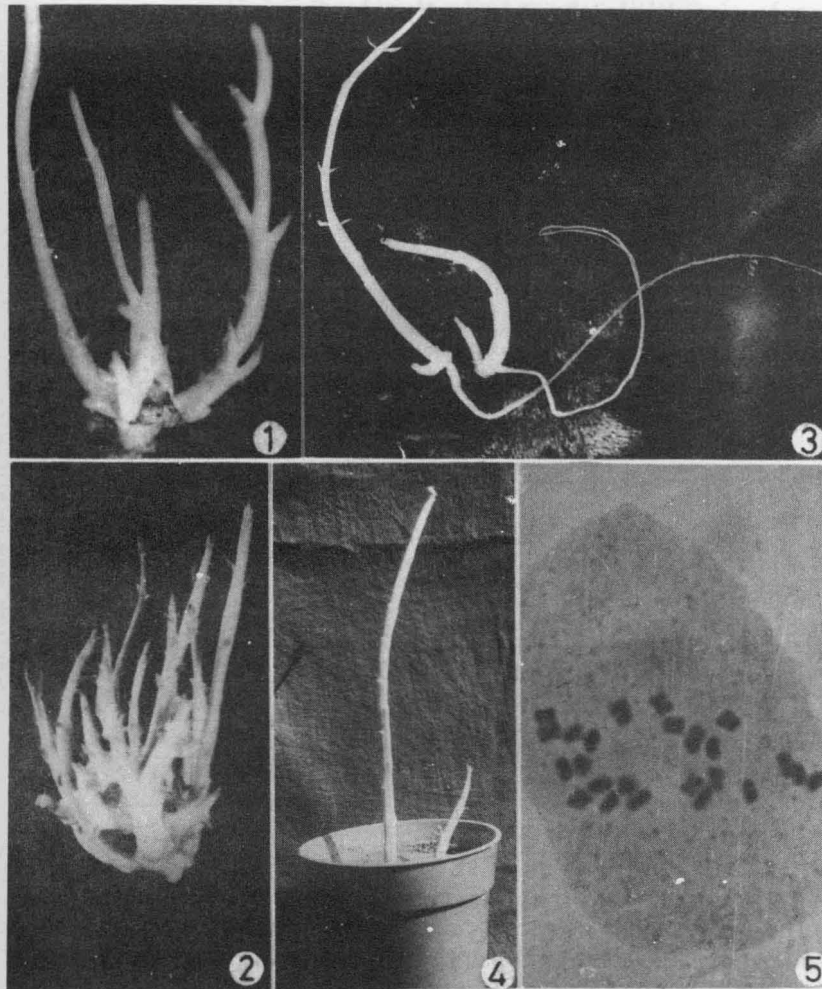
to conserve *C. edulis* germplasm. Establishment of *in vitro* cultures of *C. edulis* and its micropropagation using tissue culture technology has been discussed in this paper.

MATERIALS AND METHODS

In vitro cultures of *C. edulis* were established from shoots of plants collected from natural habitat from nearby areas in Jaisalmer. Apical and axillary shoots (each with a single node) and inflorescence segments were taken as explants. These were washed thoroughly with water containing a few drops of Tween-80 and surface sterilized with 0.1% mercuric chloride for 4 min, and washed 5-6 times with autoclaved distilled water. Explants were placed vertically or horizontally on MS (Murashige and Skoog, 1962) medium for shoot induction and multiplication. The pH of the media was adjusted to 5.8 prior to autoclaving. Various concentrations and combinations of auxins and cytokinins were incorporated. Differentiated shoots were sub-cultured after intervals of 3-4 weeks on fresh medium for further multiplication. These were kept under 12 h photoperiod ($30 \mu\text{Em}^{-2}\text{s}^{-1}$ photon flux density) at $28 \pm 2^\circ\text{C}$ and 60 per cent relative humidity. The differentiated shoots were excised and transferred to various rooting media containing different concentrations of auxins and kept in the dark for a week and later under light conditions. Plantlets were carefully removed from the agar medium without damage to the root system and were kept in distilled water for 15 min to avoid dehydration and to remove traces of agar and transferred to pots containing soil and vermiculite in the ratio of 4:1 (Fig. 4). These plants were first acclimatized in a culture room for two weeks and then to the field. Plantlets of 8-12 cm in length were later transferred in pots containing field soil. The root tips of *in vitro* produced plantlets were analysed for chromosome number using the method described by Rao *et al.* (1991).

RESULTS AND DISCUSSION

Tissue cultures were established from apical and axillary shoot explants on MS medium containing 0.25 mg l^{-1} of IAA and 2.5 mg l^{-1} of BAP. Shoot segment with a single node was found to be the best explant for induction of multiple shoots over the apical shoots and inflorescence segments. On an average, 4-6 shoots were induced (Fig. 1) from each nodal shoot segment, whereas 2-3 shoots differentiated from apical shoot segment. Inflorescence segments did not respond. The effect of growth regulators on multiple shoot



- Fig. 1. Multiple shoot induction in *Caralluma edulis* from nodal segment on MS medium supplemented with IAA (0.25 mg l^{-1}) and BAP (2.5 mg l^{-1}).
- Fig. 2. Multiplication of shoots on MS + IAA (0.25 mg l^{-1}) BAP (2.5 mg l^{-1}) + GA₃ (2.5 mg l^{-1}).
- Fig. 3. Rooted shoots of *C. edulis* on half- strength MS medium containing IBA (1.0 mg l^{-1}).
- Fig. 4. Five week old potted plant of *C. edulis*.
- Fig. 5. Chromosomes $2V = 24$) of a root tip cell of *in vitro* raised plantlet of *C. edulis*.

Table 1 : Combined effect of auxin + cytokinins on multiple shoot induction in *C. edulis*

Auxin + Cytokinin (mg l ⁻¹)	Number of shoots	Length of shoots (cm)	Callusing
IAA + BAP			
0.1 + 0.5	1.32	1.01	-
0.1 + 1.0	2.08	1.9	-
0.1 + 2.5	3.3	2.2	+
0.1 + 5.0	4.0	1.9	+
0.25 + 0.5	2.05	2.2	-
0.25 + 1.0	3.64	2.6	-
0.25 + 2.5	5.2	3.4	-
0.5 + 0.5	1.5	0.9	+
0.5 + 1.0	2.2	1.5	+
0.5 + 2.5	3.7	1.9	+
0.5 + 5.0	4.5	2.0	+
IAA + Kinetin			
0.1 + 0.5	0.91	0.7	-
0.1 + 1.0	1.72	1.0	+
0.1 + 2.5	1.79	1.2	+
0.1 + 5.0	2.24	1.3	+
0.25 + 0.5	2.9	1.5	+
0.25 + 1.0	3.0	1.8	+
0.25 + 2.5	3.2	2.3	+

inductions is summarised in Table 1. BAP and IAA combination was found better than kinetin and IAA combination for multiple shoot induction. Replacement of IAA by NAA in the shoot induction medium caused callusing of the explant and did not increase shoot number or length. Differentiated shoots were cut into small segments (2.0–2.5 cm) and cultured on fresh medium for further multiplication. The number of shoots per explant increased to 8 and the shoot length to 6–8 cm when 0.25 mg l⁻¹ IAA, 2.5 mg l⁻¹ BAP and 2.5 mg l⁻¹ of GA₃ were incorporated in the culture medium (Fig. 2). Thus, incorporation of GA₃ in shoot multiplication medium caused considerable elongation of shoots (Table 2). Among the media tested for root induction, half strength MS medium was found to be the best followed by one fourth strength MS basal and

White's basal medium (Table 3). About 85-90 per cent of the shoots rooted on half strength MS medium containing 1.0 mg l^{-1} of IBA within three weeks (Fig. 3). It is estimated on the basis of present study that 50-60 plantlets can be obtained from single explant within 60 days.

Table 2 : Effect of GA_3 on shoot elongation of *C. edulis* cultured on MS medium containing 0.25 mg l^{-1} of IAA + 2.5 mg l^{-1} of BAP

GA_3 (mg l^{-1})	Number of shoots	Length of shoots (cm)
0.1	5.2	4.97
0.5	5.85	5.43
1.0	7.7	5.93
2.5	8.06	6.91
5.0	6.49	6.05

Table 3 : Root induction and elongation on *C. edulis* shoots cultured on different media containing IBA 1.0 mg l^{-1}

Medium	Number of roots	Length of root (cm)
MS full	1-2	3-4
MS/2	2-4	5-6
MS/4	1-3	4-6
White's	1-2	2-3

In vitro produced plantlets were analyzed for chromosome number using root tips. The *in vitro* regenerated plants showed chromosome number ($2N = 24$) similar to mother plants (Fig. 5). No chromosome aberration was recorded.

In several plants of Asclepiadaceae, plant regeneration through somatic embryogenesis has been reported (Rao *et al.*, 1991; Prabhudesai and Narayanswamy, 1974; Wilson and Mahlberg, 1977). Bapat *et al.* (1986) reported regeneration of plants from protoplasts derived calli. Thus, there is strong possibility of *C. edulis* being regenerated from callus, cells and protoplasts. It will help increasing genetic variability of this rare and highly drought and heat resistant edible plant of Indian desert. It is suggested that protocol developed for micropropagation and multiplication of *C. edulis* can be used for *in vitro* conservation of germplasm of this valuable plant.

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COMPUTERIZED DATA PROCESSING AND CATALOGUING OF PLANT GENETIC RESOURCES

R.C. Agrawal and R.K. Mahajan

National Bureau of Plant Genetic Resources
New Delhi – 110012

Enormous information has accumulated over the past few decades on germplasm of various crops and their wild relatives. Awareness and importance of computerisation of database information, logging, analysis and retrieval is increasing day by day at national, regional and global levels. Various steps in preparation of a catalogue vis-a-vis recording of data, and duplication, verification, sorting, analysis, querying and listing of data are discussed in this paper. Computer program based on dBASE III Plus software for identification of duplicates as well as sorting and analysis of data are also discussed.

With tremendous pile-up of information by various global and national agencies, viz., CGIAR institutes, USDA, NBPGR etc., on the collection, characterization and evaluation, storage, *in situ* conservation and usage of the germplasm of various crops and their related wild species during the past few decades, scientists now-a-days spend at least 30 per cent of their time in taking care of the data information associated with collections (Rogers *et al.*, 1975). Their accumulation to the long-term genebanks at various stages of documentation posed serious threat to their efficient management as well as utilization by breeders. IBPGR has compiled directories of germplasm resources in various crops available with various national, regional or international organisations. In most cases, the stage of documentation is manually operated data registers or partially computerised data banks. Bettencourt and Konopka (1990) have indicated recent trends in documentation of sorghum germplasm database at 51 international centres. There is a clearcut advancement towards switching over to computerised database management. But since no standard data retrieval system

exists at different plant genetic resources organisations, except a few, e.g., GRIN of USDA, IRRIGEN of IRRI etc., the inter-institutional interaction among users becomes quite a difficult task. In the modern era, electronic computers are extensively used in different organisations for multiple purposes. Geographic Information Systems (GIS) as developed by Global Resources Information Database (GRDA) are powerful tools for integrating and analysing diverse spatial data (Burrill *et al.*, 1991). Data input, information and exchange through magnetic floppies, magnetic tapes, compact disks, etc. becomes easier through systematic use of computers. A simple and common method for exchange of such information is through crop catalogues which are the printed versions of systematically pre arranged/analysed data based on a particular set of descriptors and descriptor states decided for a crop or its related species.

Crop catalogues are valuable source of information on passport data, various agrobotanical and economic characters and other traits of interest to research workers involved in crop improvement programmes. In the present context, a crop catalogue may be considered primarily a systematic listing of different accessions of a crop, their identification source, characterisation and evaluation data alongwith additional/optional pre-analysed information using different statistical tools. Extensive data processing is involved in bringing out a catalogue. The computer data processing is a series of operations carried out in order to convert the data into useful information. The voluminous data recorded over a period of time, its tabulation etc. and lengthy calculations done manually has been a tedious task for huge pile-up of germplasm information and thus switching over to computer data processing is a good proposition. Following paragraphs relate to stepwise information required for preparation of a catalogue for efficient retrieval of information database.

CATALOGUING AND DATA PROCESSING

Cataloguing involves frequent use of many softwares and statistical packages, viz., dBASE III Plus, Fox Pro, Reflex, Lotus 1-2-3, MSTAT-C, SPSS, BMDP, MICROSTAT, Harward Graphics, Word Star, Word Perfect etc. Among these, the most frequently used package is any DBMS (Data Base Management System) package. A DBMS package is a computer program that organises large collections of interrelated data according to a well defined

scheme and produces reports by extracting and reformatting data. Reformatting refers to indexing and/or sorting on a particular field(s). It may further range from rearrangement or simple totalling to complex statistical analysis. Thus, a DBMS is a system for information storage, retrieval and analysis with emphasis on formatted data. In all the standard softwares on DBMS, we come across two terms — Field and Record. A Field can be considered as any descriptor [a widely accepted computer term for the character of plant, as well as for other units of information such as country of origin or the date of collection (Sapra and Singh, 1992)] from the list of descriptors whereas a Record is an accession with all descriptors. A collection of related records/ information constitute a file in computer environment.

Recording of data

The information about passport data (accession identifiers and information recorded by collectors) and characterisation (recording highly heritable characters capable of expressing themselves in all environments), preliminary and further evaluation is recorded on paper or on data loggers, a handy device, from which data can be subsequently transferred to a computer for further storage and analysis. To facilitate description of accessions, results of tests of accessions and to improve communication between scientists in different institutions, internationally accepted IBPGR descriptors lists decided for each crop species should be followed. These norms are well defined for qualitative as well as quantitative characters (Rogers *et al.*, 1975). For scoring in heterogeneous populations Hintum (1989) approach should be followed.

Various statistical designs are available in literature which can be extensively used depending upon the population size, availability of seed and resources. In plant genetic resources, the accessions for different crops vary invariably from hundreds to thousands. Limited seed quantity in each accession and meagre experimental land makes it difficult to replicate the accessions and thus the basic norms of statistical designs are violated. In such situations, augmented randomized design may be adopted (Federer, 1956). The design consists of one set of treatments (the check varieties) replicated a number of times and a second set of treatments (the accessions) appearing only once in the entire layout. A computer program for statistical analysis of augmented randomized complete block design was further described in simplified form (Sapra and Agrawal, 1992).

Loading of data to computer

The data is transferred to the computer system generally by data entry operators. It is normally carried out either in text mode by using some text editors, *viz.*, Norton Editor, Word Star (Non-document mode), Edit etc. or by directly using the DBMS package. Spreadsheets like LOTUS 1-2-3, Quatro etc. may also be used for this purpose. For fast data feeding, data entry machines may also be used. If data is stored on a data logger, the above steps can be skipped. These loggers minimise human error in data feeding. In text editors, the fields should be preferably separated by comma (,) which makes easy transfer of data to other software. In any DBMS package, extra care is taken while selecting the field width (the maximum width for different fields). Furthermore, a range may be defined for every numeric field so that the values outside the range will not be accepted at data feeding time.

Verification of data

For verification and subsequent use, the data loaded in the text editor should be transferred to DBMS package (preferably dBASE III Plus). The technique of transfer differs from package to package. For dBASE III Plus, the structure of fields should be defined first and then for transfer APPEND FROM command may be used. The error occurs in data recording and data feeding. Duplicate entries detected first and after manual checking from the original, such record may be deleted. Equal field width should be maintained for each accession throughout. For example two accessions, *viz.*, IC-532 and IC-1000 should be entered as IC-0532 and IC-1000 fixing a maximum field width of 7 characters. For identifying the duplicate entries, following program in dBASE III Plus can be utilised.

```
SET TALK OFF
```

```
SET EXACT ON
```

```
USE filename-1
```

```
INDEX ON fieldname-1 TO filename-2
```

```
COPY STRUCTURE TO filename-3 FIELDS fieldname-1
```

```
SELECT A
```

```
USE filename-1 INDEX filename-2
```

```
SELECT B
```

```
USE filename-3
```

```
SELECT A
```

```

GO TOP
AN=fieldname-1
SKIP
DO WHILE .NOT. EOF ( )
  IF fieldname-1=AN
  SELECT B
  APPEND BLANK
  REPLACE fieldname1 WITH AN
  ELSE
    AN=fieldname1
  ENDIF
  SELECT A
  SKIP
ENDDO
CLOSE ALL
SET EXACT OFF
SET TALK OFF

```

In this program, characters in italics can be replaced by the user according to the choice.

Characters in italics	Explanation
Filename1	datafile
Filename2	file to store the indexed information
Filename3	file to store duplicates
Fieldname1	file name defined for accessions

For major data feeding errors, indexing on different fields may be carried out which can help in identifying the maximum and minimum values of different fields. For coded fields like seed colour, pod type etc. 'UNIQUE' indexing may be done. In case some wrong entry is detected, the entire data of the record should be varified.

Example-Following data has been extracted from a catalogue on Forage Sorghum Germplasm (Mathur *et al.*, 1992) for verification of duplicates. One accession at the last has been added as a duplicate accession. This catalogue contains 3943 accessions, and thus makes physical verification of duplicates a difficult task. Field names used to store 5 descriptors in dBASE III Plus are mentioned in the following column headings (Acc_no is for accession no., P_height is for plant height and S_thick is for stem thickness).

Acc_no	Pedigree	Location	P_height	S_thick
IS-01002	Gund	Maharashtra	187.6	16.0
IS-01015	—	Haryana	200.03	21.0
IS-01018	IC-3666	Haryana	193.3	21.0
IS-01023	Delhi Local	Delhi	228.3	16.0
IS-01029	Ramkel	Maharashtra	271.3	31.0
IS-01036	Palitina Dholiao	Gujrat	109.3	31.0
IS-01047	CO18	Tamil Nadu	192.0	16.0
IS-01113	Baligaon	Bihar	199.0	31.0
IS-01015	Bhindi Loha	Maharashtra	130.0	16.0

The file names and field names used are –

1. Sorghum. dbf as filename1
2. Accession. ndx as filename2
3. Dupli. dbf as filename3
4. Acc_no as fieldname1

After replacing these file names and field names in the program of duplicates, it can be run and a list of duplicates can be taken from the database file Dupli. dbf (for the present example, only one duplicate i.e. IC-01015 will be stored in this file).

Sorting and analysis of data

Depending upon the requirement, one can disturb the sequence of data records by sorting them on a particular field(s), say arranging the data records on the basis of increasing order of accessions. Before the data is subjected to sorting and statistical analysis, it is of utmost importance to have a duplicate listing of original data on some storage device so that the original data can be further used in future or in accidental damage while processing the data. Depending upon the number of descriptors, in case of larger field length it may be separated into two parts-passport data and characterization and preliminary evaluation data.

To gather some more important information, the data should be subjected to statistical analysis using standard packages, viz., MSTAT-C, Lotus 1-2-3, Statgraf, Spar 1, Harward Graphics, Microstat etc. These packages can be utilised for presenting the information in histograms, bar diagrams, pie charts, regression analysis, correlation analysis, measures of central tendency and dispersion (mean, range, skewness, kurtosis, coefficient of variation

etc.), path analysis, stability analysis etc. Statistical analysis will enable the user in querying the database on individual and interrelated descriptors for selecting the desirable accessions for utilisation in crop improvement programs. For augmented design, the adjusted treatment means may be obtained by using Augment 1 package (Sapra and Agrawal, 1992) and may be incorporated in the data file as a separate field. These adjusted means should be used for further retrieval and querying purposes. The outcome of the analysis is presented in a suitable form by adding table headings, legends etc. Such modification is possible by using some text editor(s).

For computing the frequency distribution of qualitative descriptors e.g. country, state, district, colour, leaf type etc. the following dBASE III Plus program may be utilised.

```
SET TALK OFF
USE filename1
INDEX ON fieldname1 TO filename2
SELECT A
    USE filename1 INDEX filename2
SELECT B
    USE filename3
ZAP
SELECT A
GO TOP
temp1=fieldname1
SKIP
FRQ=1
DO WHILE .NOT. EOF ( )
    IF fieldname1=temp1
        FRQ=FRQ+1
    ELSE
        temp2=fieldname1
        SELECT B
        APPEND BLANK
        REPLACE fieldname2 WITH temp1, fieldname3 WITH FRQ
        temp1=temp2
        FRQ=1
    SELECT A
ENDIF
SKIP
ENDDO
```

```

SELECT B
  APPEND BLANK
    REPLACE fieldname2 WITH temp1, fieldname3 WITH FRQ
CLOSE ALL
SET TALK ON

```

In this program, characters in italics can be replaced by the user according to the choice.

Characters in italics	Explanation
Filename1	data file
Filename2	file to store indexed information on <i>fieldname1</i>
Filename3	file to store frequencies (must be created before using the program)
Fieldname1	field name for which frequencies are to be computed (from <i>filename1</i>)
Fieldname2	field name in <i>filename2</i> defining the field corresponding to <i>fieldname1</i> of <i>filename1</i>
Fieldname3	field name in <i>filename2</i> to store the frequencies

Example — In the earlier mentioned data (after removing the last record which is a duplicate accession), frequencies of accessions according to location can be calculated by replacing the following file and field names in the above mentioned program.

```

Sorghum. dbf as filename1
Location. ndx as filename2
Freq. dbf as filename3
Location as fieldname1
Location as fieldname2
Frequency as fieldname3

```

After the program is executed, file Freq. dbf will contain

Location	Frequency
Bihar	1
Delhi	1
Gujarat	1
Haryana	2
Maharashtra	2
Tamil Nadu	1

Querying and listing of data

To enable the user of a catalogue to select some promising accessions for important traits, some sample queries may be carried out using DBMS package and can be presented in a tabular form. For example, one can take list of accessions for forage sorghum, satisfying a query e.g. all accessions with days to 50 per cent flowering between 60 to 80 days, stem thickness less than 3 cm, number of leaves greater than 15 and forage yield greater than 2 Kg. (Mathur *et al.*, 1991). The list will include :

Accession number	Days to flowering	Stem thickness	Number of leaves	Fodder yield
IS-27087	72.0	2.83	15.2	2.2

A hard copy of the analysis part, querying part and passport and evaluation data may be taken by using some printing device. The duplication of print outs may be taken on offset printing, xerox machines etc.

The discussion above is extremely helpful in bringing out salient features of data and also systematically preparing a catalogue. Moreover, one can improve upon as per requirements and availability of resources.

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UNIQUE HIGH MOLECULAR WEIGHT GLUTENIN SUBUNITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

A.B. Damania and H. Altunji

Genetic Resources Unit
International Center for Agricultural Research in the Dry Areas
(ICARDA), PO Box 4566, Aleppo, Syria

High molecular weight (HMW) subunits of glutenin proteins in hexaploid wheats are responsible for the elasticity of the dough essential for good bread-making quality. Unique HMW subunits of glutenin were detected in certain varieties of bread wheat of Japanese origin when single seeds of the same were evaluated for their gliadin banding patterns using electrophoretic screening techniques. These glutenin subunits could be utilized for grain quality improvement of cultivars through hybridization with promising bread wheat lines possessing other desirable attributes such as tolerance to biotic and abiotic stresses.

Bread wheat, *Triticum aestivum* L., is one of the most important crops in the West Asia and North Africa with an average yearly regional production of 63.4 million metric tonnes according to the Food and Agriculture Organization of the United Nations (FAO, 1992). The improvement of its industrial quality is, therefore, one of the principal breeding objectives in most bread wheat breeding programmes. To support plant improvement, landraces, old varieties and primitive forms have been extensively collected and preserved as a valuable current and future source of variation for desirable traits.

HMW glutenin is the storage protein (prolamin) constituent of bread wheat flour which gives elasticity to the dough prior to baking and hence contributes towards good bread-making quality. It comprises at least 12 different subunits which are easily separated by sodium dodecyl sulphate (SDS)-polyacrylamide gel electrophoresis (PAGE). Some of these subunits have been extensively

studied since they are important for industrial bread-making quality (Burnouf and Bouriquet, 1980; Payne *et al.* 1979, 1980). Unique HMW subunits in certain previously cultivated Japanese bread wheat varieties were reported by Payne *et al.* (1983). These subunits had by far the lowest relative mobility and, therefore, probably the highest molecular weight of any HMW subunit of glutenin so far described in hexaploid wheat. Results of an electrophoretic evaluation of a collection of varieties of bread wheat and new sources for HMW glutenin proteins which could be used to improve bread-making quality of wheats is described in this article.

MATERIALS AND METHODS

A collection of 130 previously cultivated Japanese bread wheat varieties was donated to the Genetic Resources Unit (GRU) of the International Center for Agricultural Research in the Dry Areas (ICARDA) by the gene bank at the National Agriculture Research Center, Tsukuba, Japan. These varieties were screened electrophoretically with an aluminium lactate PAGE system, which revealed HMW gliadin storage protein banding coded by genes located on the short arm of chromosome 1D, using the method described by Tkachuk and Mellish (1980). Subsequently, the existence of the HMW glutenin subunits coded by genes located on the long arm of the 1D chromosome was confirmed experimentally using the SDS-PAGE technique described by Bietz *et al.* (1975).

RESULTS AND DISCUSSION

Using aluminum lactate PAGE analysis in our experiment it was found that the varieties Akasabi Shirazu, Aoba Komugi, and Shirasagi Komugi possessed the unique HMW gliadin subunits. The screening was repeated with SDS-PAGE when the variety Shirasagi Komugi clearly confirmed the presence of HMW glutenins (Fig. 1). Canadian bread wheat cv. Marquis and U.S. bread wheat cv. Chinese Spring, and wild relative *Aegilops umbellulata* were used for comparison.

Although such HMW glutenins have been reported previously in *Aegilops umbellulata* and other diploid *Aegilops* species such as *Ae. longissima*, and tetraploids *Ae. peregrina* and *Ae. kotschy* (Galili *et al.*, 1988), they have been detected only once in hexaploid cultivated bread wheats (Payne *et al.*, 1983). However, it is unlikely that these subunits appear in Japanese varieties owing to

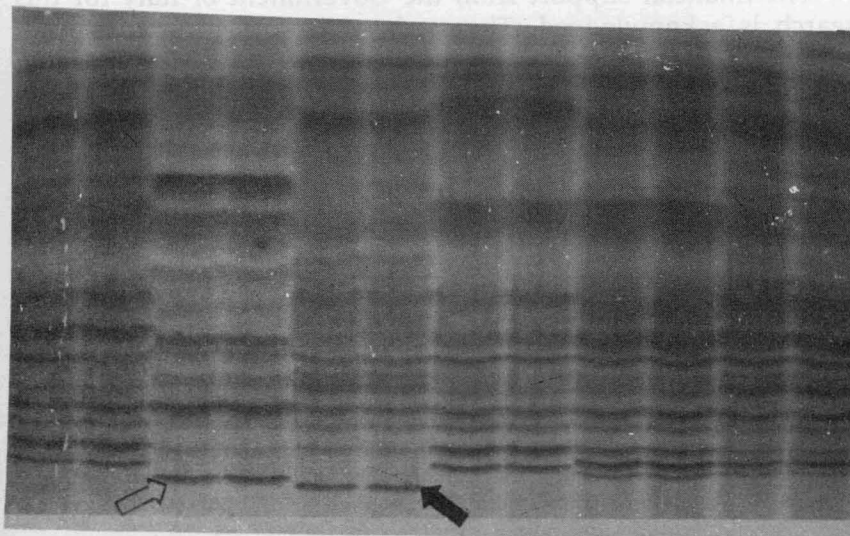


Fig. 1 : Electrophoregram of glutenins using SDS-PAGE technique. The samples are from left to right in twin tracks on the gel: *Triticum aestivum* cv. Marquis; Japanese varieties Akasabi Shirazu, Aoba Komugi, and Shirasagi Komugi (dark shaded arrow shows the very HMW glutenin band); *Aegilops umbellulata* also poses HMW glutenin but with a slightly higher mobility (unshaded arrow); and *T. aestivum* cv. Chinese Spring.

outcrossing with a diploid wild progenitor because (i) *Aegilops* species do not occur naturally in Japan (M. van Slageren, pers. comm.), and (ii) the relative mobility (R_m) of the HMW band in *Ae. umbellulata* is not sympatric with the HMW band of Shirasagi Komugi (Fig. 1). The novel subunits, it is hypothesized, may have arisen as a result of a recent gene mutation within the Japanese bread wheats rather than from any outcrossing which may have taken place in the field.

We hope to transfer these subunits through hybridization to other good quality and stress-tolerant bread wheat varieties in order to look at the possibility of improving extensibility (elasticity) of dough. After several generations of backcrossing with the selected good quality stress-tolerant breeding line parents, it could be possible to observe the positive effect of this unique HMW subunit on bread-making quality.

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**PATTERN OF GENETIC DIVERSITY AND
VARIABILITY IN PROSO MILLET
(*PANICUM MILLACEUM* L.)**

**S. Ganga Prasad, G.S. Siddaraju, A. Seetharam and
B.T.S. Gowda**

AICRP on Small Millets
UAS, GKVK, Bangalore – 560 065

*One hundred proso millet (*Panicum miliaceum* L.) germplasm which included 50 from erstwhile USSR and 50 from India, were evaluated for variability and magnitude of genetic divergence using Mahalanobis's D^2 analysis. Genetic variability was substantial for nodal, basal and main tiller yield in both Indian and USSR accessions, while for grain yield per plant, it was high in USSR accessions and moderate in Indian germplasm. In contrast, it was high for flag leaf area in Indian and moderate in USSR accessions. For number of basal tillers, it was moderate in both groups of accessions. For rest of the characters variability was low in both the groups. The D^2 analysis grouped all accessions into 8 clusters. The USSR accessions were distributed in 4 clusters and Indian in 6 clusters. The characters — days to 50 percent flowering, days to maturity, peduncle length, nodal tiller yield, basal tiller yield, main tiller yield and flag leaf area — which showed high genetic variability also contributed for genetic divergence. Geographical diversity was found associated with genetic diversity.*

Proso or common millet (*Panicum miliaceum* L.) is grown over 0.2 million hectares in India and is important because of its assured harvest in areas of low rainfall. The erstwhile USSR with an area of over 3 million hectares is the largest producer of proso millet in the world. Considering the antiquity of cultivation, it is presumed that Proso millet was first domesticated in Eurasia in the area falling in Central Asia, Afghanistan and India. Later, it moved westwards to Europe and eastwards to East Asia, during which

period gradual genetical differentiation took place (Sakamoto, 1987). Attempt has been made to compare the variability and magnitude of genetic diversity between Indian and erstwhile USSR accessions in the present studies.

MATERIAL AND METHODS

The material for the present investigations comprised 50 accessions from erstwhile USSR and 50 representative Indian accessions of proso millet. The 100 accessions were planted in 10×10 simple lattice design with two replications during summer 1988. Each accession was sown in a single row of 3 m length with a spacing of 22.5 cm between rows and 10 cm between plants within a row. Recommended agronomic practices were followed in raising the crop. Observations on the 15 metric traits were recorded on 10 random plants in each accession. Estimation of phenotypic and genotypic coefficient of variation was made as per the method suggested by Burton and Devane (1953). Multivariate analysis (Mahalanobis, 1936; Rao, 1952) was done on mean values for computing the genetic divergence between accessions and the D^2 values thus obtained were used for clustering the accessions using Tocher's method. The Wilks' lambda test criterion (Wilks, 1932) was used for testing the significance of genotypes.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the accessions for all the 15 characters in Indian and USSR accessions except main tiller yield in USSR accessions. Range, mean and coefficient of variability are presented in Table 1. The Indian accessions were superior to USSR accessions for all the fifteen characters except peduncle length and protein content. The higher GCV of 153.30 per cent was recorded for nodal tiller yield in USSR accessions as against 67.59 per cent in Indian accessions. Basal and main tiller yield recorded high GCV of around 50 per cent in both the groups. For yield per plant, the USSR accessions recorded high variability of 60 per cent compared to 36.49 per cent of Indian. The variability for basal tiller number was moderate in both the groups. The GCV was moderate for nodal tillers and peduncle length in Indian, while it was low in USSR accessions. For the remaining traits, the variability was low in both the groups.

Table 1 : Genetic parameters of 15 metric characters of USSR and Indian germplasm

Character		Range		Mean	PCV	GCV
		Min.	Max.			
Plant height (cm)	U	38.25	98.00	62.98	20.64	20.38
	I	53.71	133.60	94.41	16.47	15.60
Peduncle length (cm)	U	13.89	35.52	23.76	22.22	20.66
	I	7.24	24.99	14.26	36.26	33.74
Inflorescence length (cm)	U	8.50	23.68	15.20	25.29	22.57
	I	13.64	33.18	24.50	18.12	16.63
Number of primary inflorescence branches	U	3.62	8.87	6.64	18.96	16.39
	I	4.25	11.38	7.82	24.73	18.67
Number of nodal tillers	U	1.12	3.50	2.07	33.45	23.97
	I	0.43	5.50	2.75	49.75	37.99
Number of basal tillers	U	0.81	5.75	2.92	36.96	33.88
	I	1.08	6.69	4.05	39.69	35.84
Days to 50% flowering	U	23.00	31.50	26.26	7.86	7.49
	I	26.00	44.50	34.70	12.04	11.63
Days to maturity	U	56.00	70.55	63.05	6.46	5.48
	I	60.50	80.50	72.65	12.04	7.30
Flag leaf area (cm ²)	U	9.74	84.88	27.05	32.50	30.52
	I	15.13	92.89	39.68	54.02	53.32
Test weight (g)	U	3.60	7.60	5.06	18.77	15.31
	I	3.55	7.10	5.32	21.72	18.25
Protein content (%)	U	7.40	13.44	10.06	18.06	17.53
	I	6.90	13.10	9.86	16.76	16.59
Nodal tiller yield (g)	U	0.03	11.38	1.03	156.62	153.30
	I	0.25	4.80	1.60	73.89	67.59
Basal tiller yield (g)	U	0.18	3.33	1.69	58.43	53.55
	I	0.31	10.35	4.27	54.97	50.59
Main tiller yield (g)	U	0.30	4.43	1.29	58.75	53.67
	I	0.78	7.73	2.37	69.37	67.21
Yield/plant (g)	U	0.50	15.15	3.93	62.86	60.00
	I	2.21	17.50	8.23	39.07	36.49

U = USSR Accessions, I = Indian Accessions.

Based on D^2 values, the accessions were grouped into 8 clusters (Table 2). The 50 USSR accessions got distributed in 4 clusters and 50 Indian accessions in 6 clusters. Cluster I has been formed with 55 accessions of which 47 are of USSR origin and 8 are of Indian origin. The cluster II composed 29 accessions — 1 USSR and 28

Table 2 : Formation of clusters and accessions included in each cluster

Cluster number	No. of Strains	Accession number of entries
I	55	EC212510, EC212532, EC212512, EC212542, EC212521, EC212520, BTC-2, EC212525, EC212494, GPms 380, EC212508, EC212482, GPms 554, EC212502, EC212500, EC212483, EC212524, EC212515, EC212503, EC212492, EC212522, EC212531, EC212519, EC212530, EC212539, EC212504, EC212499, EC212498, EC212536, EC212501, EC212520, EC212527, EC212486, EC212514, EC212487, EC212495, EC212535, EC212496, GPms 589, EC212517, EC212511, EC212535, EC212540, BTS-1, EC212484, EC212518, EC212491, EC212506, EC212529, GPms 507, EC212485, GPms 510, GPms 509, GPms 383, GPms 553
II	29	GPms 446, GPms 454, GPms 387, GPms 393, GPms 365, GPms 495, GPms 398, GPms 391, GPms 399, GPms 466, GPms 390, GPms 450, GPms 430, GPms 482, GPms 438, GPms 441, GPms 396, GPms 368, GPms 397, GPms 432, GPms 514, GPms 392, GPms 575, GPms 506, GPms 570, GPms 382, EC212489, GPms 367, GPms 510
III	8	GPms 373, GPms 378, GPms 512, GPms 374, GPms 377, GPms 376, GPms 458, GPms 370
IV	3	GPms 384, GPms 388, GPms 389
V	2	GPms 372, GPms 375
VI	1	GPms 385
VII	1	BTS-3
VIII	1	EC212545

Indian. Cluster III, IV and V have 8, 3 and 2 Indian accessions, respectively. The remaining 3 clusters were solitary ones with cluster VI having one Indian accession and Cluster VII and VIII having one USSR accession each. Around 40 per cent of the D^2 were non-significant suggesting that an equal amount of the germplasm could be genetically similar. However, the remaining 60 per cent showed greater distance and greater diversity. The USSR accession EC212545 was most distant from the rest. The cluster wise mean value for the fifteen characters are presented in table 3.

The Z values obtained for character means for two nearest clusters (I and VII) and two distant clusters (III and VIII) are presented in a profile graph (Fig. 1). It could be seen from the graph that the cluster I and VII have a similar trend for most of the characters while the distant clusters III and VIII indicated an opposite trend in majority of the characters such as peduncle length,

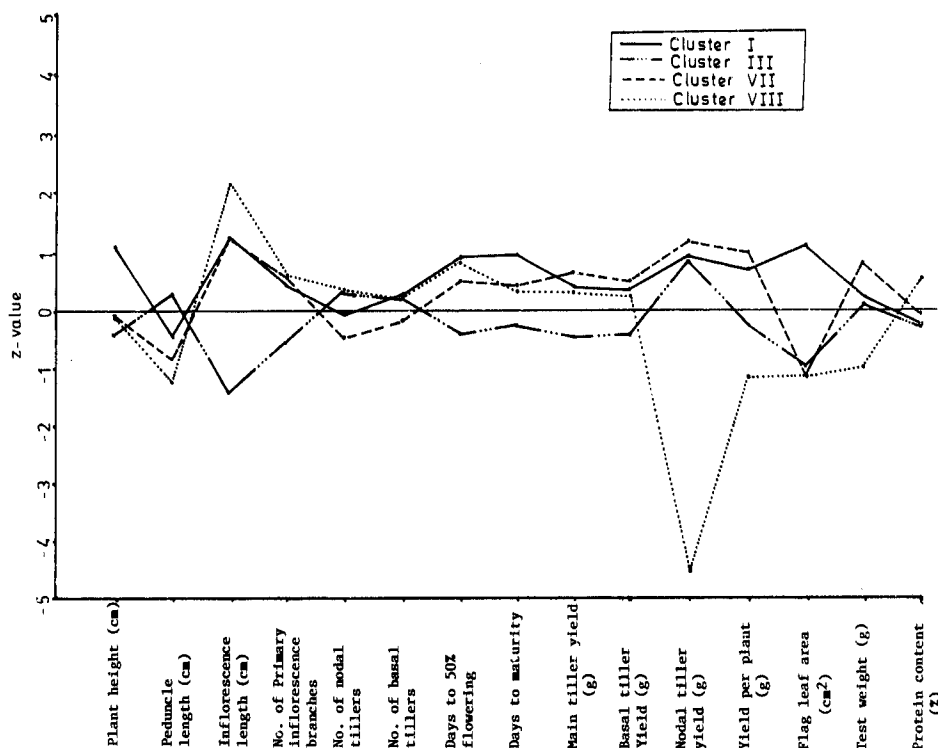


FIG. 1 : THE PATTERN OF DEVIATIONS OF MEANS OF FOUR CLUSTERS (Z values) FOR THE CHARACTERS

Table 3 : Mean values of the 15 characters for the 8 clusters

Char- acters		Plant height (cm)	-Ped- uncle length (cm)	Inflo- res- cence length (cm)	No. of primary Inflores- cence branches	No. of nodal tillers	Days to 50% flow- ering	Days to matu- rity	Main tiller yield (g/pl)	Basal tiller yield (g/pl)	Nodal tiller yield (g/pl)	Yield (g/pl)	Flag leaf area (cm ²)	1000 grain weight (g)	Protein content (%)
I		63.85	22.98	15.86	6.22	2.22	26.72	62.99	1.33	1.69	1.03	4.06	31.27	5.07	10.07
II		93.61	12.10	24.02	7.90	3.05	36.05	73.38	1.80	4.86	1.76	8.60	31.99	5.38	9.65
III		106.84	16.30	29.44	8.76	1.52	34.13	74.44	4.02	4.32	1.17	9.57	79.13	5.28	10.23
IV		93.45	12.03	24.65	7.56	3.23	37.83	72.83	4.26	4.90	1.52	8.98	27.37	6.66	12.33
V		110.01	20.79	30.24	10.58	0.78	33.25	77.75	6.00	2.59	0.67	9.26	82.70	5.45	7.47
VI		103.18	13.12	30.31	6.94	1.87	34.00	80.50	1.47	2.47	4.80	8.27	41.05	5.70	9.29
VII		98.00	26.45	15.51	5.60	3.00	26.00	68.00	0.51	1.25	0.55	2.31	82.25	3.95	9.69
VIII		99.19	30.00	10.53	5.75	1.50	27.00	69.00	1.58	2.18	11.38	15.15	82.61	7.62	7.78
Mean		96.02	19.22	22.57	7.41	2.15	31.87	72.36	2.62	3.03	2.86	8.28	57.29	5.64	9.56
Variance		791.99	79.23	30.62	6.54	3.73	32.71	93.54	10.06	12.11	3.64	35.66	521.32	3.97	8.20
S.D.		28.14	8.90	5.53	2.56	1.93	5.72	9.67	3.17	3.48	1.91	5.97	22.83	1.99	2.86

TABLE 3

inflorescence length, number of primary inflorescence branches, days to 50 per cent flowering, days to maturity, main tiller yield, nodal tiller yield, yield per plant, test weight and protein content and these were largely responsible for the genetic divergence. The plant height and basal tiller yield contributed little towards divergence.

Cluster analysis revealed certain relationship between genetic and geographic diversity. The Indian and USSR accessions forming solitary clusters VI, VII and VIII with accessions, GPms 385, BTS 3 and EC212545, respectively are genetically more diverse. The involvement of these accessions in the recombination breeding programme should be highly rewarding. Hybridization of selected USSR and Indian proso millet accessions may help in combining favourable yield contributing characters to have complementary effect on seed yield.

The promising accessions of potential breeding value for different traits are listed in table 4.

Table 4 : Promising accessions of proso millet for specific traits

Traits	Accessions
1. Tall plants	: GPms 376, GPms 432
2. Long inflorescence	: GPms 370, GPms 374, GPms 375
3. High primary inflorescence branches	: GPms 361, GPms 370, GPms 374, GPms 375, GPms 392, GPms 482
4. High nodal tillers	: GPms 368, GPms 389, GPms 438
5. High basal tillers	: GPms 390, GPms 392, GPms 396, GPms 454, GPms 466
6. Early duration	: GPms 375, GPms 388
7. Large flag leaf	: GPms 378, GPms 373, EC212542
8. Bold seeds	: EC212545, GPms 353, GPms 466
9. High protein	: EC212495, EC212496, EC212529, GPms 389
10. High nodal tiller yield	: EC212545,
11. High basal tiller yield	: GPms 368, GPms 390
12. High main tiller yield	: EC212489, GPms 379, GPms 399
13. High yield per plant	: GPms 370, EC212545

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VARIABILITY AND CORRELATED RESPONSE IN MUNGBEAN

B.R. Choudhary and P. Joshi

Agricultural Research Station,
Rajasthan Agricultural University, Mandor, Jodhpur – 342 304

Analysis of variance for nine quantitative characters in 45 genotypes of mungbean showed significant variability. Primary branches per plant, pods per plant and seeds per pod had high genotypic coefficient of variation (GCV) coupled with moderate to high estimates of heritability, expected genetic advance and maximum correlated response in yield. This shows that effective selection for improvement of these characters is possible and are important for mung bean improvement.

Mung bean (*Vigna radiata* L. Wilczek) is an important source of protein in vegetarian diet of Indian population and is particularly preferred for invalids and infants for its easy digestibility and non-flatulence properties. Though, much work has been reported on variability aspects but information on correlated response in yield (CRY) and relative selection efficiency (RSE) of different traits in this crop is lacking. Thus present studies were undertaken to assess the genetic variation in the available germplasm of mungbean alongwith the correlated response in yield and relative selection efficiency to test the suitability of various traits for making their use in improvement of this crop.

MATERIALS AND METHODS

Forty five strains of mung bean were grown at Agricultural Research Station, Mandor, Jodhpur during *kharif* rainy season of 1990 using randomized block design with three replications. The plot size was 5.0m × 1.5m with the crop geometry of 30cm × 10cm. Ten randomly selected plants from each plot of each replication were used to record observations on nine quantitative characters,

viz., days to flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 1000 seed weight (g), and seed yield per plant (g). Variability parameters such as genotypic variance (V_g), phenotypic variance (V_{ph}), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability in broad sense (H), were calculated by the method proposed by Johnson *et al.*, (1955). Expected genetic gain expressed as per cent of mean, (ΔG), correlated response in yield (CRy) and relative selection efficiency (RSE) were computed assuming 5 per cent selection intensity using the procedure suggested by Searle (1965).

RESULTS AND DISCUSSION

The statistical analysis revealed highly significant differences among the genotypes for all the attributes. Plant height and pods/plant showed wide variation (Table 1). Plant height recorded maximum phenotypic variance whereas, primary branches per plant showed minimum variation both at the genotypic and phenotypic levels. The GCV and PCV were the highest for secondary branches per plant (23.12, 35.64). The characters like pods per plant, seed yield per plant and plant height also showed comparatively higher GCV and PCV. These results are in agreement with those reported by Singh and Malhotra (1970) and Veeraswamy *et al.*, (1973). There was closeness between the GCV and PCV of 1000-seed weight, showing higher resistance to environmental influence as compared to other traits. But, seed yield per plant revealed a high degree of disparity and indicated that the yield was highly influenced by the environment. Further, the lowest values of coefficients of variation (GCV and PCV) for days to maturity indicated lesser scope of its selection.

The heritability estimates were high for 1000 seed weight and plant height suggesting the possibility of selection response based on their phenotypic expression, while heritability of seed yield and secondary branches per plant were low suggesting that these traits were highly influenced by environment. Days to flowering, days to maturity, primary branches per plant, pods per plant and seeds per pod exhibited moderate to high values of heritability. High heritability estimates were reported for plant height and pods per plant (Chowdhry *et al.*, 1971) and for days to 50 per cent flowering, plant height, branches per plant, pods per plant and 1000 seed weight (Reddy *et al.*, 1991).

Table 1 : Range, mean, variability components, correlated response and relative selection efficiency for various characters in mungbean

Characters	Range	Mean $\pm$ SE	V_g	V_{ph}	GCV (%)	PCV (%)	H (%)	(G)	CRy	RSE
Days to flowering	37.7-54.7	46.5 $\pm$ 2.16	11.53	18.55	7.30	9.26	62.15	4.48	-74.63	-0.36
Days to maturity	86.7-98.3	94.4 $\pm$ 1.45	4.51	7.67	2.25	2.93	58.83	1.70	-51.40	-0.26
Plant height (cm)	38.3-77.0	52.2 $\pm$ 2.87	18.61	93.94	17.31	18.57	86.88	7.70	8.84	0.03
Primary brachches/plant	6.0-9.0	7.5 $\pm$ 0.52	0.49	0.90	9.33	12.60	54.80	11.81	16.88	0.09
Secondary branches/plant	1.3-5.0	3.8 $\pm$ 0.75	0.61	1.45	23.12	35.64	42.10	24.34	0.52	0.01
Pods/plant	17.3-45.7	30.2 $\pm$ 3.38	40.96	58.07	21.18	25.22	70.54	10.09	40.52	0.17
Seeds/pod	8.3-13.6	10.4 $\pm$ 0.53	0.80	1.22	8.54	10.60	65.03	10.47	68.53	0.33
1000-seed weight (g)	29.4-47.2	34.6 $\pm$ 0.74	11.99	12.80	9.97	10.32	93.64	7.46	31.64	0.10
Seed yield/plant (g)	3.2-8.5	5.2 $\pm$ 1.05	0.95	2.62	18.77	31.14	36.35	14.05	—	—

The suitability of characters for direct and indirect selection may be judged by the expected genetic gain (G) and correlated response in yield (CRY), respectively (Table 1). The expected genetic gain (G) was the maximum for secondary branches per plant (24.34%) followed by seed yield per plant, primary branches per plant, seeds per pod and pods per plant; and it was the lowest for days to maturity. Maximum correlated responses in yield were expected through selection on seeds per pod (68.53%). This character also had comparatively higher value of the expected relative selection efficiency.

Primary branches per plant, pods per plant and seeds per pod had high GCV coupled with moderate to high estimates of heritability, expected genetic advance as per cent of mean and maximum correlated response in yield. It indicates that selection may effectively be based on these characters and their phenotypic expression would be good indicator of the genotypic potentiality. Therefore, these traits would deserve weightage while formulating selection programme in mungbean.

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GENETIC DIVERGENCE IN INTERSPECIFIC HYBRIDS OF SUGARCANE

O.U.K. Reddy and K.G. Somarajan

Sugarcane Breeding Institute, Coimbatore

Forty six interspecific hybrids of sugarcane derived from crosses involving various species were evaluated and grouped into eleven clusters, indicating high genetic diversity among them. Though there was no clear cut differentiation between clusters with reference to species, to some extent, dispersion of hybrids in various clusters was in accordance with their species origin. Based on inter-cluster distances and cluster means for various characters, potential parents were identified from different clusters for hybridization programme.

Breeders have constantly sought to increase the selection gains for various characters through the introduction of new genes from available germplasm. Successful exploitation of the sugarcane genetic resources in the future will require careful evaluation of interspecific hybrid (ISH) clones with reference to genetic diversity. Stevenson (1965) opined that when the nobilization from recent collections of wild forms came into general use as breeding material, seedling populations of almost unbelievable genetic complexity will be common representing a veritable treasure house of *Saccharum* forms and offering interesting possibilities of recombination. He further stated that utilization of wide range of parental material in crossing programmes leads to heterotic segregants in progenies which in turn stand as successful commercial varieties whose value depends upon balance of genes instead of getting varieties through chance. Present investigation was to test such a group of interspecific hybrids for their divergence, in order to incorporate diverse material in sugarcane breeding programmes.

MATERIALS AND METHODS

Forty six clones derived from complex crosses utilizing various *Saccharum* spp. (Table 1) were grown in randomized block design

Table 1 : Details of experimental materials

Clone	Parentage		
I. <i>S. officinarum</i> × <i>S. barberi</i> (OB)			
ISH 236	Gungera	×	Khakai
ISH 237	Gungera	×	Khakai
ISH 239	Gungera	×	Khakai
ISH 241	Gungera	×	Khakai
ISH 245	Gungera	×	Khakai
ISH 247	Keong	×	Khakai
ISH 249	Keong	×	Khakai
ISH 250	Gungera	×	Khakai
ISH 258	Keong	×	Khakai
ISH 260	Keong	×	Khakai
ISH 261	Keong	×	Khakai
ISH 264	Keong	×	Khakai
ISH 265	Keong	×	Khakai
ISH 268	Keong	×	Khakai
ISH 269	Keong	×	Khakai
ISH 270	Keong	×	Khakai
II. <i>S. officinarum</i> × <i>S. robustum</i> (OR)			
ISH 273	51 NG 131 Str.	×	57 NG 133
ISH 274	51 NG 131 Str.	×	57 NG 133
ISH 275	51 NG 134	×	NG 77-34
ISH 278	NG 77-65	×	NG 77-221
ISH 280	51 NG 131 Str.	×	57 NG 133
III. <i>S. officinarum</i> × Commercial Hybrid (OH)			
ISH 18	Keong	×	MS 68/47
ISH 229	57 NG 222	×	Co 62174
IV. <i>S. officinarum</i> × <i>S. spontaneum</i> (OS)			
ISH 284	Green German	×	51 NG 2
ISH 288	Orambo	×	SES 275
ISH 289	NG 77-63	×	Holes I
V. <i>S. barberi</i> × Commercial Hybrid (BH)			
ISH 155	Pansahi	×	Co 1307
ISH 172	Ubawhite	×	Co 775
ISH 292	Kansar	×	MS 68/47
ISH 297	Pathri (Self 3)	×	Co 62174
VI. Commercial Hybrid × <i>S. barberi</i> (HB)			
ISH 126	Q 68	×	Khakai

VII. Commercial Hybrid $\times$ *S. spontaneum* (HS)

ISH 128	Co 62174	$\times$	IMP 1532
ISH 307	Co 62174	$\times$	51 NG 2

VIII. Commercial Hybrid $\times$ *S. robustum* (HR)

ISH 282	Q 68	$\times$	28 NG 289
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IX. Hybrids from complex Crosses

ISH 1	CoC 671 $\times$ (57 NG 110 $\times$ NG 77-28)	H/OR
ISH 4	(Saipan G $\times$ Co 62174) $\times$ (51 NG 77 $\times$ 57 NG 45)	OH/OR
ISH 5	(Q 68 $\times$ Khakai) $\times$ (51 NG 199 $\times$ NG 77-55)	HB/OR
ISH 9	Co 7229 $\times$ (Mont 1585 $\times$ NG 77-28)	H/OR
ISH 10	(Q 68 $\times$ Khakai) $\times$ (Q 68 $\times$ 28 NG 289)	HB/HR
ISH 19	Co 7201 $\times$ (CP 61-39 $\times$ NG 77-170)	H/HR
ISH 20	Co 7201 $\times$ [CoC 671 $\times$ (57 NG 110 $\times$ NG 77-28)]	H/H/OR
ISH 23	Co 419 $\times$ [CoC 671 $\times$ (57 NG 110 $\times$ NG 77-28)]	H/H/OR
ISH 24	Co 7201 $\times$ (CP 61-39 $\times$ NG 77-170)	H/HR
ISH 25	Co 7201 $\times$ (CP 61-39 $\times$ NG 77-170)	H/HR
ISH 58	Co 7201 $\times$ [CoC 671 $\times$ (57 NG 110 $\times$ NG 77-28)]	H/H/OR
ISH 59	Co 7201 $\times$ [CoC 671 $\times$ (57 NG 110 $\times$ NG 77-28)]	H/H/OR

with three replications at Sugarcane Breeding Institute, Research Centre, Jamkhandi in 1990-91. Each clone was grown in a 3 row plot; each row was of 6 m length and spaced 90 cm apart. Twenty four three-budded setts were planted in a row at equal distance. The trial was harvested after 360 days and the data on 12 quantitative characters (Table 4) were recorded by adopting standard procedures.

The data were subjected to analysis of variance as well as D^2 analysis as suggested by Mahalanobis (1936). Test of significance of difference with regard to the pooled effect of all the characters was carried out by using Wilk's lambda criterion (Wilks, 1932).

RESULTS AND DISCUSSION

The dispersion between the variables was highly significant as tested by Wilk's criterion ($\chi^2_{540} = 881.05$). The D^2 values for different pairs of genotypes ranged from 1.53 to 562.68. All the 46 genotypes were grouped into 11 clusters (Table 2). Though there was no clear cut differentiation between clusters with reference to species, all complex hybrids (H/OR, OH/OR, HB/OR, HB/HR, H/HR, H/H/OR) were distributed in few clusters viz., I, II, V and VII. Clones from OB group predominantly were distributed in clusters III, V and VI. Likewise, Gupta and Singh (1970) showed that the parentage had definite effect on clustering pattern.

Table 2 : Cluster means for various characters

Sl.No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
1. NMC/plot	34.73	39.50	50.62	68.13	33.53	42.06	56.67	40.67	28.67	36.67	110.67
2. Yield (Kg/plot)	26.89	36.82	32.11	30.83	28.49	30.19	38.27	26.00	37.20	23.23	31.00
3. Brix (%)	18.78	19.26	16.79	17.34	17.70	14.21	18.56	22.88	18.79	13.29	12.49
4. Sucrose (%)	17.05	18.11	14.53	14.26	15.19	11.17	16.09	19.84	16.42	9.40	8.79
5. Purity (%)	90.52	94.02	86.30	82.25	85.66	78.42	92.50	86.81	86.80	70.71	70.31
6. CCS (%)	11.94	12.86	10.02	9.53	10.56	7.26	12.16	13.59	11.29	5.72	5.33
7. CCS (Kg/plot)	3.16	4.76	3.19	2.96	2.88	2.15	4.72	3.50	4.15	1.38	1.65
8. Cane diameter (cm)	2.50	2.63	2.20	1.75	2.48	2.22	2.28	2.13	3.17	2.20	1.57
9. S.C. Wt (Kg)	0.86	0.93	0.65	0.48	0.92	0.78	0.66	0.62	1.37	0.71	0.31
10. Cane length (m)	1.79	1.80	1.88	1.93	1.81	1.95	1.86	1.43	1.83	2.16	2.00
11. Extract (%)	46.92	49.70	46.23	37.56	50.15	45.77	53.90	44.76	51.19	34.69	34.23
12. Internode number	16.39	16.11	18.29	6.33	19.53	19.73	15.33	13.33	19.00	19.00	16.00

TABLE 2

Intra-cluster distances ranged from 3.50 to 7.28 (Table 3). The highest intra cluster distance was recorded for cluster VI followed by cluster VIII and the lowest for clusters I, II, III, IV and V respectively. Since cluster IX, X and XI were having only one clone each, their intra-cluster distances were zero. The inter-cluster distances were higher than intra-cluster distances in all cases. The highest inter-cluster distance was recorded between IX and XI cluster (23.72) and the lowest between I and II (4.22).

Table 3 : Grouping of various clones into different clusters

Cluster	Clones
I.	ISH 9, ISH 59, ISH 4, ISH 265, ISH 245, ISH 128, ISH 289, ISH 24, ISH 172, ISH 19, ISH 126
II.	ISH 229, ISH 20, ISH 25, ISH 58, ISH 1, ISH 18
III.	ISH 269, ISH 275, ISH 250, ISH 237, ISH 239, ISH 307, ISH 264
IV.	ISH 284, ISH 273, ISH 274, ISH 280, ISH 155
V.	ISH 241, ISH 10, ISH 236, ISH 270, ISH 261
VI.	ISH 260, ISH 269, ISH 258, ISH 268, ISH 247
VII.	ISH 292, ISH 23, ISH 5
VIII.	ISH 282
IX.	ISH 297
X.	ISH 278
XI.	ISH 288

Based on inter-cluster distances (D values), the clusters XI, X, IX and VIII were found to be highly divergent from all the clusters. Hence, the types from these clusters when crossed with the types from other clusters may result in high heterosis. Murthy and Anand (1966) claimed that there was a positive relationship between the specific combining ability and the degree of genetic diversity.

Cluster mean of number of millable canes was high for cluster XI followed by cluster IV (Table 4). Cluster mean of cane yield was high for cluster II followed by cluster VII. Sucrose and brix were high for cluster VIII. Such clustering pattern could be utilized in choosing parents for cross combinations likely to generate the highest possible variability for various economic characters as also

Table 4 : Inter and intra-cluster genetic distance (D values)

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	3.50	4.22	5.84	9.46	8.16	7.72	5.81	6.20	6.81	11.33	19.38
II		3.89	7.08	10.97	5.37	8.66	6.28	6.71	6.11	12.16	20.75
III			3.86	6.88	12.25	6.49	5.92	9.12	10.40	10.46	16.28
IV				3.90	9.56	9.08	8.39	11.48	14.71	11.68	12.65
V					4.25	6.97	6.44	7.72	7.00	11.25	19.46
VI						7.28	8.71	10.81	10.77	7.58	16.53
VII							5.95	7.82	10.03	12.18	18.35
VIII								6.68	8.61	13.28	20.83
IX									0.00	13.51	23.72
X										0.00	15.62
XI											0.00

reported by Endany *et al.*, (1977). As series of polycrosses based on high mean values may prove to be highly fruitful.

Hybridization programme which includes complex hybrids from cluster II, F₁s of commercial hybrid x *S. robustum* from cluster VIII and F₁s of *S. officinarum* x *S. spontaneum* from cluster XI are expected to produce superior and diverse segregants.

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GENETIC DIVERGENCE IN FRENCH BEAN (*PHASEOLUS VULGARIS* L.)^{*}

B.D. Joshi and K.L. Mehra¹

National Bureau of Plant Genetic Resources
Regional Station, Phagli, Shimla-171 004

Genetic variation providing wide opportunities for the improvement of autogamous crop plants through hybridization and heterosis is known to depend on extent of genetic diversity between the parents. In India, information on studies on genetic divergence in French bean is lacking. Hence, Mahalanobis's D^2 analysis was carried out in the present study on 42 genotypes of French bean to estimate the extent and nature of genetic diversity.

Forty two accessions of French bean were sown in single row plots, during *Kharif* (July-October) seasons of 1979 and 1980, in a randomised complete block design with four replications. The rows were 2.25m long, spaced 50cm apart and with seeds dibbled 15cm apart within rows. Five randomly selected competitive plants, in each replication, were used for recording data on days to flower, days to maturity, plant height (cm), number of leaves, number of branches, number of clusters, number of pods, pod length (cm), number of seeds, 100 seed weight (g) and seed yield per plant (g). The average values of these characters were used for statistical analysis. Mahalanobis's (1936) generalised distance was used for the estimation of genetic divergence, as outlined by Rao (1952).

There were significant differences among the forty two genotypes which could be grouped into 11 clusters. Cluster 1 was the largest having 9 genotypes from different countries. Clusters II, III, IV, V, VI, VII and VIII consisted of 8,5,4,4,3,3, and 3 genotypes respectively, whereas cluster IX, X and XI were represented by a

^{*} Parts of Ph.D Thesis of the first author, submitted to Kumaon University, Nainital (U.P.)

¹. Ex Director, NBPGR, New Delhi-110 012

Table 1 : Distribution of 42 *Phaseolus vulgaris* genotypes in different clusters

Clusters	Varieties	Number	Geographic Origin
I	EC 19038, EC 24948, EC 31230, EC 36664, EC 42960, EC57080, Premier, PLB 14-1 and PLB 256	9	Mexico, USSR, USA, Australia, India.
II	EC 22365, EC 44760, EC 57260, EC 93621, EC 93828, EC 100677, EC 100680 and EC 108101	8	USA, Holland, Colombia.
III	EC 34023, EC 44758, EC 77005, EC 94455, and EC 109975	5	USA Brazil, Bulgaria.
IV	EC 44787, EC 44790, EC 93625 and. EC 99540	4	Canada, Colombia, U.K.
V	EC 26399, EC 43893, EC 44624 and EC 109977	4	Mexico, Japan, Canada, Brazil.
VI	EC 94453, EC 99541 and PLB 10-1	3	Bulgaria, U.K. India.
VII	EC 18611(B), EC 26402 and EC 43896	3	Nepal, Mexico, Japan.
VIII	EC 43900, EC 44747 and EC 94469	3	Japan, USA, Bulgaria.
IX	EC 18600	1	Nepal.
X	EC 109508	1	Australia.
XI	PLB 440	1	India.

TABLE 1

Table 2. Cluster means for 11 characters in French bean

Cluster	No. of leaves/plant	Plant height (cm)	No. of branches/plant	No. of clusters/plant	No. of pods/plant	Pod length (cm)	No. of seeds/plant	Seed yield/plant (g)	100-seed weight (g)	Days to flowering	Days to maturity
I	16.68	36.33	3.00	6.45	9.22	10.57	36.92	9.52	25.97	43.90	90.43
II	20.02	40.85	3.51	7.46	10.51	11.47	38.08	12.64	33.70	42.38	89.43
III	30.72	63.76	3.32	10.14	15.68	10.10	75.30	16.28	22.60	53.52	99.48
IV	28.40	44.59	3.45	10.40	17.47	8.32	71.92	12.22	17.12	52.25	95.30
V	20.46	46.43	3.13	6.90	8.96	12.43	31.80	16.36	5.76	44.26	92.56
VI	26.70	62.43	3.76	8.33	10.56	12.53	33.20	16.06	50.50	45.15	94.90
VII	27.83	47.33	3.66	8.80	12.46	12.80	40.20	15.33	38.20	50.70	98.50
VIII	30.10	73.62	3.22	10.92	16.15	10.65	62.55	18.77	30.25	53.47	101.20
XI	47.24	127.29	3.68	12.98	18.18	10.67	62.80	25.33	40.98	60.70	117.20
X	41.16	64.84	3.52	14.24	22.05	9.03	112.58	14.92	14.93	58.90	110.70
XI	38.94	111.96	3.20	9.15	13.49	9.80	60.74	14.99	23.97	61.30	112.35

TABLE 2

Table 3 : Intra and inter-cluster divergence $\sqrt{D^2}$ values in 42 varieties of French bean

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	2.62	6.34	12.09	13.83	12.91	10.21	9.40	11.20	20.08	19.61	21.29
II		<u>3.16</u>	10.14	9.66	18.78	11.22	13.64	12.07	26.63	16.80	20.92
III			<u>3.28</u>	6.10	21.31	13.07	18.62	7.78	21.15	8.85	13.17
IV				<u>3.77</u>	24.58	16.10	21.68	12.68	18.29	8.85	26.94
V					<u>3.79</u>	9.74	5.78	16.93	21.86	28.28	25.78
VI						<u>4.61</u>	7.92	10.00	20.12	19.99	19.65
VII							<u>4.60</u>	14.80	22.24	26.06	24.16
VIII								<u>6.35</u>	16.43	14.14	12.20
IX									0.00	25.10	12.90
X										0.00	15.51
XI											0.00

TABLE 3

single genotype from Nepal, Australia and India respectively (Table 1).

In general, the cultivars in cluster 1 were dwarf (Table 2). Cluster X represented by single genotype having the highest mean value for number of clusters (14), number of pods (22), number of seeds (112). EC 18600 of cluster XI gave the highest seed yield (25g). The genotypes earliest to flower (42 days) belonged to cluster II. Hundred seed weight was recorded the highest in cluster VI (50.5g). The earliest maturing genotypes fell in cluster II (89 days) and longest pod bearing genotypes in cluster VII (12.8 cm). Cluster IX was characterized by having a genotype with highest number of leaves (47.2). Cluster I, II, VI, VII, IX and X had genotypes that would prove useful in obtaining desirable recombinants for improving yield and its contributing characters. The genetic divergence (Table 3) was the maximum between cluster V and X (28.28), followed by IV and XI (26.94) and II and IX (26.63). Selecting such divergent genotypes for hybridization might result in better segregants and high heterotic response. The intra-cluster distance ranged from 0.00-6.35.

Considering high mean value alongwith high genetic distance, EC 109508, EC 43625, EC 43896, EC 44760, EC 24948, EC 18600 and PLB 440 were promising. These may be crossed in several combinations or in a complete diallel fashion to achieve high yield in French bean. D² analysis showed that genotypes possessing similar characteristics, though far separated geographically, have come together. Hence geographic diversity had no relation with genetic diversity. Perhaps these genotypes were subjected to the similar selection pressure for suiting to local requirements and adaptation. The genetic architecture of such populations could be the result of prolonged selection by various natural and artificial forces. Successful use of D² analysis to assess the relative combination of different components of yield to the total divergence and to determine the nature of forces operating at intra and inter-cluster levels have been emphasised by various workers in French bean (Froussios, 1970; Pegington, 1972; Singh *et al.*, 1991 and Vaid *et al.*, 1988).

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SCREENING OF SUNFLOWER GERMPLASM FOR RESISTANCE TO *ALTERNARIA* LEAF SPOT

Nagaraju, Suma C. Mogali and K. Virupakshappa

Project Coordinating Unit (Sunflower)
University of Agricultural Sciences
GKVK, Bangalore - 560 065

Leaf spot of sunflower caused by *Alternaria helianthi* has been considered as a potentially destructive disease of sunflower all over the world (Allen *et al.*, 1983; Balasubramhanyam and Kolte, 1980; Reddy and Gupta, 1977). Yield losses as high as 80 per cent have been reported under favourable weather conditions in India due to this disease (Agrawath *et al.*, 1979; Balasubrahmanyam and Kolte, 1980). Though destructive levels of *Alternaria* leaf spot have been reported in India, no concerted efforts were made to screen the available germplasm systematically to locate the field resistance, as no resistant sources are available against this disease both in cultivated as well as in related wild species of *Helianthus* (Morris *et al.*, 1983). Significant genetic variability to *Alternaria* leaf spot has, however, been reported in sunflower (Agrawath *et al.*, 1979; Carson, 1985; Nagaraju *et al.*, 1992a). The usefulness of the available level of resistance in reducing the loss caused by this disease, therefore, is of great importance. Thus, studies were carried out to screen the available sunflower germplasm in phased manner against this disease under field conditions.

One-hundred and ninety-six sunflower germplasm accessions selected from the Germplasm Unit, GKVK, Bangalore were evaluated against *Alternaria* leaf spot under natural epiphytotic conditions in the *kharif* season of 1991 along with the susceptible check, Morden. The selected germplasm entries were sown during third week of July 1991 in a randomised complete block design with two replications. Each entry was grown in a single row of 3 m length. Row to row and plant to plant spacings were 60 cm and 30 cm, respectively. *Alternaria* leaf spot severity was monitored in

the field from germination till 50 per cent grain filling stage of the crop. Final disease severity was assessed when most plants in a particular genotype were at 50 per cent grain filling stage. Disease severity was recorded on the basis of per cent leaf area affected using 0-9 scale (Nagaraju *et al.*, 1992b).

The germplasm lines varied in disease severity levels and none of the lines could be identified as immune or highly resistant to this disease. Thirty six accessions could, however, be categorised as field resistant with less than 5 per cent disease severity. These lines included accession nos. 1381, 1389, 1391, 1394, 1421, 1424, 1425, 1431, 1439, 1440, 1442, 1445, 1447, 1454, 1456, 1462, 1467, 1473, 1474, 1483, 1484, 1485, 1497, 1499, 1500, 1514, 1515, M 4908-5, M 733-4-2, M 744-8-4, M 733-10-3, M 733-10-4, M 733-10-6, BLC 15-7-1-1, BLC 15-7-1-3 and RLC 30-11-9-4.

The resistance of these lines needs to be confirmed under field and laboratory conditions. Similar results were obtained when another set of 100 genotypes was tested by Nagaraju *et al.* (1992a). This suggested that possibilities exist for utilizing these field resistant lines, in the absence of absolute resistance to the disease, in crop improvement programme and disease management.

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