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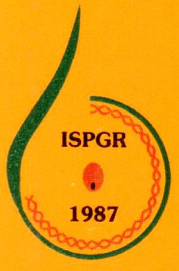

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Isolation and Characterization of Protease Inhibitor Gene by Construction of Genomic Library of Black Gram (*Vigna mungo* L.)

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Plant protease inhibitors (PIs) are small proteins abundant in storage organs such as seeds and tubers. They have been implicated in binding to proteases of insects and interfere with the digestive process, there by proving their insecticidal activity. Black gram is known to be a source of plant protease inhibitors. A genomic DNA library of Black gram variety Uttara was constructed in Fosmid vector. Primary and secondary screening of library using mung bean protease inhibitor gene as a probe resulted in isolation of recombinant clones containing protease inhibitor gene and promoter. The positive clones were further confirmed by PCR and subsequently sequenced. The nucleotide sequence of genomic clone was analyzed by Blastn algorithm of NCBI database and 5' upstream sequence was analysed *in-silico* by Place and Plant Care databases.

Key Words: Black gram, Genomic library, Plant protease Inhibitors, Promoter

Introduction

Black gram is an important pulse crop of many South Asian countries including India. In India black gram cultivation occupies 3.29 million ha and contributes 1.60 million tones to pulse production. Like other legumes black gram is also known to be a source of plant protease inhibitors. Plant protease inhibitors (PIs) are small proteins which represent a class of well studied compounds of plant defence genes and are abundant in storage organs such as seeds and tubers (Joanitti *et al*., 2006). Majority of PIs in plant kingdom occur in three main families *viz*., Fabaceae, Solanaceae and Poaceae (Ryan, 1990; Lawrence and Koundal, 2002). The PIs form complexes with proteases, thereby inhibiting their proteolytic activity. There have been many examples of PIs active against certain insect species both in *in-vitro* assays against insect gut proteases (Koiwa *et al*., 1998) and *in-vivo* artificial diet bioassays (Urwin *et al*., 1997; Vain *et al*., 1998).

A direct proof of the protective role of PIs against insect herbivores was provided by Hilder *et al.* (1987). The first transgenic tobacco plant expressing PI was reported in 1987 (Hilder *et al*., 1987). Since then a large number of transgenic plants have been developed using PIs. The genes of plant origin have added advantages, as they are correctly transcribed, translated and processed in the host plant after genetic transformation without any codon bias. Further more, it has been demonstrated that mechanical wounding, insect chewing and microbial infection enhanced the level of PIs content significantly in local as well as remote tissues (Telang *et al*., 2003, Srinivasan *et al*., 2009). Insect-resistant crops have been one of the major successes of applying plant genetic engineering technology to agriculture; Cotton (*Gossypium hirsutum*) resistant to lepidopteran larvae (Caterpillars) and maize (*Zea mays*) resistant to both lepidopteran and coleopteran larvae (rootworms) have become widely used in global agriculture and have led to reductions in pesticide usage and lower production costs increasing the crop yield substantially (Toenniessen *et al*., 2003). Single gene based genetic engineering is having major concerns of development of insect resistance. Many strategies to insect resistance management particularly to *Bt* toxins were proposed and reviewed (Gould, 1998) and holds good for all other transgenic too. Several strategies including tissue or time-specific expression of toxins, gene stacking/ pyramiding, mixtures, rotation or mosaics of transgenic plants, combination of toxins with different modes of action, refuge strategy and "trap plants" strategy were proposed for mitigating the advent of resistance in insects. Gene stacking/pyramiding demands genes and promoters for resistance management. Hence isolation and deployment of genes differing for mode of action is need of the hour. Plant protease inhibitors (PIs) which are known for insecticidal activity should be explored to have sustainable transgenic technology. Since the PIs are ubiquitous, there is tremendous scope for finding specific PI which is toxic to a particular insect pest (Marchetti *et al*., 2000, Dunse *et al*., 2010). As genetic engineering of plants increases in complexity, an increased need for

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versatile promoters for direct expression of desirable transgenes in plants has arisen and indigenous to plant system promoters adds an advantage. So, In this study we have reported successful development of genomic library of Black gram variety Uttara, and isolation of protease inhibitor gene and 5' upstream sequences of the protease inhibitor gene.

Materials and Methods

Plant Material

Seeds of black gram (*Vigna mungo* L.) variety Uttara were collected from Indian Institute of Pulse Research, Kanpur. Seeds were sown in plastic trays and seedlings were raised in dark condition, and the 10 days old etiolated seedlings were used for genomic DNA isolation.

Construction of Genomic DNA Library

Isolation and Shearing of Genomic DNA

The good quality and high molecular weight DNA (~30 - 50 Kb) was isolated by the CTAB method (Doyle and Doyle, 1990). Around 25 µg genomic DNA of black gram was randomly sheared by passing it through a 200 µl small-bore pipette tip. The DNA aspirated and expelled from the pipette tip for about 100 times. Around 1-2 µl of sheared DNA was examined on a 20 cm agarose gel using the Fosmid Control DNA as a size marker.

End-Repair of the Insert DNA and Size Selection of the End-Repaired DNA

The end repair of the insert DNA was done using End-Repair Enzyme Mix according to the EPICENTER® Biotechnologies and size fractionation (more than 25 Kb) of end-repaired DNA using GELASE method as per the manufacturer's instructions. The concentration of extracted DNA was determined by running an aliquot of the DNA on an agarose gel using dilutions of known amounts of the Fosmid Control DNA as standard.

Ligation of the Insert DNA and Packaging of Recombinant Fosmid DNA

It is suitable to clone large fragments of genomic DNA in Copy Control™ Fosmid vector. The Copy Control Cloning System combines the clone stability afforded by single-copy cloning with the advantages of high yields of DNA obtained by "on-demand" induction of the clones to high-copy number. A 10:1 molar ratio of CopyControl PCC2FOS Vector to insert DNA was optimal. To ligate more than 25 Kb inserts to the Fosmid vector, 0.25 µg of insert for every 0.5 µg of vector was used. The ligation was incubated at room temperature for 4 hours.

Tittering the Packaged Recombinant Fosmid Clones

The titter of the phage particles (Packaged Copy–Control Fosmid Clones) was determined to calculate the number of plates and dilutions required to obtain a library. Different serial dilutions of the 1 ml of packaged phage particles were made with Phage Dilution Buffer (PDB) in sterile microfuge tubes. The infected EPI300-T1^R cells spread on an LB plate + 12.5µg/ml chloramphenicol and incubated at 37°C overnight to select for the CopyControl Fosmid clones. The colonies were counted and the titter of the packaged phage particles was calculated using following formula:

$$\frac{\text{(Number of colonies) x (Dilution factor) X (1,000 µl/ml)}}{\text{(Volume of phage plated [µl])}}$$

Screening of Genomic Library

The primary screening of genomic library for isolation of black gram PI gene and promoter was done using mung bean (*Vigna radiata*) PI as probe according to the methods of Davis *et al*. (1986) and Sambrook *et al*. (1989). The recombinant fosmid clones were inoculated in 96 well ELISA plates containing LB freezing media with chloramphenicol antibiotic (Master plate and replica plate) and incubated overnight at 37°C with shaking. Master plates were stored for alignment of positive clones and replica plates were centrifuged at 10,000 rpm for 5 min and pelleted colonies were dissolved in 20 µl of autoclaved milliQ water. About 5 µl of dissolved bacterial colonies were spotted onto Hybond-N+nylon membranes (Amersham) using 96 well grids plate and dried completely. Three solutions were used for washing of membranes after air drying, denaturation solution (1.5 M NaCl, 0.5 M NaOH), neutralization solution (1.5 M NaCl, 0.5 M Tris-HCl: pH 8.0) and buffer solution (2 x SSC). Each membrane was incubated and processed in a stepwise fashion; i.e., denaturation 2-5 min, neutralization 2-5 min and 2 x buffer solution 2-5 min with occasional gentle shaking. After washing, the membranes were dried again and crosslinked the DNA on to the membranes using a UV crosslinker. For primary and secondary screening the probes were labeled with P^{32} radioisotopes by random-primer labeling kit as per manufacturer's instructions (Stratagene, La Jolla, CA). Only those colonies which showed convincing hybridization signals on the autoradiogram were marked and the reference number of each colony was noted down.

Secondary screening was done to identify truly positive clones. The positive clones were further confirmed by PCR using mung bean protease inhibitor heterologous gene specific primers and subsequently sequenced (Chromous Biotech, Pvt. Ltd, India). The nucleotide sequence of genomic clone was analyzed by BLASTn algorithm of NCBI database. Further 5' upstream sequence of genomic clone was analysed *in-silico* by Place (Higo *et al*., 1999) and Plant Care (Lescot *et al*., 1999) databases.

Results and Discussion

Construction of Genomic DNA Library Isolation and End-Repair of the Insert DNA

For genomic library construction high molecular weight DNA isolation was very crucial. After passing genomic DNA through a 200 µl small-bore pipette tip for 100 times the correct size sheared DNA of more than 25 Kb was obtained. The End repair of the insert DNA generated blunt-ended 5'-phosphorylated DNA. The size-fractionation of the end-repaired DNA was done by running on a 20-cm long, 1% LMP (Low Melting Point) agarose gel at 30-35 V overnight (Fig. 1). This electrophoresis was performed in absence of ethidium bromide. The desired size DNA (≥25 Kb) was excised from the gel and extracted by GELase method.

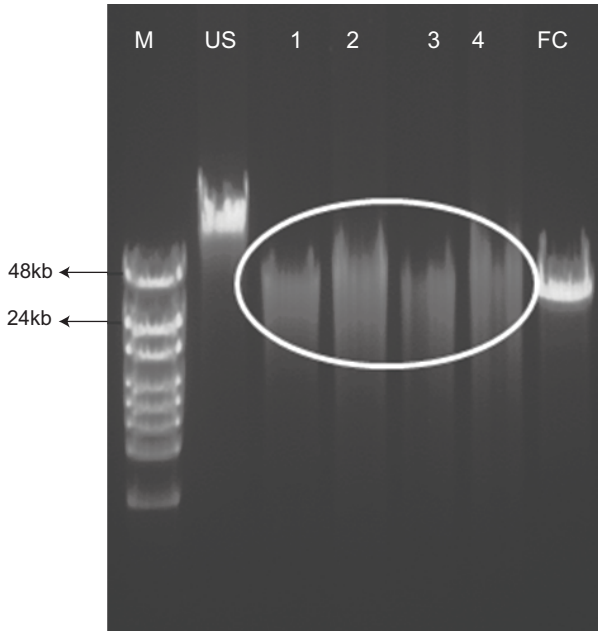

Fig. 1. Size fractionation of sheared genomic DNA

Ligation of the Insert DNA and Packaging of Recombinant Fosmid DNA

The gel extracted insert DNA was ligated with Copy Control™PCC2FOS Fosmid vector. Genomic library construction depends on efficient ligation. Since successful ligation can only be determined after infecting the phages with the host bacteria, higher the number of cfu/ml of the library, higher the efficiency of ligation. Using EPICENTRE® Biotechnologies Fast-Link DNA Ligase enzyme and buffer resulted in a titter of 3 x 10^5 to 1 x 10^6 cfu/ml, which was high. The recombined DNA was packaged using MaxPlax Lambda Packaging Extracts with high efficiency. Ligations were carried out at DNA concentrations of 0.2 µg/µl which favors concatemers and efficient packaging. The care was taken ensuring that the colony forming units were the same for every dilution. The titter of colonies of Uttara library was around 3 x 10^5 to 1 x 10^6 cfu/ml in different tubes with the same ligation product.

Screening of Genomic Library

The genomic library was screened by using mung bean PI heterologous gene specific probe. After primary screening positive signals were found and the reference number of each positive colony was traced out. The each positive colony lifted from the primary screening was passed through secondary screening with the same probe. After secondary screening each positive colonies were found to be very distinct and it was very easy to locate the individual positive colonies (Fig. 2). The positive clones were further confirmed by PCR using mung bean protease inhibitor heterologous gene specific primers and four PCR positive clones were obtained (Fig. 3). The PCR positive clones sequenced at Chromous Biotech, Pvt. Ltd, India. Based on a haploid genome size of 5.74 x 10^8 bp, the coverage of the library was estimated to be 4.5 haploid genome equivalents,

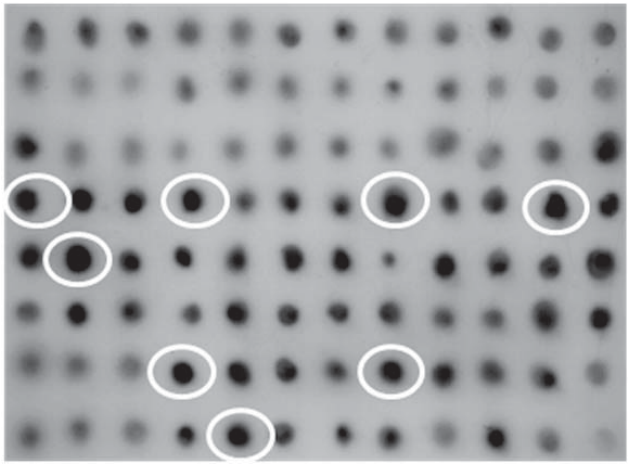

Fig. 2. Secondary screening of black gram genomic library

Fig. 3. Colony PCR confirmation of genomic clones

resulting in a 99.5 per cent probability of recovering any specific sequence (Clarke and Carbon, 1976).

Nucleotide Sequencing and Sequence Analysis

The NCBI Blastn algorithm analysis showed that 1514 bp nucleotide sequence of genomic clone contains partial coding sequence of black gram protease inhibitor gene (Fig. 4) and it showed 97 per cent homology with *Vigna radiata* trypsin protease inhibitor. Similarly it showed 93% homology with Cicer arietinum trypsin inhibitor. The 5' upstream sequence of genomic clone was analysed *in-silico* by Place and Plant Care databases. The 5' upstream sequence contains transcription control regions like TATA signals between 624-631 bases, GAAT and CAAT signals between 498-554 bases. Similarly MYB1AT dehydration responsive elements, a pollen specific expression element, endosperm specific expression elements and wound responsive elements were also found. The longest ORF analyzed in partial coding sequence was between 746 and 1414 bases in the second reading frame and the ATG for this ORF starting at 746 bp. This ORF on translation gave a protein with 222 amino acids (Fig. 4). The molecular weight of this protein was calculated to be 23.9 KD of which 21 amino acids were negatively charged, 16 positively charged with an isoelectric point of 5.0. The protein has an N-terminal signal sequence of 19 amino acids which is important in its translocation as it has been

```
 746 atgaaatccattgtattcctcctatttgcaattctaaccaatcct
     M  K  S  I  V  F  L  L  F  A  I  L  T  N  P
 791 ttatttgcattctccaataacaatgctattgagcaagtgttggat
     L  F  A  F  S  N  N  N  A  I  E  Q  V  L  D
 836 acaaatggtaacccccttatccctggtgatgaatactacatttttt
     T  N  G  N  P  L  I  P  G  D  E  Y  Y  I  F
 881 ccagcaagtgataaccctaaaactggaggactaaccctaaacaaa
     P  A  S  D  N  P  K  T  G  G  L  T  L  N  K
 926 attagtgatgcagagtgtcctgtaactgtcctacaaaataatgcg
     I  S  D  A  E  C  P  V  T  V  L  Q  N  N  A
 971 acaagaggtttaccagttaaattcaccttatcaggaagtaataac
     T  R  G  L  P  V  K  F  T  L  S  G  S  N  N
1016 actggtaataatatcttgactaatactgatcttgaaattgagttc
     T  G  N  N  I  L  T  N  T  D  L  E  I  E  F
1061 actaagaagccaaattgcgttgaatcatcaaaatggattgtgttt
     T  K  K  P  N  C  V  E  S  S  K  W  I  V  F
1106 gttgatgattttactcctcaaggttgtgttggtattggtggtcct
     V  D  D  F  T  P  Q  G  C  V  G  I  G  G  P
1151 gaaaatcatcttggtttagaaatactcaatggcaaatttttaatt
     E  N  H  L  G  L  E  I  L  N  G  K  F  L  I
1196 gtgagacatgcttctggatatgtttataggtttggatttgttttg
     V  R  H  A  S  G  Y  V  Y  R  F  G  F  C  L
1241 gatgtgagtggtgattgtggtttgcttggattgaatacttttgat
     D  V  S  G  D  C  G  L  L  G  L  N  T  F  D
1286 tcgagagaaggtggatcacgtttaatttaactatatttaattct
     S  R  E  G  G  S  R  L  I  L  T  I  F  N  S
1331 tataatgttgtatttgttgatgttgcttctgttaaatctggacgt
     Y  N  V  V  F  V  D  V  A  S  V  K  S  G  R
1376 attatgcctcttaaaggtggatttgatgcgtcagtttag 1414
     I  M  P  L  K  G  G  F  D  A  S  V  *
```

Fig. 4. The longest ORF of coding sequence of Black gram Protease Inhibitor gene (669 bp)

reported in many protease inhibitors such as soybean (Hammond *et al*., 1984), cowpea (Hilder *et al*., 1989), pea (Domoney *et al*., 1995) and maize (Rohrmeier and Lehle, 1993). Comparison for conserved domain in the protein by NCBI CD-search showed that the regions from 27-202 amino acids have the conserved domain similar to trypsin inhibitor Kunitz family of protease inhibitors. The active centre has four amino acid residues (from 85 to 93 amino acids) that are located within the conserved region (Fig 5).

In conclusion, a good quality of black gram Fosmid library representing 4.5 genome equivalents has been successfully constructed and characterized for isolation of protease inhibitor gene as well as promoter. Further this library will provide a good genomic resource for isolation of other agronomically important genes and promoters which can be further deployed for genetic transformation of crops for desired traits.

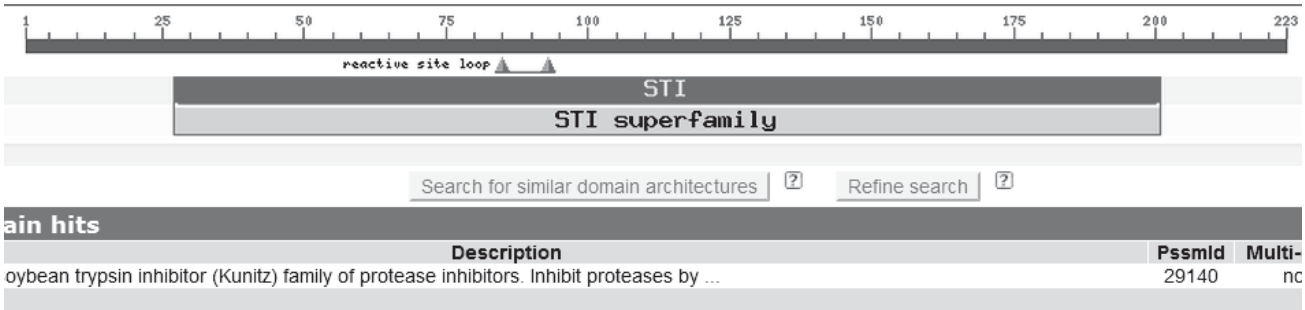

Fig. 5: Comparison for conserved domain of Protease Inhibitor gene using NCBI CD-search

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Studies on Genetic Variability and Divergence in Relation to Heterosis for Some Metric Traits in Indian Mustard

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Genetic variability and divergence were studied for some metric traits in 23 Indian mustard genotypes under timely and late sown conditions to assess the impact of environments. The results revealed presence of wide exploitable variability in the material. The high values of phenotypic coefficient of variation closely followed by genotypic coefficient of variation for seed yield per plant in both the conditions while, all the characters except oil content, days to flowering and days to maturity showed moderate to high estimates of genetic advance in (%) of mean coupled with high heritability. The genotypes were grouped into 9 clusters under timely sown (E_1) and 6 clusters under late sown conditions (E_2), where cluster I was the largest and contained 5 genotypes in E_1, 13 genotypes in E_2. Maximum inter cluster distance was noticed between the clusters IV and IX in E_1 and cluster II and VI in E_2, which could be made use of in heterosis and recombination breeding. Plant height and days to maturity contributed maximum to genetic diversity in both the conditions. The genotypes NDYR-32 and NDRE-4 genotypes do not cluster in a single cluster in both the environments, therefore could be used in breeding programme for obtaining the desirable recombinants.

Key Words: Coefficient of variability, Genetic advance, Genetic divergence, Heritability, Heterosis, Indian mustard

Introduction

Rapeseed-mustard oil is the third largest edible oil produced in the world after Soy oil and Palm oil. It accounts for about 12% of the total world's edible oil production. Indian mustard is the pre-dominant crop occupying nearly 80% of the rapeseed-mustard cropped area in the country. India is estimated to have a total mustard seed output of 5 million tons while oil is around 1.3 million tons (Damodaran and Hegde, 2005). The country also generates 2.4 million tons of oil cake. However, India exports around 400,000 tons of oil cake. Hence, increasing yield potential of the crop is imperative to enhance oilseed production. Knowledge of genetic diversity and utilization of divergent genotypes in breeding programme is the key to success in developing heterotic gene pool in Indian mustard (Chauhan *et al*., 2007; Patel and Patel, 2006; Pradhan *et al*., 1993). Genetic diversity in breeding is of paramount importance as evidenced by earlier workers (Murty and Arunachalam, 1966). Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence among biological population. Change in environments alters clustering patterns due to genotype-environment interaction (Raut *et al*., 1985). Inter crossing between more divergent parents is expected to generate a broad spectrum of variability. Therefore, study was undertaken to identify suitable stable donors having wider genetic distance among Indian mustard.

Materials and Methods

Twenty-three genotypes of Indian mustard from different geographical regions of the India were grown in two environments *viz*., timely (E_1) and late (E_2) sown conditions during *Rabi* season, 2004-05 at farm of N.D. University of Agriculture and Technology, Kumarganj, Faizabad. Eighty crosses were made during *Rabi* season, 2005-06 with 20 varieties/strains using as lines and 4 testers namely NDYR-32, Narendra Rai, NDRE-4 and a hybrid NDYR-32 x Narendra Rai for triple test cross analysis. These diverse elite strains were selected from the collection of the genetic stock available in oilseeds breeding section of Genetics & Plant Breeding of this University. The F_1 (hybrid) of NDYR-32 x Narendra Rai was produced by hand emasculation and pollination. The trials were conducted in Randomized Block Design with three replications under uniform cultural practices. Observations were recorded on 10 randomly selected plants for plant height, primary branches/plant, secondary branches/plant, length of main raceme, siliquae/plant, seeds/siliqua, seed yield/plant,

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1000-seed weight and oil content (%) while, data on days to flowering and days to maturity were recorded on whole plot basis. Multivariate analysis of genetic divergence among varieties was done using Mahalanobis D^2 statistics (1936) and grouping of varieties into clusters by Toucher method (Rao, 1952). The character wise rank totals were used to calculate the per cent contribution of each character to the total divergence. Averages inter-and intra-cluster distance, coefficient of variation, heritability in broad sense and genetic advance were estimated as per the method given by Singh and Chaudhary (1985). Heterosis expressed as per cent increase or decreases of hybrids (F_1) over better-parent (heterobeltiosis) and standard variety (standard heterosis) were calculated according to the method suggested by Hayes *et al.* (1955).

Results and Discussion

The results revealed presence of wide exploitable variability in the materials examined with respect to various morphological traits in both the environments indicating, thereby, immense scope of genetic up-gradation in Indian mustard. High values of phenotypic coefficient of variation closely followed by genotypic coefficient of variation for plant height, primary branches/plant, secondary branches/plant, length of main raceme, siliquae/plant, seeds/siliqua, 1000-seed weight and seed yield/plant indicated greater opportunities for desired gain through phenotypic selection. Earlier studies by Chaudhary *et al.* (2003) and Ahlawat *et al.* (2006) also exhibited the existence of greater natural variability for seed yield and secondary branches per plant. The high magnitude of phenotypic and genotypic coefficient of variations for 1000-seed weight has also been reported by Akbar *et al.* (2007). Simultaneously, high PCV and GCV for plant height, siliquae/plant and seed yield/plant were found by Khan *et al.* (2006). The low magnitude of phenotypic and genotypic coefficient of variations for days to flowering, days to maturity and oil content recorded in both the environments, indicated lesser opportunities for improvement through selection for these characters in the present set of material. For days to flowering, low coefficient of variability has also been reported by Pant and Singh (2001). In present study, genetic advance expressed as per cent of mean showed a wide range in its magnitude and in general, high heritability (broad sense) estimated were associated with the high genetic advance in per cent of mean (Table 1). All the

Table 1. Mean, range, coefficient of variation, heritability and genetic advance for eleven characters in Indian mustard (E_1 & E_2)

Characters	Environments	General mean ± SE	Range		Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
			Minimum	Maximum	Genotypic	Phenotypic		
Days to flowering	E_1	42.49 ±0.64	34.33	47.67	5.93	6.21	91.3	11.68
	E_2	43.06 ±0.49	39.67	46.67	4.05	4.28	89.5	7.90
Days to maturity	E_1	115.79 ±0.88	105.67	139.67	5.61	5.68	97.3	11.39
	E_2	119.21 ±0.64	108.67	127.33	2.80	2.87	94.7	5.61
Plant height (cm)	E_1	157.74 ±1.82	105.31	197.67	12.29	12.37	98.7	25.16
	E_2	174.69 ±3.13	105.00	237.67	16.70	16.84	98.3	34.10
Primary branches/plant	E_1	5.30 ±0.32	3.20	7.02	18.24	19.57	85.9	34.63
	E_2	5.55 ±0.46	4.24	7.33	9.74	14.07	87.9	13.88
Secondary branches/plant	E_1	10.96 ±0.52	2.99	16.93	30.07	30.63	96.4	60.80
	E_2	10.44 ±0.49	6.37	13.90	16.68	17.66	89.2	32.45
Length of main raceme (cm)	E_1	61.63 ±1.53	34.00	82.29	17.43	17.69	97.0	35.37
	E_2	59.12 ±2.33	41.81	79.09	14.10	14.91	89.5	27.49
Siliquae/plant	E_1	176.99 ±8.43	102.76	241.53	17.20	18.16	89.7	33.56
	E_2	180.29 ±8.35	112.93	252.73	13.18	14.35	84.4	24.95
Seeds/siliqua	E_1	12.48 ±0.26	9.67	16.82	16.69	16.89	97.7	33.98
	E_2	13.24 ±0.52	10.11	15.79	9.49	10.63	79.7	17.46
Seed yield/plant (g)	E_1	9.10 ±0.51	4.46	13.92	23.93	24.91	92.3	47.36
	E_2	9.84 ±0.93	5.61	16.54	20.88	23.88	86.5	37.62
1000-seed weight (g)	E_1	3.99 ±0.09	2.65	5.40	15.63	15.91	96.5	31.63
	E_2	3.98 ±0.12	2.52	5.88	20.09	20.44	96.6	40.67
Oil content (%)	E_1	40.01 ±0.23	37.88	43.24	2.57	2.66	92.9	5.09
	E_2	39.55 ±0.15	33.56	42.79	3.67	3.69	98.4	7.49

E_1: Timely sown condition; E_2: Late sown condition

characters except days to flowering, days to maturity and oil content in both the conditions and seeds/siliqua in E_2 demonstrated to high estimates of genetic advance in per cent of mean coupled with high heritability values. Similar results for days to flowering and oil content found by Pant and Singh (2001). Though contrast result was observed by Akbar *et al*. (2007). High heritability (broad sense) coupled with the high genetic advance in per cent of mean for 1000-seed weight and seed yield/plant was reported by Singh *et al*. (2003).

Based on D^2 values, the varieties were grouped in to 9 distinct non-overlapping clusters under E_1 and 6 under E_2. Cluster I and II contained approximately 22% of total varieties under E_1 and 56% under E_2. Interestingly, only one variety each was constituted by last three clusters in both the environments (Table 2). Similar results were reported by Vaishnava *et al*., (2006) and Khan *et al*. (2005). In both the environments, clusters included genotype from different region of India, indicating that clustering of the genotype did not follow their geographic distributions. The absence of correlation between genetic diversity and geographic diversity suggests that forces other than geographic origin, such as exchange of breeding material, genetic drift, variation, selection are responsible for diversity, as reported earlier (Alie *et al*., 2009).

The statistical distances represent the extent of genetic diversity amongst clusters. D^2 values were, in general, higher in E_2 than E_1. The average D^2 value within and between clusters revealed that intra cluster divergence was maximum in cluster IV (D^2 406.68) which include three entries in E_1 and cluster I (D^2 288.40) which comprised of 13 entries in E_2. The inter cluster distance was maximum between cluster IV and IX (1652.69) followed by IV and VII (1369.08) in E_1 and between cluster II and VI followed by III and VI (1593.44) in E_2 (Patel and Patel, 2006), while, closest cluster I and II (451.69) in E_1 and cluster II and III (373.27) in E_2 indicates that genotypes of these clusters had maximum number of common gene complexes. High statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates.

Days to maturity contributed maximum to total divergence followed by plant height in E_1 while, plant height appeared most important contributor towards divergence in E_2 (Pradhan *et al*., 1993). The developmental traits like days to maturity and plant height are known to have substantial contribution to genetic divergence in several crops (Singh *et al*., 2010). The genetic differences between the clusters were reflected in cluster means. Considering the cluster means for different characters under E_1, it was observed that cluster IV possessed dwarf plant stature, with short maturity duration, high values for length of main raceme, while, cluster IX had only one genotype (NDYR-32), with the highest values for primary branches/plant, siliquae/plant, seed yield/plant, plant height and oil content. However, under E_2, cluster III had high values for the primary branches/plant, seed yield/plant and oil content, while cluster V had highest values for length of main

Table 2. Distribution of 23 genotypes of Indian mustard in different clusters (E_1 & E_2)

Cluster No.	Environments	Number of genotypes	Genotypes included
I	E_1	5	BPR-558, RK-02-2, RAURDL-02-01, RGN-101, PR-2001-62
	E_2	13	BPR-558, RAURDL-02-01, KLM-145, Narendra Rai, RGN-101, HUJM-0202, RK-02-2, CS-611-1-3-1, JMWR-946-3-13, SEJ-2, JGM-15-02, RK-03-2, BAUSM-92-1-1
II	E_1	5	JGM-15-02, HUJM-0202, JMWR-946-3-13, RGN-74, SEJ-2
	E_2	4	NDM-87-1, PR-2001-62, RGN-74, PBR-253
III	E_1	3	RK-03-2, Narendra Rai, BAUSM-92-1-1
	E_2	3	SKM-9928, RH-0202, NDYR-32
IV	E_1	3	CS-33-4-9, NDRE-4, Kranti
	E_2	1	CS-33-4-9
V	E_1	2	NDM-87-1, CS-611-1-3-1
	E_2	1	Kranti
VI	E_1	2	SKM-9928, KLM-145
	E_2	1	NDRE-4
VII	E_1	1	PBR-253
VIII	E_1	1	RH-0202
IX	E_1	1	NDYR-32

E_1: Timely sown condition; E_2: Late sown condition

Table 3. Heterosis over better parent (BP) and standard variety (SV) for yield and yield contributing characters in Indian mustard (E_1 and E_2)

Crosses	Environments	1000-seed weight		Seed yield/plant (g)		Oil content	
		BP	SV	BP	SV	BP	SV
BPR-558 x NDYR-32	E_1	4.20*	-6.98**	17.69**	22.44**	-3.09**	3.30**
	E_2	2.14	-9.19**	1.73	6.91	-2.97**	6.56**
BPR-558 x N. Rai	E_1	2.39	2.39	25.74**	25.74**	-2.61**	3.81**
	E_2	1.44	1.44	27.58**	27.58**	2.04**	2.04**
BPR-558 x NDRE-4	E_1	-30.97**	-38.37**	-7.01	-11.83*	-1.00	3.53**
	E_2	-5.54*	-16.02**	33.47**	7.90	-0.65	1.58**
RAURDL-02-01 x NDYR-32	E_1	-2.28	-19.77	-0.27	3.81	-3.08**	2.58**
	E_2	-1.08	-9.98	-6.93	-2.91	-7.09**	2.04**
RAURDL-02-01 x N. Rai	E_1	-25.26**	-25.26**	-7.61	-7.61	-4.32**	0.92
	E_2	-7.55**	-7.55**	-12.31	-12.31	2.60**	2.60**
RAURDL-02-01 x NDRE-4	E_1	13.38**	-6.91**	37.29**	-8.03	-2.70	2.63**
	E_2	10.75**	0.79	9.68	-3.55	3.10**	-0.93*
RGN-101 x NDYR-32	E_1	-22.67**	-33.66**	-17.34**	13.92**	-1.30*	4.45**
	E_2	-12.35	-20.29**	-12.24	-7.78	2.12**	7.50**
RGN-101 x N. Rai	E_1	-0.90	-0.90	16.92**	16.92**	1.09	3.24**
	E_2	15.76**	15.76**	25.92*	25.92**	1.61**	5.39**
RGN-101 x NDRE-4	E_1	9.64**	-5.94**	-11.86**	19.00**	-4.40**	0.84
	E_2	10.32**	0.33	44.60**	-4.57	-0.82*	2.87**
RK-02-2 x NDYR-32	E_1	8.16**	-16.09**	23.24**	28.27**	-5.03**	2.88**
	E_2	-32.30**	-45.76**	-21.23	-17.22	-3.68**	5.78**
RK-02-2 x N. Rai	E_1	-20.35**	-20.35**	15.57**	15.57**	-4.13**	3.85**
	E_2	-37.69**	-37.69**	-18.98*	-18.98*	2.90**	5.10**
RK-02-2 x NDRE-4	E_1	-16.93**	-37.86**	3.47	1.04	-5.18	2.72**
	E_2	-37.95**	-50.30**	4.67	-20.46*	-2.87**	0.70

raceme, seeds/siliqua and siliquae/plant and substantial high values for seed yield/plant. Interestingly, cluster VI constituted with NDRE 4 possessed low values for seven characters *viz*., days to flowering, days to maturity, plant height, secondary branches/plant, seeds/siliqua, seed yield/plant and 1000-seed weight. In view of late sown condition, NDRE 4 serves as good donor for short duration and stature.

The genotypes like BPR-558, RK-02-2, RAURDL-02-01 and RGN-101 were found stable diverse varieties because these genotypes were grouped in the same cluster under both the environments. Noteworthy observations were that above said stable genotypes in different cross combinations, recorded significant heterosis for seed yield/plant, oil content and other characters in both the environments (Table 3). The variety Narendra Rai was used as standard variety (SV) to calculate standard heterosis. Significant levels of heterosis with respect to seed yield and its component attributes have been reported with hybrids showing greater advantage under adverse environmental conditions (Banga, 2005). The selections of the crosses based on heterotic response over standard variety could be more realistic under such a situation. There was high manifestation of heterosis over standard variety for seed yield/plant as evidenced by the significant superiority of hybrids of stable parents ranging from 13.92 to 28.27% in 7 crosses in E_1 and 2 crosses in E_2. Ten crosses in each environment, registered significant heterosis over standard variety for oil content. Results of heterobeltiosis for oil content indicated that the pool of material studied was, in general, poor combiner for oil content. Thus, there exist hardly any opportunity for transgressive segregates, beyond the better parents.

Manifestation of high amount of heterosis by a large number of crosses, thus, indicate the presence of substantial parental diversity at genetic level. The crosses of divergent genotypes in present study exhibited significant desirable heterosis for yield and yield components in both the environments (Table 4). Similar findings were reported by Pradhan *et al*. (1993) and Goswami *et al*. (2006). Furthermore, NDYR-32 and NDRE-4 genotypes do not cluster in a single constellation in any environment and crosses between these strains are expected to give promising segregates in the segregating generations.

Table 4. Prospective cross combinations of divergent genotypes based on heterosis (BP & SV) for different characters in Indian mustard (E_1 and E_2)

S.No.	Cross Combinations	Significant heterosis for different characters
E_1		
1	CS 33-4-9 x NDYR 32	PH, PB/P, SB/P and OC
2	PBR 253 x NDRE 4	DF, PH, PB/P, SB/P, S/S and OC
3	Kranti x NDYR 32	PH, PB/P, SB/P, LMR, S/P, SY/P, TW and OC
E_2		
1	NDM 87-1 x NDRE 4	PH, LMR and OC
2	PR 2001-62 x NDRE 4	S/P, S/S, DF and DM
3	RGN 74 x NDRE 4	DF, DM, LMR and S/S
4	PBR 253 x NDRE 4	DF, PH, SB/P, S/P and S/S
5	SKM 9928 x NDRE 4	DF and PH
6	RH 0202 x NDRE 4	DF, DM, SB/P, LMR and S/S

DF: Days to flowering; DM: Days to maturity; PH: Plant height (cm); PB/P: Primary branches per pant; SB/P: Secondary branches per plant; LMR: Length of main raceme (cm); S/P: Siliquae per plant; S/S: Seeds per siliqua; SY/P: Seed yield per plant (g); TW: 1000-seed weight (g), OC: Oil content (%)
E_1: Timely sown condition; E_2: Late sown condition

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Genetic Studies on Differential Expression of Mungbean Yellow Mosaic Virus Resistance Related to Trichome Density in Urd bean (*Vigna mungo* (L.) Hepper)

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In blackgram, five cross combinations were taken for generation mean analysis to study the inheritance pattern of *Mungbean yellow mosaic virus* (MYMV) disease which revealed different gene actions. It is found that the crosses Co5 x VBN (Bg) 4 and Co5 x VBG 66, the segregation was governed by digenic complementary interaction. However, in Co5 x VBG 73 the YMV incidence was governed by digenic duplicate interaction. In contrast, in the crosses KBG 98005 x VBN (Bg) 4 and KBG 98005 x VBG 73, the incidence of YMV was governed by trigenic inhibitory interaction. The putative gene symbols assigned for the five genotypes *viz.*, Co5, KBG 98005, VBN (Bg) 4, VBG 66 and VBG 73 are $r_1r_1r_2r_2r_3r_3r_4r_4$, $r_1r_1r_2r_2r_3r_3r_4r_4$II, $R_1R_1R_2R_2$ii, $R_1R_1R_2R_2$ and $R_3R_3R_4R_4$ii, respectively. Besides this, the presence of trichomes in leaf of urdbean genotypes reveals that trichomes do not hinder the activities of whitefly and the resistance to MYMV may be due to some other factors like chemical, physiological and morphological factors.

Key Words: Blackgram, Genetic studies, Inheritance, Mungbean yellow mosaic virus, Trichome density

Introduction

Mungbean yellow mosaic virus (MYMV) is the one of the most destructive diseases and is prevalent on mungbean, blackgram and soybean throughout India mainly in the *Kharif* season and rice fallow situation. The virus is transmitted by whitefly, *Bemisia tabaci.* The yield losses upto 100 % have been reported by Nair (1971) in blackgram. Khattak *et al*. (2000) reported 32.2 to 78.6% decrease in grain yield under field conditions in mungbean. Hence, the present investigation was taken up to know the inheritance pattern of MYMV, Which is the prerequisite to evolve high yielding blackgram varieties combined with resistance to MYMV. Further, the presence of trichomes on leaf was also studied to know the relationship between MYMV and trichome density.

Materials and Methods

To study the inheritance pattern of MYMV, the five cross combinations *viz*., Co5 x VBN (Bg) 4, Co5 x VBG 73, Co5 x VBG 66, KBG 98005 x VBN (Bg) 4 and KBG 98005 x VBG 73 were chosen for the study. The 'lines' (Co5 and KBG 98005) are highly susceptible and three 'testers' (VBN (Bg) 4, VBG 73 and VBG 66) are highly resistant for MYMV. Six generations *viz.*, P_1, P_2, F_1, F_2, B_1 and B_2 for each of the five crosses were generated to understand the inheritance pattern of MYMV. The six generations of the five selected cross combinations were raised at National Pulses Research Centre, Vamban, which is a hot spot area for MYMV. The above said materials were raised in ridges of two meter length spaced at 30 cm between ridges and 10 cm between plants in two replications. For every 10th row and as border rows of the experimental plot the check Co5 (highly susceptible to MYMV) was raised as infector row so as to effectively spread the inoculum.

For trichome density studies, fifth leaf from the top of the selected plants in parents alone was taken at the time of initiation of flowering. The number of trichomes per cm^2 was estimated after removing chlorophyll from the leaf samples as per the method suggested by Maite *et al.* (1980).

The MYMV incidence was recorded on all the plants based on the visual scores on 50th day while the susceptible check Co5 recorded scale 9. The classification was made into scale 1-9 as follows based on the scale adopted by Singh *et al.*, (1988) and is given below:

The plants in the F_2 and back cross generations were classified as resistant (1-3) and susceptible (5-9) following Reddy and Singh (1993).

The goodness of fit to Mendelian segregation ratio for MYMV (resistance: susceptible) in the segregating population was tested through Chi-square test.

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Scales	Percentage of plant foliage affected	Reaction
1	Mottling of leaves covering 0.1 to 5.0% of the leaf area	Resistant
3	Mottling of leaves covering 5.1 to 10.0% of the leaf area	Moderately resistant
5	Mottling and yellow discoloration of 10.1to 25.0% of the leaf area	Moderately susceptible
7	Mottling and yellow discoloration of 25.1to 50.0% of the leaf area	Susceptible
9	Severe yellow mottling on more than 50.0% and up to 100% of the leaf area	Highly susceptible

The mean disease scale of parents and $F_1$was calculated following Singh (1980).
Mean scale = $\sum$ (Infection rate x Frequency)/Total number of plants scored.

Results and Discussion

For the study of inheritance of MYMV resistance, the Chi-square test for the deviation from the expected genetic ratios of the segregating generations *viz.*, F_2, B_1 and B_2 of five crosses was made and the results are presented in Table 1.

The F_1 of the crosses *viz*., Co5 x VBN (Bg) 4), (Co5 x VBG 73) and (Co5 x VBG 66) were resistant to MYMV, while it was susceptible in the crosses KBG 98005 x VBN (Bg) 4 and KBG 98005 x VBG 73. Regarding the segregating generations, in crosses Co5 x VBN (Bg) 4 and Co5 x VBG 66 the chi-square test for the expected ratio of 9:7 (resistant: susceptible) in F_2 and 1:3 (resistant: susceptible) in B_1 was not significant. In B_2 generation, all plants were resistant. In the case of Co5 x VBG 73 cross, the chi-square test revealed that the F_2 generation showed a expected ratio of 15:1 for resistance: susceptible and B_1 showed a ratio of 3:1 (resistant: susceptible). In B_2, all plants were resistant. In the crosses KBG 98005 x VBN (Bg) 4 and KBG 98005 x VBG 73, the chi-square test was non-significant showing fitness of the expected ratios of 15:49 (resistant: susceptible) and 1:1 (resistant: susceptible) in F2 and B_2 generations respectively. All the plants in B_1 were susceptible to MYMV.

Among these five crosses, three crosses *viz.*, (Co5 x VBN (Bg) 4), (Co5 x VBG 73) and (Co5 x VBG 66) were found to be resistant to MYMV in F_1, where the female parent was Co5. Therefore, resistance is dominant over susceptibility. In black gram, Dahiya *et al.* (1977), Verma and Singh (1980) and Kaushal and Singh (1988) and in green gram Reddy and Singh (1993) Selvi (2002) and Gupta *et al.* (2005) and in mungbean, Patel *et al*. (2009) reported that the resistance was dominant over susceptibility. The segregation of YMV resistance in the present study was

Table 1. Chi-square test for inheritance of MYMV resistance in blackgram

Generation	Observed values		Expected ratio	c^2 values	Probability between
	Resistant	Susceptible			
Co5 X VBN(Bg) 4					
F_1	Resistant	–			
F_2	151	111	9:7	0.21	0.70-0.50
B_1	31	71	1:3	1.59	0.30-0.20
B_2	121	–			
Co5 X VBG 73					
F_1	Resistant	–			
F_2	254	20	15:1	0.52	0.50-0.30
B_1	80	30	3:1	0.31	0.70 – 0.50
B_2	120	–			
Co5 X VBG 66					
F_1	Resistant	–			
F_2	172	146	9:7	0.6	0.50-0.30
B_1	35	80	1:3	1.8	0.20-0.10
B_2	115	–			
KBG 98005 X VBN(Bg) 4					
F_1	–	Susceptible			
F_2	54	212	15:49	1.44	0.20-0.30
B_1	–	112			
B_2	52	56	1:1	0.15	0.70
KBG 98005 X VBG 73					
F_1	–	Susceptible			
F_2	57	218	15:49	1.13	0.2- 0.30
B_1	–	115			
B_2	57	50	1:1	0.45	0.50

Table 2. Details of the parents

Genotypes	Parentage	Reaction to MYMV	Place of origin	Special features
CO 5	Selection from Musiri local	Highly Susceptible	Coimbatore	High yielding suitable for rabi seasons
KBG 98005	Selection from Kalugumalai local.	Highly Susceptible	Kovilpatti	Suitable for rainfed situation
VBN (Bg) 4	Co 4 x PDU 102	Highly Resistant	Vamban	High yielding, suitable for all seasons
VBG 73	Vamban 1 x UK 17	Highly Resistant	Vamban	Short duration (60 days)
VBG 66	Pure line selectionfrom IPU 94-2	Highly Resistant	Vamban	Suitable for rainfed situation

appeared to be governed by digenic complementary interaction as seen from the ratio of 9:7 (resistant: susceptible) in F_2 of Co5 x VBN (Bg) 4 and Co5 x VBG 66. The pattern of segregation in B_1 (1 resistant: 3 susceptible) and B_2 (all resistant) of these two crosses (Co5 x VBN (Bg) 4 and Co5 x VBG 66) also confirmed the result of complementary interaction (duplicate recessive genes) (Table 1). A similar type of duplicate recessive genes for MYMV resistance in black gram was reported by Verma and Singh (1980), Sandhu *et al.* (1985) and Shukla and Pandiya (1985) and in green gram by Selvi (2002).

However, in the cross (Co5 x VBG 73), the segregation of F_2 showed a ratio of 15:1 (resistant: susceptible). The segregation ratio in B_1 (3 resistance: 1 susceptible) and B_2 (all resistant) also confirmed the ratio observed in F_2. This revealed that, in the cross Co5 x VBG 73 the YMV was governed by interaction of two duplicate genes (duplicate dominant genes). Shukla *et al.* (1978) and Singh (1980) reported the presence of duplicate dominant genes for YMV in black gram. From the above discussion it was found that, though the three crosses had same female parent (Co5), two different types of gene action of complimentary interaction in (Co5 x VBN (Bg) 4 and Co5 x VBG 66) and duplicate interaction in Co5 x VBG 73 were noticed. The reason for the difference in gene action may be attributed to the presence of two different sets of genes in male parents of the crosses. The male parents of the crosses (Co5 x VBN (Bg) 4 and Co5 x VBG 66) namely VBN(Bg) 4 and VBG 66, may have same alleles ($R_1R_1R_2R_2$), which act in complementation. However, the male parent of the cross Co5 x VBG 73 namely VBG 73, may have another set of non-allelic genes ($R_3R_3R_4R_4$), which act in a duplicate manner. The common female parent of all these three crosses, namely Co5, may have recessive alleles for all these four loci.

In the crosses KBG 98005 x VBN (Bg) 4 and KBG 98005 x VBG 73, the F_1 was found to be susceptible, where the female parent was KBG 98005. The segregation of F_2 was observed to be 15:49 (resistant: susceptible). It showed that the reaction to MYMV was governed by trigenic inhibitory interaction. The segregation in B_1 (all susceptible) and B_2 (1 resistant : 1 susceptible) also confirmed the trigenic inhibitory interaction. In blackgram, inhibitory gene action was reported by several workers in blackgram (Solanki *et al.*, 1982; Verma,1985; Verma and Singh, 1986; Reddy and Singh 1990); in greengram (Mishra and Asthana, 1996; Khattak *et al.*, 2000). From the above results, it could be concluded that the male parents of these two crosses namely VBN (Bg) 4 and VBG 73 respectively, may have recessive alleles for an inhibitory gene (ii) apart from two sets of alleles already indicated. The female parent KBG 98005 of these two crosses may have a set of dominant inhibitory alleles (II) at a locus apart from recessive alleles for susceptibility to MYMV at four loci.

Therefore, the following putative gene symbols are proposed for the parents involved in the five crosses:

Parent	Reaction to MYMV	Gene symbol for MYMV resistance
CO5	Susceptible	$r_1r_1r_2r_2r_3r_3r_4r_4$
KBG 98005	Susceptible	$r_1r_1r_2r_2r_3r_3r_4r_4$II
VBN(Bg) 4	Resistant	$R_1R_1R_2R_2$ii
VBG 66	Resistant	$R_1R_1R_2R_2$
VBG 73	Resistant	$R_3R_3R_4R_4$ii

However, the gene symbols are allotted subject to confirmation by allelic tests. The allelic tests may be conducted by intercrossing all the three male parents and studying the resistant pattern for MYMV resistance.

From the present investigation it was confirmed that the MYMV was controlled by two and three genes with various types of interaction. Hence, recombination breeding with two or three cycles of recurrent selection is required to obtain desirable segregants of high yielding ability coupled with MYMV resistance.

MYMV Resistance and Trichome density on leaves

Limited studies have been conducted to reveal the relationship between white fly and MYMV incidence. Earlier results reported that there was an association between trichomes on leaves and whitefly resistance (Chand and Verma, 1980). Hence, the present study was undertaken utilizing the MYMV scores and the number of

Table 3. Correlation between number of trichomes and MYMV scores in parents

Code No.	Genotypes	No. of trichomes/cm^2	Mean MYMV score	Type of trichome
L_1	Co 5	10 (3.16)	9.0	Non septate - Long
L_2	KBG 98005	2 (1.41)	9.0	Non septate - Medium
L_3	Vamban 1	10 (3.16)	2.3	Septate - Medium
L_4	Vamban 2	6 (2.45)	1.3	Non septate - Very long
L_5	Vamban 3	10 (3.16)	1.3	Septate - Small
L_6	ADT 3	16 (4.00)	7.0	Medium - Septate
L_7	ADT 5	28 (5.29)	1.0	Small - Septate (distinct septate)
L_8	T 9	12 (3.46)	1.6	Non septate - Very short
L_9	TMV 1	10 (3.16)	7.9	Non septate - Very long - Sharp
L_{10}	VBG 81	1 (1.00)	1.9	Septate - Small
L_{11}	ADB 2003	14 (3.74)	4.6	Non septate - Medium
T_1	VBN (Bg) 4	10 (3.16)	1.0	Septate - Long
T_2	VBG 73	6 (2.45)	1.0	Non septate - Medium
T_3	VBG 66	12 (3.46)	1.0	Non septate - Long - Glandular

Square root transformed values are in paranthesis
Correlation coefficient (r) = 0.006 (ns)

trichomes observed in 14 parents and results obtained are discussed. The results obtained from the present study showed that there was no correlation between number of trichomes on leaves and MYMV resistance (Table 3). There was no distinct pattern of variation between the resistant and susceptible varieties for number of trichomes. Hence it is concluded from the present study that trichomes in leaf does not hinder the activities of whitefly and the resistance to MYMV may be also due to some other factors like cuticle thickness, chemical components, wax coating, compact vascular bundles, lignification of cell walls *etc.* in leaves.

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Characterization and Evaluation of Pomegranate (*Punica granatum* L.) Germplasm under Indian Arid Ecosystem

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Thirty accessions/genotypes collected from various sources and propagated vegetatively were planted in spacing of 5m x 5m to describe and select superior pomegranate genotypes suitable for arid ecosystem of India. The following phonological growth and yielding characteristics were evaluated: tree height, tree spread, suckering, girth, leaf length and width, leaf tip, leaf base, leaf shape, thorn length, size of flowers, TSS, acidity, juice (%), fruit cracking, seed hardness, juice flavour, arid colour. Substantial variability was recorded among the genotypes/varieties. Pomegranate genotypes suitable to the specific soil and climate conditions of Indian arid region are described in detail for their morphological characteristics and physico chemical parameters of the fruits.

Key Words: Arid fruits, Conservation, Genotypes, *Punica granatum*, Variability

Introduction

The genus *Punica* has two species, *Punica protopunica* and *Punica granatum* and is cultivated in tropical and sub tropical areas of the world. Further *Punica granatum* has been classified in to two sub species, *chlorocarpa* and *porphyrocarpa*.Several types of pomegranate distinguished by shape of the fruit, colour and thickness of the skin, and taste and colour of the seed are grown throughout the world.

The fruit is known to have been cultivated in the Middle East more than 5000 years ago. However, wild pomegranate still exists in the North of Syria (Sexana *et al*., 1987) and in the Himalayan belt of India (Himachal Pradesh, Jammu & Kashmir, Uttaranchal). The fruit was featured in Eyptian mythology and art, praised in the old testaments of the Bible and in the Babylonian Talmud and it was carried by desert caravans for the sake of thirst quenching juices. It traveled to central and southern India from Iran about the first century AD and was reported growing in Indonesia in 1416. There are some commercial orchards in Israel on coastal plains and in the Jordan valley (Morton, 1987). It is found in various regions from Caucasus to Afghanistan. The wild type in Central Asia shows a wide range of variation in size of fruit, sweetness, time of ripening and proportion of seeds to flesh (Adsule and Patil, 1995). Pomegranate is grown as commercial crop in India and Iran, and is cultivated extensively in Spain, Morocco, Egypt, Afghanistan and Baluchistan. It is also grown to some extent in Burma, China, Japan and parts of the United States. The demand for pomegranate fruits for both local and export market has motivated producers, mainly in the sub tropical and semi-arid-areas of the Indian peninsula (Prasad *et al*., 1997).

Pomegranate stands out with high potential for economic exploitation due to proven importance for manufacture of juice, syrup, jam/rub as well as for consumption as fresh fruit. It has enjoyed a reputation for its healthy dietic and medicinal properties. Versatile adaptability, hardy nature, low orchard management cost, high yields and excellent keeping quality had made this fruit most lucrative and remunerative (Dhandhar and Singh, 2002). The pomegranate fruits have therapeutical value, good keeping quality and export potential.

However, few studies have been made to classify or identify types with desirable botanical and agronomical characteristics and their suitability under different ecosystems (Fadavi *et al*., 2005; Singh, 2004; Prasad and Bunker 1999; Bunker and Prasad 1992; Umrao and Singh, 1995; Feng-YZ *et al*., 1998; Levin 1994).

In spite of rich diversity existing in nature, available variability in gene banks is necessary for utilization. Therefore, it is still necessary to carry out selection of superior cultivars adapted to the area, as their edaphoclimatic characteristics are quite unique. The present study was taken for characterization and evaluation of promising types of pomegranate trees specific to arid and semi arid ecosystem of India and to develop National Repository and their further exploitation for improvement in terms of quality and production.

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Materials and Methods

This work pertaining to development of National Repository for conservation, characterization and evaluation of pomegranate germplasm was conducted at Central Institute of Arid Horticulture, Bikaner, Rajasthan, India. Climate is arid with scanty rainy season in monsoon and with an average minimum and maximum temperature of -2.5°C in winter and 50.0°C in summer (Goyal, 2004). The germplasm collection of 31 varieties/ accessions *i.e.* Jalore Seedless, Ganesh, P-26, Mridula, G-137, Jodhpur Red, Kabul, GKVK 1, Dholka, Coimbatore White, P-23, Yarcaud, Muskat, Patna-5, Jyoti, Bedana Thin Skin, Kurvi-2EL-24685, Speen Danedar, Basein Seedless, Kazaki Anar, Khog, AK Anar, Bocheka lines, Gul-e-Shah, Sirin Anar, Dorseta malus, Tabest, Kali Sirin and Tujetis EC-104347 each of which is represented in replication of 3 by plants. The germplasm was collected in the form of vegetative stock obtained by cuttings and air layering. The experimental plot was planted during 1995-96 with planting material obtained from germplasm collection of experimental stations of various National Institutes in India located in diverse climatic conditions and Exotic germplasm from Argentina, Russia, Iran, California. These were planted in the spacing of 5m x 5m. All the recommended agricultural practices for pomegranate such as fertilizer application, weed control, pest/disease management were carried out manually.

During experimental study from 2000 to 2003 data on plant growth and developmental characteristics of tree *i.e.* tree height, tree spread, suckering, girth, leaf length and width, leaf tip, leaf base, leaf shape, thorn length, size of flowers and physico chemical composition of fruits i.e. TSS, acidity, juice (%), fruit cracking, seed hardness, juice flavour, aril colour were recorded. A sample of 10 ripe fruits was used to determine characteristics and composition. TSS determination was achieved by means of direct refractometer reading while mean fruit weight was obtained by dividing plant yield by total number of fruits.

Table 1. Tree growth characteristics of pomegranate germplasm

Genotype	Type of planting material	Tree height (m)	Girth of tree (cm)	Tree spread (m)		Suckering
				Across row	Along row	
Jalore Seedless	EG	2.21	4.20	2.30	2.30	Less
Ganesh	EG	2.18	4.00	2.25	2.30	Less
Bedana Suri	EG	1.90	3.88	1.70	1.91	Less
P-26	EG	2.10	4.47	2.20	2.51	Less
Mridula	EG	2.00	3.80	2.30	2.00	Less
G-137	EG	2.18	4.30	2.25	2.50	Less
Jodhpur Red	EG	2.50	4.00	2.75	2.75	Less
Kabul	EG	2.30	4.40	2.60	3.10	Less
GKVK 1	EG	1.80	3.90	2.30	2.40	Less
Dholka	EG	2.34	4.00	2.00	2.05	Less
Cimbatore White	EG	2.20	3.50	2.30	2.50	Very Less
P-23	EG	2.20	4.10	2.60	2.40	Less
Yarcuad	EG	2.25	4.48	2.35	2.40	Less
Muskat	EG	2.00	3.85	2.10	2.40	Less
Patna-5	EG	1.89	3.71	2.16	2.05	Less
Jyoti	EG	2.08	5.45	2.37	2.68	Less
Bedana Thinn Skin	D	2.05	4.74	1.92	2.10	Very Less
Kurvi-2EL-24685	D	2.12	3.41	2.47	2.24	Less
Speen danedar	D	2.28	3.85	2.55	2.31	Medium
Basein Seedless	D	2.22	3.91	2.20	2.21	Less
Kazaki Anar	D	2.21	3.66	2.47	2.50	Medium
Khog	D	2.70	3.30	2.72	2.30	Medium
A K Anar	D	2.20	3.51	2.90	3.10	Medium
Bocheka Lines	D	2.30	4.96	2.20	2.56	Medium
Gul e Shah	D	2.16	3.81	2.28	2.47	Medium
Sirin Anar	D	2.13	4.10	2.05	1.98	Medium
Dorsetta Malus	D	2.38	4.17	2.40	2.30	Medium
Tabest	D	2.65	3.11	2.04	2.31	More
Kali Sirin	D	2.02	2.81	1.88	1.54	Less
Tujetis EC-104347	D	2.59	3.96	2.18	2.49	Less
CD at 5%		0.45	0.36	0.21	0.27	

EG: Ever Green; D: Deciduous

Results and Discussion

Under arid conditions of Bikaner, Rajasthan, Indian cultivars namely Jalore Seedless, Ganesh, Bedana Suri, P -26, Mridula, G-137, Jodhpur Red, Kabul, GKVKI, Dholka, Coimbatore White, P-23, Yarcuad, Muskat, Patna-5, Jyoti showed ever green nature of growth, while, Bedana Thin Skin, Kurvi-2EL-24685, Speen Danedar, Basein Seedless, Kazaki Anar, Khog, AK Anar, Bocheka Lines, Gul-e-Shah, Sirin Anar, Dorsetta Malus, Tabest, Kali Sirin, Tujetis EC-104347 showed deciduous nature of growth Table 1. The growth analysis shown in Table 1 is the result of measurements taken from 7-year-old plants. Highest plant height (2.70 m) was recorded in cultivar Khog, where as, minimum (1.70 cm) was recorded in Bedana Suri while the average for the germplasm was 2.29 m. This value is near the mean height recommended for pomegranate trees (2.50 cm). Bunker and Prasad (1992) also reported differences in vegetative growth of pomegranate varieties grown in different agro climatic zones. Larger height trees hinder the harvest, pest disease control and in many cases are responsible for an insignificant percentile of losses.

For the various characteristics, stem diameter/girth a variation from 2.81 cm in Kali Sirin to 5.45 cm in Jyoti was observed with an average of 3.97 cm. More stern and robust stems better support the main branches and increase sap circulation for the canopy. The cultivar AK Anar had the largest canopy (2.90 cm across row and 3.1 cm along row) while least spread (1.88 cm across row and 1.54 cm along row) was recorded in Kali Sirin. The mean average of all the pomegranate trees in this collection was 2.34 cm along row and 3.97 cm across row. Tree growth habit is determined by various factors like genetic behaviour of tree/genotype, nutritional status of the soil and other management practices as well. Canopies and spread needs to be maintained at a diameter that allows management practices without affecting the growth and development of neighbouring plant. The size of the canopies of the plants examined was acceptable for the space that was available. These values shows that after 7 years of cultivation the pomegranate germplasm had adapted well to the climate and soil, conditions of arid ecosystem and showed good growth characteristics.

Table 2. Leaf and thorn characteristics of pomegranate germplasm

Genotype	Leaf base	Leaf shape	Leaf tip	Leaf length (cm)	Leaf width (cm)	Length of thorn (cm)	Length of thorn (cm)
Jalore Seedless	Cunnate	Elliptic Entire	Cuspidate	4.8	1.8	5.9	5.9
Ganesh	Cunnate	Elliptic Entire	Obtuse	6.4	2.1	6.0	6.0
Bedana Suri	Connate	Elliptic Entire	Obtuse	5.4	2.0	4.0	4.0
P-26	Cunnate	Elliptic Entire	Mucronate	5.2	1.9	4.9	4.9
Mridula	Cunnate	Elliptic Entire	Mucronate	6.0	1.8	7.6	7.6
G-137	Cunnate	Elliptic Entire	Mucronate	6.6	2.0	7.8	7.8
Jodhpur Red	Cunnate	Elliptic Entire	Acute	4.8	2.0	5.4	5.4
Kabul	Cunnate	Elliptic Entire	Acute	5.8	1.7	3.6	3.6
GKVK 1	Cunnate	Elliptic Entire	Obtuse	5.8	2.2	5.5	5.5
Dholka	Cunnate	Elliptic Entire	Acute	6.4	2.2	6.8	6.8
Cimbatore White	Cunnate	Elliptic Entire	Obtuse	5.8	2.0	5.6	5.6
P-23	Cunnate	Elliptic Entire	Mucronate	5.7	2.2	5.8	5.8
Yarcuad	Cunnate	Elliptic Entire	Cuspidate	5.9	2.5	4.4	4.4
Muskat	Cunnate	Elliptic Entire	Acute	5.6	2.0	6.4	6.4
Patna-5	Cunnate	Elliptic Entire	Acute	6.5	2.0	5.2	5.2
Jyoti	Cunnate	Elliptic Entire	Obtuse	4.7	1.8	5.5	5.5
Bedana Thin Skin	Cunnate	Elliptic Entire	Obtuse	5.4	2.0	5.5	5.5
Kurvi-2EL-24685	Cunnate	Elliptic Entire	Cuspidate	8.2	2.7	6.0	6.0
Speen danedar	Cunnate	Elliptic Entire	Acute	5.5	1.7	4.4	4.4
Basein Seedless	Cunnate	Elliptic Entire	Obtuse	4.2	1.8	6.8	6.8
Kazaki Anar	Connate	Elliptic Entire	Acute	5.5	2.0	4.9	4.9
Khog	Cunnate	Elliptic Entire	Acute	5.4	2.2	4.8	4.8
A K Anar	Cunnate	Elliptic Entire	Acute	6.0	2.1	3.9	3.9
Bocheka Lines	Cunnate	Elliptic Entire	Mucronate	5.4	2.3	5.0	5.0
Gul e Shah	Cunnate	Elliptic Entire	Acute	5.5	1.7	3.7	3.7
Sirin Anar	Cunnate	Elliptic Entire	Acute cuneate	4.8	1.9	4.3	4.3
Dorsetta Malus	Cunnate	Elliptic Entire	Obtuse	4.8	1.8	4.2	4.2
Tabest	Cunnate	Elliptic Entire	Acute	5.7	1.9	5.0	5.0
Kali Sirin	Cunnate	Elliptic Entire	Obtuse	5.7	1.6	5.0	5.0
Tujetis EC-104347	Cunnate	Elliptic Entire	Obtuse	4.8	1.8	5.1	5.1
CD at 5%				**0.23**	**0.13**	**0.17**	**0.24**

A lot of variation was recorded in shape and size of leaf Table 2. All the varieties produced leaves having connate leaf base and elliptic entire leaf shape. Cultivar Jalore seedless, Yercuad produced leaf with cuspidate leaf tip. Cultivar Ganesh, Bedana suri, GKVK I, Jyoti, Bedana Thin Skin, Basein Seedless, Dorsetta Malus, Tujetis EC-104347 produced leaf having obtuse leaf tip, P-26, Mridula, P-23, Bocheka Lines produced leaf with Mucronate tips, Jodhpur Red, Kabul, Dholka, Muskat, Patna-5, Speen Danedar, Kazaki Anar, Khog, A.K. Anar, Gul-e-Shah and Tabest produced leaf with acute leaf tip while Sirin Anar produced acute cunate leaf tip. Maximum leaf length (8.2 cm) was recorded in Kurvi-2EL-24685 and minimum length (4.2 cm) in Basein Seedless, whereas, average was recorded as 5.61 cm. Similarly, leaf width was maximum (2.7 cm) in Kurvi-2EL-24685 and minimum (1.6 cm) in Kali Sirin and the average was 1.98 cm. Germplasm was found to have leaf size just close to the average size leaves. Foliage load is responsible for photosynthesis and carbohydrates in turn responsible for flowering and fruiting.

Wide range of variability was recorded in case of length of thorn, ranging from maximum 7.8 cm in G-137 and minimum in 3.6 cm in Kabul. Whereas, it was 5.3 cm for average of all the germplasm tested. Size of thorns is one of the characters which hinders with various farm operations being carried out.

All the varieties under gremplasm produced male flowers Table 3. Fruit set and bearing capacity of a tree depends upon size of the male, female and hermaphrodite flowers. Maximum length male flowers were recorded in Bedana Thin Skin (3.15 cm) and minimum in Mridula (1.70 cm). Whereas average/mean value was 2.38 cm. Maximum width of male fower was in Tabest (1.95 cm) and least in Gul-e-Shah (1.20 cm) and the mean value recorded was 1.34 cm. Except genotype Patna 5, all varieties under germplasm produced female flowers. Maximum length (4.20 cm) was recorded in Basein Seedless and minimum size of 2.71 cm in Bocheka Lines. Where as, maximum breadth of the flowers was recorded in Bedana Suri (1.91 cm) and the least in Tabest (1.21 cm) and the

Table 3. Flowering characteristics of pomegranate germplasm

Genotypes	Size of flowers (cm)					
	Male		Female		Intermediate	
	Length	Breadth	Length	Breadth	Length	Breadth
Jalore Seedless	2.60	1.40	3.90	1.51	2.90	1.43
Ganesh	2.65	1.52	3.607	1.60	3.52	1.51
Bedana Suri	2.18	1.29	3.38	1.91	–	–
P-26 2.80	1.30	3.80	1.62	2.70	1.28	
Mridula	1.70	1.23	3.47	1.52	2.78	1.42
G-137	2.68	1.32	3.46	1.40	2.62	1.30
Jodhpur Red	2.72	1.37	3.78	1.62	3.02	1.55
Kabul	2.36	1.36	3.52	1.34	–	–
GKVK 1	2.71	1.31	3.41	1.57	2.51	1.52
Dholka	2.81	1.53	3.82	1.69	2.66	1.29
Coimbatore White	2.11	1.36	2.83	1.41	2.21	1.25
P-23	2.50	1.28	3.79	1.59	2.79	1.38
Yarcuad	2.51	1.42	3.77	1.61	2.41	1.41
Muskat	2.70	1.39	3.22	1.34	2.85	1.10
Patna-5	2.92	1.48	–	–	2.53	1.33
BedanaThin Skin	3.15	1.41	4.13	1.36	2.84	1.60
Kurvi-2EL-24685	2..38	1.29	3.58	1.57	2.20	1.26
Speen danedar	2..33	1.31	3.01	1.60	2.31	1.32
Basein Seedless	2..93	1.64	4.20	1.77	2.93	1.55
Kazaki Anar	2..32	1.51	3.32	1.51	–	–
Khog	2.11	1.27	2.87	1.41	2.81	1.47
A K Anar	2.17	1.31	2.80	1.42	2.77	1.52
Bocheka Lines	2.26	1.47	2.71	1.41	–	–
Gul e Shah	1.90	1.20	2.93	1.23	3.08	1.18
Shirin Anar	2.21	1.40	3.33	1.68	2.60	1.86
Dorsetta Malus	2.10	1.18	2.90	1.71	2.71	1.62
Tabest	2.353	1.90	3.33	1.21	–	–
Kali Sirin	2.59	1.49	3.26	1.42	–	–
Tujetis EC-104347	2.71	1.41	3.01	1.71	3.01	1.51
CD at 5%	**0.09**	**0.07**	**0.27**	**0.05**	**0.18**	**0.06**

Table 4. Physical characteristics of friuits of pomegrante germplasm

Genotypes	Fruit skin colour	Fruit length (cm)	Fruit width (cm)	Average Fruit wt. (g)	No. of fruits/ tree	No. of arils/ fruit	Size of aril (cm)		Rind thickness (cm)	Seed hardiness	Fruit cracking (%)
							L	B			
Jalore Seedless	YRT	8.7	7.2	168	55	157	0.9	1.1	0.34	S	15
Ganesh	YRT	8.4	6.7	160	53	123	0.7	0.9	0.45	S	18
Bedana Suri	YRT	7.21	6.7	124	23	104	0.8	1.0	0.60	H	17
P-26	R	7.5	6.9	157	30	138	1.0	1.2	0.32	S	18
Mridula	R	6.8	5.7	95	80	105	1.0	1.0	0.45	VS	24
G-137	R	8.1	7.0	150	60	116	0.8	1.1	0.43	S	21
Jodhpur red	YRT	5.4	6.7	135	130	125	0.7	0.9	0.34	H	70
Kabul	YR	6.5	6.8	153	75	100	0.7	0.9	0.32	VH	10
GKVK 1	YRT	7.7	6.8	153	28	172	0.9	1.2	0.42	VH	18
Dholka	YRT	7.4	7.7	0193	50	113	0.8	1.1	0.31	SH	25
Cimbatore white	YRT	5.2	6.3	112	45	72	0.5	0.6	0.89	H	22
P-23	YRT	8.1	8.2	185	40	142	0.8	0.9	0.35	S	25
Yarcuad	R	5.5	6.0	91	55	167	0.9	1.4	0.45	VH	40
Muskat	YRT	8.5	7.5	188	20	205	0.9	1.2	0.43	VH	16
Patna-5	YRT	6.9	7.2	125	10	298	1.4	0.9	0.48	VH	11
Bedana Thin Skin	YRT	6.0	6.2	100	41	59	0.9	1.1	0.35	SH	25
Kurvi-2EL-24685	L R	5.1	5.7	135	50	89	0.7	0.9	0.45	SH	21
Speen Danedar	YRT	5.0	7.0	146	60	112	0.8	1.0	0.46	VH	31
Basein Seedless	YRT	6.8	6.7	117	40	150	0.8	1.0	0.42	VH	35
Kazaki Anar	YRT	7.5	6.8	75	40	144	0.9	1.1	0.45	S	10
Khog	R	6.1	5.2	108	80	143	0.9	1.2	0.45	SH	33
A K Anar	R	6.1.	6.8	112	30	85	0.8	0.9	0.67	H	20
Bocheka Lines	LR	5.9	5.6	90	21	70	0.7	0.9	0.23	VH	16
Gul e Shah	YRT	5.5	5.5	88	30	98	0.7	0.7	0.34	H	12
Sirin Aanar	YRT	5.8	6.1	100	140	103	1.3	1.1	0.34	VH	31
Dorsetta Malus	R	5.5	5.8	196	10	157	0.6	0.8	0.40	VH	15
Tabest	YRT	6.8	7.0	106	126	142	1.0	1.2	0.45	SH	33
Kali Sirin	YRT	5.6	5.8	102	60	112	0.8	0.8	0.34	VH	25
Tujetis EC-104347	R	5.5	5.1	143	10	115	0.9	1.1	0.36	VH	26
CD at 5%		**1.04**	**0.90**	**10.09**	**6.00**	**15.09**	**0.06**	**0.04**	**0.08**		**2.57**

YRT = Yellow Red Tinge; R = Red; YR = Yellow Red; LT = Light Red

S = Soft; H = Hard; VS = Very Soft; VH = Very Hard; SH = Semi Hard

mean value was 1.47 cm. Martinez *et al*. (2000) also observed that heterosity in terms of flower characteristics is a common occurrence in different clones of pomegranate.

Except Bedana Suri, Kabul, Kazaki Anar, Bocheka Lines, Tabest, Kali Sirin, all the cultivars in germplasm produced hermaphrodite flowers. There was wide range of diversity in case of the size of Hermaphrodite flowers. Maximum size (3.52 cm) was recorded in Ganesh and least length (2.20 cm) in Kurvi-2EL-24685, where as, mean value recorded was 2.61 cm. Maximum breadth of hermaphrodite flowers was 1.86 cm found in Sirin Anar and minimum breadth 1.10 cm in Muskat and mean value was 1.36 cm.

With regard to fruit shape wide range was observed. In cultivars GKVK, Speen Danedar, Bocheka Lines, Dosetta Malus and Tujetis EC-104347 fruits were flat round whereas, rest of varieties produced round fruits. Similarly, there was lot of difference and variation in fruit skin colour, which ranges from red (P-26, Mridula, G-137, Khog, Yarcuad, AK Anar, Dorsetta Malus, Tujetis EC-104347) to yellowish red ting (Jalore Seedless, Ganesh, Bedana suri, Jodhpur red, GKVK-1, Dholka, Coimbatore White, P-26, Muskat, Patna-5, Bedana Thin Skin, Speen Danedar, Basein Seedless, Kazaki Anar, Gul-e-Shah, Sirin anar, Tabest, Kali sirin) and light red (Kurvi-2EL-24685 and Bocheka Lines).

Table 4 shows the physical characteristics of the fruits. With regard to length of fruit it was maximum (8.7 cm) in Jalore Seedless and minimum in Speen Danedar (5.0 cm), whereas, mean value was 6.50 cm in. Similarly maximum fruit width was 7.7 cm recorded for Dholka and mean value was 6.51 cm.

Average fruit weight was maximum (196.0 g) in Dorsetta Malus and minimum (75.0 g) in Kazaki Anar while its mean value was 131.13 g.

Owing to great incidence of fruit cracking, day night fluctuation of temperature, hot summer and cold winter, it was necessary to select promising genotypes for producing

healthy and sound fruits. Number of fruits/tree ranged from 130 in Jodhpur red to minimum of 10.0 in Patna-5 and Dorsetta Malus while mean value was 48.48.

There was quite a wide range of variability in number of arils/fruit, which ranged from 298 in Patna-5 to 70.0 in Bocheka Lines and mean value was 128.20.

Maximum length of aril was recorded in Patna-5 (1.4 cm) and minimum (0.5 cm) in Coimbatore White, and the average value was 0.84 cm. Maximum breadth (1.4 cm) of aril was recorded in Yercaud and minimum (0.6 cm) in Coimbatore White, whereas, mean value was 1.09. Maximum thickness of the rind (0.89 cm) was recorded in Coimbatore White and minimum (0.23 cm) in in Bocheka Lines.

There was difference in seed hardiness among various cultivars varying from very soft (Mridula), soft (Jalore Seedless, P-26, G-137, P-23, Kazaki Anar), Semi Hard (Dholka, Bedana Thin Skin, Kurvi-2 EL-24685, Khog, Tabest), Hard (Bedana suri, Jodhpur Red, Coimbatore White, AK Anar, Gul-e-Shah) and Very Hard (Kabul, GKVK-I, Yarcuad, Muskat, Patna-5, Speen Danedar, Basein Seedless, Bocheka Lines, Dorsetta Malus, Kali Sirin, Tujetis EC-104347).

Maximum cracking (70%) was found in Jodhpur Red and minimum in Kabul and Kazaki Anar (10.0%), Patna-5 (11.00) Gul-e-Shah (12.0%), Dorsetta Malus and Jalore Seedless (15.0%). Singh (2007) and Mali and Prasad (1999) also reported similar cracking in Jodhpur Red genotype1. Cracking may be attributed to weather conditions, particularly prevalence of high temperature and moisture stress condition of the soil (Singh *et al.*, 2003). A positive correlation of primary nutrients (leaf and fruit), leaf gas exchange properties, leaf water potential and other fruit characteristics with the ration and tendency of cracking was found by Hepaksoy *et al.* (2000).

A lot of variation was found in case of colour of arils; varying from White (Patna-5), Light Pink (Bedana Suri, P-26, G-137, Kabul, GKVK-I, Dholka, Coimbatore White, P-23, Muskat, Bedana Thin Skin, Kazaki Anar, Khog, Ak Anar, Pink (Jalore Seedless, Ganesh), Red (Yercuad, Kurvi-2EL-24685, Bocheka Lines, Gul-e-Shah, Tujetis EC-10437) and Blood Red (Mridula, Jodhpur Red, Sirin Anar, Tabest, Kali Sirin) (Table 5).

Quality of fruits and adaptability to climate decides the selection of particular variety or genotype. Juice recovery is the character which determines processing potential of cultivar/genotype. Enormous variation was observed in juice content of the fruits. Maximum juice percentage (52.0%) was recorded in Mridula followed by Jalore Seedless (51.0%), P-26 (51.0%) and least (36.0%) in Kali Sirin, whereas, average was 45.10%.The results are in line with the findings of Malhotra *et al*. (1983), Mali and Prasad (1999), and Singh (2004). With regards to TSS of fruits in pomegranate presented enormous variability was recorded. Fruits with high TSS and less acidity can be consumed raw as well as processed, while fruits with high acidity can be exploited for making dehydrated arils (anardana) and acidulant used for culinary and confectionary purpose (Singh *et al.*, 2007). Maximum TSS (21.0°B) was recorded in AK Anar, Speen Danedar (20.5°B) and least in Jodhpur Red (15.6°B), whereas, average value for TSS was 18.3°B. Acidity was recorded in the range of maximum (3.70%) Tujetis EC-104347, Dorsetta Malus (3.41%), Sirin Anar (2.30%), Kali Sirin (2.88%), whereas, minimum was recorded in Bedana Thin Skin (0.68%). Mali and Prasad (1999) reported good performance of variety Jalore Seedless, Ganesh and G-137 under arid climate while Godhara *et al.* (1989) reported that Chawla and Nabha varieties are suitable under Hissar

Table 5. Chemical composiotion of fruits of pomegranate genotypes.

Genotypes	Aril colour	Juice (%)	TSS (% B)	Acidity (%)
Jalore Seedless	Pink	51	18.5	0.76
Ganesh	Pink	50	18.0	0.76
Bedana Suri	Light pink	36	18.5	0.80
P-26	Light pink	51	19.0	0.72
Mridula	Blood red	52	18.0	0.76
G-137	Light pink	49	17.0	0.70
Jodhpur Red	Light red	49	15.6	0.70
Kabul	Light pink	42	18.0	0.72
GKVK 1	Light pink	43	18.5	0.72
Dholka	Light pink	50	19.0	0.70
Cimbatore White	Light pink	49	18.0	0.83
P-23	Light pink	51	18.5	0.73
Yarcuad	Red	49	17.5	1.50
Muskat	Light pinkp	43	19.0	0.78
Patna-5	White	40	20.0	1.00
Bedana Thin Skin	Light pink	42	17.0	0.68
Kurvi-2EL-24685	Red	43	19.5	1.08
Speen Danedar	Light pink	40	20.5	0.89
Basein Seedless	Light pink	45	17.5	1.08
Kazaki Anar	Light pink	48	17.5	1.21
Khog	Light pink	41	18.0	2.30
A K Anar	Light pink	45	21.0	0.83
Bocheka Lines	Red	43	19.5	1.50
Gul e Shah	Red	41	18.5	1.98
Sirin Anar	Blood red	47	18.0	2.30
Dorsetta Malus	Red	41	19.0	3.41
Tabest	Blood red	47	19.5	1.98
Kali Sirin	Blood red	36	17.5	2.88
TujetisEC-104347	Red	44	16.5	3.70
CD at 5%		**4.08**	**0.79**	**0.07**

conditions and Umrao *et al*. (1995) reported that Dholka and Ganesh performed better in north Indian conditions. This detailed study and information on genetic variability and evaluation of pomegranate germplasm under arid ecosystem will ensure and confirm the suitability of some promising pomegranate genotype. Long term conservation of these genotypes will provide the genetic stock for commercial exploitation and doing research for further improvement of varieties.

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Access to Crop Wild Relatives and Their Use: An Overview

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The Crop Wild Relatives (CWR; wild species closely related to crop taxa) have the potential to contribute beneficial traits to crop plants. They are at great risk of threats due to habitat loss, degradation and climate change and hence require immediate collection and conservation to make use of their potential value. The plant genetic resource programmes at the national, regional and global levels provide strong recommendations for conservation and use of CWR. The present account mainly deals in the Indian context and provides a wide array of information on importance, approach, access and utilization of this group of genetic resources for various users.

Key Words: Access, Crop wild relatives, Legal issues, Utilization

Introduction

Increasing recognition of the value of crop wild relatives (CWR) as a source of genetic material for crop improvement has enhanced the plant genetic resource management activities in different parts of the world. The CWR are species closely related to crop taxa which have the potential to contribute beneficial traits such as pest or disease resistance, wider adaptability/ tolerance/ resistance to disease, insect-pests, quality attribute, yield and wider adaptability to the crop. However, CWR, like any other group of wild species, are subject to increasing threats due to habitat loss, degradation and land use patterns, over-exploitation for use and climate change and hence require immediate collecting to make use for their value.

The utilization of CWR requires a multidisciplinary linkage at various levels *viz*. researchers, conservators, policy makers, partners, local communities and many other end users. The conservation programmes at the national, regional and global levels provide strong recommendations for conservation and use of CWR (Heywood *et al.*, 2008). However, activities on collection/augmentation, characterization, conservation and utilization of CWR have been given less focused as compared to crop plants. The present account mainly dealt in the Indian context and provides a wide array of information on importance, approach, access and utilization of CWR. Information on thrust, issues and concerns on legal aspects on this group of plant genetic resources included in this paper are the views of authors in light of current developments and not of National Bureau of Plant Genetic Resources.

Why Important?

In early part of the 20th century, there was a speculation that hybridization may play a major role in adaptive evolution (Stebbins, 1950). Artificial hybridization in recent times between crop plants and their wild progenitors, as well as wild relatives has led to variation in many crops. The CWR have been the donors of many useful traits such as resistance/tolerance to diseases, insect-pests and other stress (Sharma *et al*., 2003). Some of which include wild annual rice (*Oryza nivara*), the only source of resistance to rice tungro virus, wild lady's finger (*Abelmoschus tuberculatus*) for yellow vein mosaic virus and wild urd (*Vigna mungo* var. *silvestris*) for resistance to yellow vein mosaic virus (Arora and Pandey, 1996).

During 1970s, the great devastation caused by the grassy stunt virus in rice fields, from India to Indonesia, damaged the world's most important food crop. After a critical screening of over 17,000 accessions of cultivated and wild rices, a sample of *O. nivara*, collected from Gonda, Uttar Pradesh was found to contain gene for disease resistance. Presently rice containing gene for resistance to this virus is cultivated over a large part of Asia. Similarly, the muskmelon crop, threatened by a downy mildew outbreak was saved by a wild species of Indian muskmelon (*Cucumis*) which provided the gene for resistance to downy mildew (Rana, 1993).

Deliberate introduction of genes from wild progenitors is now being employed in all major crop improvement programmes (Khush and Brar, 1988). Identification of CWR of many crop plants and establishing their close

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genetic affinities with crops have made it possible to utilize them as potential source of genetic variation by the breeders (Kalloo and Bergh, 1993; Sharma *et al.*, 2003).

Introgression of genes from more distantly related species to a crop taxa is difficult due to crossability barriers, hybrid incompatibility, sterility, etc. (Newell and Hymowitz, 1982). However, successful introgression of useful genes from distantly related species to wild or cultivated species depends on cross-compatibility, production of hybrid seeds, normal development of F_1 hybrids, partial seed production (by natural or by back-crossing) and no hybrid break down in the segregating generations. The traits with biotic and abiotic stresses have made CWR a special category of plants for utilization in improvement of cultivated types (Kalloo and Chowdhary, 1992).

Some researchers observed that CWR are less vulnerable to genetic erosion, provided their environment is protected (Kalloo and Chowdhary, 1992). Their indiscriminate/over-exploitation for commercial use, large-scale deforestation, changing land use are the major causes of depletion of species from nature.

Access to CWR: How?

In the Indian context information pertaining to distribution, potential traits and crossability/hybridization potential of wild species with their crops is scattered. The knowledge on role of secondary genepool in crop evolution and potential/ desirable traits is insufficient. There is a need for evaluation/ characterization and cataloguing of CWR for desirable traits through the following steps:

a) Assessment of diversity
b) Identification (source, availability, potential traits)
c) Augmenting diversity
d) Evaluation/ characterization; multiplication/ conservation
e) Utilization

a) Assessment of Diversity

Diversity Distribution in CWR in India: The Indian gene centre, a major centre of domestication and diversity of crop plants (Zeven and de Wet, 1982; Arora, 1991) has three of the world's major hot-spots (Myers *et al.*, 2000; www.conservation.org.). It has over 47,000 plant species, including vascular plants (a dominant component) representing over 17,500 species of the angiosperms. High rate of endemism and intra-specific variation in Indian species (5,725 endemic taxa) is represented from three major phyto-geographical areas namely the Himalaya (3,471 species), the peninsular India (2,015 species) and the Andaman and Nicobar Islands (239 species) (Nayar, 1997). Amongst these the most significant component related to crop genepool is the CWR (Arora, 1991; 2000).

The Indian gene centre harbours about 166 species of native cultivated plants. The crops with primary, secondary and regional centers of diversity represent a part of native and introduced species which account for over 480 species (Nayar *et al.*, 2003). Diverse agro-climate and agricultural practices have led to rich diversity of crop species (landraces and cultivars) and the diversity in over 320 CWR (Arora, 1991; Arora and Nayar, 1984) along with wild economic species and weedy taxa that constitute a wild useful genepool (Box 1).

Crop wild relatives are component of agro-biodiversity on one side and floristic diversity occurring in biotically disturbed habitats on the other side. The CWR by and large, occur in grasslands, scrub vegetation and open degraded forest areas, disturbed habitats and farmer's fields as weedy components, within the major vegetation types. Seven botanical areas/centers have been identified in India: Western Himalaya, Eastern Himalaya, North-Eastern Region, Upper Gangetic Plains, Indus Plains, Western Peninsular Region and Deccan/ Eastern Peninsular Region (Arora and Nayar, 1984; Arora, 2000)· Maximum concentration of species is observed in the Western Ghats, North-eastern Region and the high altitude of the Western Himalaya. The taxonomic identification of CWR requires a skill on systematic botany. This is perhaps the reason why wild relatives are meagerly collected and represented in the germplasm collections of many germplasm holdings.

Box 1. Crop wild relatives (CWRs)

- ***Cultivated plants*** have been derived from the crop wild relatives through the process of selection followed by hybridization for bringing desired improvement.
- ***CWR*** have contributed significantly towards improvement of crop plants such as paddy, wheat, sugarcane, potato, brinjal and tomato.
- ***CWR*** are economically important for edible, medicinal and other uses: *Allium, Cicer, Citrus, Coix, Crotalaria, Dioscorea, Prunus, Rubus, Solanum*, etc. This class may include undomesticated wild species utilized by man.

National Inventories on CWR: During 1980s efforts for synthesis of information based on floristic data and exploratory studies brought out a scientific monograph "Wild Relatives of Crop Plants in India" (Arora and Nayar, 1984) and revisionary works in subsequent status papers (Arora, 2000; Arora and Nayar, 1984, Arora and Pandey, 1996). This monograph included information on about 320 species of CWR distributed in different phytogeographical regions of India namely, Western Himalaya (125); Eastern Himalaya (82); North-eastern region (132); Gangetic Plains (66); Indus Plains (45); Malabar/ Western Peninsular region/ Western Ghats (145), and Deccan/ Eastern Peninsular region/ Eastern Ghats (91). Of these species, 60 are endemic and rare taxa. Different crop-groups based on their agri-horticultural importance (number of species given in parenthesis) were: cereals and millets (51), legumes (31), oilseeds (12), fibres (24), vegetables (54), fruits (109), spices and condiments (27) and miscellaneous (26).

Systematic documentation using passport information generated through exploratory studies, literature, etc. will help in compiling scientific database and updated information on distribution, phenology, ecology, cytological, evolution studies for potential traits, etc., of CWR. This would provide a baseline for planning and execution of germplasm exploration and collection programmes, sorting out the priority areas/species for collection, multiplication, evaluation, utilization, *vis-à-vis* effective management and adopting suitable strategies. Updating and bringing out forthcoming publications on "Potential Value and Utilization of CWR of India" would be desirable in this context.

b) Identification (Source, Availability, Potential Traits)

The wild relatives, semi-domesticated and distantly related taxa occurring in developing countries have contributed significantly towards improvement of major crop species (Witt, 1982). Identification and utilization of a single gene of importance has played a major role in crop improvement. For example, an accession of wild and weedy tomato from Peruvian Andes in 1962 has been the source of high sugar content in modern tomato (Khoshoo, 1988). Source material (if exotic) requires channeling through specific procedures (import into India as per the provisions of the Plant Quarantine Order 2003). Collection of germplasm of an indigenous material from the source locality (protected habitat or site for endangered/threatened/rare species) requires prior permission of the Biodiversity Authorities.

c) Augmenting CWR

The germplasm of CWR is augmented through exotic and indigenous sources. The access to indigenous CWR germplasm is through collection that requires considerable skills. National Bureau of Plant Genetic Resources (NBPGR) as a national nodal organization, over the last three decades has been actively engaged in germplasm collecting and conservation of such biodiversity from exotic and indigenous sources (Arora *et al.*, 1975; Dhillon *et al.*, 2001). Realizing the importance of CWR in crop improvement, domestication and use of native diversity, these activities got further impetus with implementation of a mission-mode sub-project on "Sustainable Management of Plant Biodiversity' under the National Agricultural Technology Project (NATP)" (Pandey *et al.*, 2004; Pareek *et al.*, 2006).

During 1976-2004, collective national efforts have resulted in germplasm collecting from diverse phytogeographical regions/habitats of 23,118 accessions of wild species (including wild/weedy relatives of crop plants) belonging to 124 genera and 389 species. The diversity was augmented in genera *Piper* (18 species), *Dioscorea* and *Vigna* (16 species each), *Curcuma* (14 species), *Solanum* (12 species), *Citrus*, *Syzygium* and *Zingiber* (11 species each), *Cinnamomum* (10 species), *Allium* (9 species), *Momordica*, *Oryza* and related genera, *Trichosanthes* and *Sesamum* (6-7 species each). Major thrust in collections was made under National Agricultural Technology Project (NATP) during 1999-2004.

d) Evaluation, Multiplication, Conservation

The CWR for all their proven value and obvious potential have not been fully utilized principally due to lack of awareness about the potential of wild material, pattern of variability, reproductive biology, the knowledge and aptitude for identification, etc. The problem of taxonomic delineation is more serious for utilization of CWR. Conventional germplasm holdings are unable to represent full spectrum of variations and useful trait(s)/represented in the diversity.

Important examples of CWR with identified traits in India are *Oryza nivara*, a wild relative of cultivated *Oryza* (paddy), having resistance to grassy stunt virus from Uttar Pradesh; *O. coarctata*, a weedy relative with hardiness traits for saline/marshy habitats from Sunderban delta

region in West Bengal; *Eleusine compressa*, a wild relative of *E. coracana* (finger millet) from north western arid tracts, having traits for hardiness and drought tolerance; *Vigna mungo* var. *silvestris* and *V. radiata* var. *sublobata*, wild relatives of cultivated *V. mungo* (urd) and *V. radiata* (mung), respectively from Ghats and adjacent areas, exhibiting tolerance to yellow mosaic virus; *Cicer microphyllum*), a wild relative of *C. arietinum* (chickpea) having cold hardiness and more seeds/ pod from high altitudes of Himalayas; *Sesamum laciniatum* from coastal Andhra and Tamil Nadu, a wild relative of cultivated *S. indicum* (sesame) having resistance to leaf phyllody disease; *L. perenne*, a wild relative of cultivated *Linum usittatissimum* (linseed) with cold hardy traits from Lahaul and Spiti region and other parts of Western Himalayas; *Citrus latipes*, a wild relative of cultivated *Citrus* species (lemon and limes) with cold resistance from the Shillong plateau, Khasi hills; *Abelmoschus tuberculatus* and *A. manihot*, wild relatives of *A. esculentus* (lady's finger) tolerant/resistant to yellow vein mosaic virus and fruit borer from northern India.

The multiplication of germplasm of wild relatives in newer habitats (to which it is poorly adapted) is in itself a major cause of loss. For example wild relatives of *Vigna* collected from Western Ghats may be very poorly adapted to conditions of north India and thus are difficult to maintain and multiply under normal field conditions. Multiplication, evaluation and characterization should be done at least at 2-3 geographical locations of similar latitude/longitude for conservation and future utilization.

At the time of maintenance of CWR, seed shattering during field operations (evaluation/characterization) results in soil infestation which may lead to appearance of unwanted plants in subsequent seasons. Hot-spots and critical habitats should be used for conservation and for protection of wild species. Role models for *in situ*/ *on farm* conservation may be developed on regional basis. For this, community involvement and less dependence of local people on the natural stock (wild genetic resources) may be emphasized.

The NBPGR networks with its regional stations and 59 National Active Germplasm Sites (NAGS) representing crop-based institutes, national research centres (NRCS), State Agricultural Universities (SAUS) for multiplication, evaluation, conservation and distribution of active collections of CWR. The current holdings of wild species conserved in the national genebank are meagerly represented from Indian region. Accessions from widely distributed habitats are required to be augmented and conserved. Special collection missions are needed in areas of occurrence of diversity and conserved using *ex situ* and *in situ* approaches.

e) Utilization

Utilization of CWR involves: Identification of wild genepool of the crop; availability of sufficient material for screening and evaluation of desirable trait; and appropriate method for gene transfer. Based on genetic affinities between the crop species and CWR they can be classified into exploitable and unexploitable types. The first group includes the wild progenitors of crops, wild and weedy forms that were called the primary genepool of crops (Harlan and de Wet, 1971). This also includes the distantly but cross compatible wild related species, leading to partly fertile cross-progenies (secondary genepool). The unexploitable category of CWR includes the tertiary genepool that has little direct value. They can be used to trap valuable genes by application of gene transfer techniques.

By utilizing modern techniques such as DNA fingerprinting and molecular techniques to identify the genepool and tissue culture technique (embryo's rescue), the desired traits of wild species can be exploited. Through these approaches/applications, utilization of secondary and tertiary genepool has now become possible. However, our knowledge of CWR of most crops is still fragmentary. Basic information on species delimitation, distribution and diversity of desirable traits and genetic variation, chromosome numbers, crossability aspects, etc. in many species is either incomplete or totally lacking.

The utilization of crop wild relatives (CWR) genes to improve crop performance has been known for more than six decades. The improved interspecific hybridization techniques have led to an increase in use of secondary and tertiary genepool of many crops in the past (Hajjar and Toby, 2007). There has been steady increase in rate of release of cultivars containing genes from CWR. Introduction of genes from CWR into crops of major global food security are met with basic sources i.e. from '*in situ*', the farmers' fields and uncultivated land. Majority of new breeding materials or germplasm held in national gene bank, or organizations and the 'in trust' collections are maintained by the International Centers of the CGIAR.

Accomplishment of interspecific crosses between crops and CWR has opened new dimensions in the utilization of wild relatives in various crop improvement

programmes. The value of wild relatives was better recognized with findings of *Zea diploperennis*, a new teosinte from Mexico (Iltis, 1979) and *Oryza nivara* from India (Govindaswami *et al.*, 1966). Crossability of *Allium cepa* and *A. sativum* with *A. roylei* (a accession of Indian origin) has opened a new avenue for utilization of Indian alliums. This species has been used for transferring resistance for powdery mildew and leaf blight in the cultivated taxa (de Vries *et al.*, 1992).

The CWR resources have also been utilized as crude product in traditional medicine and traded worldwide in different regions of the globe. Over 20 per cent of these medicinal plants traded in Germany are naturalized outside their region of economic utilization and only 40 per cent are native, for example, Chinese Ginseng (*Panex ginseng*), from Afghanistan, orchids from India, etc. (Kerry Kate and Laird, 1999).

Problems Associated with CWR

While collecting the germplasm of wild relatives from natural population, problems are encountered due to asynchronized seed maturity, availability of insufficient material due to poor density of plant population and dormancy in the bud woods (trees and vegetatively propagated species). Seed germination and lack of suitable agro-climatic conditions for multiplication, often result in loss of germplasm during the process of seed multiplication. The asynchronised seed maturity and shattering habit are problematic traits associated with wild species in the natural habitats, collection sites and during evaluation and characterization. Seed dormancy problem may be overcome by breaking dormancy, using elaborate and time-consuming protocols. Using standard seed treatment protocols, which require expertise, financial inputs and manpower, this problem, may be overcome. The germplasm of wild relatives is too often represented by a few accessions available with the institutions and are considered inadequate to represent wild germplasm.

Access to CWR: Legal Issues

Enforcement of Convention on Biological Diversity CBD (1992) and provisions of Trade Related Aspects of Intellectual Property Rights (TRIPS) have led to the apprehension that exchange of germplasm would get restricted. In the post-CBD era, there was an overall decline in per cent introduction of PGR (Arjunl Lal *et al.*, 2009). Exchange of CWR in the post-CBD era is imperative as the use of exotic species is much desired for crop improvement, such as successful use of CWR of tomato, potato, etc. that have been build up through vast range of diversity and a systematic plan of addition to the diversity by collection and introduction. This activity is now restricted due to the condition for prior permit for access of germplasm (Lal *et al.*, 2009). The trend may however change after the International Treaty on Plant Genetic Resources for Food and Agriculture (IT-PGRFA), a legally binding (Kerry Kate, 1999; Gadgil *et al.*, 1996) which envisages a facilitated access to plant genetic resources for food and agriculture held by countries through multilateral system (MS) of exchange. This access under the Treaty would be only for utilization, conservation, research, breeding and training. However an access for chemical, pharmaceutical and other non-food and non-feed purpose is not covered under the Treaty. The exchange of genetic resources (Annex 1 crops of the Treaty: including 35 Food crop genera and 29 Forage Crop Species) would be under the conditions of a standard material transfer agreement (SMTA).

The mechanism of access to genetic resources from India as envisaged in the Biological Diversity Act 2002 is as follows. Section 3 of the Biological Diversity Act 2002 provides mandatory prior approval by all non-Indians (as defined in the Act) from the National Biodiversity Authority (NBA) for obtaining any biological resources occurring in India or associated knowledge for commercial or any other use. However, there are exemptions from seeking approval of NBA for exchange of genetic resources under collaborative research projects approved by the Government of India, including bilateral/MoU/multilateral agreements. Further, section 6 of the NBA grants such approvals subject to terms and conditions so as to secure equitable sharing of benefits arising out of the use of accessed biological resources, and associated knowledge. Similarly Indian industry is required to provide prior intimation to the concerned State Biodiversity Board (SBB) about the use of biological resource, and the SBB has the power to restrict any such activity which violates the objectives of conservation, sustainable use and equitable sharing of benefits. The NBA as well as the SBB is required to undertake mandatory consultation of the concerned local level Biodiversity Management Committees (BMCs) for decision making process relating to access and benefit sharing, thereby formalizing the prior informed consent by communities for access and benefit sharing. Under the Plant Varieties and Farmers' Rights Act, 2001 the rights are shared on use of any traditional varieties/landrace of a cultivar developed through selection and identification

for traits/ usefulness, and wild species or a wild relative about which the farmer possess the common knowledge, through recognition of farmers and benefit sharing of provisions from the ' Gene Fund'.

Concerns: CWR Access for Utilization

In the present international scenario, global climatic changes, unsustainability of high input agriculture, search for novel genes for biotic and abiotic stress have increased the focus on access, conservation and utilization of potential diversity in the years to come. To meet these challenges more plant species have to be tested against the threat of nature. The modern agricultural practices indirectly favour reduction of diversity by supporting crop subsidies for cultivating high yielding varieties of crops, use of herbicides to eliminate CWR, weedy relatives of crop plants. For effective implementation of biodiversity conservation programmes, involvement of local communities by providing positive incentives is desirable (Gadgil et al., 1996).

Indiscriminate harvest can be avoided by dissemination of information on sustainable harvesting tips in relation to ensuring public confidence, to maximize economic benefits and to minimize negative impacts on habitats and species diversity from use of wild genetic resources at local level. Over-exploitation of commercially important CWR as *Dioscorea, Allium, Rauvolfia* adopting precautionary measures for controlled grazing, organizing environmental education programmes and by harvesting only after maturation/ shedding of seeds, for retaining some part for perpetuation and by practicing scientific methods of storage can help to save biodiversity including CWR. Through formal and informal educational curricula, emphasis can be laid on environmental education to conserve the biodiversity. Special training courses should include issues such as diversity and management strategy, knowledge on potentials of wild relatives and promotion of biodiversity conservation.

Gaps identified on management of CWR relatives should be bridged through appropriate research and development. Communication links among relevant national/ international institutions and rapport between scientists and administrators, Non-Governmental Organizations (NGOs) and local communities can facilitate the networking in the present era.

Conclusions

The genetic erosion has increased alarmingly in all parts of the world. The national and international concern for systematic management of wild and weedy relatives of crop plants has necessitated collection and conservation for immediate and future use in breeding programmes. In response to the CBD regime, there has been a need to assess the potential of wild wealth available with us. In view of these provisions, CWR, with valuable traits and hidden potential need to be collected, conserved, characterized and documented on priority basis.

Emphasis needs to be given on target collection, conservation and sustainable management of CWR using *ex situ* and *in situ* measures especially for rare/endangered species. Collaborative/networking approaches through inter-institutional linkage can help in periodic monitoring of the status of wild genepool. For this, Botanical Surveys, Ministry of Environment and Forests, Government of India and NGOs may actively collaborate to perform the task effectively.

Keeping in view the importance of CWR in the national context, the following thrust areas have been identified:

- Assessment of gaps in collection; survey and collection of CWR through special exploration missions in priority areas/ for priority traits
- Characterization/ evaluation for desirable traits for utilization of CWR
- Establishing linkages between organizations involved in *ex situ* and *in situ* conservation
- Developing documentary information and data bases, and
- Awareness generation at various levels

The above account briefly highlights the access to CWR for utilization with special reference to the Indian gene centre. The information contained would help in understanding the basics of CWR in general and also help in assessing and evaluation/ validation of these resources with particular reference to PGRFA and rights to access and benefit sharing with global terms.

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Evaluation of Exotic Mandarin Germplasm under Mid-Hills of Sikkim Himalayan Region

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Eight exotic mandarin germplasm were evaluated on the basis of physico-chemical properties of fruit at ICAR Research Complex, Sikkim Centre, Tadong, Gangtok, during 2009 and 2010. Cultivar 'Dancy' had the longest fruit development period and maximum oil gland density, whereas, Thorny showed precocity in fruit development. Except 'Page', all mandarin germplasm had loosely adhered flavido which is the desired character for table type variety. 'Kinnow' and 'King' mandarins have relatively bigger and heavier fruit, whereas, 'Page' has the smallest and 'Fortune' has medium size fruit. Except 'Fortune', other cultivars could not develop deep orange colour in their fruit. Fortune had maximum juice content (51.3%), TSS (10.4° Brix), TSS/acid ratio (11.07), sugar content (7.86%) and sugar/acid ratio (8.45). It also had intermediate number of seeds/fruit (10.2). Whereas, 'Dancy' has the minimum juice content (42.6%), TSS (8.2° Brix), TSS/acid ratio (5.77), sugar/acid ratio (4.45%) and seeds/fruit (7.3). Physico-chemical properties of mandarin germplasm clearly indicated that 'Fortune' mandarin possesses desired qualities for table type cultivar and hence deserves adoption after further field evaluation trial.

Key Words: Fruit, Juice content, Mandarin, Sugar/acid ratio

Introduction

Citrus is cultivated under varied latitudes of tropical and subtropical regions of the world as well as of India. India ranks forth in world citrus production (Anon., 2010) and citrus industry is mainly dominated by sweet orange (*Citrus Sinensis* Osbeck), mandarin (*Citrus Reticulata* Blanco), lemon (*C. limon*) and lime (*Citrus Rurantifoli*a Swingle), however, other citrus groups are cultivated at limited scale (NHB, 09-10). The northeastern region is rich treasure of various Citrus species and varieties (Bhattacharya and Dutta, 1956). Manipur and Assam are major citrus producing state, accounting for more than 60 % of citrus production in the region (NHB, 09-10). Among citrus, mandarin is considered as the most important horticultural fruit crop of the regions, which plays vital role in sustaining the livelihood of farmers. Mandarin shows minor variation in physico-chemical properties due to its adaptability under different climatic conditions (Singh *et al.*, 2001). In Sikkim, mandarin (*Citrus reticulata* Blanco) is mainly cultivated in the mid hills under the subtropical temperate humid climatic conditions with the altitudinal variations of 3000 -4200 feet.

The North-eastern region is recognized globally as an area of citrus diversity but the genetic erosion of valuable citrus species warrants for an urgent step for conservation of exceptionally well performing germplasm under specific climatic conditions. Sharma *et al.* (2004) studied in detail the genetic resources of citrus of north eastern India and put emphasis on their systematic conservation and potential use. Furthermore, Malik *et al.* (2006) characterized the endangered potential citrus root stocks of northeastern region and perceived the potential threat of erosion if not conserved. Many potential exotic citrus species/varieties have been introduced and some of them have well adapted and some has the potential to be grown at larger scale. Initially germplasm should be characterized, evaluated and screened against biotic and abiotic stresses for future utilization for improvement. Other strategies include *ex-situ* conservation facilities such as gene banks. The later has received considerable importance after perceiving the threat of rapid genetic erosion.

The physico-chemical and sensorial attributes of mandarin cultivated in different areas of Sikkim has been studied (Kishore *et al*., 2009) however, evaluation of performance of exotic mandarin germplasm under mid hills of Sikkim has not been done so far. This study will be helpful not only in giving an overview of the potential of exotic mandarin germplasm but also in conserving them.

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Moreover, the potential germplasm may be suggested for step-wise adoption in the region due to poor productivity of Sikkim mandarin.

Materials and Methods

A total of eight mandarin germplasm; Dancy, Thorny, Fox, Fortune, Afourer, Page, King (Citrus nobilis Lour.) and Kinnow (*C. nobilis* Lour. x *C. deliciosa* Ten.) were collected under Sikkim Foundation Programme from Catherin Research Institute, Australia. Germplasm were planted in 2001 in the research farm of ICAR Sikkim Centre, Tadong, Gangtok located at latitude of 27°20' N, longitude of 88° 4' E and altitude of 1300m amsl. The prevailing climate is temperate humid with annual rainfall of 2850 mm and mean minimum and maximum temperature ranges of 11.5 and 24.6°C, respectively. Plants were planted in randomized block design with three replications and evaluated in 2009 and 2010 on the basis of their yield attributes and fruit characters. Data on flower and fruit characters were recorded as per the descriptor for Citrus (IPGRI, 1999). Physical characters of fruit were measured by considering mean value of ten fruits; however, data on chemical characters were calculated by taking mean value of five fruits under different replications during 2009 and 2010. The juice percentage was calculated by dividing the juice content with fruit weight and by multiplying the resultant with 100. The total soluble solids (TSS) were recorded by hand refractometer (0-32° Brix), whereas, titrable acidity, vitamin C, reducing sugar and total sugar were determined by following the methods of Ranganna (1991). The TSS/acid ratio was calculated by dividing TSS and titrable acidity and similarly sugar/acid ratio was calculated by dividing sugar and acid. Data collected on various attributes during 2009 and 2010 were averaged and subjected to analysis of variance (ANOVA) to test the significance among variables and Duncan multiple range test at $P<0.05$ to compare the means by using SPSS statistical package (11.5 version).

Table 1. Physical characters of mandarin germplasm

Citrus species	Variety	IC No.	Time of flowering	Duration from flower to fruit maturity (days)	Fruit base	Fruits apex	Fruit shape	Flavido colour	Flavido adherence	Nature of oil glands	Oil glands/ mm^2	Albedo colour
C. reticulata	Dancy	586981	Feb. 1st fortnight	287.5[a]	Convex	Flat	Obloid	Light orange	Loose	Conspicuous	6.3[a]	White with yellow tinge
C. nobilis	King	586982	Feb. 2nd	278.3[b]	Truncate	Flat	Spherical	Light orange	Loose	Conspicuous	5.4[ab]	Creamish
C. reticulata	Thorny	586983	Mar. 1st fortnight	252.7[e]	Convex	Flat	Spherical	Orange	Slightly tight	Conspicuous	5.7[a]	White with orange tinge
C. reticulata	Fox	586984	Feb. 2nd fortnight	270.3[c]	Truncate	Flat	Obloid	Greenish with yellow tinge	Loose	Conspicuous	4.2[bc]	Creamish
C. reticulata	Fortune	586985	Feb. 2nd fortnight	265.3[d]	Convex	Convex	Obloid	Deep	Slightly tight	Highly Conspicuous	5.6[a]	Creamish
C. reticulata	Afourer	586986	Feb. 1st fortnight	267.7[d]	Convex	Flat	Spherical	Orange	Slightly tight	Conspicuous	5.1[ab]	Creamish
C. reticulata	Page	–	Feb. 2nd fortnight	277.7[b]	Convex	Flat	Spherical	Orange	Strong	Conspicuous	5.4[ab]	White with orange tinge
C. nobilis x *C. deliciosa*	Kinnow	–	Mar. 1st fortnight	271.7[c]	Truncate	Flat	Obloid	Orange	Slight tight	Conspicuous	4.6[bc]	White with orange tinge
CD at 5%			–	6.6	–	–		–	–	–	0.8	

Data with the same superscripted letter in a column are statistically non-significant (p=0.05)

Table 2. Physico-chemical characterization of mandarin germplasm

Citrus species	Variety	IC No.	Fruit size (mm)	Fruit wt. (g)	Peel thick-ness (mm)	Fruit firm-ness (lb/ inch$^{2)}$	No. of seg-ments	Juice (%)	TSS (^{o}B)	Acidity (%)	TSS/ acid ratio	Vit. C (mg/ 100 g)	Red. sugar (%)	Total sugar (%)	Sugar/ acid ratio	Seeds/ fruit
C. reticulata	Dancy	586981	63 x 54	98.5^{c}	3.5 ^{a}	5.6^{c}	10^{a}	42.6^{c}	8.2^{b}	1.42^{a}	5.77^{d}	62.5^{a}	4.82^{c}	6.32^{d}	4.45^{e}	7.3^{c}
C. nobilis	King	586982	65 x 57	108.6 ^{b}	3.2 ^{b}	6.2^{a}	10^{a}	43.4^{c}	8.8^{b}	1.12^{b}	7.85^{c}	55.2^{b}	5.10^{b}	6.54^{c}	5.83^{c}	18.3^{b}
C. reticulata	Thorny	586983	62 x 52	90.3^{d}	3.2 ^{b}	5.5^{c}	11^{a}	47.5^{b}	9.3^{a}	0.98^{c}	9.48^{b}	47.3^{d}	5.24^{a}	6.84^{c}	6.97^{b}	7.9^{c}
C. reticulata	Fox	586984	63 x 53	95.6^{d}	3.6 ^{a}	5.8^{b}	10^{a}	46.2^{b}	8.4^{b}	0.96^{c}	8.75^{b}	48.2^{d}	4.65^{c}	6.23^{d}	6.48^{b}	21.4^{a}
C. reticulata	Fortune	586985	60 x 52	87.6^{e}	3.2 ^{b}	5.6^{c}	8^{b}	51.3^{a}	10.4^{a}	0.93^{c}	11.07^{c}	45.3^{d}	5.62^{a}	7.86^{a}	8.45^{a}	10.2^{c}
C. reticulata	Afourer	586986	58 x 51	82.6^{f}	3.2 ^{b}	5.6^{c}	9^{ab}	47.6^{b}	8.5^{b}	1.21^{b}	7.02^{c}	48.4^{d}	4.75^{c}	6.21^{d}	5.13^{d}	17.4^{b}
C. reticulata	Page	–	56 x 50	64.5^{g}	3.5 ^{a}	5.7^{c}	10^{a}	44.3^{c}	10.2^{a}	1.22^{a}	8.36^{b}	52.7^{c}	5.12^{b}	7.42^{b}	6.08^{bc}	16.6^{b}
C. nobilis x *C. deliciosa*	Kinnow	–	66 x 58	113.5 ^{a}	3.7^{a}	6.1^{b}	10^{a}	50.6^{a}	9.8^{a}	1.28^{a}	7.65^{c}	56.4^{b}	4.95^{c}	7.30^{b}	5.70^{c}	18.1^{b}
CD at 5%				3.4	0.2	0.3	1.4	1.9	1.6	0.2	0.8	3.5	0.4	0.4	0.6	3.1

Data with the same superscripted letter in a column are statistically non-significant (p=0.05)

Results and Discussion

The qualitative and quantitative traits varied with germplasm (Table 1 and 2). The flowering time varied from February to March, however, Dancy and Afourer showed precocious flowering, whereas, Kinnow and Thorny were late in flowering under the temperate humid climate of Sikkim. Thorny mandarin had the shortest fruit development cycle and got matured in 252.7 days whereas, Dancy had the longest fruit development period of 287.5 days. Most of the germplasm had oblate fruit shape with convex fruit base and flat apex, however, the fruit base of King and Fox mandarin was truncate. Flavido colour of germplsm varied from light orange to deep orange colour except Fox mandarin which had greenish colour flavido with yellow tinge , whereas, albedo colour of germplasm varied from creamish to whitish. As regard to adherence of flavido with albido, except Page other mandarin germplasm were loosely adhered. Nature and density of oil gland are considered important variables for germplasm characterization. All germplasm had conspicuous oil gland the maximum oil gland density recorded in Dancy (6.3/ mm^{2}) and minimum in Fox mandarin (4.2/mm^{2}), whereas other germplasm had intermediate density.

Physical properties of fruits of different germplasm clearly indicate that King and Kinnow bear relatively bigger and heavier fruits, whereas Page mandarin has the smallest and lightest fruits. Peel thickness varied marginally with germplasm and the maximum peel thickness was recorded in Kinnow followed by Fox mandarin. Thorny had the maximum segments, whereas Fortune had the minimum. Juice content varied from 42.5-51.3% and the highest percentage of juice was recorded in Fortune (51.30%), whereas Dancy had the minimum.

The chemical analysis of fruit showed that Fortune had the highest TSS and lowest acidity that resulted highest TSS/acid ratio (11.8), whereas fruit of Dancy had the lowest TSS, highest acidity and consequently lowest TSS/acid ratio. The highest vitamin C content was recorded in Dancy and lowest in Fortune. In contrast, Fortune had the highest reducing sugar, total sugar and sugar acid ratio followed by Thorny mandarin, whereas, Dancy had the minimum reducing sugar, total sugar and sugar acid ratio. The highest sugar acid ratio suggests high sweetness and preferred variety for table purpose. Varietal preference is also based on the number of seeds/fruit and generally fruits with less seed are preferred. Fox had the maximum number of seeds/ fruit (21.4) and Thorny had the minimum number (7.9). Preliminary evaluation studies clearly indicated that Fortune mandarin has potential to become the table variety of this region, as its fruit possesses most of the required physicho-chemical properties. However, before suggesting for adoption further multilocational field evaluation is required to be undertaken. Citrus diversity of northeastern region has been studied by various workers (Hore *et al*., 1997; Malik *et al*., 2006; Singh *et al*., 2001) and they suggested proper exploitation of potential germplasm in crop improvement. This effort will further strengthened by more concentrated efforts to characterize document and conserve the native and exotic species of citrus in North-eastern India.

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Genetic Variability of Guava (*Psidium guajava* L.) and its Prospects for Crop Improvement

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Diverse germplasm of guava (*Psidium guajava* L.) assembled at Horticulture Farm, Maharana Pratap University of Agriculture and Technology; Udaipur was evaluated with respect to morphometric characteristics, yield attributes and quality parameters for further utilization in improvement programme. The 47 guava genotype showed range of variability in respect to plant growth, yield attributes and yield and quality parameters. The average fruit weight ranged from 65 to 281 g, seed content 1.21 to 3.26 g and seed number 125 to 450/fruit in the different genotypes. Further, TSS and ascorbic acid contents ranges from 11 to 18.2 per cent and 129 to 268 mg/100 g pulp respectively. Out of the 47 genotypes two genotypes (MPUAT/47, MPUAT/43 recently named as MPUAT S-1 & MPUAT S-2, respectively) were identified as superior in respect to yield and quality. Further, MPUAT/6 and MPUAT/41 were also observed as potential genotype for the yield. This paper discuss the performance of promising guava genotypes and status of the conservation of guava genotypes in the field repository being maintained and evaluated under sub humid southern plains and Aravalli hills of Rajasthan.

Key Words: Evaluation, *Psidium guajava*, Variability

Introduction

Guava is also known as the "Apple of the Tropics" and belongs to family Myrtaceae. Important guava growing states in the country are Uttar Pradesh, Bihar, Madhya Pradesh and Maharashtra. Allahabad district of Uttar Pradesh has the reputation of growing the best quality of guava fruits in the world (Mitra and Bose, 1990). In Rajasthan major guava growing pockets are Sawaimadhopur, Udaipur, Kota, Bundi etc. The importance of guava is due to the fact that it is the hardy fruit which can be grown in alkaline and poorly drained soil. Tropical America is supposed to be centre of origin of guava where it is found in wild as well as cultivated forms. Most of the cultivars of Indian guava belong to the genus *Psidium* and *species guajava*. Based on the shape of common guava fruits, they are classified into two groups, *i.e. Psidium pyriferum* and *Psidium pomiferum* (De Candolle, 1886). Genus *Psidium* contains about 150 species (Hayes, 1970) all cultivated guava varieties are either diploid 2n=2x=22 or triploid 2n=3x=33 (Atchinson, 1947). As per the inheritance pattern bold seed is found to be dominant over soft seed and governed monogenically, red flesh colour is dominant to white and is known to bealso governed monogenically, red fleshed cultivars are supposed to be heterozygous and there is linkage between red flesh colour and bold seed size. Further, triploidy and some other genetic factors are responsible for female sterility (Subramanyam and Iyer; 1982, Shukla *et al*., 2004).

The evaluation and improvement of guava for Rajasthan need to be intensified with superior quality and dwarf growth habit. Keeping in view the above facts present programme was launched to evaluated and utilize the existing variability of the guava for crop improvement.

Materials and Methods

Guava is mainly a self-pollinated crop but occurrence of cross pollination resulted in great variation in the seedling population. At present, 210 seedling germplasm of guava are being maintained at Horticulture Farm, of Maharana Pratap University of Agriculture and Technology, Udaipur, collected through exploration from different parts of Rajasthan particularly Sawaimadhopur, Kota, Bundi and Udaipur, and these were evaluated for plant growth characteristics, fruiting behaviour, fruit quality and fruit yield. Selective sampling method was adopted for the identification of the promising genotype. Age of the plants was ten years and planted at the spacing of the 6m x 6m. The fruit sample comprising of 15 mature fruits of each genotype from winter season (Mrig bahar) were used for the physico-chemical analysis. Total Soluble Sugars (TSS) content was recorded with help of hand refractometer and readings were corrected at 20^{o}C with the help of

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Table 1. Range of variability in plant and fruit characters of guava germplasm

A. Plant phenology		Range
Plant height (m)		3.10-5.18
Canopy spread	E-W (m)	5.10-6.48
	N-S (m)	5.18-7.25
Girth (cm)		28.00-64.00
Leaf Size	Length (cm)	9.2-13.45
	Width (cm)	4.24-5.65
B. Fruit yield and quality		
Fruit weight (g)		65.00-281.00
Fruit size (cm) (L x B)		4.40 x 8.61-3.60 x 8.24
Fruit yield (kg/tree)		25.00-68.00
Seed weight (g/fruit)		1.21-3.26
Number of seeds/fruit		125.00-450.00
TSS (%)		11.00-18.20
Reducing sugar (%)		3.96-4.75
Non reducing sugar (%)		3.45-4.68
Total sugars (%)		7.41-9.43
Acidity (%)		0.5-1.01
Ascorbic acid (mg/100 g pulp)		129.00-268.00
Organoleptic score		7.00-9.00

temperature correction chart. However, titrable acidity and vitamin C contents were determined as per standard method described by AOAC (1990). Organoleptic score was obtained by a panel of five judges following zero to ten hedonic scale.

Results and Discussion

It is evident from the data presented in Table 1, 2 and variability exists with respect to plant growth characteristics, fruit yield and fruit quality in the analysed germplasm accessions. From the observations it was noticed that the plant height varied from 3.10 to 5.18 m, canopy spread 5.10 to 6.48 m (E-W), 5.18 to 7.25 m (N-S), girth of main branch 28 to 64 cm, leaf length 9.20 to 13.45 cm and width 4.24 to 5.65 cm. Further, average fruit weight varied from 65 to 281 g and fruit length and breadth showed variability range from 4.40 to 8.61 cm and 3.60 to 8.24 cm, respectively. However, seed weight/fruit varied

Table 2. General characteristics of fruits of guava germplasm

Collector No.	Fruit characters	Collector No.	Fruit characters
MPUAT/1	Smooth surface, seedy & milky white pulp	MPUAT/23	Shining surface, pear shape, sweet taste, seed big size.
MPUAT/2	Smooth surface. Inside cavity & white pulp	MPUAT/24	Oblong shape, soft and little seed , milky white pulp
MPUAT/3	Smooth surface, sweet taste, low seed but hardy	MPUAT/25	Smooth surface with line depressions , hollow cavity, seedy but soft seed, milky white pulp
MPUAT/4	Smooth surface, creamish yellow pulp, less & soft seed		
MPUAT/5	Smooth surface, creamish green pulp, hard seed	MPUAT/26	Round shape, whitish pulp, 5 locular but hard seed
MPUAT/6	Rough surface, pyriform shape, less & soft seed with white pulp	MPUAT/27	Greenish background with red colour pigmentation, low seed density.
MPUAT/7	Slight roughish surface, creamish yellow pulp small seed with soft.	MPUAT/28	Greenish white pulp, large or bold seeds
		MPUAT/29	Golden colour, acidic taste, low & soft seed
MPUAT/8	Shining smooth surface, few & soft seed, milky white pulp	MPUAT/30	Golden colour, milky white pulp, high but soft seed with 5 seed cavity locules.
MPUAT/9	Smooth surface, soft seed, good aroma & white pulp	MPUAT/31	Red colour pulp, good sugar acid blend
MPUAT/10	Rough surface, pyriform shape, creamish yellow pulp	MPUAT/32	Rough shape, low & soft seed with good taste, milky white pulp
MPUAT/11	Shining smooth surface, round shape, seed medium hardy, white milky pulp	MPUAT/33	Light green surface, milky white pulp, low but hard seed
		MPUAT/34	Ridge to smooth surface, golden colour, white pulp, low seed but hard
MPUAT/12	Pronounced ridges on surface, small & little seed but comparatively hard	MPUAT/35	Greenish fruit skin, white pulp, big size fruit, low seed but hard with 5 locules.
MPUAT/13	Smooth surface with greenish yellow colour, milky white pulp	MPUAT/36	Smooth green surface, white pulp, soft & low seed.
MPUAT/14	Smooth and golden colour surface, extra milky white pulp	MPUAT/37	Rough karela shape, little seed, good acidic blend with high pulp content
MPUAT/15	Round shape, greenish yellow colour, smooth & soft pulp with whitish colour	MPUAT/38	Golden colour, smooth surface, milky white pulp with coconut biting, low and soft seed
MPUAT/16	Smooth surface with slight ridges, low seed but soft good texture	MPUAT/39	Golden colour with apple like pigmentation, taste sweet and coconut biting but hard seed
MPUAT/17	Rough surface, ridge on it, creamish white pulp, negligible seed but hard	MPUAT/40	Pulp white, low seed but hard
		MPUAT/41	Light green fruit surface, whitish pulp with 5 locules in it.
MPUAT/18	Smooth surface with six line depressions on it, seedy but soft in nature, milky white pulp	MPUAT/42	Extra smooth surface, low but hard seed
MPUAT/19	Ridge surface with hallow cavity, greenish yellow surface colour, white pulp	MPUAT/43	Oblong shape, greenish yellow skin colour, white pulp good appealing overall with 2 locular segmentation..
MPUAT/20	Bright surface with round shape, high sweet with 4-5 locules, white pulp with soft seed	MPUAT/44	Smooth green surface, white pulp with hallow cavity& 6 locules and soft seed
MPUAT/21	Bright surface with round shape, high sweet with 6 loculer cavity, white pulp with soft seed	MPUAT/45	Rough surface, white pulp, bold and soft seed.
		MPUAT/46	Golden green colour, milky white pulp, low and soft seed
MPUAT/22	Bright & slight ridges on it, tiny hole cavity, 4 locules & soft pulp	MPUAT/47	Red Skin surface look like apple, creamish pulp, slight hard seed with good organoleptic score

Table 3. Physico-chemical properties of fruits of guava germplasm

Collectors No.	Fruit weight (g)	Fruit width (cm)		TSS (%)	Acidity (%)	Vitamin C (mg/100 g pulp)	Seed weight (g)/fruit	Organoleptic score (0 to 10)
		Length	Breadth					
MPUAT/1	185	6.95	8.24	11.0	0.80	145	2.00	8.0
MPUAT/2	136	6.14	7.76	12.0	0.75	130	1.85	7.5
MPUAT/3	115	5.85	6.25	13.0	0.64	134	1.79	8.0
MPUAT/4	121.5	6.21	5.87	11.5	0.78	142	1.76	7.25
MPUAT/5	138	6.37	6.63	12.0	0.73	154	2.10	7.5
MPUAT/6	281	9.17	7.65	13.2	0.75	210	2.45	8.5
MPUAT/7	200	7.78	7.32	11.0	0.85	190	3.00	7.0
MPUAT/8	130	6.81	6.34	12.0	0.72	175	1.89	8.5
MPUAT/9	160	6.47	7.10	13.0	0.69	163	1.90	9.0
MPUAT/10	200	8.61	6.68	12.8	0.72	197	2.89	8.0
MPUAT/11	115	6.44	5.91	12.8	0.76	149	2.10	7.0
MPUAT/12	115	6.30	5.24	16.0	0.65	170	3.10	6.2
MPUAT/13	170	5.72	5.30	13.0	0.72	183	3.34	7.0
MPUAT/14	95	5.85	5.44	12	0.78	185	2.10	7.0
MPUAT/15	75	5.35	4.67	14	0.70	145	2.00	7.0
MPUAT/16	106	5.70	5.70	16.0	0.64	176	2.14	7.5
MPUAT/17	195	6.90	6.23	17	0.68	178	2.90	7.0
MPUAT/18	157.5	6.60	6.65	15.5	0.64	179	2.76	7.0
MPUAT/19	76	5.25	4.87	17	0.62	134	1.98	7.5
MPUAT/20	110	5.9	5.5	16	0.59	138	1.76	8
MPUAT/21	200	7.4	6.9	15	0.54	210	3.14	8
MPUAT/22	187	7.2	5.9	16	0.53	205	2.89	8
MPUAT/23	90	5.25	5.70	17	0.52	178	1.75	8.5
MPUAT/24	104	5.7	5.9	15	0.61	175	1.68	7.5
MPUAT/25	122.5	6.3	6.0	16	0.60	168	1.70	7.5
MPUAT/26	191	7.1	6.8	16	0.59	190	2.00	7.5
MPUAT/27	95.0	6.5	4.0	17	0.57	180	1.98	8.0
MPUAT/28	128	6.35	6.7	16	0.53	129	3.00	7.5
MPUAT/29	65.0	4.4	3.6	17	1.01	180	1.45	7.5
MPUAT/30	121.5	6.4	5.8	17.0	0.54	175	3.26	8.0
MPUAT/31	100	5.4	5.7	17	0.54	180	2.10	8.0
MPUAT/32	82	5.4	5.1	17	0.55	172	1.98	8.0
MPUAT/33	155	6.4	6.3	17	0.54	210	1.76	8
MPUAT/34	100	5.9	5.2	17	0.50	199	1.65	8.0
MPUAT/35	200	7.1	6.3	16	0.57	193	2.30	7.5
MPUAT/36	123	5.4	5.5	16	0.60	192	1.76	7.5
MPUAT/37	200	6.9	7.5	17	0.59	199	3.00	8.0
MPUAT/38	88	5.35	5.5	17	0.58	139	1.68	8.0
MPUAT/39	85	5.6	4.5	17.2	0.57	167	1.74	8.0
MPUAT/40	71	5.25	4.2	17	0.55	150	1.49	8.0
MPUAT/41	200	6.5	6.2	17	0.58	237	2.89	8.5
MPUAT/42	75	4.8	4.3	16	0.68	160	1.72	7.5
MPUAT/43	204	7.12	7.77	18	0.52	240	2.10	8.0
MPUAT/44	71	5.98	4.89	17	0.54	157	1.21	8.0
MPUAT/45	141	6.65	5.94	17	0.57	150	1.48	7.5
MPUAT/46	75	4.79	4.17	17	0.58	149	1.39	8.0
MPUAT/47	175	5.35	5.40	18.2	0.50	268	1.72	9.0

from 1.21 to 3.26 g and seed number 125 to 450. Seed content was considered to be a most important fruit character for determining the quality of the guava fruits, lower seed content was a desirable trait for judging the palatability of the fruits (Khehra and Bal, 2006). The genotypes MPUAT S-1 (MPUAT/47) and MPUAT S-2 (MPUAT/43) have the lower and soft seed content and can be used for the donor parent in hybridization programme. The range of the TSS was 11.00 to 18.20% and highest TSS content was noticed in MPUAT S-1(MPUAT/47) 18.2% followed by MPUAT S-2 (MPUAT/43) 18% and minimum in MPUAT/01(11%) and MPUAT/07 (11%).

The acidity content varied from 0.5 to 1.01% and ascorbic acid content range from 129 to 268 mg/100 g pulp.

Further, total sugar, reducing sugars and non reducing sugars also ranged from 7.41 to 9.43%, 3.96 to 4.75% and 3.45 to 4.68%, respectively. Variation in fruit yield was also noticed and fruit yield ranged from 25 to 68 kg/tree. The pulp colour of the fruit varied from white, creamy white to red. Further, skin colour at the time of ripening also varied from red, yellowish green and straw yellow to greenish yellow. On the basis of organoleptic scoring TSS and ascorbic acid content MPUAT S-1 and MPUAT S-2 were most promising. The fruit skin colour is red in MPUAT S-1 and greenish yellow in MPUAT S-2 (Shukla *et al.*, 2008). MPUAT/6 and MPUAT/41 were also observed as potential genotypes for yield.

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Association Analysis for Morphological and Biomass Traits in *Albizzia lebbeck* Seedlings

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Seeds of *Albizzia lebbeck* Benth from 20 different seed sources were collected from different eco-geographic regions of Uttar Pradesh to study of the morphological and biomass traits in the experimental area of the school of Forestry and Environment, green house and natural field conditions. The traits studied were seedling height, collar diameter, internodal length, branches/seedling, leaf area, shoot and root fresh and dry weight, shoot/root ratio and seedling biomass. Out of total 55 correlation combinations in both environments, 26 and 10 were positive and highly significant, 10 and 9 positive and significant. Seedling height showed positive and significant correlation with collar diameter, leaf area, shoot fresh weight and root dry weight. Shoot dry weight and root dry weight showed positive and significant correlation with seedling biomass under both environments. This suggests that there exits a strong inherent association between these characters.

Key Words: *Albizzia lebbeck*, Genotypic correlation, Phenotypic correlation

Introduction

Albizzia lebbeck Benth. is commonly known as Siris belongs to the family Fabaceae and sub family mimosoideae. *Albizzia* is a large tropical genus containing 150 species, mainly shrubs and trees (Allen and Allen, 1981) and is native to deciduous and semi-deciduous forests of Asia from Eastern Pakistan, throughout India and Sri Lanka to Myanmar (Everist, 1969). It occurs naturally in the sub-Himalayan tract from the Indus eastwards to the Khasi hills throughout the Indian peninsula and Andamans. It grows in the tropical rain forest of Burma and in the Himalayan valleys up to an altitude of 1600 m, with an annual rainfall range of 600-2500 mm and a temperature range 5ºC to 46ºC (Streets, 1962).

A. lebbeck is a well known leguminous fodder tree with very palatable leaves (Negi, 1977). It is extensively grown as a shade tree and which makes it a potentially valuable species for pasture development (Anonymous, 1980). It has soil-binding ability and tolerance to saline soil (Sommen, 1981). Paste of stem bark of *A.lebbeck* has been claimed to be useful in respiratory problem (asthma), snake bite, scorpion sting and malarial/intermittent fever (Chopra and Nayar, 1956). The flowers and leaves of the plant is reported to have antiseptic, anti dysenteric and anti tubercular properties. The bark, leaves, flowers, pods and seeds are employed medically. Bark extracts have documented anti-inflammatory activity (Lowry, 1989).

The ultimate goal of the tree breeder is to improve tree species in terms of the quality and the quantity of wood produced. This can be achieved through the selection of superior genotypes for which an indirect selection is often performed. The expression of a character is sum total of the contribution of so many other characters and therefore, screening/selection should be done on the basis of components contributing towards that character. The biometrical tool used for this is correlation which gives the nature and degree of association between various traits. So, the knowledge of association of different characters is the first hand information for any improvement programme (Searle, 1961). The species, therefore, offers an opportunity to study existing variation and also to select the superior seed sources for adaptability and growth pattern. Due to longer rotation period of the tree, there is very less information available on its genetic improvement (Zobel and Talbert, 1984).

Materials and Methods

The present study was carried out in the nursery of College of Forestry and Environment, Allahabad Agricultural Institute-Deemed University, Allahabad, Uttar Pradesh, India. The area is situated at 28.87º N latitude and 81.15º

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Table 1. Passport data of collections from U.P.

Notation	District	Latitude*	Longitude*
S_1	Meerut	29 º01'N	77º45'E
S_2	Ghaziabad	28 º40'N	77º28'E
S_3	Bulandshahar	28º24'N	77º54'E
S_4	Aligarh	27º53'N	78º05'E
S_5	Bareilly	28º22'N	79º27'E
S_6	Mathura	27º28'N	77º41'E
S_7	Etah	28º20'N	78º11'E
S_8	Hathras	37º36'N	78º06'E
S_9	Agra	27º10'N	78º05'E
S_{10}	Jhansi	25º27'N	78º37'E
S_{11}	Kanpur	26º28'N	80º20'E
S_{12}	Sitapur	27º35'N	79º37'E
S_{13}	Lucknow	26º55'N	80º59'E
S_{14}	Unnao	26º48'N	80º43'E
S_{15}	Fatehpur	27º05'N	77º39'E
S_{16}	Pratapgarh	25º34'N	81º59'E
S_{17}	Allahabad	28º87'N	81º 15'E
S_{18}	Ghazipur	25º35'N	83º34'E
S_{19}	Varanasi	25º20'N	83º03'E
S_{20}	Mirzapur	25º10'N	82 º37'E

* Encarta U.S. geological survey

E longitude at an elevation of 78 m above mean sea level on Northern aspect. Mature pods from different parts of the crown for the present study was procured by selecting, the twenty phenotypically superior trees in the natural distribution zones of Uttar Pradesh on the basis of different morphological characters of fruit and seed character mentioned below: (a) tree height, (b) tree diameter, (c) leaf area, (d) pod length, (e) pod width, (f) number of seeds/pod, (g) seed weight/pod. Five phenotypically superior trees of same size and free from any disease and pest were selected and observations were made. Out of these, the best one was considered as plus tree. Uniform and healthy seeds from mature pods of plus trees from twenty representing stands were collected to constitute the seed lot. The passport data of the plus trees is given in Table 1. For experimental purpose, the seeds were sown in a Complete Randomized Design under green house and Randomized Block Design under field conditions. Seeds of plus trees were sown in three replicates in polybags (10 x 25 cm) filled with a mixture of soil, sand and farm yard manure (1:1:1) at a depth of 0.5 cm. The observations were made for till 12-mo-old seedlings for different morphological and biomass traits *viz*., seedling height, collar diameter, inter-nodal length, branches per seedling, leaf area, shoot fresh weight, root fresh weight, shoot dry weight, root dry weight, shoot: root ratio and seedling biomass. The data were statistically analyzed for each character in a Completely Randomized Design under green house and Randomized Block Design under field condition. Karl Pearson's correlation coefficient was worked out as per Panse and Sukhatme (1967). The significance of correlation coefficients was tested against 'r' values as given by Fisher and Yates (1963).

Table 2. Progeny mean for morphological and biomass traits of 20 superior trees of *A. lebbeck* in greenhouse environment

Traits → / Sites ↓	Seedling height (cm)	Collar diameter (cm)	Internodal length (cm)	Branches/ seedling	Leaf area (cm^2)	Shoot fresh weight (g)	Root fresh weight (g)	Shoot dry weight (g)	Root dry weight (g)	Shoot/ root ratio	Seedling biomass (g)
S_1	47.05	1.184	3.85	11.23	5.24	8.62	4.21	2.66	1.57	1.69	12.83
S_2	43.25	1.067	4.52	10.57	5.63	8.66	4.71	1.98	1.59	1.25	13.37
S_3	41.04	1.079	3.69	11.01	5.35	10.52	4.99	2.89	1.32	2.19	15.51
S_4	39.15	0.856	3.74	11.46	5.57	7.20	3.05	1.91	1.19	1.61	10.25
S_5	49.12	1.180	5.35	13.23	4.52	12.67	5.01	4.18	1.63	2.56	17.68
S_6	41.51	0.967	4.08	11.12	5.68	11.21	5.01	2.46	1.58	1.56	16.22
S_7	43.68	1.012	3.96	12.12	5.74	10.42	4.24	2.96	1.33	2.23	14.66
S_8	35.35	0.893	4.46	12.79	4.29	8.58	3.35	2.07	1.61	1.29	11.93
S_9	61.37	1.245	5.81	16.12	6.91	14.19	5.28	4.74	1.77	2.68	19.47
S_{10}	46.30	1.079	3.52	10.79	5.52	11.88	4.27	3.20	1.41	2.27	16.15
S_{11}	53.62	1.023	4.31	11.34	5.18	12.94	4.72	3.21	1.54	2.08	17.66
S_{12}	58.95	1.189	4.16	14.68	5.91	12.42	3.64	3.05	1.21	2.52	16.06
S_{13}	52.74	0.901	3.93	12.12	5.41	10.66	3.47	2.55	1.58	1.61	14.13
S_{14}	48.53	0.922	4.62	11.57	5.79	10.73	3.31	3.06	1.34	2.28	14.04
S_{15}	48.06	0.801	4.32	12.34	5.63	9.13	3.29	1.98	1.29	1.53	12.42
S_{16}	40.12	0.656	4.34	10.23	4.63	10.15	4.10	2.30	1.54	1.49	14.25
S_{17}	51.01	0.756	4.03	13.23	5.57	9.13	4.08	1.59	1.42	1.12	13.21
S_{18}	46.23	0.734	4.42	13.91	4.41	10.66	3.24	2.42	1.19	2.03	13.90
S_{19}	55.27	0.856	3.83	11.96	5.85	10.39	3.50	3.10	1.24	2.50	13.89
S_{20}	47.80	0.901	4.37	15.01	4.37	9.39	3.01	1.86	1.18	1.58	12.40
Mean	47.51	0.966	4.27	12.34	5.36	10.48	4.02	2.71	1.77	1.90	14.50
Range	61.37-35.35	0.656-1.245	3.52- 5.81	10.23-16.12	4.29-6.91	7.2-14.19	3.01-5.28	1.59-4.74	1.18-1.77	1.12-2.68	10.25-19.47
S.E. ±	4.27	0.092	0.16	0.22	0.18	2.21	0.72	0.81	0.29	0.31	4.13
C.D. 5%	8.54	0.184	0.32	0.44	0.36	4.41	1.44	1.62	0.58	1.92	8.26

Table 3. Progeny mean for morphological and biomass traits of 20 superior trees of *A. lebbeck* in field

Traits → / Sites ↓	Seedling height (cm)	Collar diameter (cm)	Internodal length (cm)	Branches/ seedling	Leaf area (cm^2)	Shoot fresh weight (g)	Root fresh weight (g)	Shoot dry weight (g)	Root dry weight (g)	Shoot/ root ratio	Seedling biomass (g)
S_1	13.54	0.873	2.4	7.98	4.43	2.46	1.52	0.42	0.44	0.95	3.98
S_2	14.73	0.973	2.51	8.12	4.71	2.90	2.06	0.63	0.84	0.75	4.96
S_3	14.71	0.907	2.66	8.31	4.44	2.44	1.74	0.43	0.52	0.83	4.18
S_4	10.47	0.784	2.12	7.76	4.1	1.53	1.67	0.38	0.54	0.70	3.20
S_5	12.67	0.884	2.32	8.23	4.65	2.73	1.15	0.50	0.73	0.68	3.88
S_6	15.16	0.996	2.48	8.64	5.15	3.38	2.38	0.84	1.03	0.82	5.76
S_7	13.35	0.873	2.65	8.26	4.71	2.8	1.93	0.61	0.81	0.75	4.73
S_8	14.51	0.851	2.39	8.53	5.21	2.74	1.94	0.57	0.78	0.73	4.68
S_9	14.52	0.984	2.63	8.42	4.82	2.76	1.84	0.6	0.72	0.83	4.6
S_{10}	11.89	0.807	2.31	7.03	4.6	2.55	1.71	0.36	0.61	0.59	4.26
S_{11}	24.01	1.029	2.93	9.94	5.66	4.04	2.43	0.89	1.13	0.79	6.47
S_{12}	17.47	0.707	2.27	8.32	4.18	2.24	1.27	0.41	0.45	0.91	3.51
S_{13}	12.9	0.662	1.77	7.23	4.37	1.98	1.24	0.23	0.33	0.70	3.22
S_{14}	18.96	0.707	2.61	8.56	4.54	2.45	1.46	0.47	0.37	1.27	3.91
S_{15}	14.28	0.729	2.24	7.64	4.10	2.36	1.2	0.45	0.38	1.18	3.56
S_{16}	19.17	0.762	2.71	9.23	4.38	3.69	2.22	0.86	1.05	0.82	5.91
S_{17}	20.95	1.016	2.88	9.82	5.54	3.99	2.31	0.77	1.12	0.69	6.30
S_{18}	19.94	0.962	2.86	8.21	4.43	3.57	2.23	0.53	0.91	0.58	5.80
S_{19}	20.27	1.004	2.64	8.42	4.32	3.64	2.26	0.61	0.93	0.66	5.90
S_{20}	13.23	0.718	2.23	8.62	4.6	2.53	1.13	0.35	0.29	1.21	3.66
Mean	15.84	0.861	2.48	8.36	4.65	2.84	1.78	0.55	0.70	0.82	4.62
Range	10.47-24.01	0.662-1.029	1.77-2.93	7.03-9.94	4.1-5.66	1.53-4.04	1.13-2.43	0.23-0.89	0.29-1.13	0.58-1.27	3.20-6.47
S.E.±	1.06	0.043	0.18	0.34	0.11	0.20	0.20	0.06	0.10	0.12	0.38
C.D. 5%	3.14	0.129	0.53	1.00	0.34	0.61	0.58	0.18	0.29	0.35	1.13

Results and Discussion

The mean, range and variation under green house and field condition of twenty superior tree progeny are presented in Table 2 and 3. Range of seedling height varied between 35.35-61.37 cm under green house condition and 10.47-24.01 cm under field environment; collar diameter 0.656-1.245 cm and 0.662-1.029 cm; inter-nodal length 3.52-5.81 cm and 1.77-2.93 cm; branches/seedling 10.23-16.12 and 7.03-9.94; leaf area 4.29-6.91 cm^2 and 4.1-5.66 cm^2; shoot fresh weight 7.2-14.19 g and 1.53-4.04 g; root fresh weight 3.01-5.28 g and 1.13-2.43 g; shoot dry weight 1.59-4.74 g and 0.23-0.89 g; root dry weight 1.18-1.77 g and 0.29-1.13 g; shoot/root ratio 1.12-2.68 and 0.58-1.27; seedling biomass 10.25-19.47 g and 3.2-6.47 g, respectively. Collar diameter and leaf area recorded similar variation under both the environments and there was not much difference in the range for these traits in all the genotypes. However, seedling height, branches/seedling, shoot fresh weight, shoot dry weight and seedling biomass varied greatly and it was recorded maximum for S_9 collection under green house whereas, under field environment it was found highest for S_{11} followed by S_{17}.

Estimation of phenotypic and genotypic correlation between various traits provide better understanding to the improver/breeder during selection especially when selection is based on two or more characters. The intensity and direction of association between two or more characters may be measured by genotypic and phenotypic coefficients of correlation depending on the type of materials studied. The knowledge of genotypic interrelationship between characters may be either due to pleiotropic action of genes or due to linkage or more likely both. The main genetic cause of such correlation is pleiotropy, which refers to the manifold effects of the gene.

It is clear from the Table 4 and 5 that phenotypic correlation coefficients were lower than the genotypic correlation coefficients. This suggests that it could be either due to the modifying effect of environment or the strong inherent association of characters at genetic level. Seedling height showed positive and significant correlation with collar diameter, leaf area, shoot fresh weight and root dry weight. Collar diameter with branches/seedling. Inter-nodal length showed positive and significant correlation with branches/seedling. Branches/seedling with leaf area and shoot dry weight. Leaf area with shoot dry weight. Shoot fresh weight with root fresh weight, shoot dry weight, root dry weight and seedling biomass. Root fresh weight showed positive and significant correlation with seedling biomass but negative and significant correlation with shoot: root ratio. Shoot dry weight and root dry weight showed positive and significant correlation with seedling biomass under both environments. A positive genetic correlation

Table 4. Phenotypic (r_p) and genotypic (r_g) correlation coefficients between morphological and biomass traits of *A. lebbeck* in Greenhouse

Characters		Seedling height	Collar diameter	Internodal length	Branches/ seedling	Leaf area	Shoot fresh weight	Root fresh weight	Shoot dry weight	Root dry weight	Shoot/ root ratio	Seedling biomass
Seedling height (cm)	r_p	1.000	0.865**	0.385	0.323	0.652*	0.869**	0.658*	0.850**	0.703*	0.323	0.747**
	r_g	1.000	0.883**	0.964**	0.214	0.697*	0.484	0.667*	0.890**	0.850**	0.466	0.851**
Collar diameter (mm)	r_p		1.000	0.417	0.276	0.285	0.787**	0.715*	0.732*	0.779**	0.079	0.846**
	r_g		1.000	0.725*	0.972**	0.843**	0.218	0.793**	0.854**	0.862**	-0.198	0.889**
Internodal length (cm)	r_p			1.000	0.782**	0.717*	0.406	0.263	0.384	0.303	0.343	0.374
	r_g			1.000	0.886**	0.912**	0.183	0.656*	0.401	0.442	0.463	0.536
Branches/seedling	r_p				1.000	0.756*	0.273	0.089	0.367	0.151	0.468	0.340
	r_g				1.000	0.870**	0.329	0.517	0.756*	0.283	0.773*	0.976**
Leaf area (cm^2)	r_p					1.000	0.445	0.118	0.421	0.106	0.435	0.364
	r_g					1.000	0.857**	0.342	0.672*	0.528	0.546	0.627*
Shoot fresh weight (g)	r_p						1.000	0.755*	0.871**	0.724*	0.257	0.935**
	r_g						1.000	0.774*	0.973**	0.756*	0.367	0.973**
Root fresh weight (g)	r_p							1.000	0.434	0.919**	-0.247	0.873**
	r_g							1.000	0.536	0.978**	-0.756*	0.932**
Shoot dry weight (g)	r_p								1.000	0.505	0.456	0.746*
	r_g								1.000	0.619	0.943**	0.852**
Root dry weight (g)	r_p									1.000	0.658*	0.808**
	r_g									1.000	0.715*	0.921**
Shoot/root ratio	r_p										1.000	0.256
	r_g										1.000	0.329
Seedling biomass (g)	r_p											1.000
	r_g											1.000

* Significant at 5% level of significance; ** Significant at 1% level of significance

Table 5. Phenotypic (r_p) and genotypic (r_g) correlation coefficients between morphological and biomass traits of *A. lebbeck* in field

Characters		Seedling height	Collar diameter	Internodal length	Branches/ seedling	Leaf area	Shoot fresh weight	Root fresh weight	Shoot dry weight	Root dry weight	Shoot/ root ratio	Seedling biomass
Seedling height (cm)	r_p	1.000	0.665*	0.245	0.373	0.742*	0.674*	0.374	0.643*	0.453	-0.220	0.578
	r_g	1.000	0.739*	0.351	0.458	0.783*	0.798*	0.426	0.783*	0.521	-0.198	0.431
Collar diameter (mm)	r_p		1.000	0.374	0.473	0.193	0.338	0.225	0.453	0.125	-0.167	0.267
	r_g		1.000	0.532	0.692*	0.284	0.484	0.473	0.578	0.367	-0.045	0.088
Internodal length (cm)	r_p			1.000	0.483	0.327	0.148	0.135	0.367	0.042	0.050	0.092
	r_g			1.000	0.863**	0.439	0.322	-0.389	0.583	0.274	0.250	0.134
Branches/seedling	r_p				1.000	0.594	0.158	-0.197	0.452	-0.257	0.246	-0.029
	r_g				1.000	0.953**	-0.252	-0.280	0.767*	-0.382	0.533	-0.254
Leaf area (cm^2)	r_p					1.000	0.136	-0.182	0.412	0.251	0.279	0.072
	r_g					1.000	0.261	-0.231	0.759*	0.364	0.291	0.053
Shoot fresh weight (g)	r_p						1.000	0.853**	0.653*	0.856**	-0.634*	0.870**
	r_g						1.000	0.932**	0.856**	0.937**	-0.825**	0.902**
Root fresh weight (g)	r_p							1.000	0.635*	0.932**	-0.751*	0.868**
	r_g							1.000	0.743*	0.963**	0.793*	0.974**
Shoot dry weight (g)	r_p								1.000	0.761**	-0.316	0.628*
	r_g								1.000	0.793**	-0.424	0.706*
Root dry weight (g)	r_p									1.000	-0.676	0.646*
	r_g									1.000	-0.843**	0.928**
Shoot/root ratio	r_p										1.000	-0.723*
	r_g										1.000	-0.901**
Seedling biomass (g)	r_p											1.000
	r_g											1.000

*Significant at 5% level of significance; **Significant at 1% level of significance

between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously because any one of the two characters would be a reliable measure of the other. This also suggests that there exists a strong inherent association between these characters. Therefore, these trait seems to be under strong genetic control and is quite amenable for selection. Root dry weight showed negative but significant correlation with shoot:

root ratio under both, green house and field environment. These non significant associations between two characters advocate that they are independent of each other and could be selected separately. The above findings support the results of Manga and Sen (1998) in *Prosopis cineraria*, Chauhan and Verma (1993) in *Acacia catechu*, Thakur *et al.* (2000) in *Alnus nitida*, Raj *et al.* (2006) in *Bambusa bambos* and Wani *et al.* (2008) in *Bauhinia variegata.*

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Cultivated Grasses and their Wild Relatives in Andhra Pradesh and Their Conservation Concerns

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The study was carried out during 2007-2009. The information on the crops was collected from primary sources with the help of a planned and structured interview schedule in three regions of Andhra Pradesh. There are 65 wild relative grass species belonging to 18 genera of 24 cultivated grasses in Andhra Pradesh. Commercial grasses are represented maximum with 11 grasses and 23 wild relative species, which is followed by small millets with 7 species and 22 wild relatives, millets with 2 crop species and 12 wild relative species, cereals with four cultivated crops species and 8 wild relatives. Out of all *Panicum* having maximum of 10 wild relatives followed by bamboo (9) and *Cymbopogon* (9), *Pennisetum* (7), *Oryza* (6), *Sorghum* (5) and *Setaria* (5), *Zea* (2) and 4 crops showed minimum with one wild relative each. The wild relatives of Andhra Pradesh, particularly those occurring in the Eastern Ghats zone have narrowed distributional. Systematic efforts must be taken to conserve these wild relatives through *in-situ* means.

Key Words: Conservation concerns, Grasses, Wild relatives

Introduction

The Indian gene centre harbors about 166 species of native cultivated plants. The crops with primary, secondary and regional centers of diversity represent a part of native and introduced species which account for over 480 species (Nayar *et al.*, 2003). Wild relatives are an important genetic resource on which the sovereign rights exist for a country in the post-Convention on Biological Diversity (CBD) regime. The crop wild relatives are an important genetic resource gaining significance in crop species (Arora, 1996). The cultivated grass species are derived from centre of diversity from areas of cultivation. They are developed through different breeding methods *viz.*, pure line selections, mutants, polyploids and inter-generic/inter-specific hybrids. They are also directly selected as good performance for specific and/multiple traits (may not be yield superior). The wild relatives of crop plants constitute a part of the crop genepool, and posses a big reservoir of untapped genes that have potential to be utilized in crop improvement programmes. The wild relatives and distantly related taxa occurring in developing countries have contributed significantly towards improvement of major crop species (Witt, 1982). Identification and utilization of a single gene of importance has played a major role in crop improvement. In India, 80% of cultivated area is under food crops, of which rice covers about 30%, millets 28% and wheat 15%. Minor millets account for less than one per cent of the food grains produced in the world today (FAO, 1999). Cereals and millets were popular in the Andhra Pradesh region for hundreds of years and remained a staple food for a long time. Thus they are not important in terms of India food production, but they are essential as food crops in their respective agro-ecosystems. They are mostly grown in marginal areas or under adverse agricultural conditions where major cereals fail to give sustainable yields.

Andhra Pradesh is the fifth largest state in India with an area of 275,068 km^2. The state has 23 districts which are grouped into three zones *i.e.*, Circar or Coastal Andhra comprising the districts of Srikakulam, Vijayanagaram, Visakhapatnam, East Godavari, West Godavari, Krishna, Guntur, Prakasam and Nellore, Rayalaseema region consists of Kurnool, Kadapa, Anantapur and Chittoor districts and Telangana region includes Adilabad, Hyderabad, Karimnagar, Khammam, Mahbubnagar, Medak, Nalgonda, Nizamabad, Rangareddy and Warangal districts.

Andhra Pradesh state constitutes a total of 2,601 species belong to 1,035 genera and 173 families of angiosperms, 4 species of gymnosperms, 72 species of pteridophytes (Pullaiah and Karuppusamy, 2007). Of the 2,601 angiosperms species, 531 are tree taxa species

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(representing 245 shrubs, and 290 climbers), 1,972 dicotyledons species and 674 monocots species. The ratio of monocot to dicot families is 1:4 (34:139 families). The genetic resources of wild relatives of 73 major cultivated crops belonging to crop-groups of cereals, small millets, pulses, oilseeds, vegetables, tubers, fruit crops and spices in Andhra Pradesh are represented by 71 genera and 203 species of 36 plant families. In which, Poaceae is represented maximum with 13 genera and 34 species (Pandravada *et al*., 2008).

Materials and Methods

The present study was carried out during 2007-2009 as part of research work on "Quantitative Assessment and Mapping of Plant Resources of Eastern Ghats". The information on the crops was collected from primary sources with the help of a planned and structured interview schedule. Farmers were randomly selected from Coastal Andhra, Telangana and Rayalaseema regions of Andhra Pradesh. In each selected village, 10 per cent households were randomly selected for interview. The farmers and respondents were interviewed thoroughly and their statements were recorded in the interview schedule. A quadrate of 5×5m was layout for enumerate shrubs and herbs were recorded from 1×1m quadrates. All the taxa were identified upto species level by using available state, regional and local floras (Gamble and Fischer, 1915-1935; Ellis, 1987; Pullaiah, 1997; Pullaiah and Alimoulali, 1997; Pullaiah and Chennaiah, 1997). The wild relatives of crop plants were recorded and specimens were made into herbarium following standard methodology and finally validated through reference material at the herbarium of Botanical Survey of India (BSI), Coimbatore.

Results and Discussion

In Andhra Pradesh, 24 grass species are cultivated which belong to the different crop groups of cereals, millets, small millets and commercial grasses. There are 65 wild wild relative grass species belongs to 18 genera of 24 cultivated grasses exists in the state (Table.1). Among the group, commercial grasses are represented maximum with 11 grasses and 23 wild relative species, which is followed by small millets with 7 species and 22 wild relatives. The millets with minimum 2 crop species and 12 wild relative species. The cereals showed 4 cultivated crops species and minimum with 8 wild relatives. *Panicum* has maximum 10 wild relatives followed by *bamboos* (9) and *Cymbopogon* (9), *Pennisetum* (7), *Oryza* (6), *Sorghum* (5) and *Setaria* (5), *Zea* (2) and four crops showed minimum with one wild relative (Table 2).

Table 1. Status of diversity in wild relatives of cultivated grasses in Andhra Pradesh

Crop group	No. of cultivated grasses	Diversity in wild relatives	
		No. of genera	No. of species
Cereals	4	5	8
Millets	2	2	12
Small millets	7	5	22
Commercial grasses	11	6	23
Total	24	18	65

Table 2. Diversity of cultivated grasses (bold) and their wild relatives, chromosome number/genome, common and local names

Species	Chromosome number/genome	Common name	Local name
Oryza sativa L.	2n=24 AA	Rice	Vari, Vadlu
Hygroryza aristata (Retz.) Nees ex Wight & Arn.	2n=24		
Leersia hexandra Swartz.	2n=48, 2n=4x=60	Southern cut grass	
*Porteresia coarctata (*Roxb.) Tateoka	2n=48		
O. officinalis Wall. ex Watl. ssp. malampuzhaensis (Krish. et Chandr.) Tateoka.	2n=24, 2n=4x=48 GG		
O. meyeriana (Zollin. & Mor.) Baill. ssp. *granulata* Tateoka.	2n=24 GG		
O. rufipogon Griff.	2n=24, AA		
Triticum aestivum L.	2n=6x=42, AABBDD	Wheat	Godhumalu
Triticum dicoccum L.	2n=4x=28, AABB	Wheat	Godhumalu
Zea mays L.	2n=20	Maize, Corn	Mokkajonna
Tripsacum laxum Nash.	2n=72		
Chionachne koenigii (Spr.) Thw.	2n=20		
Pennisetum glaucum (L.) R.Br.	2n=14	Pearl millet	Sajjalu, saddalu
Pennisetum americanum (L.) Schum.	2n=14		
P. clandestinum Hochst. ex Chiov.	2n=36		
P. hohenackeri Hochst. ex Steud.	2n=18		

Table 2. Contd.

Table 2. Contd.

Species	Chromosome number/genome	Common name	Local name
P. pecidellatum Trin.,	2n=14		
P. polystachyon (L.) Schult.	2n=36		
P. purpureum Schum.	2n=14		
P. setosum (Sw.) Rich.			
Sorghum bicolor (L.) Moench	2n=20	Great millet	Jonna
S. deccanense			Gaddijanu, gaddi jonna
S. halepense (L.) Pers.	2n=40		
S. nitidum (Vahl) Pers.	2n=40		
S. subglabrescens (Steud.) Schweinf. & Asch. var. *rubidium* (Burkill ex Benson)			
Echinochloa colonum (Linn.) Link	2n=36	Shama millet	Ooda gaddi, Bontha gaddi
Echinochloa frumentacea Link			Bonta Shama, Sawa, Hamalu
E. crus-galli (Linn.) P. Beauv.	2n=4x=54		Pedda windu
E. oryzoides (Ard.) Fritsch.			
E. picta (Koenig) P.W.Michael.			
E. stagnina (Retz.) P. Beauv.			
Eleusine coracana (L.) Gaertn.	2n=4x=36 AABB	Finger millet	Ragi, ragulu, chodulu, thaidalu
E.indica (Linn.) Gaertn.	2n=18 AA		
Panicum milaceum L.	2n=4x=36	Proso millet, Common millet	Warigalu, barigalu
Panicum sumatrense Roth. ex Roem et Schult.	2n=40		Gangasamalu, samalu,Chamalu
P. brevifolium L.	2n=18		
P. fischiri Bor.			
P. maximum Jacq.	2n=32		
P. milare L.	2n=40		
P. notatum Retz.	2n=36		
P. paludosum Roxb.	2n=54		
P. psilopodium Trin (related to *P. milare*)			
P. repens L.	2n=18,4x=36		Ladda gaddi, hasi gaddi
P. trypheron Schult.	2n=42		
P. walense Mez.	2n=36		
Paspalum scrobiculatum L.	2n=40	Kodo millet	Arikelu, aarkalu, nitari gaddi
P. canarae (Steud.) Veldk.			
P. paspaloides (Michx.) Scribner.	2n=20		
Setaria italica (L.) P. Beauv	2n=18	Foxtail millet, Italian millet, German millet, Hay millet	Korralu
Setaria intermedia Roem. & Schult.	2n=36		Arranki gaddi
S. palmifolia (Koen.) Stapf.			
S. paniculifera (Seud.) Fourn. ex Hems.	2n=34		
S. pumila (Poir.) Roem. & Schult.	2n=18,4x=36	Kavetta grass	Nakkathoka gaddi, chinna korralu
S. verticellata (L.) P. Beauv.	2n=18	Bristyl fox tail	Chiklenta gaddi
Bambusa arundinacea (Retz). Roxb.	2n=72	Thorney bamboo	Mulla veduru, mulla bongu
B. bambos			
B. tulda Roxb.	2n=70		
Dendrocalamus strictus (Roxb).Nees.	2n=72	Hard bamboo, solid bamboo	Veduru, sanna veduru, pillanagrovi veduru
D. membranous			
D. hamiltonii			
D. giganteous			
D. longispathus			
D. hookeri			
Desmostachya bipinnata (L.) Stapf.			Sadanapu veduru
Coix lacryma-jobi L.	2n=30	Job tears	Golugulu, gulbay gaddi
Coix aquatica Roxb.	2n=10		
C. gigantea Koenig ex Roxb.	2n=40		
Cymbopogon flexuosus Stapf.	2n=20	Lemon grass	Nimmagaddi
Cymbopogon citratus Stapf.	2n=60	Lemon grass	Nimmagaddi, vasana gaddi
Cymbopogon martini (Roxb.) Wats	2n=20	Palm rose	Nimma gaddi
Cymbopogon nardus (L.) Rendle.			
C. caesius (Hook. f.) Stapf.			Kasi gaddi
C. coloratus (Hook. f.) Stapf.			Boda gaddi

Table 2. Contd.

Table 2. Contd.

Species	Chromosome number/genome	Common name	Local name
C. flexuosus (Nees ex Steud.) Wats. var. flexuosus.	2n=20	Malabar lemongrass, ginger grass	
C. gidarba (Ham. ex Steud).	2n=20, 4x=40		Adavi kanchi, seetha kasigaddi, thigavomigaddi
C. jwarancusa (Jones) Schult.	2n=20		
C. nardus (L.) Rendle. var. confertiflorus (Steud) Staf.			
C. nardus var. naruds	2n=40	Citronella grass	Ganjini
C. schoenanthus	2n=20		
C. winterianus	2n=20		
Saccharum officinarum L.	2n=80	Sugarcane	Cheraku
S. spontaneum Linn.	2n=64	Tatch grass, Buffello reed, crow bamboo, dog's bamboo	Rellu gaddi, billu gaddi, naga saramu
Vetiveria zizanioides (L.) Nash.	2n=20	Vetiver, Khus khus grasss	Vattivellu, vattiveru
V. lawsonii (Hook. f.) Blatt.&McCann.	2n=20		Itta gaddi

Diversity in Wild Relatives

The wild species/related genera of important cultivated grass species, their diversity and affinities among the species have been dealt with for the crop groups of cereals, millets, small millets and commercial grasses in the state of Andhra Pradesh as follows:

Cereals

In Andhra Pradesh, three cereals *viz*., paddy, wheat (fewer amounts) and maize are cultivated. Paddy and maize are grown in all the three regions of the state.

Rice *(Oryza sativa* L.*)*

Rice is commonly called *Vari, Vadlu* in Andhra Pradesh. Rice is the staple food of half of the world's population. Roschevicz (1931) proposed a polyphyletic origin for rice, and that rice might have arisen in the region of India, China and Indo-China. He proposed that majority of *sativa* varieties to have arisen from *O. spontanea* (*O. rufipogon* annual type) some of the seeded varieties from minuta and some of the West African cultivated forms grouped under *glaberrima* arising from *breviligulata*. All these wild relatives are present in Andhra Pradesh. *Hygroryza aristata* (Retz.) Nees ex Wight & Arn., *Leersia hexandra* Swartz, *Porteresia coarctata* (Roxb.) Tateoka, *O. officinalis* Wall. ex Watl. ssp. *malampuzhaensis* (Krish. et Chandr.) Tateoka, *O. meyeriana* (Zollin. & Mor.) Baill. ssp. granulata Tateoka, *O. rufipogon* Griff. Within this *O. officinalis* is resistant to insects, grassy stunt virus, and tropical strain of bacterial blight, brown plant hopper, and green leaf hopper. Others such as *O. meyeriana* ssp. granulata and *O. officinalis* ssp. *malampuzhaensis* based on taxonomic and cytological studies are reported to be distantly related to *O. sativa* (Sampath and Rao, 1951; Morishima and Oka, 1960).

Oryza rufipogon has similar distribution as that of *O. sativa* especially near ditches, ponds and in the paddy fields as off types/introgressed forms mainly in Adilabad, Warangal, Chittoor, Khammam, Medak, Nellore, Nizamabad and Srikakulam districts (Pandravada and Reddy, 1990; Pandravada and Sivaraj, 1996; Sivaraj *et al.*, 2000) and may be source of red coloured rice (Sastry and Sharma, 1974). *Lersia hexandra* occurred at higher altitudes, *Porteresia coarcata* occurred in brackish waters and *Hygroryza aristata* in moist coastal areas (Bor, 1960; Pullaiah, 1997).

Wheat *(Triticum aestivum* L. *and Triticum dicoccum* L.*)*

Wheat is commonly called as *Godhumalu* in Andhra Pradesh. There are no wild relatives found in Andhra Pradesh. This crop is cultivated in few pockets of the state.

Maize *(Zea mays* L.*)*

Maize is called as *Mokka jonna* in Andhra Pradesh. It is widely cultivated in all the three regions. Two wild relatives of maize *viz*., *Tripsacum laxum* Nash. and *Chionachne koenigii* (Spr.) Thw. are present in Andhra Pradesh.

Millets

In Andhra Pradesh, two millets are cultivated *i.e*., great millet and pearl millet. These are cultivated in the drier parts of the Telangana and Rayalseema regions. In coastal area these are cultivated for fodder purposes.

Pearl Millet *(Pennisetum glaucum* (L.) R.Br.*)*

Pearl millet is known as *sajjalu, saddalu*. It is third important cereal after rice, sorghum in Andhra Pradesh. It is a source of protein, calcium, phosphorous, iron, thiamine,

riboflavin and niacin. In India these species are present, *Pennisetum americanum* (L.) Schum., *P. clandestinum Hochst.* ex Chiov., *P. hohenackeri* Hochst. ex Steud., *P. pecidellatum* Trin., *P. polystachyon* (L.) Schult., *P. purpureum* Schum., *P. setosum* (Sw.) Rich. These are resistant to floral diseases. *P. hohenackeri* generally occurs in the sandy soils near the ponds, ditches and streams mostly in the Telangana especially in the Medak districts (Pandravada, 1992a).

Grate Millet (*Sorghum bicolor* (L.) Moench)

It is locally known as *Jonna*. In India there are five basic races present *i.e., bicolor, caudatum, durra, guinea,*and *kafir* (Harlan and de Wet, 1972). It is further divided into these sub-races *durra caudatum, durra guinea, durra kafir, durra bicolor, caudatum guinea, caudatum kafir, caudatum bicolor, guinea kafir, guinea bicolor, and karir bicolor*. The main species in Andhra Pradesh are Sorghum deccanense, *S. halepense* (L.) Pers., *S. nitidum* (Vahl) Pers., and *S. subglabrescens* (Steud.) Schweinf. & Asch. var. rubidium (Burkill ex Benson) Snowden. *S. subglabrescens* var. rubidium is reported form Krishna district (Lakshminarayana *et al.*, 1997) and S. nitidum from Araku valley of Vishakhapatnam district.

Small Millets

Shama Millet (*Echinochloa colonum*) and Barnyard Millet *(Echinochloa frumentacea)*

These are commonly known as *Shamalu, Bontha samalu*. It is divided into sub species colona and frumentacea and races are stolonifera, intermedia, robusta and laxa. In Andhra Pradesh four wild relatives are present *i.e., Echinochloa crus-galli* (Linn.) P. Beauv., *E. oryzoides* (Ard.) Fritsch., E. picta (Koenig) P.W.Michael., E. stagnina (Retz.) *P. Beauv*. But E. crus-galli is widely distributed and variants of this species occur in the rice fields and in water logged habitats (Arora and Nayar, 1984). *E. oryzoides* and *E. picta* is reported from Karimnagar district only (Naqui and Raju, 1998).

Finger Millet (*Eleusine Coracana* (L.) Gaertn.)

Finger millet is commonly known as *Ragi, Chodulu* and *Chollu*. It is a staple food for many people. There are two sub species - *E. africana* and *E. coracana*. Each sub-species is derived into races and sub-races. Elongata, plana, compacta and vulgaris are main races available in Andhra Pradesh. *Eleusine* having only one wild relative in Andhra Pradesh *Eleusine indica* (L.) Gaertn. *E. indica* is the only wild species widely occurring which is morphologically and cytologically similar to *E. coracana* (Krishnaswamy, 1951). *E. indica* is of Indian origin and may be the immediate ancestor of finger millet (Mehra, 1963).

Prosomillet (*Panicum milaceum* L.) and Little Millet (*Panicum Sumatrense* Roth. ex Roem et Schult.)

Prosomillet is commonly called *Warigelu, Barigelu*. It is supposed to be one of the oldest grain crops and is grown extensively in India. It is a quick growing drought resistance crop. It has two sub-species psilopodium and sumatrense. It is classified as race- nana and robusta, sub races-laxa, erecta and compacta. In Andhra Pradesh, *Panicum brevifolium* L., *P. fischiri* Bor., *P. maximum* Jacq., *P. milare* L., *P. notatum* Retz., *P. paludosum* Roxb., *P. psilopodium* Trin (related to P. milare), *P. repens* L., *P. trypheron* Schult., and *P. walense* Mez. are present. Out of these species, *P. psilopodium* which is similar to the wild forms of *P. sumatrense* from which the later species might have originated (Anonymous, 1966).

Kodo Millet (*Paspalum scrobiculatum* L.)

Koda millet is locally called Arikelu. It has three races *viz*., regularis, irregularis and variables. In Andhra Pradesh wild related species, *Paspalum canarae* (Steud.) Veldk., *P. paspaloides* (Michx.) Scribner. are present.

Foxtail Millet (*Setaria italica* (L.) *P. beauv*)

Foxtail millet is considered to be sweet, acrid and aphrodisiac and is used as a sedative to the gravid uterus. The grain is said to posses heating properties and when taken alone sometimes causes diarrhoea. The grain is astringent, diuretic and laxative and is useful externally in rheumatism. It is a popular remedy for alleviating the pains of parturition (Kirtikar and Basu, 1935). Foxtail millet is locally called as Korralu. It is also known as Italian, German, Hungarian or Siberian millet. Cultivation of foxtail millet dated back to the third millennium BC. *S. italica* is not known in the wild state except as a weed which escapes from cultivation. *S. italica* is divided into sub species viridis and italica. *S. italica* is further classified into three races moharia, maxima and indica, and further classified into nine subraces-aristata, fusiformis, glabra, compacta, spongiosa, assamese, erecta, nana and profusa. *S. viridis* is the ancestral form of *S. italica* on the basis of chromosome number.

In the state, *Setaria* has these wild and weedy relatives *i.e., Setaria intermedia* Roem. & Schult., *S. palmifolia*

(Koen.) Stapf., *S. paniculifera* (Seud.) Fourn. ex Hems., *S. pumila* (Poir.) Roem. & Schult., *S. verticellata* (L.) *P. beauv.*

Commercial Grasses

Bamboos: Bamboos are commonly called *Veduru, Veduru* and *Bongulu*. They are perennial, woody plants of the family Poaceae. They combine the best of both worlds - it grows speedily like a grass and in much the same way and at the same time, it produces a considerable amount of strength and easily to process for woody material with similar properties. Bamboos are important ecologically because of the vast area over which they are distributed, the total quantum of the resources, on the diversity of the species and ecological habitats they occupy.

Common Bamboo (*Bambusa arundinacea* (Retz). Roxb.) and *Sadhanapu veduru* (*Dendrocalamus strictus* (Roxb). Nees.)

In Andhra Pradesh, bamboos have following wild relatives, *Bambusa arundinacea*, *B. bambos*, *B. tulda* Roxb., *Dendrocalamus membranous*, *D. hamiltonii*, D. giganteous, *D. longispathus*, *D. hookeri* and *Desmostachya bipinnata* (L.) Stapf.

Job's Tears (*Coix lacryma-jobi* L.)

It is cultivated throughout the world tropics. The panicles bear attractive, shiny white grains resembling tears and often used ornamentally as beads. In Andhra Pradesh, *Coix* have two wild relatives *viz*., *Coix aquatica* Roxb. and *C. gigantea* Koenig ex Roxb.

Lemon Grass (*Cymbopogon flexuosus* Stapf. and *Cymbopogon citratus* Stapf.)

The cultivated lemon grass in India mostly belongs to the above two species. These are distinguished in commerce, the distinction being based on properties of oil.

Palm Rose (*Cymbopogon martini* (Roxb.) Wats.)

Palm rose is a source of palmarosa. It yields grass oil and contains large amount of geraniol which can be used to adulterate otto of roses.

Citronella Grass (*Cymbopogon nardus* (L.) Rendle.)

Citronella is known as *Nimmagadd*, *Vasanagaddi* in Andhra Pradesh. This is also called 'oil of citronella'. It is pale yellow oil much used for inexpensive soaps and perfumes as insect repellent also containing 80-90% of geraniol which makes the oil an important substitute for otto of roses. In Andhra Pradesh, *Cymbopogon* wild relatives, *C. caesius* (Hook. Arn.) Stapf., *C. coloratus* (Hook. f.) Stapf., *C. flexuosus* (Nees ex Steud.) Wats. var. *flexuosus*., *C. gidarba* (Ham. ex Steud)., *C. jwarancusa* (Jones) Schult., *C. nardus* (L.) Rendle. var. *confertiflorus* (Steud) Staf., *C. nardus* var. nardus, *C. schoenanthus* and *C. winterianus* are present.

Pogonatherum paniceum (Lam.) Hack.

This grass is extensively cultivated as an ornamental in gardens due to its peculiar tillering and foliage. *Pogonatherum crinitum* (Thunb.) Kunth. is the wild relatives.

Sugarcane (*Saccharum officinarum* L.)

Sugarcane is derived from the sanskrit word shakkara. This crop from the east provides a linguistic evidence of Indian origin of sugarcane. In Andhra Pradesh, many sweet based products are prepared from sugarcane. There is only one wild relative *Saccharum spontaneum* L. is present in Andhra Pradesh.

Vetiver (*Vetiveria zizanioides* (L.) Nash.)

Vetiver is known as *Vattivellu* or *Vatti verlu* in Andhra Pradesh. It is a source of vativer oil. The oil obtained by distillation of these roots and useful as a fixer of 'violet' odours. The roots are made into mats for air cooling (Khaskhas mats). Andhra Pradesh has only one wild relative *Vetiveria lawsonii* (Hk. f.) Blatt. & Mc Cann.

Conservation of Wild Relatives

Conservation of wild relatives of crops is the most important task to match the challenges of erosion of species. The existence of these wild relatives are shrinking fast due to various bio-edaphic factors and disturbed habitats. In the present rate of threat of genetic erosion, we must collect all requisite information of the wild relatives to make use of their wider adaptability/tolerance/resistance to diseases and insect-pests, yield, quality attributes and other biotic and abiotic characters. In comparison to the cultivated landraces, these wild relatives are given less emphasis for collection/augmentation, characterization, conservation and utilization. Specific programmes on collection, conservation and utilization of wild relatives and related taxa need to be intensified in areas of species (Arora and Nayar, 1984).

Collection and conservation of wild species are generally most effective when there is a specific requirement for research or crop improvement programmes (Bothmer and Seberg, 1995). Conservation of diversity of

cultivated plants on private land using on-farm approach and their wild relatives in the landscape has been strongly recommended (Gadgil *et al.*, 1996). The modern agricultural practices strongly favour reduction of diversity by providing crop subsidies for replacement of landraces of crops by uniform stands of high yielding varieties and use of herbicides to eliminate weedy relatives of crop plants.

We can utilize these wild relatives for conventional breeding programmes. Though hard to develop resistant varieties by conventional breeding procedures to withstand the pest pressure under diverse farmer conditions.

A great number of plant species including several unique and irreplaceable taxa have faced extinction and some of these have already disappeared from the earth in nature's own process of evolutionary changes. The wild relatives of Andhra Pradesh, particularly those occurring in the Eastern Ghats zone have shown narrow distribution.

The endemic diversity in wild relatives are *O. officinalis* ssp. *Malampuzhaensis* reported from Nallamalais of Eastern Ghats only. *Bambusa arundinacea* var. *gigantea* (Gigantic bamboo, distributed in north coastal districts), *Cymbopogon coloratus*, *C. gidarba*, *Panicum fischeri* and *Vetiveria lawsonii* are endemic to peninsular India in Andhra Pradesh. These wild species need immediate attention for collection and conservation *in situ/ex situ*.

Conservation of wild relatives using in situ/on-farm can be successfully achieved by providing special incentives to farmers/local people for growing difficult or uneconomical material on private land or domestic gardens. The village communities may get the benefits through watershed management, wild life habitats and environmental stabilization. Complementary conservation strategies include the protection of wild species, plant populations and traditional crop varieties where they have evolved (*in situ*) with the collection and preservation of inter and intra-specific diversity in gene banks and botanical gardens (*ex situ*). National gene banks, research institutes should collect and conserve the wild/weedy relatives of these cultivated crops. Scientists, individuals, departments, and institutions in particular State Agricultural Board, State Biodiversity Board should come forward and work together in coordination to protect these natural resources.

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Assessment of Genetic Diversity of Barnyard Millet Accessions using Molecular Markers

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Present study was conducted to access genetic diversity among 33 accessions of two cultivated species of barnyard millet *i.e.*, *Echinochloa crus-galli* (15 accessions) and *E. frumentacea* (18 accessions). Though crop possesses great nutritional value, little attention has been paid for the improvement of this crop. We assessed genetic diversity on the basis of morphological and RAPD analysis. Morphological analysis suggested that EC-545 is superior for grain yield, whereas VRS-MB-1202 and VRS-MB-889 were found to be good for fodder yield. On the other hand, RAPD primers were able to segregate the accessions in two groups at a similarity level of 34% with clear demarcation of inter and intra species diversity. The data would be important in detailing the level of variation and relationship within and between species to plan future domestication trials and to manage the wild species collection that is available in the gene banks.

Key Words: Barnyard millet, Genetic diversity, RAPD

Introduction

Barnyard millet (*Echinochloa* sp.) is one of the oldest domesticated millets in the semi-arid tropics of Asia and Africa. The genus *Echinochloa* includes some 20 species that are distributed widely in the warmer parts of the world. Two of the main species, *E. crus-galli* and *E. frumentacea* are grown as cereals. In addition to these two domesticated species, the genus includes about 30 annual and biennial wild species distributed worldwide (Clayton and Renvoize, 1986). These millet species are morphologically very dissimilar. Indian barnyard millet (*E. frumentacea*) can easily be distinguished from Japanese barnyard millet (*E. crus-galli*) by its panicle, thinner texture of the glumes and lower lemma (Yabuno, 1971).

The crop is valued for its drought tolerance, good yield and superior nutritional value. It is the fastest growing crop among all millets and can be harvested in a short period of nine weeks. Barnyard millet is an important dual-purpose crop. Its grains contain 6.2% protein, 9.8% crude fiber, 65.5% carbohydrates and are consumed just like rice (Ruiz-santaella *et al.*, 2006). Also it is a nutritive fodder for animals. These aspects make barnyard millet a valuable crop.

Being one of the traditional crops, barnyard millet (*E. frumentacea*) is cultivated at almost all farming situations in Uttarakhand hills even in rainfed areas. But, the cultivation area of the crop has reduced tremendously in past decades because of one or other reasons, among which main are, the poor productivity and susceptibility to diseases like collar rot and seed rot etc. Moreover, in absence of wide genetic diversity among local cultivars and released varieties, the selection for adaptation to cold temperature is discouraging (Gullord *et al*., 1975). On the other hand Japanese millet (*E. crusgalli*) is high yielding, shows better adaptability to cold temperature and disease resistant. So the accessions posses better morphological characters and wide genetic diversity should be evaluated for this region.

Genetic diversity of common morphological traits is difficult to measure in a natural population since the traits are influenced by environmental factors to a large degree. On the other hand, their expression is largely governed by different interacting genes. Assessment of genetic diversity with molecular markers overcomes this problem because these molecular traits have virtually no environmental component and large numbers of variables are produced. As a result, qualitative and quantitative traits can be more efficiently introduced into plant breeding programmes. Molecular techniques for evaluating genetic diversity have been improved in the last decades, complementing the use of morphological markers. Measurement of genetic diversity with molecular markers is relevant to assessment of ecological conditions because it allows estimation of

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important population parameters *e.g.*, characterization of the geographic structure or connectivity of populations. Molecular markers such as SDS-PAGE, isozymes and DNA markers have been found more useful to study genotypic diversity in many plant species (Tanksley *et al.*, 1989; Paterson *et al.*, 1991).

In the present study we evaluated genetic diversity among 33 different accessions of two cultivated species of barnyard millet (*E. crus-galli* and *E. frumentacea*) on the basis of morphological and molecular (RAPD) markers.

Materials and Methods

Plant Material

Two sets of different accessions of both the species (*E. crus-galli* and *E. frumentacea*) were examined. 15 accessions of *E. crus-galli* were procured from ICRISAT, Hyderabad (Andhra Pradesh, India) and 18 accessions of *E. frumentacea* were collected from VPKAS, Almora (Uttarakhand, India).

Morphological Characters

All the 33 genotypes were sown in the fields in a Randomized Block Design (RBD) at GBPUA&T, Hill Campus, Ranichauri, Tehri Garhwal (Uttarakhand) for two consecutive years 2004 and 2005. Crop management was done according to the recommended agronomic practices. Sowing was done in the plots (3m × 1m), plant to plant distance was maintained 10 cm., while row to row distance was kept 22.5 cm. Eight morphological characters including, germination (%), days to 50% flowering, plant height, number of fertile tillers, length of spikelet, days to maturity, 1000 grain wt and yield/plant were taken to assess genetic variability in accessions.

DNA Isolation and PCR Amplification

Seeds were grown in the green house and leaf material was harvested from 3-4 week old seedlings. Total cellular DNA was isolated from leaf material of individual plants following the procedure of Saghai-Maroof *et al.* (1984) with few modifications. Samples for PCR amplification were diluted to 15 ng/µl with deionized distilled water.

Fifty random decamer primers were used to study polymorphism. Out of these, 21 primers gave polymorphic bands and were used for further study. The PCR amplifications were carried out in a 25 µl reaction mixture containing 15 ng of genomic DNA, 100 ng primer, 1X PCR reaction buffer (Banglore Genie, India), 0.8 mm DNTP mix (Banglore Genie) and 1.5 U Taq polymerase (Banglore Genie). Amplifications were carried out in a thermal cycler (Eppendorf), programmed for one initial denaturation 95°C for 5 min. followed by 49 cycles of 92°C for 10 sec., 36°C for 1 min., 72°C for 2 min. and synthesis 72°C for 2 min. Amplifications were repeated twice in order to check reproducibility.

PCR amplification products were analyzed by electrophoresis on 1.5% agarose gel and run in TBE buffer at 80 Volt for approximately 5hrs. Gels were stained in ethidium bromide solution (0.5 $\mu g/ml^{-1}$) and documentation was done using Gel Doc system (Bio-Rad).

Data Analysis

Field data for morphological characters was evaluated by the analysis of variance (ANOVA) using RBD to calculate the significance by magnitude of F value (P= 0.01) and D^2 statistics as suggested by Rao (1952) using computer software. The calculation of D^2 values involved the steps followed by Murthy and Arunachalam (1996).

RAPD-PCR data was evaluated for pair-wise similarity and cluster analysis was done on the basis of presence and absence of bands. Computer software (Gel-Compar-II, ver. 3.5, Applied Maths, USA) was used to perform the similarity matrix analysis using 'UPGMA' with 'Dice' coefficient of similarity.

Results and Discussion

Estimation of Genetic Diversity Based on Morphological Characters

On the basis of D^2 analysis, all the accessions of two species were grouped into three clusters (Table 1). Cluster-I comprised of accessions of *E. frumentacea,* cluster-II consists of *E. crus-galli*, while cluster-III had two accessions of *E. crus-galli* and rest ten were of *E. frumentacea* (Table 1).

The average intra- and inter-cluster genetic distance (d values) shown in Table 1. Inter-cluster centeroids distance ranged from 0.00 to 3.14 and Intra-cluster distance ranged from 1.76 to 1.9. Comparison of these morphological clusters revealed that maximum intra-cluster distance (D=2.25) was observed in cluster-II whereas, maximum inter cluster centeroids distance (D=3.41) was observed in between cluster-III and cluster-II (Table- 1). It has previously been suggested that genetic drift and selection in different environments can produce greater diversity (Raje and Rao, 2001). We observed that accessions of *E. crus-galli* showed genetic superiority to *E. frumentacea* in different agronomic characters. The findings get support by Bandyopadhyay (1998, 1999). He

Table 1. D^2 statistics* based clustering pattern and average inter and intra cluster d values of the different accessions of two different species of *Echinochloa*

Clusters	Accessions grouped in different clusters	d values of Clusters		
		I	II	III
I	RS-MB-1554, VRS-MB-1839, VRS-MB-886, VRS-MB-846, VRS-MB-1361, VRS-MB-1535, VRS-MB-1377, VRS-MB-871 **(n=8)**	1.76		
II	IEC-530, IEC-531, IEC-540, IEC-545, IEC-546, IEC-547, IEC-548, IEC-549, IEC-555, IEC-556, IEC-542, IEC-533, PRB-9404 **(n=13)**	3.40	2.25	
III	IEC-535, IEC-538, VRS-MB-1202, VRS-MB-893, VRS-MB-889, VRS-MB-1506, VRS-MB-882, VRS-MB-1546, VRS-MB-1508, VRS-MB-1543, VRS-MB-858, VRS-MB-1372 **(n=12)**	2.50	3.41	1.91

* The D^2 analysis was done according to Murthy and Arunachalam, 1996.
IEC and PRB: Accession number for the accessions of *E. crus-galli*, VRS-MB: Accession number for the accessions of *E. frumentacea*.

Table 2. Cluster mean for different morphological characters

S. No.	Characters	Clusters		
		I	II	III
1.	Germination (%)	89.93	91.49	92.69
2.	Days to 50% flowering.	71.92	83.65	67.47
3.	Plant height (cm)	173.25	135.40	186.56
4.	Number of fertile tillers	2.74	3.43	3.26
5.	Panicle length (cm)	10.76	15.66	14.54
6.	1000 seed weight (g)	3.51	4.26	2.88
7.	Days to maturity	123.71	128.62	116.94
8.	Yield / plant* (g)	116.00	206.00	125.00

* Data represents average of total grain weight of five plants from each accession.

reported that the accessions of *E. crus-galli* were better adapted for Uttarakhand hills and were promising for high grain yield. Average inter-cluster and intra-cluster distance (D) values presented in Table- 2 indicated that the maximum variability was present in cluster-II and cluster-III for agronomic characters. So the clusters showing greater genetic diversity can be used in further crop improvement programme. Several workers suggested selection of parents for hybridization from two clusters having wide inter-cluster and intra-cluster distance to get maximum heterosis (Pradhan and Rao, 1990; Mehta *et al*., 2005).

Molecular Diversity Based on RAPD Markers

In this study only 21 primers were used after a two-step selection of polymorphic primers. First, 50 random primers were prescreened with the four barnyard millet accessions VRS-MB 1508, VRS-MB 1546, IEC-530 and IEC-540. 21 primers revealed polymorphism and were used in further study. Polymorphic primers detected 7 to 15 bands with an average of 12 bands from each accession.

Genetic diversity among 33 accessions was calculated on the basis of DNA fingerprints generated with a set of 21 oligo-decamer primers using UPGMA method based on 'Dice' similarity coefficient. On the basis of Dice coefficient of similarity (Fig.1) among 33 genotypes, similarity ranged from 20.5 to 78.4. At 34% similarity two major groups are formed, which clearly separate 15 accessions of *E. crus-galli* and 18 accessions of *E. frumentacea*. At 48% similarity 8 clusters were formed and two genotypes remained ungrouped (Fig.1). Six clusters were formed within accessions of *E. crus-galli* and four were in *E. frumentacea*.

The marker system successfully resulted in classifying of the two species of barnyard millet as both the species grouped separately in two different groups (Fig.1). Within species variability revealed by RAPD marker was evident but diversity among accessions of same species was low. Similarity observed among accessions of *E. crus-galli* was up to 75 %, whereas accessions of *E. frumentacea* showed higher genetic similarity (upto 80%). This might be due to the collection of the accessions from a small area. Variability within species may be less due to high inbreeding nature of these crops (Yabuno, 1966). Similarly, Salimath *et al*., (1995) reported only 10% polymorphism in the 17 accessions of *Eleucine coracana* and explained the low polymorphism in finger millet because of high inbreeding nature of the crop. The low degree of variability in RAPD markers was observed within *E. frumentacea*, while high degree of morphological variability was observed in this

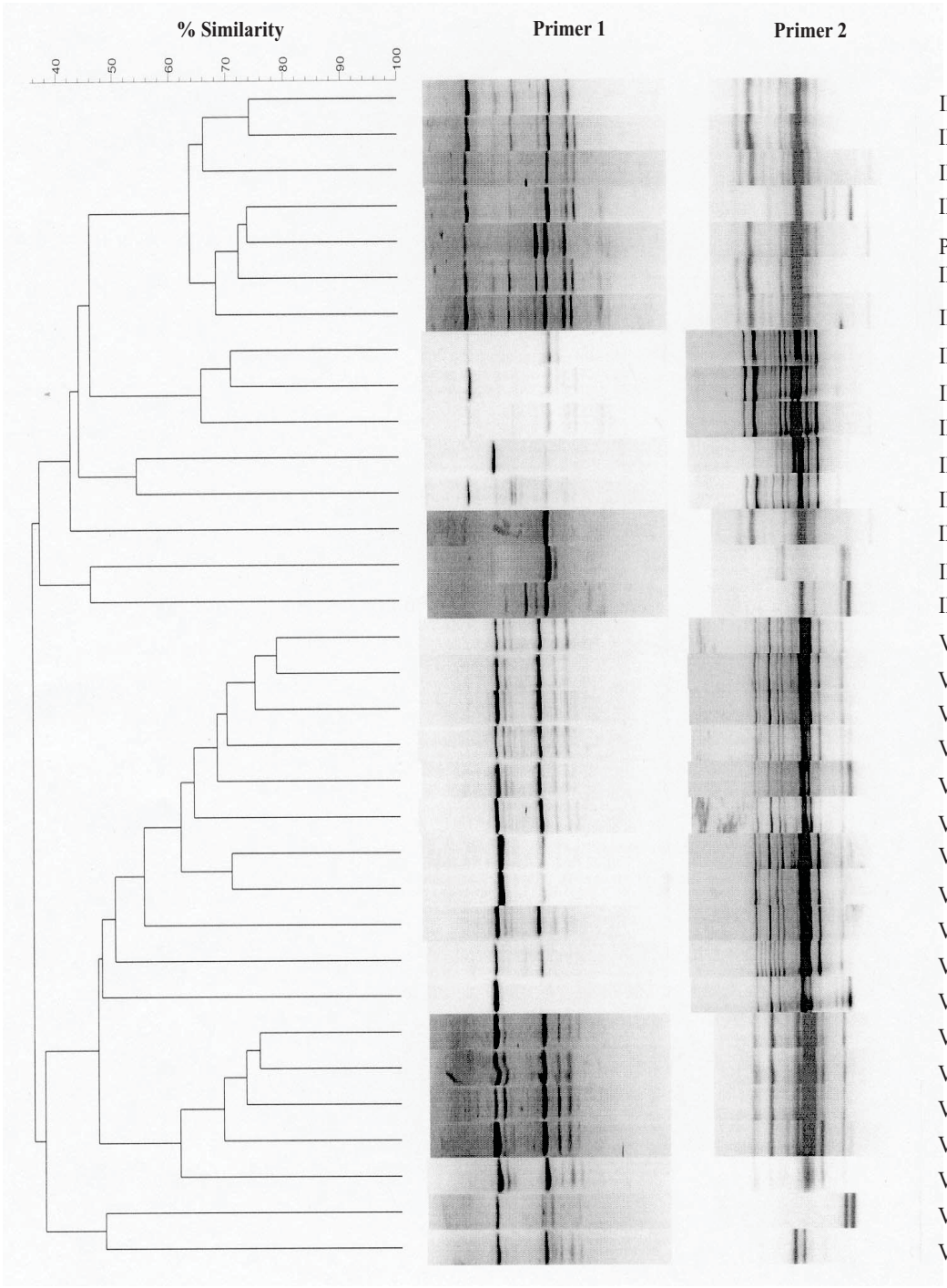

Fig. 1: Random amplified polymorphic DNA cluster analysis of fingerprint patterns generated with a set of 21 oligodecamer primers from genomic DNA of 33 accessions belonging to two cultivable species of Barnyard millet (*Echinochloa crus-galli* and *Echinochloa frumentacea)*

species. Crop domestication represents relatively recent (about 10,000 years) evolutionary process from a few wild populations, so low genetic variability within species of barnyard millet is not surprising (Hilu and Johnson, 1991).

Variability in RAPD marker was evident in both the domesticated species. The similarity index showed about 64% diversity between two species. The study was supported by Hilu (1994). Polymorphism in RAPD markers has been reported in several domesticated species of wheat (Devos and Gale, 1992; He *et al*., 1992) finger millet (Hilu,

1994), *Gossypium* (Rana and Bhat, 2005) and barnyard grass (Roy *et al*., 2000), etc.

The clear-cut segregation of the two species, *E. frumentacea and E. crus-galli* is in marked contrast within considerable overlap in morphological markers, where specimen identification can sometimes become difficult (De Wet *et al*., 1983). The two species differ in inflorescence morphology, spikelet size and texture, and presence of awns.

RAPD marker represents an efficient and inexpensive way to generate molecular data and have been used successfully in various taxonomic and phylogenetic studies (Wilkei *et al*., 1993; Kazan *et al*., 1993). RAPD marker was used for *Hordeum* phylogeny and as a result two main branches were identified at 20% similarity. One was containing sections of *Anisolepis* and *Hordeum* and the second containing sections *Criterion* and *Stenostachys*. Similarly, RAPD markers were more efficient than the ISSR marker with regards to polymorphism detection in *Jatropha curcas*, as 84.26% polymorphism was detected by RAPD marker as compared to 76.54% by ISSR markers (Gupta *et al.*, 2008).

Thus, the RAPD approach is particularly useful to assess genetic diversity in germplasm resources of agricultural crops at intra-specific and inter-specific levels. The molecular character provided by the RAPD approach outlined a pattern of genetic affinities among the species of *Echinochloa* that is well supported by molecular data from cytogenetic, isozymes, chloroplast and nuclear genomes (Yabuno, 1962, 1966; Roy *et al*., 2000). Morphological markers grouped the accessions in three clusters, but some overlapping was observed. RAPD bands, which could mark individual plants, subspecies and species, are very valuable for germplasm resource studies and plant breeding. Two species of barnyard millet are showing wide genetic diversity. Accessions of *E. crus-galli* showed more genetic diversity within species on the basis of morphological and molecular markers. Similar findings were reported by Tabacchi *et al*., (2006). They revealed a good correlation between AFLP and morphological traits in the classification of *Echinochloa* species present in Italian rice fields. Also they showed considerable genetic diversity.

Clear demarcation of inter and intra species diversity among 33 accessions of two species *E. frumentacea* and *E. crusgalli* was observed. When these results were compared with morphological markers we found that the set of 21 RAPD primers were able to differentiate the two species according to their plant hight, no. of fertile tillers, panicle length and 1000 seed weight (Table 3). All the four characters are the major characters in respect to fodder and grain yield. On the basis of yield accessions IEC-530, IEC-533 and PRB-9404 and on the basis of fodder yield accessions VRS-MB-1202, VRS-MB-889 and VRS-MB-1508 were found good. The accession showed both the characters up to optimum level should be selected as the cultivated land is decreasing we need the maximum output from the minimum input. Accession IEC-555 was alone in group 5; this accession shows the average value of all the studied morphological characters. IEC-555 was the best accession for yield as well as for fodder.

With such improvements, primers can be utilized to develop specific marker system to identify the species from the admixture. Selection of better genotypes can be made for species improvement on the basis of percent similarity with other species. Two more similar but

Table 3. Groups formed on the basis of RAPD are differentiated on the basis of morphological characters

Groups*	Germination (%)	50% Flowering (Days)	Plant height (cm)	No. of fertile tiller	Panicle length (cm)	1000-seed weight (g)	Days to maturity	Yield/ plant (kg)
1.	92.70	91.24	135.25	3.21	15.91	4.05	133.48	0.20
2.	90.55	81.11	141.67	2.97	16.79	4.83	126.55	0.18
3.	92.83	63.50	130.53	4.40	15.92	4.22	114.12	0.15
4.	89.00	76.33	134.67	4.60	15.10	3.30	122.67	0.15
5.	92.66	79.33	140.00	3.10	14.10	4.10	123.00	0.18
6.	94.33	64.00	156.00	3.60	14.23	3.47	112.00	0.11
7.	91.79	65.19	187.06	3.02	14.57	3.56	123.53	0.15
8.	90.00	73.33	220.00	2.63	14.60	1.42	126.00	0.12
9.	91.80	67.66	184.87	3.01	13.01	2.67	112.80	0.14
10.	92.17	74.83	171.83	2.99	11.79	3.22	127.67	0.12

Data shown in the table is average of triplicates. Accessions were grown in the field in the plots of 3m x 1m. Plant to plant distance was maintained 10 cm., while row to row distance was kept 22.5 cm. Crop was harvested after maturity.
*Groups were made at similarity of 48% according to Dice coefficient of similarity.
†Data represents average of total grain weight of five plants from each accession.

possessing distinct characters can be chosen for the purpose. Studies of the kind presented here are important in detailing the level of variation and relationship within and between species in order to plan future domestication trials and to manage the wild species collection, which is available in the gene banks.

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Stability Analysis for Biomass and Essential Oil Yield in Basil (*Ocimum basilicum*) Germplasm

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The essential oil of basil (*Ocimum basilicum* L.) is used for flavoring foods, dental and oral products. Stability analysis was conducted on 30 accessions of basil germplasm (exotic as well as indigenous). These accessions were augmented from different countries namely, India (10), USA (10), USSR (7), Germany (1), Hungary (1) and Poland (1). These were evaluated under four diverse environments comprising two locations and two years (2004 and 2005). The mean performance and stability parameters of 30 accessions were analyzed under four environments for nine characters, namely, number of primary branches/plant, lamina length (cm), lamina width (cm), leaf-stem ratio, plant height (cm), fresh herbage yield/plant (g), dry herbage yield/plant (g), essential oil content (%) and essential oil yield/plant (ml). All 30 genotypes had squared deviation equivalent to zero (S^2 di=0) showing consistent performance of the genotypes among all the environments. Essential oil is the economic product of basil. Five genotypes *viz.* EC388788, IC333332, IC336833, IC388891 and EC338773 were identified as desirable and stable in relation to essential oil yield per plant. Two genotypes (EC388788 and IC333332) were found superior for essential oil yield, fresh herbage yield and dry herbage yield/plant over the four environments. Hence, these genotypes could be recommended for their direct utilization across the environments.

Key Words: Accession, Adaptability, Basil, Environment, Essential oil, Herbage yield, Stability

Introduction

The genus *Ocimum* is an annual aromatic herb, having 160 species and belongs to family Lamiaceae (Balyan and Pushpangadan, 1988). It is widely distributed and cultivated throughout India (Pushpangadan and Bradu 1995; Verma *et. al.*, 1989 and Pandey and Chowdhary, 2002). The diversity in this genus is observed in the tropical rain forests of Africa with the largest 59 reported species followed by the subtropical regions of Africa (19 species), Arabia and Brazil (11 species each), India, Ethiopia and Madagascar with 9, 8 and 7 species, respectively (Pushpangadan and Bradu, 1995). Its aromatic leaves are used fresh and dried as salad dressing, vegetables, flavouring in sauces, vinegar and confectionary products. The essential oil of basil is used to flavour foods, dental and oral products, in fragrances and in traditional rituals and medicines (Guenther, 1949 and Simon *et al.*, 1984). The variable performance of the genotypes under varying environments creates problem in the adaptation and spread of a crop/varieties for large scale cultivation. Realizing the importance of this new crop, the efforts have been made to generate information on influence of environment, adaptability and stability of genotypes.

Materials and Methods

The experimental materials comprised of 30 accessions of basil, augmented from different indigenous as well as exotic sources through National Bureau of Plant Genetic Resources (NBPGR), New Delhi. These accessions were grown under four diverse environments at two locations during *kharif* 2004 and 2005. These environments were created through different locations and years. The NBPGR Experimental Farm, Issapur, New Delhi (latitude 28°36'N, longitude 76°50'E) is of semi-arid climate with average annual rainfall/400 mm. The ground water is highly saline having EC of over 4m mhos/cm. The soil varies from sandy loam to loamy sand having pH around 8.0. The Research Farm, JV College Baraut, District Baghpat, Uttar Pradesh (latitude 29°06'N, longitude 77°15'E) is of sub-tropical nature having loamy humus rich soil and average annual rainfall over 600 mm. It has good irrigated water condition. All the accessions were sown in nursery and transplanted after 30 days of sowing. In each environment, these accessions were planted in Randomized Block Design (RBD) with three replications. Each entry was allotted a plot of three rows (3m) with spacing 45 x 30 cm. Before transplanting, a dose of 10 tones of FYM, 80 kg N, 40 kg P and 40 kg K/ha was applied. Half of the N and whole of P and K were applied as basal dose. The remaining half of the nitrogen was mixed in two equal doses as top dressing after 30 and 45 days of transplanting between the rows in wet soil by hand-hoeing. Irrigation and weeding were done regularly. Observations on five randomly selected plants

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in each genotype for nine characters *viz.* number of primary branches/plant, lamina length (cm), lamina width (cm), leaf-stem ratio, plant height (cm), fresh herbage yield/plant (g), dry herbage yield/plant (g), essential oil content (%), essential oil yield/plant (ml) were recorded at full-bloom stage. The stability analysis was carried out on mean performances of four environments accomplished by two locations and two years for nine characters following the Eberhart and Russell Model (1966) and variability parameters were estimated as per standard procedures.

Results and Discussion

The analysis of variance (Table 1) revealed that all the genotypes differed significantly for all the characters indicating the presence of genetic variability in the genotypes. Environmental variance was significant for all the characters except leaf-stem ratio, lamina length, lamina width, essential oil content and oil yield suggesting the influence of the environment. However, G x E interaction was significant for plant height, fresh herbage yield/plant and dry herbage yield/plant. Environment (linear) was significantly pronounced for all the characters whereas Environment and G x E interaction (linear) were significant for number of primary branches, fresh herbage yield and dry herbage yield/plant. The traits having significant G x E interaction namely plant height, fresh herbage yield/plant and dry herbage yield per plant were considered for analysis of stability parameters (Table 2). For plant height, the mean performance of the different genotypes ranged from 44.95 (EC387837) to 81.70 (EC338785) with population mean 54.14. Out of 30 genotypes, thirteen genotypes have shown regression coefficient (bi#1) showing better adaptation to favorable environments and 16 genotypes had shown regression coefficient (bi#1) showing poor response to the environments. In respect of fresh herbage yield/plant, the results indicated that the mean performance ranged from 223.58 g (EC388896) to 346.92 g (IC333332) with population mean 290.97. Four genotypes namely IC110267, EC388788, EC388891 and EC338794 had b_i values closer to unity and these genotypes are stable and can be suggested for all the environments. Similarly, four genotypes, namely, IC110267, EC388788, EC388891 and EC338794 had higher values of regression coefficient (b_i <1.0) may be suitable for favourable environment. Similarly, in case of dry herbage yield/plant, the mean performance of different genotypes ranged from 49.16 g (IC201233) to 75.78 g (IC333332) with population mean 63.39 g. Three genotypes (EC338893, EC388788 and EC338794) had b_i values closer to unity and favorable for all kind of environments. Nine genotypes had higher values of regression coefficient (b_i <1.0) and suitable for favourable environment.

Stability is an important parameter to decide the suitability of a genotype under vide range of environments. In the present study on basil, almost all the characters except lamina length, lamina width, leaf-stem ratio, essential oil content and essential oil yield influenced by the environment. It showed the sensitivity of the crop toward environments. However, genotype and environment (G x E) interaction was significant on plant height, fresh herbage yield/plant and dry herbage yield/plant. Environment (linear) was significantly pronounced for all the nine characters studied, whereas E+(G x E) were significant for number of primary branches/plant, number of spikes/plant, fresh herbage yield/plant, dry herbage yield /plant and seed yield/plant. The stability parameters like population mean, regression coefficient (bi) and squared deviation from regression (S^2di) for plant height, fresh herbage yield/plant and dry herbage yield/plant where the G x E interaction was significant.

In respect of plant height, four genotypes namely IC110267, EC388788, EC388891 and EC338794 best suited for all the environments. For fresh herbage yield/plant, four genotypes namely IC110267, EC388788, EC388891 and EC338794 had b_i values closer to unity

Table 1. Analysis of variance (ANOVA) for stability in basil germplasm for nine characters under four environments

Source of variance	d.f.	No. of primary branches/plant	Lamina length (cm)	Lamina width (cm)	Leaf stem ratio	Plant height (cm)	Fresh herbage yield/plant (g)	Dry herbage yield/plant (g)	Essential oil content (%)	Essential oil yield/ plant (ml)
Genotype (G)	29	1.06	0.49	0.11	0.350	197.67 **	5041.17 **	232.79 **	0.0022	0.024
Environments (E)	3	11.57 **	0.46	1.19	0.005	41.15 **	19653.23 **	1136.76 **	0.0004	0.083
G x E	87	0.45	0.09	0.04	0.005	4.99 **	576.15 **	28.81 **	0.0004	0.005
Pooled error	232	0.41	0.09	0.02	0.002	11.09	298.25	20.03	0.0007	0.006
E + (G x E)	90	0.83	0.10	0.08	0.005	6.20 **	1212.05 **	65.74 **	0.0004	0.008
Environment (linear)	1	34.72 **	1.39	3.58	0.014	123.38 **	58960.44 **	3410.39 **	0.0013	0.249
(G x E) (linear)	29	0.56	0.10	0.05	0.006	10.99	916.88	51.74	0.0004	0.009
Pooled deviation	60	0.39	0.08	0.03	0.004	1.93	392.24	16.76	0.0004	0.003

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

Table 2. Estimates of stability parameters basil germplasm during *kharif* 2004 and 2005 at New Delhi and Baraut locations

Genotype	Fresh herbage yield/plant (g)			Dry herbage yield/plant (g)			Plant height (cm)		
	Mean	b_i	S^2d_i	Mean	Mean	S^2d_i	Mean	b_i	S^2d_i
IC110267	321.76	0.96	356.91	46.41	46.41	13.35	0.71	1.37	0.00
EC338785	344.92	1.27	11.89	81.70	81.70	-3.25	0.50	0.13	0.00
EC388890	326.92	0.29	83.48	58.65	58.65	-6.62	0.70	0.27	0.00
EC388895	298.92	2.48	644.16	57.90	57.90	38.96	0.50	2.09	0.00
EC388893	238.83	1.18	208.51	55.07	55.07	0.88	0.53	1.29	0.00
EC387838	320.00	1.42	446.95	54.28	54.28	29.96	0.46	2.71	0.00
EC388788	335.00	1.01	-82.94	56.53	56.53	-6.44	0.53	0.78	0.00
EC338794	330.58	1.03	38.26	50.98	50.98	-4.84	0.57	1.65	0.00
IC326735	255.33	0.43	189.47	53.45	53.45	-5.37	0.46	0.61	0.00
IC333332	346.25	1.20	166.40	50.30	50.30	11.47	0.62	0.98	0.00
IC336833	287.00	0.83	50.22	46.06	46.06	3.44	0.54	0.54	0.00
EC312264	321.67	2.23	1171.98	53.28	53.28	36.76	0.55	2.39	0.00
EC388891	264.92	0.96	51.29	58.18	58.18	-6.36	0.56	1.23	0.00
EC338782	313.25	0.63	186.78	51.55	51.55	28.35	0.58	1.41	0.01
EC128730	341.25	2.24	952.66	56.16	56.16	-6.41	0.59	3.00	0.00
EC338772	297.75	2.15	1386.55	49.76	49.76	17.63	0.56	2.64	0.01
IC344638	281.33	1.38	349.04	50.38	50.38	2.12	0.50	-0.44	0.02
EC174527	293.17	1.39	483.38	50.43	50.43	22.67	0.49	2.08	0.00
EC387837	275.50	0.46	324.33	44.95	44.95	-4.23	0.58	-0.28	0.02
IC201233	224.42	0.18	231.55	47.71	47.71	-1.91	0.39	0.00	0.00
EC388896	223.58	0.42	309.67	51.87	51.87	1.90	0.47	1.32	0.00
EC338773	304.58	0.21	129.98	58.90	58.90	3.18	0.59	0.65	0.00
IC326711	232.17	0.09	-23.86	63.14	63.14	-3.97	0.49	-0.46	0.00
EC338775	297.75	0.29	-66.78	57.84	57.84	-0.39	0.54	0.42	0.00
EC338776	258.92	0.25	628.65	58.64	58.64	48.67	0.44	-0.08	0.00
IC211313	275.42	0.86	-90.60	52.38	52.38	-0.73	0.44	0.74	0.00
IC326732	275.75	0.77	68.06	46.48	46.48	10.43	0.63	-1.18	0.01
EC388887	296.58	0.47	-48.57	47.04	47.04	7.70	0.63	1.93	0.00
EC388889	277.83	2.06	705.47	54.83	54.83	66.74	0.45	1.40	0.00
IC338959	267.92	0.87	-78.09	59.22	59.22	8.81	0.44	0.81	0.00
Pop. (mean)	290.97			54.14	54.14		0.53		
S.E. (mean)	11.43			0.80	0.80		0.032		
S.E. of B	0.44			0.68	0.68		0.611		

and these genotypes are stable and can be suggested for all the environments. Similarly, three genotypes (EC338893, EC388788 and EC338794) identified for all kind of environments. The genotype EC388788 was found stable for most of the traits and got wider adaptability. Therefore, the genotype EC388788 could be recommended for direct utilization across the environments by farmers.

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SHORT COMMUNICATION

Genetic Divergence Studies in Puddle Wetland *Boro Rice*

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The nature and magnitude of genetic divergence was estimated in forty nine early maturing rice varieties suitable for *boro* ecosystem using Mahalanobis D^2 statistics. All the genotypes were grouped into five distinct non overlapping clusters. Cluster II was largest group which accommodated 21 genotypes. Cluster IV exhibited maximum intra cluster distance (D^2= 85.01) followed by cluster V (74.48) and cluster I (55.80). Cluster II and cluster IV were found to be the most divergent clusters as indicated by maximum D^2 value (453.69).

Key Words: Genetic divergence, *Boro* rice, Direct seeded rice

The present study was taken up to assess the genetic diversity in early maturing varieties of rice suitable for *boro* ecosystem. For this purpose forty nine early duration genotypes were evaluated in Simple Lattice Design during 2008 and 2009 Dry seasons. The field was puddled and pre-germinated seeds were sown in 5 x 3 m^2 plots. In each plot, 150 g seed was sown @ 100 kg/ha with fertilizer doses of 80:40:40 kg ha^{-1} N:P:K. Standard cultural practices and need based plant protection measures were adopted. Observations on plant height (cm), panicle bearing tiller/m, panicle weight (g), test weight (g) and grain yield/plant (g) were recorded. Multivariate analysis of genetic divergence among the genotypes was done using Mahalanobis (1936) D^2 statistics and grouping of genotypes into clusters was done by Tocher's method (Rao, 1952).

It has been recorded that direct seeded *boro* rice matures earlier than the transplanted rice by 7-10 days. Therefore, it is important to characterize *boro* rice varieties and their genetic divergence adaptive to this growing condition of eastern India, which is gaining popularity in India and Bangladesh (Pande and Singh, 2004). Data presented in Table 1 revealed that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied. It was highest for grain yield/plant(g) followed by panicle weight and panicle bearing tiller/m^2, while GCV was highest for grain yield. Similar results were also reported by Singh *et al*. (2007). Test weight (g) showed lowest values for GCV and PCV. Genotypic coefficient of variation was slightly lower than corresponding PCV for all the characters because of more influence of environment in the expression of these characters.

Present study revealed high heritability coupled with high genetic advance for plant height. Days to 50 per cent flowering, test weight and grain yield showed high heritability, this observation confirmed the earlier findings of Singh *et al*. (2007). Panicle weight, grain yield and test weight exhibited low genetic advance indicating the major role of non fixable gene action.

Based on the D^2 analysis, all genotypes were grouped into five distinct non overlapping clusters (Table 2). Cluster II was largest which accommodated 21 genotypes followed by cluster I which accommodated 11 genotypes. Cluster

Table 1. Mean, Range, Genotypic and Phenotypic Coefficient of Variation, Heritability and Genetic Advance for six characters in 49 Rice Genotypes

Characters	Days to 50% flowering	Plant height (cm)	Panicle bearing tiller/m^2	Panicle weight (g)	Test weight (g)	Grain yield/ plant (g)
General Mean	102.94SE ±0.99	92.86SE ±1.11	401.08SE ±26.17	2.33SE ±0.20	23.48SE ±0.37	6.78SE ±0.42
Range	80.00-115.50	70.00-113.00	276.00-500.00	1.31-2.85	17.10-28.20	3.60-11.90
h^2 (Broad sense)	98.00	98.22	58.30	51.68	94.71	88.46
Genetic Advance	21.24	22.44	68.83	0.43	4.45	3.19
Genetic Advance as per cent of mean	20.63	24.17	17.16	18.55	18.95	47.01
Genotypic Coefficient of Variation (GCV)	10.11	11.85	10.91	12.52	9.45	24.26
Phenotypic Coefficient of Variation (PCV)	10.20	11.97	14.29	17.42	9.71	25.80

Table 2. Distribution of 49 rice genotypes in different clusters

Cluster No.	No. of genotypes	Name of the genotypes
I	11	Pusa Basmati 1, Sugandha, Lalat, CRK12, Shatabdi, Lachit, IRRBB 44, Gautam, CRK18, Khitish, CRK 15
II	21	CRAC2222-255, WITA1, IR 64, CRAC2222-537, CRK27, CRAC2224-1048, CRAC2224-969, CRAC2224-913, CRAC2224-916, CRAC2224-914, CRK14, CRK21, CRK22, CRK26, CRAC2224-910, Naveen, CRK28, PUSA 44, CRAC2222-533, Bishmprasad, WITA12
III	8	CRK16, Gitanjali, Ratna, CRK7, CRK10, CRAC2222-257, IR 36, CRK13
IV	4	Annada, Heera, Parijat, Khandagiri
V	5	WARDA33, WARDA39, WARDA44, Kalaboro, Vandana

Table 3. Intra and inter-cluster D^2 and D values (parenthesis) among five clusters

Cluster	I	II	III	IV	V
I	55.80 (7.47)	135.96 (11.66)	100.80 (10.04)	175.30 (13.24)	130.65 (11.43)
II		43.69 (6.61)	136.19 (11.67)	453.69 (21.30)	175.30 (13.24)
III			43.17 (6.57)	240.25 (15.50)	283.92 (16.85)
IV				85.01 (9.22)	348.57 (18.67)
V					74.48 (8.63)

Note: Diagonal values for intra cluster and rest inter-cluster

Table 4. Cluster mean for six agro-morphological traits in 49 rice genotypes

Clusters	Days to 50 % flowering	Plant height (cm)	Panicle bearing tillers m^{-2}	Panicle weight (g)	Test weight (g)	Grain yield/ plant (g)
I	96.45	90.77	404.36	2.20#	23.13	5.87
II	111.05+	98.43	414.00+	2.37	24.17	7.86+
III	107.50	79.38	400.94	2.23	22.33	6.18
IV	83.00#	77.63#	390.00	2.25	20.26#	5.15#
V	91.80	107.80+	348.70#	2.66+	25.75+	6.50

Note: #, + Indicates lowest and highest values, respectively.

III and V consisted of eight and five genotypes, respectively, while cluster IV contained four genotypes. This indicates that a wide diversity existed among the genotypes for different traits studied.

Intra- and inter-cluster distance were presented in Table 3. Cluster IV exhibited maximum intra-cluster distance (D^2 = 85.01) followed by cluster V (74.48) and cluster I (55.80). So far as the inter cluster divergence is concerned, cluster II and cluster IV were found to be highly divergent as indicated by maximum D^2 value (453.69). This was followed by cluster IV and V (348.57), cluster III and V (283.92) and cluster III and IV (240.25). High inter-cluster distance are likely to produce maximum heterobeltiosis and variability in hybridization programme (Pradhan and Roy, 1990). The minimum inter-cluster distance was observed between cluster I and III which indicated that genotypes in those clusters have maximum number of common gene complexes. All the anther culture derived materials (CRAC lines) except CRAC 2222-257 were clubbed into one cluster. The short duration upland varieties Annada, Heera, Parijat and Khandagiri were in cluster IV showing their genetic similarity. Similarly all the three cultures from Africa (WARDA33, WARDA39 and WARDA44) were present in one cluster (cluster V).

The genetic differences between the clusters are reflected in cluster means (Table 4). Cluster II is characterized by highest value for days to 50% flowering, ear bearing tillers/m^2 and grain yield/plant. Cluster IV had genotypes with shortest duration, lowest plant height, lowest test weight and lowest grain yield/plant. Cluster V is characterized by tallest genotypes, highest panicle weight, highest test weight and lowest panicle bearing tillers/m^2.

Cluster II and IV are not only the most divergent clusters, but also the store house of many desirable traits. Cluster II is characterized by two most important traits such as ear bearing tillers/m^2 and grain yield/plant, while cluster IV is characterized by lowest duration and plant height. Hence, hybridization among the genotypes of these two clusters will help in developing early maturing, short statured, high yielding varieties suitable for various cropping systems under *Boro* ecosystem.

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SHORT COMMUNICATION

Identification of Restorers and Maintainers for CMS lines of Rice (*Oryza sativa* L.)

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Three cytoplasmic-genic male sterile (CMS) lines of rice having wild abortive (WA) cytoplasmic male sterility source were crossed with 60 genotypes to identify their restorer/maintainer nature. Most of the genotypes expressed differential fertility reactions when crossed with CMS lines. Among the genotypes tested, 16 were found to be common as effective restorers for all the three CMS lines. These genotypes may be tested for heterosis for development of rice hybrids. Three genotypes viz; Narendra Usar-3, CR2340-5 and Maleshiya produced completely sterile hybrids with all the three CMS lines which may be used in developing new male sterile lines.

Key Words: CMS lines, Fertility restoration, Maintainers, Rice, Wild abortive

Heterosis breeding in rice is effective only when promising restorers are identified for different sources of cytoplasmic-genic male sterile (CMS) lines. The CMS source of Wild Abortive (WA) is being used most extensively in China and India for development of hybrids (Lin and Yuan, 1980).

Restorers for different cytosterile lines will increase the cytoplasmic diversification, which in turn can prevent genetic vulnerability due to the use of single CMS source (Pradhan *et al*., 1992). The restorers and maintainers for WA cytoplasm were reported earlier by Rangaswamy *et al*. (1987), Yogesha and Mahadevappa (1994), Rosamma and Vijayakumar (2005), Ingale *et al*. (2005), Raju Ram *et al*. (2006), Sabar *et al*. (2007) and Akhter *et al*. (2008). Considering the importance of heterosis breeding the present investigation was undertaken with the objective to identify different restorers and maintainers for 3 CMS lines from among the local and high yielding rice (*Oryza sativa* L.) genotypes.

Three CMS lines; IR58025A, IR68897A and Pusa 6A from wild abortive (WA) sources and 60 different test genotypes were grown in a source nursery at the Agricultural Research Farm, Banaras Hindu University, Varanasi during rainy season of 2007. Staggered planting of the CMS lines were done to ensure synchronous flowering. Each CMS line was planted in twin rows, with 10 plants alternating pollen parents (in single rows at 20 x 15 cm spacing). All CMS lines were tested for pollen sterility using 2% iodine-potassium iodide stain and the pollen shedders were removed. Panicles of CMS lines were bagged prior to anthesis. Pollen from male parents were collected at the time of anthesis and dusted separately on the bagged panicles. All possible cross combinations (180) were attempted and mature seeds were collected from 180 F_1 hybrids for further evaluation. The F_1 hybrids were grown at Banaras Hindu University, Varanasi, during rainy season 2008 in single rows having 15 plants. Before anthesis three panicles of each F_1 plant were bagged so as to avoid contamination. Pollen fertility and spikelet fertility were recorded from bagged panicles and the test entries were classified into effective maintainers (<1% pollen fertility), partial/weak maintainers (1 to 20% pollen fertility), partial restorers (21 to 80% pollen fertility) and effective restorers (81 to 100% pollen fertility).

The present observations revealed that F_1 hybrids produced by crossing different rice genotypes with CMS lines behaved differently with regard to pollen fertility Table 1. Out of the 180 F_1 hybrids, 28 were completely sterile and 77 completely fertile. The remaining 75 hybrids expressed varying degrees of fertility, eighteen of them were partial maintainers and the remaining 57 were partial restorers.

Genotypes; CR 2340-1, Type-3, Basmati-370, Pant Dhan-11, Pusa Sugandh-3, Krishna Hansa, HUBR 2-1, Narendra-359, HUR 3022, Taraori Basmati, MTU-7029, BPT 5204, Sarju-52, Malviya-36, Badshabhog and Pusa Sugandh-4 produced higher fertile hybrids and are hence considered as effective restorers for all the three CMS lines (Table 1). Genotypes; IDR-763, Pant-12, CR-2340-7, Pusa Basmati-1, IR-64, GR-32, Kalanamak, Sona Choor, Tulsiparsad and Super Basmati were found to be effective

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Table 1. Classification of rice genotypes into restorers (R), maintainers (M), partial maintainers(PM) and partial restorers for different cytosterile lines

S.No	Genotypes	IR 58025A	IR 68897A	Pusa 6A
1.	Vishnuprag	PR	M	PM
2.	CR 2340-1	R	R	R
3.	Rupali	PR	R	M
4.	Pant Dhan-10	PR	PR	PR
5.	Pant Dhan-4	M	R	PR
6.	Type-3	R	R	R
7.	Basmati-370	R	R	R
8.	Manhar	PR	M	PR
9.	Pant Sugandh Dhan-17	PR	PR	PR
10.	Pant Dhan-11	R	R	R
11.	Annada	PM	R	PR
12.	Pusa Sugandh-3	R	R	R
13.	Pant Dhan-6	PR	PR	M
14.	Gautam	PR	R	PR
15.	Krishuna Hansa	R	R	R
16.	HUBR 2-1	R	R	R
17.	NDR-118	PR	R	PR
18.	IDR-763	R	PR	R
19.	Pant-12	R	PR	PR
20	Narendra-359	R	R	R
21	Narendra-80	PR	R	R
22	Narendra2026	PR	PR	PM
23	Narendra Usar-3	M	M	M
24	Narendra-97	PR	R	PM
25	Kanak Jeer	M	PR	PR
26	Anjali	PM	M	PM
27	Naveen	M	PR	PR
28	HUR 3022	R	R	R
29	Narendra Usar-2	PR	PM	PR
30	GR-2340-7	R	PM	R
31.	CR2340-5	M	M	M
32.	BAU-170-90	PR	PR	PM
33.	Pusa Basmati-1	R	PR	PR
34.	IR-64	R	R	PR
35.	Taraori Basmati	R	R	R
36.	G R-32	R	R	PR
37.	Kalanamak	R	R	PR
38.	Jaya	PR	M	R
39.	M T U-7029	R	R	R
40.	BPT 5204	R	R	R
41.	Sarju-52	R	R	R
42.	Malviya-36	R	R	R
43.	Maleshiya	M	M	M
44.	Lalmati	M	PM	PR
45.	Heera	M	PM	M
46.	Vandana	PR	R	PM
47.	Sona Choor	R	R	M
48.	Badshahbhog	R	R	R
49.	Tulsiparsad	R	PM	PR
50.	Pusa Sugandh-2	PR	PR	R
51.	Super Basmati	R	R	PR
52.	Pusa-44	PR	PR	R
53.	Pusa Sugandh-4	R	R	R
54.	CR 2340-3	PR	M	PM
55.	Kalinga 1	PM	M	M
56.	Barni Deep	PR	PR	PR
57.	Khilish	M	PM	M
58.	Sulk Smarat	PR	M	PR
59.	Birsa Dhan 101	PR	PR	PM
60.	BVD 109	PM	PR	PR

restorers for IR58025A while Rupali, Pant Dhan-4, Annada, Gautam, NDR-118, Narendra-80, Narendra-97, IR-64, GR-32, Kalanamak, vandana, Sona Choor, Super Basmati showed effective restoration for IR68897A and IDR-763, Narendra-80, CR-2340-7, Jaya, Pusa Sugandh-2 and Pusa-44 were effective restorers for Pusa 6A.

Narendra Usar-3, CR2340-5 and Maleshiya produced sterile hybrids when crossed with all the three CMS lines while Pant Dhan-4, Kanak Jeer, Naveen, Lalmati, Heera and Khilish produced sterile hybrids when crossed with IR58025A. Vishnuprag, Manhar, Anjali, Jaya, CR2340-3, Kallinga-I and Sulk Smarat produced sterile hybrids when crossed with IR688897A and Rupali, Pant Dhan-6, Heera, Sona Choor, Kallinga-I and Khilish produced sterile hybrids when crossed with Pusa 6A, these genotypes could be utilized in back cross breeding programmes for the development of new male sterile lines. Conversion of genotypes which are well adapted in a particular agroclimatic region into CMS lines can be of great use in the development of rice hybrids for Uttar Pradesh. As observed in the present study, the differential raction to fertility restoration by different genotypes, earlier worker have also reported the similar results. For instance, Rosamma and Vijay kumar (2005) found that 'Aruna' and 'Ptb10' were maintainers for five CMS lines where as these were found effective restorers for some others CMS lines, Oka (1974) suggested that the genetic background of a female parent could influence pollen and spikelet fertility of F_1 hybrids in inter-varietal rice hybrids.

The genotypes, Narendra Usar-3, CR2340-5 and Maleshiya could be said to be perfect maintainers as these genotypes produced sterile hybrids in all the three CMS lines. These genotypes may be converted into new CMS lines through back cross breeding programmes. Genotypes showed effective restoration with promising heterosis in this area could be exploited for development of hybrids, rice varieties.

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SHORT COMMUNICATION

Proximate and Mineral Composition Analysis of Little Millet Collected from Some Millet Growing Areas in Tamil Nadu

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Eighteen accessions of little millet (*Panicum sumatrense* Roth ex Roem. & Schult.) collected from different locations across millet growing regions of Tamil Nadu were analysed for their variation in nutrient and mineral composition using AOAC method and quantification of metals using ICP spectroscopic method. Among the 18 accessions analyzed, maximum proximate content of moisture (MSSRF-BD2), protein (MSSRF-BD11), carbohydrate (MSSRF-BD5), total ash (MSSRF-BD9), fibre (MSSRF-BD18), fat (MSSRF-BD12) and energy (MSSRF-BD12) were listed. High mineral content of calcium (MSSRF-BD8), iron (MSSRF-BD1), magnesium (MSSRF-BD14), phosporus (MSSRF-BD14), potassium (MSSRF-BD15) and zinc (MSSRF-BD6) were observed in the collections.

Key Words: Intra-species variation, Little millet, Mineral composition, *Panicum sumatrense*, Proximate composition

Millet cultivation in India extends from sea level and the Deccan plateau (Mazhar *et al*., 2007) in southern peninsula to almost 2438 m altitude in western and eastern Himalaya and north-eastern hill regions (ICAR, 1999). Seeds of eighteen accessions were collected from farmers field across five millet cultivating locations in Tamil Nadu *i.e.* Dharmapuri, Salem, Thiruvannamalai, Vellore and Theni districts. Different accessions, identified by specific local names in the pockets of cultivation displayed variability in seed colour. The present investigation was under taken to analyse the samples for their nutritional and mineral composition.

The study was conducted in the year 2009-2010 crop season when 18 seed samples of little millet (locally called *Samai*) were collected from the farmers in millet growing areas of Pachamalai Hills (726-826 m), Javadu Hills (706-809 m), Yelagiri Hill (563-588 m), Megamalai (323 m), and Dharmapuri distict (458-525 m) in the state of Tamil Nadu (Table 1). Seeds were ground into fine powder separately and moisture analysis was carried out before storing at 4°C.

Proximate composition (AOAC, 2006) of moisture was determined at 95°-100°C under pressure ≤100mm Hg (ca 5 h) Ref. 934.01, crude protein Ref. 984.13, fat (ether extract) Ref. 920.39, total ash was determined at 600°C for 2 h Ref. 942.05, crude fibre Ref. 962.09, total carbohydrate [100 – (crude protein+crude fat+ash+crude fibre)]. The energy value was calculated by Pearson's method (Kirk and Sawyer, 1991).

The calcium, magnesium, potassium, phosphorus and zinc metal analysis of millets were performed using AOAC method, Ref. 985.01 (AOAC, 2006). Quantification of metals was done by Inductively Coupled Plasma (ICP) spectroscopic method as indicated at the following wavelengths, calcium (317.9 nm), magnesium (279.5 nm), potassium (766.5), phosphorus (214.9), Iron (372.0 nm) and zinc (213.8 nm). Results calculated from triplicate data were expressed as mean ± standard deviation.

The proximate composition of the samples, their mean and standard deviation are presented in Table 2. The moisture content ranged from 9.33 to 12.70 g/100 g. Higher moisture content was observed in MSSRF-BD2. The protein content among the accessions ranged from 6.36 to as high as 9.15 g/100 g found in MSSRF-BD11. The carbohydrate value ranged between 61.48 to 68.57 g/100 g. The sample MSSRF-BD5 showed the highest percentage of carbohydrate content among the accessions. The total ash value ranged from 3.15 to 9.07 g/100 g and the accession MSSRF-BD9 showed higher percentage. Fibre content ranged from 5.54 to 7.84 g/100 g and content was rich in MSSRF-BD18. The percentage of fat content ranged between 3.61 to 5.56 g/100 g and MSSRF-BD12 showed

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Table 1. Locations of collection, local name and seed colour

Districts	Sample Code	Locations	Altitude (m)	Latitude and longitude	Local name	Seed colour
Salem and Trichy	MSSRF-BD1	Pachamalai Hills	726	11º22'36.49"N 78º34'08.55"E	Samai	White and brown mixed
Salem and Trichy	MSSRF-BD2	Pachamalai Hills	768	11º21'27.69"N 78º37'15.48"E	Ilansamai or Vella samai	Light brown
Salem and Trichy	MSSRF-BD3	Pachamalai Hills	732	11º19'35.77"N 78º36'32.15"E	Vella samai	Light honey dew
Salem and Trichy	MSSRF-BD4	Pachamalai Hills	826	11º16'28.91"N 78º35'08.51"E	Perumsamai	Light brown
Salem and Trichy	MSSRF-BD5	Pachamalai Hills	791	11º18'19.99"N 78º37'54.38"E	Ilansamai	White and brown mixed
Dharmapuri	MSSRF-BD6	Pennagaram	458	12º09'15.12"N 77º54'48.33"E	Samai	Brown
Dharmapuri	MSSRF-BD7	Pennagaram	493	12º06'50.91"N 77º56'14.95"E	Samai	Brown and black mixed
Dharmapuri	MSSRF-BD8	Pennagaram	525	12º06'12.42"N 77º52'22.29"E	Samai	Light brown
Vellore	MSSRF-BD9	Yelagiri Hills	588	12º43'06.79"N 78º44'486.07"E	Ella samai	White and brown mixed
Vellore	MSSRF-BD10	Yelagiri Hills	563	12º42'55.05"N 78º45'10.61"E	Samai	Light black
Vellore	MSSRF-BD12	Yelagiri Hills	740	12º29'36.03"N 78º50'05.62"E	Sittansamai	Dull white
Vellore	MSSRF-BD13	Yelagiri Hills	779	12º38'21.86"N 78º56'07.45"E	Sittansamai	Medium black
Vellore	MSSRF-BD14	Javadhu Hills	740	12º29'36.03"N 78º50'05.62"E	Sittansamai	Medium black
Vellore	MSSRF-BD15	Javadhu Hills	706	12º37'20.85"N 78º54'43.86"E	Perumsamai	Brown
Vellore	MSSRF-BD16	Javadhu Hills	809	12º38'16.60"N 78º56'57.46"E	Sirusamai or Koluthanan Samai	Brown and white mixed
Vellore	MSSRF-BD17	Javadhu Hills	706	12º37'20.85"N 78º54'43.86"E	Sittansamai	Medium black
Vellore	MSSRF-BD18	Javadhu Hills	809	12º38'16.60"N 78º56'57.46"E	Perumsamai or Vella Samai	Dull white
Theni	MSSRF-BD11	Megamalai	323	9º58'53.66"N 77º22'43.64"E	Chinnasamai	White brown mixed

higher value. The energy values obtained across accessions and ranged from 317.17 to 349.40 kcal/100 g and highest value observed in MSSRF-BD12.

The mineral composition of the samples, their mean and standard deviation are presented in Table 3. Potassium ranged from 199.2 to 303.4 mg/100 g and higher content was found in MSSRF-BD15. Phosphorous had a value ranging from 184.3 to 308.9 mg/100 g and was high in MSSRF-BD14. Magnesium varied from 131.3 to 186.6 mg/100 g and the maximum found in MSSRF-BD14. The iron content ranged from 7.84 to 90.8 mg/100 g and MSSRF-BD1 showed maximum content. Calcium content ranged from 22.6 to 56.4 mg/100 g and accession MSSRF-BD8 showed the highest. Zinc ranged from 1.52 to 2.14

Table 2. Proximate composition of little millet (g/100g)[1]

Sample	Moisture ($\%_{f.w.}$)	Protein ($\%_{d.w.}$)	Fat (ether extract) ($\%_{d.w.}$)	Total ash ($\%_{d.w.}$)	Fibre (crude) ($\%_{d.w.}$)	Carbohydrates ($\%_{d.w.}$)	Energy (kcal/100 g)
MSSRF-BD1	10.58±0.32	7.10±0.27	4.81±0.26	4.08±0.23	7.44±0.31	65.99±1.94	335.65±4.33
MSSRF-BD2	12.70±0.44	7.12±0.35	4.73±0.24	7.73±0.36	6.41±0.23	62.0±2.34	317.17±2.12
MSSRF-BD3	11.21±0.43	7.16±0.23	4.76±0.25	3.27±0.22	6.43±0.34	67.17±1.55	340.16±4.34
MSSRF-BD4	10.71±0.39	6.88±0.26	4.53±0.26	3.30±0.25	6.50±0.37	68.08±2.24	340.61±3.28
MSSRF-BD5	10.28±0.41	6.36±0.34	4.42±0.23	3.57±0.24	6.80±0.25	68.57±1.42	339.5±4.25
MSSRF-BD6	10.64±0.47	7.83±0.35	4.48±0.25	5.48±0.23	6.67±0.32	64.9±2.29	331.24±3.32
MSSRF-BD7	11.47±0.44	8.17±0.36	4.35±0.24	6.61±0.32	6.27±0.24	63.13±2.21	324.35±3.45
MSSRF-BD8	10.86±0.38	7.64±0.24	4.35±0.27	7.31±0.21	6.11±0.17	63.73±1.32	324.63±2.72
MSSRF-BD9	9.91±0.26	8.66±0.26	4.34±0.29	9.07±0.23	6.54±0.24	61.48±2.23	319.62±3.42
MSSRF-BD10	10.96±0.42	8.62±0.34	4.66±0.25	4.06±0.24	7.36±0.33	64.34±1.64	333.78±4.34
MSSRF-BD11	9.46±0.28	9.15±0.23	4.74±0.14	3.83±0.15	6.68±0.28	66.59±1.23	345.62±3.32
MSSRF-BD12	9.33±0.36	7.46±0.24	5.56±0.13	4.73±0.14	5.54±0.25	67.38±2.12	349.40±2.17
MSSRF-BD13	11.97±0.37	8.07±0.27	4.45±0.16	4.09±0.12	7.16±0.26	64.26±2.34	329.57±4.18
MSSRF-BD14	10.43±0.27	7.90±0.25	4.69±0.14	5.07±0.13	6.40±0.23	65.51±1.23	335.85±3.12
MSSRF-BD15	11.29±0.22	6.46±0.17	3.61±0.17	4.35±0.24	7.45±0.35	66.91±1.18	326.69±3.37
MSSRF-BD16	10.04±0.41	8.46±0.22	5.04±0.33	3.44±0.15	6.72±0.22	66.3±2.11	344.4±4.52
MSSRF-BD17	9.73±0.37	6.65±0.26	4.72±0.24	6.05±0.27	7.31±0.25	65.54±2.32	331.24±3.23
MSSRF-BD18	10.64±0.26	8.08±0.35	4.32±0.23	3.15±0.17	7.84±0.26	65.97±2.12	335.08±3.32

[1]Values are expressed as means ± SD of three replicates; f.w.: fresh weight; d.w.: dry weight

Table 3. Mineral composition of little millet (mg/100 g)[1]

Sample	Calcium	Iron	Magnesium	Phosphorous	Potassium	Zinc
MSSRF-BD1	29.5±0.97	90.8±1.77	149.5±3.32	209.9±2.47	214.1±2.71	1.78±0.03
MSSRF-BD2	29.1±1.12	75.5±2.11	165.9±2.91	251.1±2.82	222.3±2.89	1.98±0.02
MSSRF-BD3	23.5±1.06	29.7±1.35	135.5±2.69	208.3±2.94	222.9±2.31	1.96±0.04
MSSRF-BD4	24.1±1.47	14.6±0.86	132.3±2.23	224.9±2.31	263.2±2.79	1.75±0.02
MSSRF-BD5	22.6±1.68	40.8±1.45	139.8±2.21	226.4±2.33	252.8±1.72	1.52±0.03
MSSRF-BD6	30.8±1.57	14.8±0.94	167.5±3.12	227.8±2.84	267.3±2.43	2.14±0.03
MSSRF-BD7	36.6±1.19	10.5±1.27	165.3±2.63	218.1±2.22	244.5±2.67	2.10±0.03
MSSRF-BD8	56.4±2.13	45.2±1.73	166.3±2.55	254.2±3.27	250.5±2.42	1.89±0.04
MSSRF-BD9	27.8±1.12	42.3±1.21	132.2±2.14	184.3±2.24	257.9±2.63	1.98±0.03
MSSRF-BD10	26.3±1.18	24.5±1.22	167.2±2.83	277.2±3.31	239.6±2.42	1.82±0.04
MSSRF-BD11	30.4±1.32	28.9±1.18	131.3±2.31	201.1±2.13	199.2±1.84	1.95±0.03
MSSRF-BD12	22.9±1.71	24.1±1.29	155.9±2.16	272.7±3.14	278.5±2.38	1.69±0.04
MSSRF-BD13	24.4±1.28	32.0±1.27	162.3±2.71	242.9±2.26	224.9±2.22	2.06±0.02
MSSRF-BD14	26.1±1.32	54.4±1.88	186.6±2.38	308.9±3.23	257.8±2.17	1.74±0.03
MSSRF-BD15	36.0±1.76	50.5±1.74	183.5±2.63	289.5±2.87	303.4±2.71	1.97±0.05
MSSRF-BD16	25.0±1.17	13.6±0.95	172.9±2.85	263.8±2.38	247.4±1.92	2.09±0.03
MSSRF-BD17	25.7±1.36	36.8±1.14	161.6±2.31	211.1±2.46	245.2±2.17	1.85±0.04
MSSRF-BD18	23.1±1.19	7.84±0.63	141.7±2.42	239.0±2.44	259.0±1.16	2.06±0.03

[1]Values are expressed as means ± SD of three replicates

mg/100 g, with accession MSSRF-BD6 having the highest. Over all analysis of the mineral composition of little millet showed that they contained minerals in varying amounts in the following order, K>P>Mg>Fe>Ca>Zn.

The samples collected from different locations indicated a high level of variability in terms of their proximate and mineral composition. Accessions having high nutrient content can possibly be used in breeding programmes, promotion of large scale cultivation and consumption. Under-utilized species like little millet are likely to be useful in fighting malnutrition and hidden hunger, both in the areas of cultivation and urban locations.

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SHORT COMMUNICATION

Naturalization of *Solanum chacoense* Bitter: An Exotic Species in the Shimla Hill, Himachal Pradesh

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Solanum chacoense Bitter is native to South America, but has also naturalized in some other countries outside its original habitat due to its invasive weedy nature. It has naturalized in the Shimla, Himachal hill forest after its escape from the wild potato germplasm collection at the Central Potato Research Institute, Shimla (Himachal Pradesh). It is an important source of genes for charcoal rot, late blight, various types of nematode etc. and could be an important genetic resource in future.

Key Words: Exotic species, Naturalization, *Solanum chacoense*, Shimla hill, Wild potato

The process of naturalization of plant species in new areas away from their original habitats presents an interesting case history, showing thereby what might have happened during the early spread of economically useful species of plants. It was around 1936 that a set of wild relatives of potato was planted at Agriculture Research Institute field station at Phagli (Shimla), for their potential use in the breeding of resistant varieties for the Indian subcontinent, but during that time there was not much known about these species in the absence of targeted evaluation of these species. Since then one of the wild potato species, namely, *Solanum chacoense* Bitter, escaped to the Shimla woods and now it can be seen in all parts of Shimla hills. It flowers and bears berries in abundance with a high percentage of viable seed setting. It also bears small sized tubers underground. The author believed that the monkeys (*Macaca mullata*) and langurs (*Semnopithecus entellus*) consume the mature berries near maturity and it is through their faecal matter seeds are dropped on the ground in different parts and after the break of dormancy the seeds germinate in high percentage, may be that the digestive enzymes help in high per cent germination. This is because the station at Phagli (Shimla) is located at an elevation of 1925 m and from there it has spread upward up to an elevation of 2100 m and laterally it has not gone into the areas beyond the disconnected forest areas. Moreover there are frequent vertical rather than lateral movements of monkeys and langurs, and that too, in forest areas only. It also appears that it has a direct relationship with their continuous presence in the area. Nayar and Gohal (1970) have suggested the spread by birds, which, if accepted then the spread of this species cannot be confined to a particular area of forest, because its distribution has not gone beyond Bolleaugunja and Dhalli in Shimla town due to discontinuity of forest.

S. chacoense is an important source of resistant genes for charcoal rot disease of potato, which occurs widely in areas with high temperature. It also has resistance to late blight disease, which is among the most injurious diseases of potato crop, because of its sudden spread and very high damage to the foliage and causing severe rot of tubers. When the fungal spores gain entry in the tubers, they may cause rotting of tubers even during the storage conditions. Generally two strains of *S. chacoense* are seen growing in the forests, one with purple pigmented stems and the other with green stems. *S. chacoense* is native to southern Bolivia, northern Argentina, south-west Uruguay, southern Paraguay, low lands of south-central Chile, and southern Brazil; at elevations ranging from near sea level to more than 2000 m and on sandy slopes even up to 2200 m. It generally grows in areas with very high rainfall (over 1000 mm/year) and prefers soils rich in organic matter, well drained with pH from 6.0-6.5. It can tolerate shade of trees and low temperatures up to 5°C as well as cloudy weather for extended periods (Terzioglu & Ansin, 2001). In its native areas, it occupies a wide range of habitats. In Shimla, it grows well under the trees of *Cedrus deodara* and has association with *Prinsepia utilis, Mirabilis jalapa, Physalis nicandra, Achyranthes aspera, Fagopyrum cymosum, Girardinia heterophylla, Bidens pilosa, Ficus palmata,*

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Fig. 1. *S. chacoense* colonistaion in Shimla forests

Prunus puddum (*P. cerasoides*), *Strobilanthes dalhousianus* and various species of grasses. *Solanum chacoense* plants form rosettes or sub-rossettes, erect or spreading, glabrous or sparsely pubescent over all parts. Stems are 30-70 cm, angular, and are usually light green or occasionally irregularly pigmented, branches winged, flowers white (Fig.1). It has single locus homomorphic self-incompatiblity, which is gametophytic type and is operative at late stylar stage (Franklin-Tong & Franklin, 2003). However, in some clones of *S. chacoense* (e.g. CPC1760), a pseudo-self incompatibility also occurs. Such sporadic self incompatibility may be due to partial breakdown of the self incompatibility which may not be owing to gene 'F' responsible for fertility. Though there are scanty in-depth studies on this plant species, of about 110 tuber bearing *Solanums*, *S. chacoense* has probably the greatest potential for use in potato improvement programmes. Plants of this species are little attacked by aphids, *Myzus persicae*, an important insect vector responsible for spread of potato virus, PVX; has resistance to *Empoasca fabae* (leaf hopper); seldom damaged by Colorado potato beetle (*Leptinotarsa decemlineata*); has some resistance to potato viruses, PLRV (potato leaf roll virus) and PVY (potato virus Y); and has resistance to *Synchytrium endobioticum* (potato wart or black scab) as well as to *Corynebacterium sepedonicum* (ring rot). It also shows resistance to various types of nematode (Anonymous, 1975, 1978). Evaluation studies conducted at the International Potato Centre (CIP), Lima, Peru indicated that *S. chacoense* possesses resistance to broad spectrum diseases and has a high degree of resistance to bacterial wilt caused by *Pseudomonas solanacearum*, a serious potato disease all over the world (Ochao, 1990).

It is note worthy to mention here that *S. chacoense* has been introduced widely outside its natural range of habitats (Reinhard *et al.*, 2010) and because of its better adaptability and aggressive weedy nature, it has spread and acquired as a weedy status. It is more so when neither wild nor cultivated potato is known to spread outside of its native range. *Solanum chacoense*, however, has become established in eight sites around the world, in Himachal Himalaya (Shimla) in India, eastern China, England, New Zealand, the United States, Central Peru, and east-central Argentina. A literature review reveals that although *S. chacoense* possesses traits typical of an invasive species, yet all populations, in these sites, appear to be confined to their site of introduction. In fact, the spread of this species in Shimla appears to be due to congenial climatic conditions and its ability to defend itself against enemies, as well as it has large ecological tolerance, which enables it to live in other ecosystems and compete with the indigenous taxa (Reinhard *et al.*, 2010). In Shimla, the species can be seen growing in frequent large colonies on the hill slopes, along the road, and water channels and near the cultivated fields

on grassy bunds (Fig. 2). It bears large number of berries producing number of viable seeds. Usually the plants forming colonies are found growing luxuriantly and are invariably free from diseases and pests. Recently it was also reported that plants of *S. chacoense* contained acetylated glycoalkaloids (leptine) providing high resistance against the potato beetle (Wink, 1988). So, no insect-pest can be seen feeding on its foliage. Taxonomically, *S. chacoense* contains one subspecies, *S. chacoense* ssp. *subtilis* (Bitt.) Hawkes, and three varieties viz. *S. chacoense* var. *angustisectum* Hassl., *S. chaconse* var. *latisectum* Hassl. f. *glabrescens* and *S. chacoense* var. *latisectum* f. *plurijugum* Hassl. This species is self-incompatible and can be readily crossed with many varieties of cultivated diploid potato species namely *S. phureja* and *S. goniocalyx*. But it cannot be crossed directly with *S. tuberosum*, however its colchicines induced tetraploids are crossable.

Fig. 2. *S. chacoense* plant with tuber

In conclusion, it is pointed out that this naturalized species in Shimla hill has become a weed and has no other worth than its potential use in breeding, when it has been evaluated for several useful traits by now. While *S. chacoense* is an important source of genes responsible for resistance to a number of diseases and insect-pests, it has not been much used in the breeding of improved varieties, because of two reasons. Firstly, it is a diploid species and the cultivated potato is tetraploid and hence direct crosses were not possible Secondly, it contains a new glycoalkaloid or high glycoalkaloids posing a health hazard. This has been the case with a variety called Lenape, which had *S. chacoense* as one of the parent and was found to exceed the safety levels of glycoalkaloids and had to be withdrawn from the commercial cultivation (Wink, 1988). The use of this species in breeding was limited in the conventional methods, which is not the case, now, when new biotechnological breeding tools are available. So, the naturalized species may serve as an important genetic resource in the years to come.

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SHORT COMMUNICATION

Oenothera laciniata Hill (Onagraceae): Addition to the Flora of North-western Plains

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Oenothera laciniata Hill was collected from wheat and brassica fields in Delhi during late winters of 2008-2011. The plants formed large rosettes with pinnatifid leaves on branches and set seed in early summer (April-May). Good establishment of plants was also noted in pot cultures. This species warrants attention for its potential for further spread as a weed of *rabi* crops in the Indian region.

Key Words: *Oenothera laciniata*, Punjab, Rosette, Weed

Oenothera laciniata Hill (Onagraceae) was collected from fields of the Indian Agricultural Research Institute (IARI), New Delhi (28º38'23" N, 77º09'27" E). This species was not earlier reported from Delhi (Maheshwari, 1963; Prithipalsingh, 2002). Its presence was recorded in the area of collection over a period of three years (2008-2010) where it formed conspicuous sparsely distributed rosettes (in fields of wheat and brassica), bearing pinnatifid leaves on the side branches. However, in other nearby areas (fields and road sides), the plants were absent indicative of restricted occurrence and no rapid spread. The species appeared in late winter and flowered and fruited in early summer.

Observations on the plants in the field, in transplants and pot cultures indicate that this species changes its habit in relation to moisture availability (Hilty, 2010) and achieves high seed production over a short growth season. These are characteristics of a successful invasive species but not of a noxious weed. Besides populations from Delhi, we have also located and examined specimens collected from fields of Punjab Agricultural University, Ludhiana. Furthermore, this species has been intercepted in wheat imports into India (http://www.plantquarantineindia.org/docfiles.Appendix-8.htm). *Oenothera laciniata*, therefore, is an important alien invasive species whose occurrence (Khan *et al*., 1984; Sasidharan, 2004) and spread must be monitored within the Indian region, taking into consideration, its wide global distribution and potential for spread as a crop contaminant (GRIN, 2009), its persistence in the 'soil seed bank' (Western Australian Herbarium, 1998-) and the high genetic diversity reported in the species (Ellstrand and Levin, 1982).

A brief taxonomic description along with useful ecological information is provided below. This information would enable research workers in plant genetic resources to identify this potentially invasive species and record its spread.

Oenothera laciniata Hill in Veg. Syst. 12 (app.): 64, t. 10. 1767 (Hort. Kew. 172 (4), t. 6. 1768); *Oenothera sinuata* Linn., Mant. Pl. 2: 228. 1771. Fig. 1A.

Diagnostic characters: Plants forming conspicuous rosettes; initial leaves oblanceolate, forming a basic rosette, cauline leaves smaller, distinctively pinnatifid, alternate, sessile; long calyx tube produced much beyond the ovary, reflexed calyx lobes subtending yellow petals which become pinkish-orange after pollination; pubescent ovary forming a long capsule, splitting from apex downwards; small, dark-brown seeds abundant in four locules (Fig. 1, A-D).

Flowering and Fruiting: April-May

Distribution: South America, Europe, South Africa, Iran, China, Taiwan, Korea, Japan (Wu Zheng-yi and P. H. Raven *et al.*, 1994; Amini and Habib, 2003). Within India in the north western plains [Bijnor, Uttar Pradesh (Khan *et al*., 1984); Delhi and Ludhiana, Punjab (RN & KP, 2008 to 2010)] and southern India [Idukki, Kerala (Sasidharan, 2004)].

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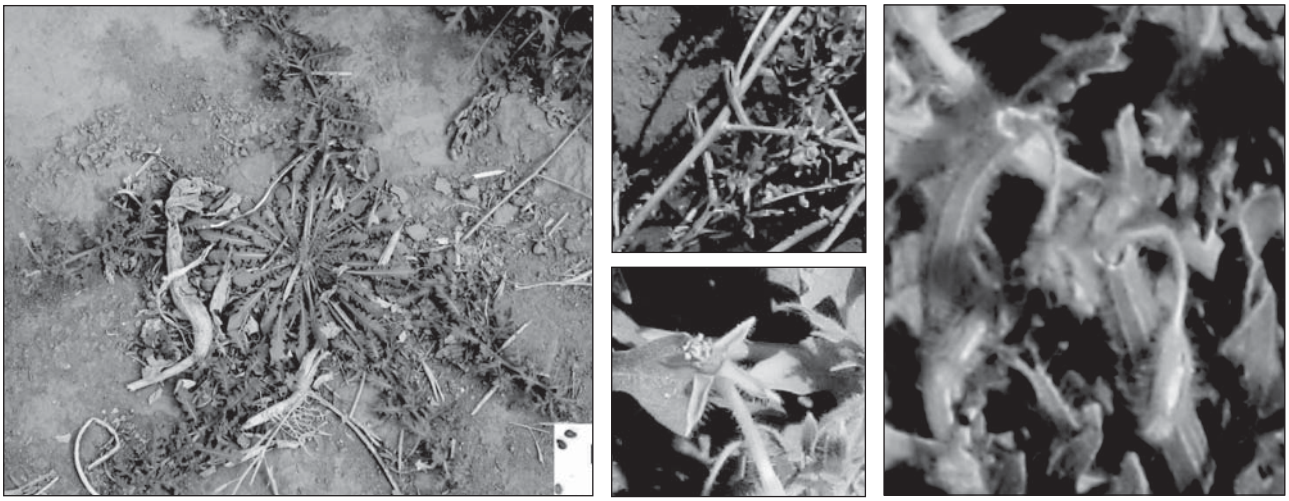

Fig. 1: *Oenothera laciniata*: (a) plant in the field; (b) close-up of flowers; (c) calyx and corolla drying up after pollination; (d) capsule splitting from apex downwards (seeds in inset, less than 0.2cm)

Origin: South eastern parts of North America (GRIN, 2009).

Habitat and Ecology: Weed found in wheat and brassica, restricted to a few adjacent fields, absent in others; fairly large populations recorded over consecutive years from 2008-2010, and co-occurring with some other rosette-forming species *viz*. *Tribulus terrestris* Linn. and *Coronopus didymus* (Linn.) Sm. and few common weeds such as *Amaranthus viridis* Linn., *Chenopodium album* Linn., *C. murale* Linn., *Heliotropium supinum* Linn., etc. in loose-textured sandy-clayey soil. Ploughing leads to elimination of plants unlike most other co-occurring weeds.

Seedling establishment high in pot cultures; plants raised from seeds flowered and set seed in similar season as in the field. Erect habit and occasional branching noted in pot culture, unlike its decumbent rosette-forming habit in field conditions.

Specimens Examined: INDIA, Delhi, IARI: 9 May 2008, RN/2008/HS19687 (NHCP); INDIA, Delhi, NBPGR: 13 April 2010, RN/2010/HS20239 (NHCP); INDIA, Delhi, IARI: 17 May 2008, RN/2008/HS20240 (NHCP); Ludhiana, Punjab: 18 May 2010, KP/2010/HS20249 (NHCP); USA, Florida, 3 April, 1987, L. C. Anderson, 10338 (http://www.herbarium.bio.fsu.edu/view-specimen.php?RecordID=9784); USA, Texas, H. Cliff 343, Bexar Herbarium, NPSOT San Antonio Chapter).

Acknowledgement

The authors thank the Director, National Bureau of Plant Genetic Resources, New Delhi, for facilities to carry out the investigations.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXIII meeting held on July 18, 2011 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 36 germplasm lines out of 105 proposals considered. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. T3-2, T3-3, T3-4 and T3-5 (IC0587407-IC0587410 and INGR11001-INGR11004), a Paddy (*Oryza sativa* L.) Germplasm, with High Yielding Pyramid Lines of Type 3 Basmati, Two Bacterial Leaf Blight Resistance Genes and a Semi-dwarfing Gene

D Rajpurohit, A Awasthi, P Paul, S Kumar, R Kumar, K Singh and HS Dhaliwal*
Eternal University, Baru Sahib via Rajgarh, Sirmour-173101, Himachal Pradesh.
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A traditional Type 3 Basmati rice cultivar grown in Uttarakhand possesses long, slender, translucent grains with strong and pleasant aroma and excellent cooking quality. It is, however tall and lodges even under low nitrogen fertilizer dose. In addition to lodging, it is highly susceptible to several diseases and pests including bacterial blight (BB). Efforts to evolve semi-dwarf basmati cultivars with aroma and cooking quality comparable to those of traditional basmati cultivars through conventional breeding methods have not met with much success. With the availability of series of molecular markers, construction of high density molecular maps and tagging of genes of economic importance it has been possible to improve rice cultivars through marker assisted backcross breeding (Joseph *et al.*, 2004; Sundaram *et al.*, 2008).

Type 3 Basmati also known as Dehraduni Basmati was taken as the recurrent parent in crosses with a non-basmati rice donor line PR106-P2 with semidwarf *sd-1* gene and three bacterial leaf blight resistance genes *xa5, xa13* and *Xa21* pyramided through marker assisted selection (Singh *et al.*, 2001).

A number of BC_2F_6 semidwarf and bacterial leaf blight resistant pyramid lines of Type 3 Basmati with *sd-1, xa13* and *Xa21* genes were developed through marker assisted foreground selection for markers linked to the genes (Fig.1) and background selection using SSR and ISSR markers. About 17 selected lines with more than 85% Type 3 Basmati background recovery, reduced plant height, BB resistance against a mixture of *Xanthomonas oryzae* pv. *oryzae* isolates of northern

Table1. Morphological, yield and quality characteristics of BC2 F6:7 pyramid lines of Type 3 Basmati grown at IIT Roorkee in 2010

Pyramid lines/Parents	Pedigree	Plant height (cm)	Days to 50% flowering	No. of tillers per plant	L/W ratio of milled rice	L/W ratio of cooked rice	% Amylose	Aroma	Paddy Yield kg/ha
T3-2	31-4-2-6-1⊗	117.0^{b}	116^{b}	13.4^{a}	3.61^{c}	5.20^{c}	22.02^{b}	Strong	5170^{a}
T3-3	36-3-8-5-4⊗	121.5^{c}	116^{b}	15.6^{c}	3.88^{f}	5.00^{b}	21.74^{b}	Mild	5877^{b}
T3-4	36-5-4-2-13⊗	130.8^{d}	123^{d}	18.5^{d}	3.82^{e}	5.76^{c}	20.13^{b}	Strong	5993^{b}
T3-5	38-5-2-5⊗	139.0^{e}	121^{c}	13.1^{a}	3.82^{e}	5.95^{c}	20.05^{b}	Strong	5263^{a}
Type 3	-	172.3^{f}	115^{b}	12.0^{a}	3.82^{e}	4.80^{b}	21.50^{b}	Strong	4611^{a}
PR106-P2	-	91.0^{a}	110^{a}	12.7^{a}	3.20^{a}	3.44^{a}	26.07^{d}	None	6537^{b}

Critical difference for paddy yield at 5% level of significance= 1125kg/ha
Different superscript letters on mean values of various traits denote significant differences among pyramid lines and control as based on t-test.

***Compiled and edited by:** *Anjali Kak and RK Tyagi, Division of Germplasm Conservation, National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012*

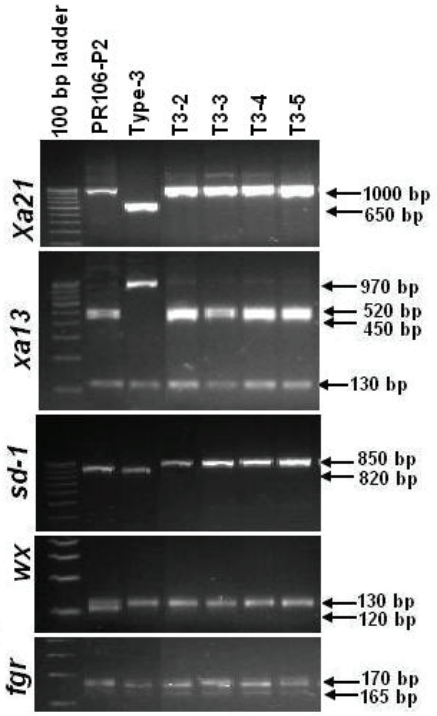

Fig.1: PCR analysis of the parental lines and foreground selection of BC2F6 pyramid lines of Type 3 Basmati using pTA248 primers linked to *Xa21*, RG136 linked to *xa13* (digested with HinfI) and 'h', RM190 and RM42 linked to semidwarfing (*sd-1*), intermediate amylose content(*wx*), and fragrance(*fgr*) genes, respectively

India, desirable kernel length/width ratio and cooking quality (Rajpurohit *et al.*, 2011) were tested in a replicated trial at the Indian Institute of Technology, Roorkee in 2010 using the recommended package of practices for basmati cultivation. Detailed data of four high yielding pyramid lines T3-2, T3-3, T3-4 and T3-5 with significantly higher yield than the recurrent parent Type 3 Basmati, reduced plant height, higher tillering, BB resistance, similar or better uncooked and cooked kernel length/width ratio and strong aroma is given in Table 1.

Registration of the pyramid lines of Type 3 Basmati will help the rice breeders to use the pyramid lines as such or as donors in their ongoing breeding programmes for development of semi-dwarf, high yielding, disease resistance and photosensitive basmati varieties with strong aroma and excellent cooking quality for export and indigenous markets.

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Rajpurohit D, R Kumar, M Kumar, P Paul, A Awasthi, PO Basha, A Puri, T Jhang, K Singh and HS Dhaliwal (2011) Pyramiding of two bacterial blight resistance and a semidwarfing gene in Type 3 Basmati using marker-assisted selection. *Euphytica* **178:** 11-126.

2. KML-29, KDTML-3, KDTML-19 and KDTML-66 (IC0589129- IC0589132 and INGR11005–INGR11008), a Maize (*Zea mays*) Germplasm, with Drought and Water Logging Tolerance and Higher Number of Rows Per Cob and High Test Weight

MV Nagesh Kumar[1], K Sumalini[2], A Srinivas[3], T Sobha Rani[4], R Sai Kumar[5] and G Manju Latha[2]
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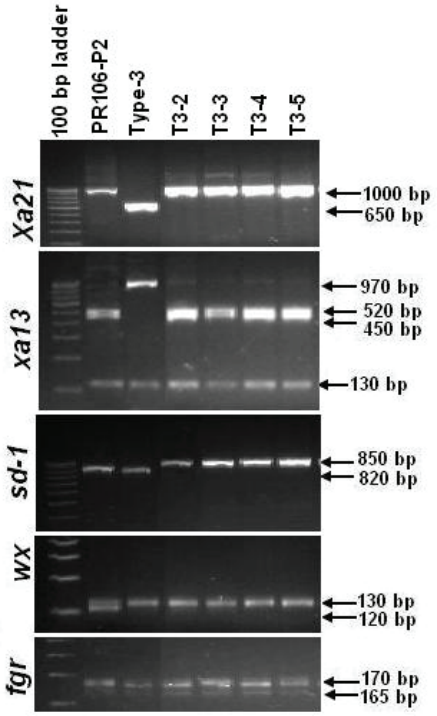
Drought is a major source of grain yield instability in maize (*Zea mays* L.) grown in Peninsular India and use of cultivars with improved drought tolerance may be the only affordable option for many small scale farmers. Among various abiotic stresses, inadequate water availability at critical stages of crop growth and



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2. KML-29, KDTML-3, KDTML-19 and KDTML-66 (IC0589129- IC0589132 and INGR11005–INGR11008), a Maize (*Zea mays*) Germplasm, with Drought and Water Logging Tolerance and Higher Number of Rows Per Cob and High Test Weight

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Drought is a major source of grain yield instability in maize (*Zea mays* L.) grown in Peninsular India and use of cultivars with improved drought tolerance may be the only affordable option for many small scale farmers. Among various abiotic stresses, inadequate water availability at critical stages of crop growth and

development is the major limiting factor for maize production and productivity. Global warming is likely to increase the incidence of drought in many established maize growing areas. Rosenzweig *et al.* (1995) revealed that decline in yield will result largely from temperature induced acceleration of crop growth and development, hastened crop maturity and reduced soil moisture. Maize is very sensitive to stress at tasseling and silking stage. Schussler and Westgate (1995) established that stress due to limited moisture can play significant role in reducing yield of Maize. Understanding the nature of the higher grain potential and enhanced yield stability especially in stress prone environments will provide opportunities to improve the breeding process for selection of stress tolerant genotypes. Hence, a systematic study was conducted at Agricultural Research Station, ANGRAU, Karimnagar, to identify the genotypes tolerant to mid-season drought conditions based on desirable traits and subsequently their seed was increased.

KDTML-3: KDTML-3 is genetically uniform inbred line derived from Tuxpeno sequia population (Temperate material). Six cycles of full-sib recurrent selection (2004-2007) were carried out in the population, Tuxpeno sequia during the rain free winter season at Agricultural Research Station, Karimnagar under controlled moisture stress to coincide either in flowering or grain filling. Among the total germplasm present, promising inbred lines were identified for secondary traits such as Short Anthesis-Silking Interval (ASI), functional stay greenness at grain filling, delayed leaf senescence and less number of barren plants. Further, the line was maintained by inbreeding.

Studies on different morphological traits revealed that KDTML-3 is a late maturing line. The angle between leaf blade and stem is wide with drooping blade attitude. The line takes 72 days for anthesis and 75 days for silk emergence during *rabi*. Purple colouration of brace roots. The study of tassel traits highlighted that there is no pigmentation at the base of the glume, glume excluding base as well as anthers. The spikelets are dense, the angle between main axis and lateral branches is wide and the attitude of lateral branches is curved. The leaves are medium in size, there is purple pigmentation on the silk and no pigmentation on the glumes of the cob. It has short plant height (120 cm) with medium ear placement. The cobs are bold, conico-cylindrical and having many number (14) of rows of grains with irregular grain row aarangement. Grains are orange in colour with yellow cap and flint grain type. It has small 1000 kernel weight. Grains are round in shape. Recorded Anthesis-silking interval of 4-5 days under drought situations with barren ness of about 20%.

KDTML-19: KDTML-19 is genetically uniform inbred line derived from Tuxpeno sequia population (Temperate material). Six cycles of full-sib recurrent selection (2004-2007) were carried out in the population, Tuxpeno sequia during the rain free winter season at Agricultural Research Station, Karimnagar under controlled moisture stress to coincide either in flowering or grain filling. Among the total germplasm present, promising inbred lines were identified for secondary traits such as Short Anthesis-Silking Interval (ASI), functional stay greenness at grain filling, delayed leaf senescence and less number of barren plants. Further, the line was maintained by inbreeding.

Studies on different morphological traits revealed that KDTML-19 is a late maturing line. It has erect plant type with medium sized leaves. The angle between leaf blade and stem is small with straight blade attitude. The line takes 69 days for anthesis and 71 days for silk emergence during *rabi.* The study of tassel traits displayed that there is no pigmentation at the base of the glume and as well as anthers but, purple pigmentation of glumes excluding base. The spikelets are sparse, the angle between main axis and lateral branches is wide and the attitude of lateral branches is curved. There is no pigmentation on the silk as well as glumes of the cob. It has medium plant height (142 cm) with medium ear placement. The cobs are long and conico-cylindrical in shape and having medium number (12-14) of rows of grains with irregular grain row arrangement. It has light Orange flint grain colour and medium 1000 kernel weight. Grains are round in shape. Recorded Anthesis-silking interval of 4-5 days under drought situations with zero percent barren ness. Plant is highly stay green in nature till late grain filling stage.

KDTML-66: KDTML-66 is genetically uniform inbred line derived from Tuxpeno sequia population (Temperate material). Six cycles of full-sib recurrent selection (2004-2007) were carried out in the population, Tuxpeno sequia during the rain free winter season at Agricultural Research Station, Karimnagar under controlled moisture stress to coincide either in flowering or grain filling. Among the total germplasm present, promising inbred lines were identified for secondary traits such as Short Anthesis-Silking Interval (ASI), functional stay greenness

at grain filling, delayed leaf senescence and less number of barren plants. Further, the line was maintained by inbreeding.

Studies on different morphological traits revealed that KDTML-66 is a late maturing line. It has erect plant type. The angle between leaf blade and stem is small with straight blade attitude. The line takes 71 days for anthesis and 72 days for silk emergence during *rabi.* The study of tassel traits revealed that there is no pigmentation at the base of the glume, glume excluding base and as well as anthers. The spikelets are sparse, the angle between main axis and lateral branches is wide and the attitude of lateral branches is curved. There is no pigmentation on the silk as well as glumes of the cob. It has medium plant height (150 cm) with medium ear placement. The cobs are long and conico-cylindrical in shape and large sized having medium number (12-14) of rows of grains. The kernel row arrangement is straight and grains are light orange and flint. It has medium 1000 kernel weight and grains are round in shape. Recorded Anthesis-Silking interval (ASI) of 3-4 days under drought situations with 25% barrenness.

KML-29: KML-29 is genetically uniform inbred line derived from CIMMYT material (Temperate material). Tropicalized plant from CIMMYT material was subjected to inbreeding followed by ear-to-row selection. The inbreeding was done at Agricultural Research Station, Karimnagar. The productive ears with desirable traits were selected in each generation and after seven generations of selfing, this line became uniform. Selection for traits such as texture, ear shape, row number and configuration, kernel shape and colour and husk appearance was effectively practiced during inbreeding.

Studies on different morphological traits revealed that KML-29 is a late maturing line. It has erect plant type with narrow leaves. The angle between leaf blade and stem is small with straight blade attitude. The line takes 69 days for anthesis and 71 days for silk emergence during rabi. The study of tassel traits revealed that there is no pigmentation at the base of the glume, glume excluding base and as well as anthers. It has compact tassel with dense spikelets and longevity of pollen shedding for 7-8 days. A very good pollen shedder. The angle between main axis and lateral branches is narrow and the attitude of lateral branches is straight. The leaves are dark green in colour and there is pigmentation on the silk and no pigmentation on the glumes of the cob. It has short plant height (115 cm) with medium ear placement. The cobs are medium in size and conical in shape having medium number (12) of rows of grains. The kernel row arrangement is straight and grains are orange and flint. It has small 1000 kernel weight and grains are round in shape.

These lines may be involved in on- going single cross hybrid breeding program for development of drought tolerant maize hybrids.

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3. DDW 12 (IC0589133; INGR11009), a Wheat (*Triticum durum*) Germplasm, with Highest Iron (45.9 ppm), Zinc (47.4 ppm), Manganese (941.6 ppm) Contents; Resistance to Rusts and Karnal Bunt

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The durum wheat genotype DDW 12 has the higher Iron, Zinc, Manganese contents in comparison to the best available variety PDW 233. This stock was developed from the progeny of cross RASCON 3 / RAJ 1555 following pedigree selection method at Directorate of Wheat Research, Karnal. The first parent (Rascon3) is a high yielding genotype, while the other parent Raj 1555 is known for wider adaptation and quality attributes. This genotype was evaluated for three years under All India Wheat Coordinated trials during 2007/08 to 2009/10

at grain filling, delayed leaf senescence and less number of barren plants. Further, the line was maintained by inbreeding.

Studies on different morphological traits revealed that KDTML-66 is a late maturing line. It has erect plant type. The angle between leaf blade and stem is small with straight blade attitude. The line takes 71 days for anthesis and 72 days for silk emergence during *rabi.* The study of tassel traits revealed that there is no pigmentation at the base of the glume, glume excluding base and as well as anthers. The spikelets are sparse, the angle between main axis and lateral branches is wide and the attitude of lateral branches is curved. There is no pigmentation on the silk as well as glumes of the cob. It has medium plant height (150 cm) with medium ear placement. The cobs are long and conico-cylindrical in shape and large sized having medium number (12-14) of rows of grains. The kernel row arrangement is straight and grains are light orange and flint. It has medium 1000 kernel weight and grains are round in shape. Recorded Anthesis-Silking interval (ASI) of 3-4 days under drought situations with 25% barrenness.

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3. DDW 12 (IC0589133; INGR11009), a Wheat (*Triticum durum*) Germplasm, with Highest Iron (45.9 ppm), Zinc (47.4 ppm), Manganese (941.6 ppm) Contents; Resistance to Rusts and Karnal Bunt

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The durum wheat genotype DDW 12 has the higher Iron, Zinc, Manganese contents in comparison to the best available variety PDW 233. This stock was developed from the progeny of cross RASCON 3 / RAJ 1555 following pedigree selection method at Directorate of Wheat Research, Karnal. The first parent (Rascon3) is a high yielding genotype, while the other parent Raj 1555 is known for wider adaptation and quality attributes. This genotype was evaluated for three years under All India Wheat Coordinated trials during 2007/08 to 2009/10

for yield, quality and resistance. Initially it was tested in NIVT-4 for one year (2007-08) and then in Advance Varietal Trial (AVT) for irrigated, timely sown durum trial for two crop seasons (2008-09 and 2009-10). DDW 12 performed as a high yielding genotype along with resistance to rusts and Karnal bunt and also found very good for quality traits as indicated by highest Iron (45.9 ppm), Zinc (47.4 ppm), Manganese (941.6 ppm) contents.

Therefore, it can be used as the genetic stock for these unique characteristics in future breeding programs to improve the nutrition quality in wheat. In addition, this genotype pertains many other characteristics like least mottled grain percent, good hectoliter weight, and resistance to all the three rusts and also for Karnal Bunt. The quality parameters for some of the traits of the coordinated trial entries including DDW 12 were tested at IARI, New Delhi and salient data for quality attributes in comparison to the best check (PDW 233), disease reactions and other agro-morphological traits are presented below.

Quality attributes of DDW 12 under coordinated trials

Parameter	DDW 12	PDW 233 (Available best quality check)
Iron content	45.90	43.80
Zinc	47.40	43.40
Manganese	41.60	34.30
Copper	6.06	4.05
Protein Content (%)	12.51	11.70
Hectolitre weight (Kg/hl)	81.20	79.30
Yellow berry incidence (%)	0.80	3.10

Disease and other agronomic characteristics of DDW 12

Characteristics	Observation
Brown rust	Resistant to all pathotypes
Yellow rust	Resistant to predominant pathotypes
Black rust resistance	Resistant to predominant pathotypes
Karnal Bunt	Resistant
Average plant height	100 cm
Days to maturity	130 days
1000 grain weight	50.0g

4. DBW 51 (IC0589135; INGR11011), a Wheat (*Triticum aestivum*) Germplasm, with Very High Iron Content (50.4 ppm), *Chapatti* Quality Score (8.06), Protein Content (12.84%) and High Biscuit Spread Factor (7.87cm); High Yield and Resistance to Diseases Particularly Rusts and Leaf Blight

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Bread wheat (*Triticum aestivum* L.) genotype DBW 51 was developed out of cross SITE/MILAN following the modified pedigree-bulk method of breeding. Under All India Coordinated Trials, it showed yield potential up to 52.1q/ha during 2008-09, thereby indicating that under better management conditions it can give very high yields even under late sown conditions. Besides, this genotype has wider adaptability and stable yields under late as well as very late sown conditions at various locations of north-eastern India in the coordinated trials as compared to the checks.

For quality parameters, DBW 51 has highest protein content (13.51%), good grain appearance (5.1), high Glu-1 score (10), and has a rare combination of suitability for three major end products (*chapati*, bread and biscuit) of wheat. DBW 51 has the best *chapati* score (8.06) at par with best available variety (C 306), bread quality score (7.49), highest bread loaf volume (583) and highest biscuit quality spread factor (7.87) thus making it suitable for *chapati*, bread and also biscuit quality. Regarding nutritional qualities, DBW 51 has shown highest iron (50.4 ppm), high yellow pigment (4.07), zinc (35.6 ppm), copper (5.50 ppm) and also high content of manganese (45.0 ppm) as compared to the best check variety. This indicates that the variety DBW 51 has potential to accumulate more micro-nutrients even under the most commonly followed and exhaustive crop rotation of rice-wheat.

for yield, quality and resistance. Initially it was tested in NIVT-4 for one year (2007-08) and then in Advance Varietal Trial (AVT) for irrigated, timely sown durum trial for two crop seasons (2008-09 and 2009-10). DDW 12 performed as a high yielding genotype along with resistance to rusts and Karnal bunt and also found very good for quality traits as indicated by highest Iron (45.9 ppm), Zinc (47.4 ppm), Manganese (941.6 ppm) contents.

Therefore, it can be used as the genetic stock for these unique characteristics in future breeding programs to improve the nutrition quality in wheat. In addition, this genotype pertains many other characteristics like least mottled grain percent, good hectoliter weight, and resistance to all the three rusts and also for Karnal Bunt. The quality parameters for some of the traits of the coordinated trial entries including DDW 12 were tested at IARI, New Delhi and salient data for quality attributes in comparison to the best check (PDW 233), disease reactions and other agro-morphological traits are presented below.

Quality attributes of DDW 12 under coordinated trials

Parameter	DDW 12	PDW 233 (Available best quality check)
Iron content	45.90	43.80
Zinc	47.40	43.40
Manganese	41.60	34.30
Copper	6.06	4.05
Protein Content (%)	12.51	11.70
Hectolitre weight (Kg/hl)	81.20	79.30
Yellow berry incidence (%)	0.80	3.10

Disease and other agronomic characteristics of DDW 12

Characteristics	Observation
Brown rust	Resistant to all pathotypes
Yellow rust	Resistant to predominant pathotypes
Black rust resistance	Resistant to predominant pathotypes
Karnal Bunt	Resistant
Average plant height	100 cm
Days to maturity	130 days
1000 grain weight	50.0g

4. DBW 51 (IC0589135; INGR11011), a Wheat (*Triticum aestivum*) Germplasm, with Very High Iron Content (50.4 ppm), *Chapatti* Quality Score (8.06), Protein Content (12.84%) and High Biscuit Spread Factor (7.87cm); High Yield and Resistance to Diseases Particularly Rusts and Leaf Blight

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For quality parameters, DBW 51 has highest protein content (13.51%), good grain appearance (5.1), high Glu-1 score (10), and has a rare combination of suitability for three major end products (*chapati*, bread and biscuit) of wheat. DBW 51 has the best *chapati* score (8.06) at par with best available variety (C 306), bread quality score (7.49), highest bread loaf volume (583) and highest biscuit quality spread factor (7.87) thus making it suitable for *chapati*, bread and also biscuit quality. Regarding nutritional qualities, DBW 51 has shown highest iron (50.4 ppm), high yellow pigment (4.07), zinc (35.6 ppm), copper (5.50 ppm) and also high content of manganese (45.0 ppm) as compared to the best check variety. This indicates that the variety DBW 51 has potential to accumulate more micro-nutrients even under the most commonly followed and exhaustive crop rotation of rice-wheat.

Salient quality attributes of DBW 51 as compared to best checks

Quality trait	DBW 51	Promising check varieties		
		NW 2036	HD 2985	DBW 14
Iron content	50.4	44.4	39.1	44.2
Chapati quality score	8.06	7.63	7.83	7.67
Biscuit spread factor	7.87	7.87	7.82	7.84
Protein Content (%)	14.4	12.2	12.1	13.4

The *per se* performance of DBW 51 could be attributed to its wider adaptability desirable plant height, heading and maturity duration and overall superiority for quality, resistance along with high yield potential.

Salient grain, quality and other morphological features of DBW 51

Parameter	Value
Days to heading	72 days
Days to maturity	107 days
Plant height	89 cm
1000- grain weight	39 g
Yield potential	52.1 q/ha

This genotype has shown resistance to both brown and yellow rusts under natural as well as artificial conditions. DBW 51 was found resistant against all the presently virulent pathotypes of yellow (46S 119 & 78S 84) and brown (77-5 & 104-2) rusts as supported by its adult plant response (APR) at Ludhiana and Delhi, locations, thereby indicating the presence of wide spectrum of genes to protect this genotypes for a longer time. The genotype has the highest tolerance level against leaf blight (23 score). In addition, DBW 51 has shown lowest incidence of loose smut (2.8) and acceptable level of Karnal Bunt (KB) and foliar head blight.

The registration of DBW 51 as a genetic stock especially for quality attributes will help as potential donor for improving nutritional qualities in future wheat genotypes and might reduce the problem of malnutrition.

5. DBW 46 (IC0589134; INGR11010), a Wheat (*Triticum aestivum*) Germplasm, with a High Level of Resistance to Most Prevalent Races of Yellow Rust (46S119, 78S84), Brown Rust (77-5, 104-2) and Leaf Blight (*Bipolaris sorokiniana*)

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Directorate of Wheat Research, Karnal-132001, Haryana (E-mail: gysingh@gmail.com)

Bread wheat (*Triticum aestivum* L.) Genotype DBW 46 was developed out of cross PBW 343/INQ 21 following modified pedigree-bulk method of breeding. Under all india coordinated trials, it showed yield superiority during 2008-09 & 2009-10 over ruling check varieties. The yield potential of DBW 46 under multilocational test was recorded up to 64.5 q/ha thereby meaning that under better management conditions it can give even very high yields. In coordinated trials, DBW 46 has shown highest 1000-grain weight under timely sown condition and minimum reduction in the grain weight under late sown situation thereby indicating that it has some degree of heat tolerance. This genotype has shown resistance to brown and yellow rusts under natural as well as artificial conditions in general and specific resistance against the presently virulent pathotypes of yellow (46s 119 & 78s 84) and brown (77-5 & 104-2) rusts. It also showed highest tolerance level against Karnal bunt as compared to checks. Besides, DBW 46 showed high degree of resistance to leaf blight (24 score) and foliar head blight.

Magnitude of disease resistance in DBW 46 against yellow and brown rusts and leaf blight disease

Location	Characters	Pathotypes	2009	2010
Ludhiana & Delhi	Yellow rust	46S119	0	0
		78S84	0	0
Controlled artificial conditions at Shimla	Brown rust	77-5	TS	0
		104-2	TS	0
Coordinated locations	Leaf Blight (Average score)	-	24	24

In addition, DBW 46 has good combination of quality attributes for *chapati,* bread and biscuit making. DBW 46 showed highest bread loaf volume (573), bread quality score (7.22), and very high biscuit spread factor (7.85). It has desirable protein content, good grain appearance, desirable hectoliter weight and sedimentation value. For nutritional attributes, DBW 46 showed very high gluten index (71) and moderate nutritional quality attributes *viz;* zinc (35.6 ppm), iron (44.2 ppm), copper (5.14 ppm) and manganese (40.1 ppm).

Salient quality attributes of DBW 51 as compared to best checks

Quality trait	DBW 51	Promising check varieties		
		NW 2036	HD 2985	DBW 14
Iron content	50.4	44.4	39.1	44.2
Chapati quality score	8.06	7.63	7.83	7.67
Biscuit spread factor	7.87	7.87	7.82	7.84
Protein Content (%)	14.4	12.2	12.1	13.4

The *per se* performance of DBW 51 could be attributed to its wider adaptability desirable plant height, heading and maturity duration and overall superiority for quality, resistance along with high yield potential.

Salient grain, quality and other morphological features of DBW 51

Parameter	Value
Days to heading	72 days
Days to maturity	107 days
Plant height	89 cm
1000- grain weight	39 g
Yield potential	52.1 q/ha

This genotype has shown resistance to both brown and yellow rusts under natural as well as artificial conditions. DBW 51 was found resistant against all the presently virulent pathotypes of yellow (46S 119 & 78S 84) and brown (77-5 & 104-2) rusts as supported by its adult plant response (APR) at Ludhiana and Delhi, locations, thereby indicating the presence of wide spectrum of genes to protect this genotypes for a longer time. The genotype has the highest tolerance level against leaf blight (23 score). In addition, DBW 51 has shown lowest incidence of loose smut (2.8) and acceptable level of Karnal Bunt (KB) and foliar head blight.

The registration of DBW 51 as a genetic stock especially for quality attributes will help as potential donor for improving nutritional qualities in future wheat genotypes and might reduce the problem of malnutrition.

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Magnitude of disease resistance in DBW 46 against yellow and brown rusts and leaf blight disease

Location	Characters	Pathotypes	2009	2010
Ludhiana & Delhi	Yellow rust	46S119	0	0
		78S84	0	0
Controlled artificial conditions at Shimla	Brown rust	77-5	TS	0
		104-2	TS	0
Coordinated locations	Leaf Blight (Average score)	-	24	24

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Salient grain, quality and other morphological features of DBW 46

Parameters	Value
Grain protein	11.80
Chapati quality (max score 10)	7.71
Bread loaf volume (ml)	573.00
Bread quality (max score 10)	7.22
Biscuit quality spread factor	7.85
Sedimentation value (ml)	50.00
Gluten index	71.00
Grain hardness index	74.00
Average plant height (cm)	98.00
Days to maturity (days)	122.00
1000 grain weight (g)	40.00

In view of the above merits, DBW 46 was found a suitable genotype for utilizing as a donor parent for improving yield, disease resistance, quality and variety of products.

6. HTW 6 (IC029007A; INGR11012), a Wheat (*Triticum aestivum* L) Germplasm, with Terminal Heat Tolerance; Suffers Only 7% Reduction in Thousand Grain Weight Under Heat Stress; 1000-Grain Weight (39 g) and HTW 11 (IC035117; INGR11013), a Wheat (*Triticum aestivum* L) Germplasm, with Terminal Heat Tolerance with Only 9% Reduction in 1000-Grain Weight Under Late Planting (heat stress); 1000-Grain Weight is 38 g (37-40 g) Under Heat Stress; The Heat Susceptibility Index is 0.83 and Heat Tolerance Index is 0.94

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HTW6: Terminal heat is one of the stress factors for wheat production. A significant wheat growing area in South Asia is affected by heat stress and majority of this area lies in Eastern Gangetic Plains, central and peninsular parts of India (Joshi *et al*., 2007a, b). Both the proximity to the equator and the popular rice-wheat cropping systems, which involve late sowing of wheat, are the major causes of exposure of wheat in India and other neighboring countries to high temperatures during grain filling (Rane *et al*., 2000). The threat of terminal heat stress is increasing due to global warming also. In order to meet the challenging temperature ahead of global warming, there is need to incorporate heat tolerance into wheat germplasm and develop genotypes which are suitable to such stressed environments. The indigenous wheat germplasm accessions which bear heat tolerance as well as reasonable thousand grain weight can be used directly in breeding programme targeting for stressed environments.

Seventy-seven germplasm accessions were evaluated for terminal heat tolerance under late planting during 2008-09. Fifteen heat tolerant and eight susceptible accessions were identified on the basis of heat sensitivity index and reduction in thousand grain weight under late planting. These accessions along with two checks WH 730 (Heat tolerant) and HUW 510 (Heat susceptible) were evaluated again during 2009-10 under late planting in field as well as temperature controlled polyhouse. The morpho-agronomic trats of the genotype are given in Table 1. It suffered less than 20% reduction in grain yield, 2.1% in thousand grain weight. The heat sensitivity and tolerance index of the accession was 0.13 and 1.03 respectively (Table 2).

The genotype was evaluated at four locations during 2010-11 under late planting. The data pooled over locations revealed that the genotype suffers 7% reduction in thousand grain weight (Table 3). Thousand grain weight under late sown conditions is 39g. The heat sensitivity and tolerance index under multilocation testing is 0.64 and 0.95 respectively (Table 4).

Salient grain, quality and other morphological features of DBW 46

Parameters	Value
Grain protein	11.80
Chapati quality (max score 10)	7.71
Bread loaf volume (ml)	573.00
Bread quality (max score 10)	7.22
Biscuit quality spread factor	7.85
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Gluten index	71.00
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Table 1. Morpho-agronomic characteristics of IC029007A and IC035117

Trait	IC 29007 A	IC035117
Coleoptile colour	Green	Green
Growth habit	Semi Erect	Semi Erect
Auricle colour	Absent	Absent
Auricle pubescence	Medium	Absent
Waxiness Leaf sheath	Weak	Strong
Waxiness Leaf blade	Absent	Weak
Waxiness Ear	Absent	Absent
Waxiness Peduncle	Weak	Strong
Foliage Colour	Pale green	Green
Days to heading	95	97
Days to maturity	132	137
Plant height	105	121
Flag leaf attitude	Erect	Drooping
Thousand grain weight	45	43
Ear colour	White	White
Ear shape	Tapering	Parallel
Ear density	Dense	Dense

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Table 2. Average Increase/ decrease (%) in grain traits, grain growth duration over control under high temperature conditions and heat sensitivity index and heat tolerance index

GENOTYPE	Grain yield	Grain no./spike	Grain weight/spike	1000- grain weight	Grain growth duration	HSI	HTI
IC 28585	21.3	15.1	22.3	5.3	6.8	2.88	1.19
IC 28620 B	32.9	10.4	16.4	7.1	16.0	2.58	0.82
IC 28913	37.7	2.3	3.1	1.1	12.6	0.88	0.80
IC 28940 A	23.2	4.4	12.2	7.7	10.9	1.79	0.95
IC 28951 A	34.5	18.2	21.7	3.2	13.1	2.80	0.85
IC 29007 A	**19.1**	**-0.5**	**4.8**	**2.1**	**9.3**	**0.13**	**1.03**
IC 29017 A	24.2	4.6	11.3	-5.6	23.3	2.11	0.87
IC 29040	19.9	2.2	10.3	10.5	6.2	1.23	1.25
IC 32508 A	42.4	15.7	17.8	1.7	7.4	2.59	1.33
IC 35037	32.5	1.9	-13.9	-17.4	19.0	-2.18	0.57
IC 35117	**31.6**	**0.6**	**-1.4**	**-0.6**	**9.5**	**0.53**	**0.96**
IC 36725	47.6	5.7	6.5	10.1	11.3	0.36	0.70
IC 45437	5.0	3.1	1.2	-0.5	13.7	0.37	1.01
IC 47073 B	39.8	5.5	12.9	6.2	10.5	2.32	0.99
IC 47585 A	14.0	3.4	-1.8	-3.5	10.3	-0.72	0.90
IC 47793 A	17.8	4.9	8.8	6.3	9.9	1.26	0.99
IC 55665	22.4	-7.1	-1.8	6.1	4.0	-1.23	0.71
IC 55707 A	23.2	4.1	3.1	2.2	9.2	-0.57	0.84
IC55707 B	22.7	-16.7	-11.9	-0.9	9.4	-1.86	0.64
IC 57985	25.9	2.6	10.4	9.3	17.2	1.25	0.89
IC 59534	29.5	-11.0	4.7	11.5	16.0	0.25	0.79
IC 73598	40.8	-10.2	-5.6	5.4	11.0	-0.81	0.71
IC 78094 B	43.0	0.6	2.6	3.9	11.0	-0.08	1.10
HUW 510	37.5	17.6	23.9	11.4	4.4	3.15	0.89
WH 730	38.6	0.6	6.4	1.5	-5.4	0.96	0.99
Mean	29.1	4.3	6.6	3.4	11.0	1.07	0.90

Table 3. Data on average reduction in various traits under heat stress during 2010-11(Pooled over 4 locations)

Genotype	% Reduction in Germination							
	Germination	Grain filling duration	Plant height	Productive tillers	Grain yield	1000- grain weight	Grain number/ spike	Grain weight/ spike
IC 28913	20.7	19.2	13.3	17.4	42.2	19.8	20.4	34.6
IC 29007 A	6.1	15.0	6.3	36.6	28.4	**7.1**	**-2.9**	**7.5**
IC 29017 A	19.3	16.5	6.6	21.5	18.4	18.8	3.0	26.0
IC 35117	**5.6**	20.3	22.7	27.9	40.5	**9.3**	**10.3**	24.2
IC 45437	14.0	9.3	-10.6	20.5	19.6	3.7	11.9	26.6
IC 47585 A	5.7	13.4	14.1	29.6	37.4	21.4	29.7	45.5
IC 47793 A	31.1	23.4	18.3	33.7	25.3	8.1	23.5	38.3
IC 55665	7.4	19.2	7.6	34.7	30.4	12.2	8.0	25.5
IC 55707 A	10.6	9.0	16.4	22.3	22.5	11.8	12.4	28.8
IC55707 B	7.3	7.7	8.8	26.4	33.6	13.4	13.0	30.0
IC 59534	10.5	12.9	7.8	24.9	13.4	-3.8	19.8	15.8
IC 73598	6.2	24.0	13.5	29.2	21.4	7.6	23.5	23.4
WH 730	20.9	27.7	32.0	42.2	10.8	13.6	**8.8**	12.2
HUW 510	13.7	18.9	45.7	45.0	40.1	33.6	51.9	31.6

Table 4. Data on grain yield & 1000 grain weight under timely and late sown conditions and their heat susceptibility and heat tolerance index during 2010-11 (Pooled over locations)

Genotype	Timely sown		Late sown		Heat susceptibility index		Heat tolerance index	
	Grain yield	1000-grain wt.	Grain yield	1000- grain wt.	Grain yield	1000- grain wt.	Grain yield	1000- grain wt.
IC 28913	46.6	42.7	26.9	34.2	1.49	1.77	0.88	0.86
IC 29007 A	36.5	41.5	26.1	38.6	1.00	**0.64**	0.67	**0.95**
IC 29017 A	34.9	44.0	28.5	35.7	0.65	1.68	0.69	0.93
IC 35117	38.5	41.9	22.9	38.0	1.43	**0.83**	0.62	**0.94**
IC 45437	33.5	38.4	27.0	37.0	0.69	0.33	0.63	0.84
IC 47585 A	42.7	46.6	26.7	36.7	1.32	1.91	0.80	1.01
IC 47793 A	35.2	39.1	26.3	35.9	0.89	0.73	0.65	0.83
IC 55665	35.6	43.6	24.8	38.3	1.07	1.09	0.62	0.99
IC 55707 A	35.3	41.5	27.4	36.6	0.79	1.05	0.68	0.90
IC55707 B	37.7	41.0	25.0	35.5	1.19	1.20	0.66	0.86
IC 59534	36.0	32.7	31.2	33.9	0.47	-0.34	0.78	0.66
IC 73598	40.6	40.4	31.9	37.4	0.76	0.68	0.91	0.89
WH 730	32.0	42.2	28.5	36.5	**0.30**	**0.89**	0.65	0.87
HUW 510	45.7	45.0	27.0	30.0	1.75	2.30	0.70	0.78
SE	1.6	0.9	1.8	1.5				
5%LSD	4.7	2.5	5.0	4.2				

The genotype was evaluated at four locations during 2010-11 under late planting. The data pooled over locations revealed that the genotype suffers 9.3% reduction in thousand grain weight (Table 3). Thousand grain weight under late sown conditions is 38g (37–40g). The heat sensitivity and tolerance index under multilocation testing is 0.83 and 0.94 respectively (Table 4).

References

Joshi AK, R Chand, B Arun, RP Singh and G Ortiz Ferrara (2007a) Breeding crops for reduced-tillage management in the intensive, rice–wheat systems of South Asia. *Euphytica* **153:** 135-151.

Joshi AK, B Mishra, R Chatrath, G Ortiz Ferrara and RP Singh (2007b) Wheat improvement in India: Present status, emerging challenges and future prospects. *Euphytica* **157:** 431-446.

Rane J, J Shoran and S Nagarajan (2000) Heat stress environments and impact on wheat productivity in India: Guestimate of losses. *Indian Wheat Newslet.* **6:** 5-6.

Salient grain, quality and other morphological features of DBW 46

Parameters	Value
Grain protein	11.80
Chapati quality (max score 10)	7.71
Bread loaf volume (ml)	573.00
Bread quality (max score 10)	7.22
Biscuit quality spread factor	7.85
Sedimentation value (ml)	50.00
Gluten index	71.00
Grain hardness index	74.00
Average plant height (cm)	98.00
Days to maturity (days)	122.00
1000 grain weight (g)	40.00

In view of the above merits, DBW 46 was found a suitable genotype for utilizing as a donor parent for improving yield, disease resistance, quality and variety of products.

6. HTW 6 (IC029007A; INGR11012), a Wheat (*Triticum aestivum* L) Germplasm, with Terminal Heat Tolerance; Suffers Only 7% Reduction in Thousand Grain Weight Under Heat Stress; 1000-Grain Weight (39 g) and HTW 11 (IC035117; INGR11013), a Wheat (*Triticum aestivum* L) Germplasm, with Terminal Heat Tolerance with Only 9% Reduction in 1000-Grain Weight Under Late Planting (heat stress); 1000-Grain Weight is 38 g (37-40 g) Under Heat Stress; The Heat Susceptibility Index is 0.83 and Heat Tolerance Index is 0.94

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HTW6: Terminal heat is one of the stress factors for wheat production. A significant wheat growing area in South Asia is affected by heat stress and majority of this area lies in Eastern Gangetic Plains, central and peninsular parts of India (Joshi *et al*., 2007a, b). Both the proximity to the equator and the popular rice-wheat cropping systems, which involve late sowing of wheat, are the major causes of exposure of wheat in India and other neighboring countries to high temperatures during grain filling (Rane *et al*., 2000). The threat of terminal heat stress is increasing due to global warming also. In order to meet the challenging temperature ahead of global warming, there is need to incorporate heat tolerance into wheat germplasm and develop genotypes which are suitable to such stressed environments. The indigenous wheat germplasm accessions which bear heat tolerance as well as reasonable thousand grain weight can be used directly in breeding programme targeting for stressed environments.

Seventy-seven germplasm accessions were evaluated for terminal heat tolerance under late planting during 2008-09. Fifteen heat tolerant and eight susceptible accessions were identified on the basis of heat sensitivity index and reduction in thousand grain weight under late planting. These accessions along with two checks WH 730 (Heat tolerant) and HUW 510 (Heat susceptible) were evaluated again during 2009-10 under late planting in field as well as temperature controlled polyhouse. The morpho-agronomic trats of the genotype are given in Table 1. It suffered less than 20% reduction in grain yield, 2.1% in thousand grain weight. The heat sensitivity and tolerance index of the accession was 0.13 and 1.03 respectively (Table 2).

The genotype was evaluated at four locations during 2010-11 under late planting. The data pooled over locations revealed that the genotype suffers 7% reduction in thousand grain weight (Table 3). Thousand grain weight under late sown conditions is 39g. The heat sensitivity and tolerance index under multilocation testing is 0.64 and 0.95 respectively (Table 4).

Table 1. Morpho-agronomic characteristics of IC029007A and IC035117

Trait	IC 29007 A	IC035117
Coleoptile colour	Green	Green
Growth habit	Semi Erect	Semi Erect
Auricle colour	Absent	Absent
Auricle pubescence	Medium	Absent
Waxiness Leaf sheath	Weak	Strong
Waxiness Leaf blade	Absent	Weak
Waxiness Ear	Absent	Absent
Waxiness Peduncle	Weak	Strong
Foliage Colour	Pale green	Green
Days to heading	95	97
Days to maturity	132	137
Plant height	105	121
Flag leaf attitude	Erect	Drooping
Thousand grain weight	45	43
Ear colour	White	White
Ear shape	Tapering	Parallel
Ear density	Dense	Dense

HTW 11: Terminal heat is one of the stress factors for wheat production. A significant wheat growing area in South Asia is affected by heat stress and majority of this area lies in Eastern Gangetic Plains, central and peninsular parts of India (Joshi *et al*., 2007a, b). Both the proximity to the equator and the popular rice-wheat cropping systems, which involve late sowing of wheat, are the major causes of exposure of wheat in India and other neighboring countries to high temperatures during grain filling (Rane *et al*., 2000). The threat of terminal heat stress is increasing due to global warming also. In order to meet the challenging temperature ahead of global warming, there is need to incorporate heat tolerance into wheat germplasm and develop genotypes which are suitable to such stressed environments. The indigenous wheat germplasm accessions which bear heat tolerance as well as reasonable thousand grain weight can be used directly in breeding programme targeting for stressed environments.

Seventy-seven germplasm accessions were evaluated for terminal heat tolerance under late planting during 2008-09. Fifteen heat tolerant and eight susceptible accessions were identified on the basis of heat sensitivity index and reduction in thousand grain weight under late planting. These accessions along with two checks WH 730 (Heat tolerant) and HUW 510 (Heat susceptible) were evaluated again during 2009-10 under late planting in field as well as temperature controlled polyhouse. The morpho-agronomic trats of the genotype are given in Table 1. It suffered less than 31.6% reduction in grain yield, -0.6% in thousand grain weight. The heat sensitivity and tolerance index of the accession was 0.53 and 0.96 respectively (Table 2).

Table 2. Average Increase/ decrease (%) in grain traits, grain growth duration over control under high temperature conditions and heat sensitivity index and heat tolerance index

GENOTYPE	Grain yield	Grain no./spike	Grain weight/spike	1000- grain weight	Grain growth duration	HSI	HTI
IC 28585	21.3	15.1	22.3	5.3	6.8	2.88	1.19
IC 28620 B	32.9	10.4	16.4	7.1	16.0	2.58	0.82
IC 28913	37.7	2.3	3.1	1.1	12.6	0.88	0.80
IC 28940 A	23.2	4.4	12.2	7.7	10.9	1.79	0.95
IC 28951 A	34.5	18.2	21.7	3.2	13.1	2.80	0.85
IC 29007 A	**19.1**	**-0.5**	**4.8**	**2.1**	**9.3**	**0.13**	**1.03**
IC 29017 A	24.2	4.6	11.3	-5.6	23.3	2.11	0.87
IC 29040	19.9	2.2	10.3	10.5	6.2	1.23	1.25
IC 32508 A	42.4	15.7	17.8	1.7	7.4	2.59	1.33
IC 35037	32.5	1.9	-13.9	-17.4	19.0	-2.18	0.57
IC 35117	**31.6**	**0.6**	**-1.4**	**-0.6**	**9.5**	**0.53**	**0.96**
IC 36725	47.6	5.7	6.5	10.1	11.3	0.36	0.70
IC 45437	5.0	3.1	1.2	-0.5	13.7	0.37	1.01
IC 47073 B	39.8	5.5	12.9	6.2	10.5	2.32	0.99
IC 47585 A	14.0	3.4	-1.8	-3.5	10.3	-0.72	0.90
IC 47793 A	17.8	4.9	8.8	6.3	9.9	1.26	0.99
IC 55665	22.4	-7.1	-1.8	6.1	4.0	-1.23	0.71
IC 55707 A	23.2	4.1	3.1	2.2	9.2	-0.57	0.84
IC55707 B	22.7	-16.7	-11.9	-0.9	9.4	-1.86	0.64
IC 57985	25.9	2.6	10.4	9.3	17.2	1.25	0.89
IC 59534	29.5	-11.0	4.7	11.5	16.0	0.25	0.79
IC 73598	40.8	-10.2	-5.6	5.4	11.0	-0.81	0.71
IC 78094 B	43.0	0.6	2.6	3.9	11.0	-0.08	1.10
HUW 510	37.5	17.6	23.9	11.4	4.4	3.15	0.89
WH 730	38.6	0.6	6.4	1.5	-5.4	0.96	0.99
Mean	29.1	4.3	6.6	3.4	11.0	1.07	0.90

Table 3. Data on average reduction in various traits under heat stress during 2010-11(Pooled over 4 locations)

Genotype	% Reduction in Germination							
	Germination	Grain filling duration	Plant height	Productive tillers	Grain yield	1000- grain weight	Grain number/ spike	Grain weight/ spike
IC 28913	20.7	19.2	13.3	17.4	42.2	19.8	20.4	34.6
IC 29007 A	6.1	15.0	6.3	36.6	28.4	**7.1**	**-2.9**	**7.5**
IC 29017 A	19.3	16.5	6.6	21.5	18.4	18.8	3.0	26.0
IC 35117	**5.6**	20.3	22.7	27.9	40.5	**9.3**	**10.3**	24.2
IC 45437	14.0	9.3	-10.6	20.5	19.6	3.7	11.9	26.6
IC 47585 A	5.7	13.4	14.1	29.6	37.4	21.4	29.7	45.5
IC 47793 A	31.1	23.4	18.3	33.7	25.3	8.1	23.5	38.3
IC 55665	7.4	19.2	7.6	34.7	30.4	12.2	8.0	25.5
IC 55707 A	10.6	9.0	16.4	22.3	22.5	11.8	12.4	28.8
IC55707 B	7.3	7.7	8.8	26.4	33.6	13.4	13.0	30.0
IC 59534	10.5	12.9	7.8	24.9	13.4	-3.8	19.8	15.8
IC 73598	6.2	24.0	13.5	29.2	21.4	7.6	23.5	23.4
WH 730	20.9	27.7	32.0	42.2	10.8	13.6	**8.8**	12.2
HUW 510	13.7	18.9	45.7	45.0	40.1	33.6	51.9	31.6

Table 4. Data on grain yield & 1000 grain weight under timely and late sown conditions and their heat susceptibility and heat tolerance index during 2010-11 (Pooled over locations)

Genotype	Timely sown		Late sown		Heat susceptibility index		Heat tolerance index	
	Grain yield	1000-grain wt.	Grain yield	1000- grain wt.	Grain yield	1000- grain wt.	Grain yield	1000- grain wt.
IC 28913	46.6	42.7	26.9	34.2	1.49	1.77	0.88	0.86
IC 29007 A	36.5	41.5	26.1	38.6	1.00	**0.64**	0.67	**0.95**
IC 29017 A	34.9	44.0	28.5	35.7	0.65	1.68	0.69	0.93
IC 35117	38.5	41.9	22.9	38.0	1.43	**0.83**	0.62	**0.94**
IC 45437	33.5	38.4	27.0	37.0	0.69	0.33	0.63	0.84
IC 47585 A	42.7	46.6	26.7	36.7	1.32	1.91	0.80	1.01
IC 47793 A	35.2	39.1	26.3	35.9	0.89	0.73	0.65	0.83
IC 55665	35.6	43.6	24.8	38.3	1.07	1.09	0.62	0.99
IC 55707 A	35.3	41.5	27.4	36.6	0.79	1.05	0.68	0.90
IC55707 B	37.7	41.0	25.0	35.5	1.19	1.20	0.66	0.86
IC 59534	36.0	32.7	31.2	33.9	0.47	-0.34	0.78	0.66
IC 73598	40.6	40.4	31.9	37.4	0.76	0.68	0.91	0.89
WH 730	32.0	42.2	28.5	36.5	**0.30**	**0.89**	0.65	0.87
HUW 510	45.7	45.0	27.0	30.0	1.75	2.30	0.70	0.78
SE	1.6	0.9	1.8	1.5				
5%LSD	4.7	2.5	5.0	4.2				

The genotype was evaluated at four locations during 2010-11 under late planting. The data pooled over locations revealed that the genotype suffers 9.3% reduction in thousand grain weight (Table 3). Thousand grain weight under late sown conditions is 38g (37–40g). The heat sensitivity and tolerance index under multilocation testing is 0.83 and 0.94 respectively (Table 4).

References

Joshi AK, R Chand, B Arun, RP Singh and G Ortiz Ferrara (2007a) Breeding crops for reduced-tillage management in the intensive, rice–wheat systems of South Asia. *Euphytica* **153:** 135-151.

Joshi AK, B Mishra, R Chatrath, G Ortiz Ferrara and RP Singh (2007b) Wheat improvement in India: Present status, emerging challenges and future prospects. *Euphytica* **157:** 431-446.

Rane J, J Shoran and S Nagarajan (2000) Heat stress environments and impact on wheat productivity in India: Guestimate of losses. *Indian Wheat Newslet.* **6:** 5-6.

7. KBRL76-3 (IC0589136; INGR11014), a Wheat (*Triticum aestivum* L.) Germplasm, with a Karnal Bunt Resistant Near Isogenic Line of Bread Wheat Variety PBW343

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The wheat line KBRL 76-3 is a Near Isogenic Line (NIL) of wheat variety PBW 343, which is resistant to Karnal Bunt disease of wheat. This disease is of great importance due to its implications on international wheat grain market. The wheat genotypes infested with this disease cannot be exported outside the country. Wheat variety PBW 343, a major variety in Indian context has shown susceptibility to Karnal Bunt. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. A KB resistant stock KBRL 22 has already been identified and is best suited source for incorporation in to PBW 343. Thus a backcross approach and simultaneous screening for the disease resistant lines was adopted, with PBW 343 as recurrent parent. Using this method a large number of Near Isogenic Lines were developed in the background of PBW 343. KBRL 76-3 is one such line which is as high yielding as PBW 343 and also resistant to KB.

The parental variety PBW 343 was tested under All India Coordinated Wheat and Barley Improvement Programme (AICW&BIP) from 2005 to 2007 for Karnal Bunt resistance which showed that this genotype is affected by this disease. Also the NIL KBRL 76-3 when tested for resistance to this disease was found to be highly resistant. Also this line carries good agronomic characteristics and yield of PBW 343.

Therefore the line KBRL 76-3 can be used as the genetic stock for Karnal Bunt resistance along with its good agronomic characteristics, in future breeding programs. The multilocation evaluation of Near Isogenic Lines of PBW 343 during 2010-11 is given below:

Multilocation evaluation of Near Isogenic Lines of PBW 343

Entry	% KB incidence				
	Hisar	Ludhiana	Karnal	Dhaulakuan	Average
Near Isogenic Line 76	0	0	0	7.20	1.80
Near Isogenic Line 76-1	2.41	0	0	1.50	0.97
Near Isogenic Line 76-2	2.21	0	0	1.20	0.85
Near Isogenic Line 76-3	1.67	0	0	1.00	0.67
Near Isogenic Line 76-4	1.78	0	0	7.80	2.39

8. PT-0012 (IC0587711; INGR11015), a Pigeonpea (*Cajanus cajan*) Germplasm, with Early Maturity (133 days)

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(E-mail: mbedis68@yahoo.co.in)

Early maturing (133 days) genotype derived by crossing ICP-332 x BSMR-736.

Morpho-agronomic characteristics

Entries	Zone/ Maturity group	AVT-2 (2010-2011)			AVT-1 (2009-10)			IVT (2008-09)			Weighted mean			Yield % increase over the check		
		Yield (kg/ha)	Maturity days	100 seed (wt.)	Yield (kg/ ha)	Maturity days	100 seed (wt.)	Yield (kg/ha)	Maturity days	100 seed (wt.)	Yield (kg/ ha)	Matu- rity days	100 seed (wt.)	UPAS 120	CORG 9701	GC 11-39
PT0012*	CZ/ (E)	1321	162	11.4	1727	153	10.9	1612	155	9.9	1547	157	10.7	21.7	48.5	31.7
UPAS 120		1065	149	8.9	1444	136	8.2	1332	144	8.5	1274	143	8.6	–	–	–
ICPL 87		1019	150	10.5	1072	136	9.8	1041	143	9.8	1042	143	10.0	–	–	–
GGT 101		907	155	12.0	1416	144	11.3	1232	152	10.9	1175	151	11.6	–	–	–

*Percent increase of grain yield over best check (UPAS 120) across CZ and SZ = 22.6

Entries	Zone/ Maturity group	AVT-2 (2010-2011)			AVT-1(2009-10)			IVT(2008-09)			Weighted mean			Yield % increase over the check		
		Yield (kg/ha)	Matu- rity days	100 seed (wt.)	Yield (kg/ha)	Matu- rity days	100 seed (wt.)	Yield (kg/ha)	Matu- rity days	100 seed (wt.)	Yield (kg/ha)	Matu rity days	100 seed (wt.)	UPAS 120	CORG 9701	GC 11-39
PT0012*	SZ/ (E)	1126	140	10.3	1268	133	11.3	1355	148	9.7	1258	141	10.4	24.6	40.6	55.3
PT 04-31		1099	147	9.7	1254	130	11.4	1239	151	10.00	1200	143	10.3	18.8	34.1	48.1
UPAS 120		932	129	8.7	950	129	9.9	1121	136	8.3	1010	132	8.9	–	–	–
CORG 9701		859	124	9.3	857	129	10.3	953	129	8.8	895	127	9.4	–	–	–
GC 11-39		859	133	9.5	732	134	12.4	832	130	10.0	810	132	10.6	–	–	–

*Percent increase of grain yield over best check (UPAS 120) across CZ and SZ = 22.6

Source: Annual. Prog. Rep. (2010-2011). All India Research Project on pigeonpea (ICAR). Annual group meet: 31st May to 2nd June, 2011 held at ANGRAU, Hyderabad (A.P.). 67p

Morphological characterization of pigeonpea variety Phule T 0012 on the basis of DUS test

Character	Salient features	Character	Salient features
Early plant vigour	Good	No. of pods per plant	230 to 415
Growth habit	Semi- spreading	Pod colour	Mixed, green & purple
Plant height(cm) at maturity	230-240cm	Pod form	Flat
Number of branches a) Primary :	5-7	Pod bearing length of branch	80-90cm
b) Secondary :	15-25	Pod hairiness	Pubescent
Stem colour	Green	Pod waxyness	Present
Stem thickness	Intermediate	No. of seeds/pod	3 to 4
Leaflet shape	Broad-elliptic	Seed colour	Reddish brown
Leaf hairiness	Pubescent	Seed shape	Globular
Days to 50 % flowering	90 to 105	100 seed weight(g)	10.6g to 11.4 g
Days to maturity	142 to 156 days	Biotic stress	Moderately resistant to wilt and sterility mosaic disease
Base flower colour	Yellow		
No. of flowers & pods per peduncle	1	Nematode resistance	Moderately resistant to root knot nematode (*M. incognita* and *M. javanica*) and cyst nematode (*H. cajani*).
Pattern of streaks on dorsal side of standard petal	Medium amount of streaks		
Flowering pattern	Indeterminate		

Associated Characters and cultivated practices

Early maturity (133 days), Average yield is 15.47q/ha. across the Central Zone and 12.58 q/ha. across the South Zone .Over all PT- 0012 recorded 22.60 % higher yield than the check UPAS-120 under Central and South Zone 43.00 q/ha. Bold seed size (11.0 g/100 seeds) with attractive red seed colour. Moderately resistant to *Fusarium* wilt, sterility mosaic and tolerant to pod borer, pod fly, root knot & cyst nematode.

References

Annual Progress Report on pigeonpea (2010-2011) All India Research Project on pigeonpea (ICAR), Annual group meet: 31st May to 2nd June, 2011 held at ANGRAU, Hyderabad (A.P.).

9. PT-04-31 (IC0587712; INGR11016), a Pigeonpea (*Cajanus cajan*) Germplasm, with Early Maturity (130 days)

MR Bedis

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Early maturing (130 days), selection from ICP No. 13171.

Morpho-agronomic haracteristics

Entries	Zone/ Maturity group	AVT-2 (2010-2011)			AVT-1(2009-10)			IVT(2008-09)			Weighted mean			Yield % increase over the check		
		Yield (kg/ha)	Maturity days	100 seed (wt.)	Yield (kg/ha)	Maturity days	100 seed (wt.)	Yield (kg/ha)	Maturity days	100 seed (wt.)	Yield (kg/ha)	Maturity days	100 seed (wt.)	UPAS 120	CORG 9701	GC 11-39
PT0012*	SZ/ (E)	1126	140	10.3	1268	133	11.3	1355	148	9.7	1258	141	10.4	24.6	40.6	55.3
PT 04-31		**1099**	**147**	**9.7**	**1254**	**130**	**11.4**	**1239**	**151**	**10.00**	**1200**	**143**	**10.3**	**18.8**	**34.1**	**48.1**
UPAS 120		932	129	8.7	950	129	9.9	1121	136	8.3	1010	132	8.9	–	–	–
CORG 9701		859	124	9.3	857	129	10.3	953	129	8.8	895	127	9.4	–	–	–
GC 11-39		859	133	9.5	732	134	12.4	832	130	10.0	810	132	10.6	–	–	–

*Percent increase of grain yield over best check (UPAS 120) across CZ and SZ = 22.6

Source: *Annual. Prog. Rep.* on pigeonpea (2010-2011). All India Research Project on pigeonpea (ICAR). Annual group meet: 31st May to 2nd June, 2011 held at ANGRAU, Hyderabad (A.P.).

Morphological characterization of pigeonpea variety Phule T 04-31 on the basis of DUS test

Character	Salient features	Character	Salient features
Early plant vigour	Good	Pod form	Flat
Growth habit	Semi- spreading	Pod bearing length of branch	75-80cm
Plant height(cm) at maturity	220-230 cm	Pod hairiness	Pubescent
Number of branches a) Primary :	6-7	Pod waxyness	Present
b) Secondary :	14-22	No. of seeds/pod	3 to 4
Stem colour	Green	Seed colour	Reddish brown
Stem thickness	Intermediate	Seed shape	Globular
Leaflet shape	Broad-elliptic	100 seed weight(g)	10.30 g
Leaf hairiness	Pubescent	Biotic stress	Moderately resistant to wilt and sterility mosaic disease
Days to 50% flowering	73 to 104		
Days to maturity	130 to151 days		
Base flower colour	Yellow	Nematode resistance	Moderately resistant to r oot knot nematode (*M. incognita, M. javanica*) and cyst nematode *(H. cajani*) and reniformis nematode (*R. reniformis*)
No. of flowers & pods per peduncle	1		
Pattern of streaks on dorsal side of standard petal	Medium amount of streaks		
Flowering pattern	Indeterminate		
No. of pods per plant	148 to 268 cm		
Pod colour	Mixed, green & purple		

Associated Characters and cultivated practices

Early maturity (133 days), Average yield is 15.47q/ha. across the Central Zone and 12.58 q/ha. across the South Zone .Over all PT- 0012 recorded 22.60 % higher yield than the check UPAS-120 under Central and South Zone 43.00 q/ha. Bold seed size (11.0 g/100 seeds) with attractive red seed colour. Moderately resistant to *Fusarium* wilt, sterility mosaic and tolerant to pod borer, pod fly, root knot & cyst nematode.

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Early maturing (130 days), selection from ICP No. 13171.

Morpho-agronomic haracteristics

Entries	Zone/ Maturity group	AVT-2 (2010-2011)			AVT-1(2009-10)			IVT(2008-09)			Weighted mean			Yield % increase over the check		
		Yield (kg/ha)	Maturity days	100 seed (wt.)	Yield (kg/ha)	Maturity days	100 seed (wt.)	Yield (kg/ha)	Maturity days	100 seed (wt.)	Yield (kg/ha)	Maturity days	100 seed (wt.)	UPAS 120	CORG 9701	GC 11-39
PT0012*	SZ/ (E)	1126	140	10.3	1268	133	11.3	1355	148	9.7	1258	141	10.4	24.6	40.6	55.3
PT 04-31		**1099**	**147**	**9.7**	**1254**	**130**	**11.4**	**1239**	**151**	**10.00**	**1200**	**143**	**10.3**	**18.8**	**34.1**	**48.1**
UPAS 120		932	129	8.7	950	129	9.9	1121	136	8.3	1010	132	8.9	–	–	–
CORG 9701		859	124	9.3	857	129	10.3	953	129	8.8	895	127	9.4	–	–	–
GC 11-39		859	133	9.5	732	134	12.4	832	130	10.0	810	132	10.6	–	–	–

*Percent increase of grain yield over best check (UPAS 120) across CZ and SZ = 22.6

Source: *Annual. Prog. Rep.* on pigeonpea (2010-2011). All India Research Project on pigeonpea (ICAR). Annual group meet: 31st May to 2nd June, 2011 held at ANGRAU, Hyderabad (A.P.).

Morphological characterization of pigeonpea variety Phule T 04-31 on the basis of DUS test

Character	Salient features	Character	Salient features
Early plant vigour	Good	Pod form	Flat
Growth habit	Semi- spreading	Pod bearing length of branch	75-80cm
Plant height(cm) at maturity	220-230 cm	Pod hairiness	Pubescent
Number of branches a) Primary :	6-7	Pod waxyness	Present
b) Secondary :	14-22	No. of seeds/pod	3 to 4
Stem colour	Green	Seed colour	Reddish brown
Stem thickness	Intermediate	Seed shape	Globular
Leaflet shape	Broad-elliptic	100 seed weight(g)	10.30 g
Leaf hairiness	Pubescent	Biotic stress	Moderately resistant to wilt and sterility mosaic disease
Days to 50% flowering	73 to 104		
Days to maturity	130 to151 days		
Base flower colour	Yellow	Nematode resistance	Moderately resistant to r oot knot nematode (*M. incognita, M. javanica*) and cyst nematode *(H. cajani*) and reniformis nematode (*R. reniformis*)
No. of flowers & pods per peduncle	1		
Pattern of streaks on dorsal side of standard petal	Medium amount of streaks		
Flowering pattern	Indeterminate		
No. of pods per plant	148 to 268 cm		
Pod colour	Mixed, green & purple		

Associated Characters and cultivated practices

Early maturity (130 days), high averages yield of 12.0 q/ha. High yield potential (43.00 q/ha), bold seed size (10.3 g/100 seeds). Attractive red seed colour and moderately resistant to *Fusarium* wilt, sterility mosaic and tolerant to pod borer, podfly, root knot and cyst nematode.

References

Annual. Progress Report on pigeonpea (2010-2011) All India Research Project on pigeonpea (ICAR), Annual group meet: 31st May to 2nd June, 2011 held at ANGRAU, Hyderabad (A.P.).

10. CRHG-6 (IC0587786; INGR11017), a Horsegram (*Macrotyloma uniflorum*) Germplasm, with Tolerant to Anthracnose

P Raghu Ram Reddy, V Maruthi, BMK Reddy, S Desai, M Maheshwari, B Venkateswarlu and SS Shishodia
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Colletotrichum lindemuthianum is a major disease of horsegram and can infect other pulse crops like cow pea, blackgram, beans etc .The fungus may attack all plant parts if not controlled, at any stage of plant growth .Spots with dark centre and bight red with orange margines may occur more often on under surface of the leaf than on the upper surface and also occur on petioles and stems and may in severe case spread to pods results in yield losses. (Purushothaman *et al,* 2006. The disease incidence in the field can be managed with carbendazim 0.1% spray (Thakur and Khare 1990).

A mutant line, CRHG-6 developed by γ-ray's irradiation of K-42 seed showed tolerance to Anthracnose as evidenced by three years of testing by the National Network Research Project on Arid legumes along with National Checks viz; 2006-07, 2007-08 and 2008-09.

During 2006-07, CRHG-6 showed a disease of 1.4 rating which was better to that of all three checks *viz;* AK-21, PHG-9 and BJPL-1 with a rating of 1.7, 2.2 and 2.3 respectively. (Annual Progress Report, 2006-07, National Network Research Project on Arid Legumes, CAZRI, Jodhpur).

During 2007-08, CRHG-6 showed a rating of 4.6 while the checks AK-21, PHG-9 and BJPL-1 showed 4.2, 6.8 and 4.8 respectively. (PP 226 of Annual Progress Report, 2007-08, National Network Research Project on Arid Legumes, CAZRI, Jodhpur).

During 2008-09, CRHG-6 revealed a superior rating of 1.2 over the checks AK-21, PHG-9 and AK-42 with 3.2, 2.2 and 2.8 respectively. (PP 288 of Annual Progress Report, 2008-09, National Network Research Project on Arid Legumes, CAZRI, Jodhpur).

The three year testing revealed CRHG-6 to be better than the checks for tolerance to Anthracnose and hence can be a source of tolerance in future crop improvement programmes of the country.

Morpho-agronomic characters	Observations
Plant type	Semi Compact
Plant height (cm)	40
Branching Pattern	Semi erect
No of Branches/plant	4
Pods/plant (no)	32.6
Seeds/pod (no)	6
100 seed weight (g)	3
Seed colour	Brown
Associated Characters	
Days to 50% flowering	53
Days to to Maturity	96

References

Anonymous (2007) *Annual Prog. Rep.* (2006-07) National Network Research Project on Arid Legumes. CAZRI, Jodhpur, 247p.

Anonymous (2008) *Annual Prog. Rep.* (2007-08) National Network Research Project on Arid Legumes. CAZRI, Jodhpur, 226p.

Anonymous. (2009) *Annual Prog. Rep.* (2008-09) National Network Research Project on Arid Legumes. CAZRI, Jodhpur, 288p.

Purushothaman S, M Manichellappan, E Sreenivasan and K Karthikeyan (2006) Plant protection. *In:* D.Kumar (ed) *Horsegram in India.* pp 71-86.

Thakur MP and MN Khare (1990) Efficacy of different fungicides on the severity of mungbean anthracnose. *Indian J. Pulses Res.* **3:** 94-96.

Associated Characters and cultivated practices

Early maturity (130 days), high averages yield of 12.0 q/ha. High yield potential (43.00 q/ha), bold seed size (10.3 g/100 seeds). Attractive red seed colour and moderately resistant to *Fusarium* wilt, sterility mosaic and tolerant to pod borer, podfly, root knot and cyst nematode.

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Branching Pattern	Semi erect
No of Branches/plant	4
Pods/plant (no)	32.6
Seeds/pod (no)	6
100 seed weight (g)	3
Seed colour	Brown
Associated Characters	
Days to 50% flowering	53
Days to to Maturity	96

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Thakur MP and MN Khare (1990) Efficacy of different fungicides on the severity of mungbean anthracnose. *Indian J. Pulses Res.* **3:** 94-96.

11. CRHG-8 (IC0587788; INGR11018), a Horsegram (*Macrotyloma uniflorum*) Germplasm, with High Fodder Yield

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Horsegram [(*Macrotyloma uniflorum* (Lam.)Verdc.)] is an important drought resistant dual purpose crop cultivated mainly in the tropics (Asha, *et al*, 2006). The biomass of Horsegram is highly nutrition and is used as fodder for cattle and buffalows. Horsegram hey commonly known bhusa usually fed to cattle is also highly palatahle along with nutrition. A mutant line CRHG-8 was developed by γ-ray irradiation of K-42 resulting in high fodder yield. In breeding programmes, the crop needs to be improved not only as a pulse, but also as a forage plant (Hanet, 2001). This variety was tested during the years 2005-06 and 2006-07 by the National Network Research Project on Arid legumes along with National Checks. During 2005-06, CRHG-8 showed highest fodder yield of 1332.0 kg/ha when tested over four southern locations of India, while the checks AK-21, AK-42 and PHG-9 yielded 929.8, 568.3 and 531.0 kg/ha respectively showing significantly superior fodder yield. (PP 117 of Annual Progress Report of National Network Research Project on Arid Legumes, 2005-06). During 2006-07, CRHG-8 revealed a fodder yield of 590 kg/ha, while the checks AK-42 and PHG-9 showed 518 and 586 kg/ha respectively. (PP 115 of Annual Progress Report of National Network Research Project on Arid legumes 2006-07).

The results have shown that CRHG-8 can be a source of high fodder yield in future crop improvement programmes.

Morpho-agronomic characteristics

Morpho-agronomic Characters recorded	Observations
Plant type	Compact
Plant height (cm)	40
Branching Pattern	erect
No of Branches/plant	5
Pods/plant (no)	24
Seeds/pod (no)	4.5
100 seed weight (g)	3.3
Seed colour	Brown
Associated Characters	
Days to 50% flowering	53
Days to to Maturity	99

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Hanet P (2001) *Mansfelds Encyclopedia of Agricultural and Horticultural Crops* (Except Ornamentals), Spinger, Berlin.

12. PT-03-142 (IC0588674; INGR11019), a Pigeonpea (*Cajanus cajan*) Germplasm, with Resistance to Wilt and Sterility Mosaic

GP Deshmukh

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The two diseases *viz*., *fusarium* wilt and sterility mosaic are important in Pathology. To overcome this, one of resistant genotype in breeding programme is essential. The genotype PT-03-142 is such a genotype having resistant to both of these diseases. It is medium late maturing genotype (195 days) with resistance to wilt and sterility mosaic

Morpho-agronomic characteristics of PT-03-142

Entries	Year	Yield (kg/ha)	Maturity days	Plant height	Plant spread	No. of branches/ plant	Pods/plant	100- seed wt.
PT-03-142	2004-05	2292	207	236.60	45.60	14	159	11.10
	2006-07	1975	183	242.30	80.50	11	246	10.80
	2007-08	2928	195	276.30	44.30	13	388	11.70
	Mean	2398.33	195	251.73	56.80	12.66	264.33	11.20

Per cent incidence of *Fusarium* wilt and sterility mosaic on Phule Tur -03-142 in wilt sick plot and sterility mosaic disease nursery during the following years.

Entries	Year	Wilt (%)	SM (%)
PT-03-142	2004-05	0.00	0.00
	2006-07	6.11	3.77
	2007-08	9.77	8.66
	2008-09	8.18	9.52
	2009-10	0.00	7.90
	Mean	4.81	5.97
ICP-2376 (Wilt Susceptible check)		100	--
ICP-8863 (SM Susceptible check)		--	100

Morphological characterization of Pigeonpea variety: Phule T 03-142.

Sr. No.	Character	Salient features
1	Early plant vigour	Good
2	Growth habit	spreading
3	Plant height (cm) at maturity	220-230 cm
4	Number of branches a) Primary : b) Secondary :	6-7 14-22
5	Stem colour	Green
6	Leaflet shape	Broad-elliptic
7	Leaf hairiness	Pubescent
8	Days to maturity	195 days
9	Base flower colour	Yellow
10	No. of flowers & pods/peduncle	1
11	Pattern of streaks on dorsal side of standard petal	Medium amount of streaks
12	Flowering pattern	Indeterminate
13	No. of pods/plant	159 to 388 cm
14	Pod colour	Mixed, green & purple
15	Pod form	Flat
16	Pod bearing length of branch	75-80cm
17	Pod hairiness	Pubescent
18	Pod waxyness	Present
19	No. of seeds/pod	3 to 4
20	Seed colour	Reddish brown
21	Seed shape	Globular
22	100- seed weight(g)	11.20 g
23	Biotic stress	Resistant to wilt and sterility mosaic disease

References

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13. PRR 2007-1 (IC0589127; INGR11020), a Ricebean (*Vigna umbellata*) Germplasm, with Narrow Leaf; Early Maturity; Determinate Growth Habit

M Dutta
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The plant is having narrow leaf, early maturing, determinate growth habit and moderate yield.

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15. AKG 18-1 (IC0587384; INGR11022), a Groundnut (*Arachis hypogaea*) Germplasm, with Multi-foliate Leaves, 5-8 Leaflets in 30% of Leaves, Reticulated Two Seeded Pods

SN Deshmukh, MY Ladole and NS Shrikhandkar
Dr Panjbrao Deshmukh Krishi Vidyapeeth, Akola-444104, Maharashtra (E-mail: srsoilseeds@pdkv.ac.in)

A Spanish groundnut mutant with multifoliate leaves. Derived from the cross Jyoti x EC76446 (292), this mutant exhibits multifoliate leaves on the upper portion of the main stem and primary branches. The mutant bred true in the next season, 30% of leaves having 5-8 leaflets/petiole.

16. Cardozo Mankurad (IC587716; INGR11023), a Mango (*Mangifera indica*) Germplasm, with Regular Bearing Nature, Attractive Fruit Colour and Bigger Fruit Size, Higher Contents of Fibers, Pulp, Higher Fruit Yield and Better Shelf Life

AB Cardozo, PA Mathew, DG Dhandar, AR Desai, NP Singh, Fausto Cardozo, Ivo Coardozo and Maria Do Ceu Cardozo
ICAR Research Complex for Goa, ELA, Old Goa-403402 (E-mail: desaiavars@gmail.com)

Among several mango varieties of Goa, "Mankurad" is the most popular variety in the state (Desai and Dhandar, 2000). Due to continuous stone-propagation of Mankurad variety for several decades, there exists tremendous variability having desired traits within the population of this variety. Cardozo Mankurad is one such chance seedling selected for several superior characters over the parental variety (Dhandar *et al.*, 1997). This important germplasm was located in a homestead garden of Cardoso family in Mapusa city of Bardez Taluka in North Goa and selected for its regular bearing tendency, attractively coloured fruits with higher contents of fibreless pulp and better storage quality (Mathew and Dhandar, 1997). Clonal progeny was developed from the mother tree

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and evaluated at ICAR Research Complex for Goa, for validating the desired traits. Progeny orchard of this new selection is being developed at ICAR Research Complex for Goa, Old Goa. Morpho-agronomic Characteristics of the new selection are presented here in the table.

S. No.	Trait	Mankurad (parent)	Cardozo Mankurad (Selection)
1.	Bearing	Alternate to irregular	Regular
2.	Yield	Medium	Heavy
3.	Fruit size	Small to medium (278.0 g)	Medium to large (320.0 g)
4.	Fruit skin colour	Yellowish orange with pink blush, seen mostly on ventral shoulder	Yellowish orange with deep pink seen on both shoulders or throughout.
5.	Fruit pulp		
a	Texture	Melting	Firm, melting
b	Aroma	Strong aromatic	Aromatic (Rose)
c	Colour	Yellowish orange	Deep Orange
d	Fibre	Scanty	None
e	Flesh (%)	75.98	78.29
f	TSS	21.0 ° Brix	22.0 – 25.0 ° Brix
6	Quality	Excellent	Excellent
7	Shelf life	Poor (3days)	Better (about one week)
8	Stone weight (g)	28.5	22.67

The soft wood grafting is a suitable propagation method for multiplication of grafts of this promising selection. One to one and half-year old grafts can be used for planting in the main field. The pits of one cubic metre size spaced at 10 m x 10 m distance are to be filled with top soil mixed with 15 kg FYM, 1.0 kg mussorie phosphate and 1.0 kg neem cake well before planting and kept ready for planting with onset of monsoon.

After one year, first year fertilizer dose of 150:50:50g of N, P_2O_5 and K_2O along with 10 kg/graft of FYM has to be applied to each young graft. Doubled quantity of nutrients should be applied for two year old grafts and from third year onwards, the first year dose be added to the previous year's dose till 9th year. For ten year old trees, nutrients comprising of 1500 g N, 500 g P_2O_5 and 500 g of K_2O along with 50 kg/tree of FYM need to be applied for better performance. Full dose of recommended nutrients has to be given in circular rings, 0.5-2.0 m away from the trunk, in the month of August for rainfed gardens and incorporated into soil. The trees of Cardozo Mankurad commence flowering during November-December and fruits become ready for harvesting during March-April. About 1500-2000 fruits may be harvested from each tree at tenth year and onwards. The grafts of this new selection are in great demand in the state, especially for taking up new commercial plantations.

References

Desai AR and DG Dhandar (2000) Variation in physico-chemical and morphogenetic characters of some mango varieties of Goa. *Acta Hort.* **509:** 243-251.

Dhandar DG, PA Mathew and S Subramanian (1997) Mangoes of Goan Origin With Propagation and Culture. Technical Bulletin No.1, ICAR Research Complex for Goa, 63p.

Mathew PA and DG Dhandar (1997) Cardozo Mankurad: A breakthrough in mango (Mangifera indica L.) selection. *Acta Hort.* **455:** 236-240.

17. CISH J – 42 (IC0587714; INGR11024), a Jamun (*Syzygium cuminii*) Germplasm, with Seedlessness and Pulp Content (97-98%) and High TSS (14-15º Brix)

AK Singh, A Bajpai and H Ravishankar

Central Institute for Subtropical Horticulture, Rehmankhera, P.O. Kakori, Lucknow-227107, Uttar Pradesh (E-mail: singhakcish@gmail.com)

Seedless accession of jamun was selected by Central Institute for Subtropical Horticulture, Lucknow during 2008 in a survey conducted for selecting best Jamun genotypes from the country. The seedless jamun accession CISH J-42 was identified in wild road side avenues at Navgarh road (Near Vindhya Hills), Chakia, Chandauli, U.P. Its uniqueness lies in seedlessness (rudimentary seed). It was multiplied by softwood grafting and established in the field gene bank.

The superiority of the accession is due to rudimentary seed leading to seedlessness in fruit, with high pulp content (97-98 %) and fairly high TSS (14-16º Brix). The seedlessnes imparts great processing potential and product diversification opportunity for Jamun. Enhanced shelf-life 5-7 days of fruits at ambient temperature as compared to 3-4 days of local types make the accession commercially important.

and evaluated at ICAR Research Complex for Goa, for validating the desired traits. Progeny orchard of this new selection is being developed at ICAR Research Complex for Goa, Old Goa. Morpho-agronomic Characteristics of the new selection are presented here in the table.

S. No.	Trait	Mankurad (parent)	Cardozo Mankurad (Selection)
1.	Bearing	Alternate to irregular	Regular
2.	Yield	Medium	Heavy
3.	Fruit size	Small to medium (278.0 g)	Medium to large (320.0 g)
4.	Fruit skin colour	Yellowish orange with pink blush, seen mostly on ventral shoulder	Yellowish orange with deep pink seen on both shoulders or throughout.
5.	Fruit pulp		
a	Texture	Melting	Firm, melting
b	Aroma	Strong aromatic	Aromatic (Rose)
c	Colour	Yellowish orange	Deep Orange
d	Fibre	Scanty	None
e	Flesh (%)	75.98	78.29
f	TSS	21.0 ° Brix	22.0 – 25.0 ° Brix
6	Quality	Excellent	Excellent
7	Shelf life	Poor (3days)	Better (about one week)
8	Stone weight (g)	28.5	22.67

The soft wood grafting is a suitable propagation method for multiplication of grafts of this promising selection. One to one and half-year old grafts can be used for planting in the main field. The pits of one cubic metre size spaced at 10 m x 10 m distance are to be filled with top soil mixed with 15 kg FYM, 1.0 kg mussorie phosphate and 1.0 kg neem cake well before planting and kept ready for planting with onset of monsoon.

After one year, first year fertilizer dose of 150:50:50g of N, P_2O_5 and K_2O along with 10 kg/graft of FYM has to be applied to each young graft. Doubled quantity of nutrients should be applied for two year old grafts and from third year onwards, the first year dose be added to the previous year's dose till 9th year. For ten year old trees, nutrients comprising of 1500 g N, 500 g P_2O_5 and 500 g of K_2O along with 50 kg/tree of FYM need to be applied for better performance. Full dose of recommended nutrients has to be given in circular rings, 0.5-2.0 m away from the trunk, in the month of August for rainfed gardens and incorporated into soil. The trees of Cardozo Mankurad commence flowering during November-December and fruits become ready for harvesting during March-April. About 1500-2000 fruits may be harvested from each tree at tenth year and onwards. The grafts of this new selection are in great demand in the state, especially for taking up new commercial plantations.

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17. CISH J – 42 (IC0587714; INGR11024), a Jamun (*Syzygium cuminii*) Germplasm, with Seedlessness and Pulp Content (97-98%) and High TSS (14-15º Brix)

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The superiority of the accession is due to rudimentary seed leading to seedlessness in fruit, with high pulp content (97-98 %) and fairly high TSS (14-16º Brix). The seedlessnes imparts great processing potential and product diversification opportunity for Jamun. Enhanced shelf-life 5-7 days of fruits at ambient temperature as compared to 3-4 days of local types make the accession commercially important.

Morpho-agronomic characteristics

The identified accession is 10-11.5 m tall, trunk girth being 1.50 m, with canopy spread E-W 10.20 m and N-S 11.70 m in the indigenous state, yield is 180-250 kg/ tree (age being 65 years old) and mid season maturity falling during the second week of June. The fruit is round shaped and has average weight 6.87 g, length 2.57 cm, pulp 97.9 per cent, TSS 14.7º Brix, ascorbic acid 34.14 mg/100g and total antioxidant value 15.54 mg AEAC/g of fresh weight and shelf life of 5-7 days at ambient temperature (Singh *et al.*, 2009).

Associated characters and cultivated practices

The jamun tree occurs in the tropical and sub-tropical climates under a wide range of environmental conditions. Due to wider adaptability jamun is valuable for reforestation programmes. It is hardy and can tolerate both short periods of drought as well as heavy rainfall and can also withstand floods (Chovatia and Singh, 2000). It can be grown successfully in semi-arid subtropical regions with an annual rainfall varying from 350 to 500 mm. However, in early periods of growth, protection from frost is needed. Its cultivation can be introduced in arid and semiarid, resource-poor and wasteland areas where other crops are difficult to grow. It requires dry weather at the time of flowering and fruit setting. In sub-tropical areas, early rain is beneficial for proper development of fruit size, colour, maturity and taste. Vigorous growth and high yield, however, could be obtained only when grown on deep loam and well drained soils that have the capacity to retain good soil moisture.

Reference

Chovatia RS and SP Singh (2000) Effect of time on budding and grafting success in jamun (*Syzygium cuminii* Skeels). *Indian J. Hort.* **57:** 255-258.

Singh AK, A Bajpai and H Ravishankar (2009) National Network Project on Underutilized Fruits. *Annual. Prog. Rep.,* Central Institute for Subtropical Horticulture, Lucknow.

18. CISH J-37 (IC0587715; INGR11025), a Jamun (*Syzygium cuminii*) Germplasm, with Bold Fruit and High Pulp Quality (Pulp Content 90-92% and TSS 16-17º Brix)

AK Singh, A Bajpai and H Ravishankar

Central Institute for Subtropical Horticulture, Rehmankhera, P.O. Kakori, Lucknow-227107, Uttar Pradesh (E-mail: singhakcish@gmail.com)

An elite and superior bold type jamun was identified by Central Institute for Subtropical Horticulture, Lucknow during exploration carried out in 2006. The jamun accession CISH J–37 (Syzygium cuminii Skeels) selected from Gaderiankhera, Lucknow, U.P. on road side avenue. This accession has superiority due to its bold large sized bunches with attractive deep purple colour. High pulp: seed ratio (90–92 %) and TSS (16–17º Brix) are other key features of this accession.

Morpho-agronomic characteristics

The identified tree was 12–15 m tall with trunk girth 1.95 m, canopy spread E–W and N–S being 14.10 m and 12.70 m respectively. The accession is high yielder (200–300 kg plant^{-1}) of about 45 years old and mid season maturity during the second week of June. The fruit is bold, oblong and has average weight of 24.05 g, length 3.90 cm, diameter 3.03 cm, pulp (92.26 %), TSS (16.4 ºBrix). High nutraceutical benefits accrue from this accession due to relatively high ascorbic acid (49.88 mg/100g) and total antioxidant value (38.30 mg AEAC/g) (Singh *et al.*, 2009).

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The jamun tree occurs in the tropical and sub-tropical climates under a wide range of environmental conditions. Due to wider adaptability jamun is valuable for reforestation programmes. It is hardy and can tolerate both short periods of drought as well as heavy rainfall and can also withstand floods (Chovatia and Singh, 2000). It can be grown successfully in semi-arid subtropical regions with an annual rainfall varying from 350 to 500 mm. However, in early periods of growth, protection from frost is needed. Its cultivation can be introduced in arid and semiarid, resource-poor and wasteland areas where other crops are difficult to grow. It requires dry weather at the time of flowering and fruit setting. In sub-tropical areas, early rain is beneficial for proper development of fruit size, colour, maturity and taste. Vigorous growth and high yield, however, could be obtained only when

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19. DWS-327 (IC0588697; INGR11026), an Ashwagandha (*Withania somnifera*) Germplasm, with Dwarf Plant Type

P Manivel, V Kumar, NA Gajbhiye and S Maiti
Directorate of Medicinal & Aromatic Plant Research, Boriavi, Anand-387310, Gujarat
(E-mail: manivelp@yahoo.com)

Ashwagandha (*Withania somnifera*) is an important medicinal herb also known as Indian ginseng, belong to the family Solanaceae. The medicinal properties of this plants is attributed due to the presence of several classes of withanolides, steroidal lactones, which are widely used; as an antioxidant, adaptogen, aphrodisiac, anti-inflammatory agent and recently proved to combat against ulcer, arthritis, venom toxine and cancer like diseases. It is being cultivated in India as post rainy season crop (August sowing and harvesting in March). So for only two varieties (JA 20 and JA 13405) have been released for commercial cultivation through AICRMAP. Both these varieties are longer duration (6-7 months). The demand for this crop is increasing both in national and international market. Hence, the demand has to be mainly met out through developing high yielding, dwarf and early maturing varieties with high active ingredients. At DMAPR, Anand a dwarf pure line DWS 327 with plant hight of less than 30 cm which mature by 120-130 days and having high withanolide-A content (>1.75 mg g^{-1} dry weight) as compared to its parent JA 134 (0.477 mg g^{-1} dry weight) has been identified. The genetic diversity studies of the selected pure lines (along with its parent JA 134) using molecular markers (RAPD) indicated the line DWS 327 is genetically divergent from all other pure lines including its parent. Hence, this could be used as variety after assessing its performance in multilocation trails and also as parent in the hybridization programme to develop high yielding and early maturing varieties with high 'Withonolide-A' content.

20. DMRHO 57 (IC0589137; INGR11027), a Maize (*Zea mays*) Germplasm, with High Oil Line (6.34%)

R Sai Kumar, JC Shekhar, J Kaul, S Dass, D Pal, P Shanti and SK Vasal
Directorate of Maize Research, Pusa Campus, New Delhi-110012
(E-mail: kauljyoti1@yahoo.co.in)

With the urbanization, specialty corn has gained a great acceptability among the masses. With rapid changes in life style, popcorn is gaining its market in India. High oil corn with added advantages in feed ration has significant importance as cooking oil due to high level of unsaturated fatty acid in it. Over the years, the demand for specialty corn in Indian market is increasing. The composites of popcorn that have been released so far have low productivity and hence not accepted by the farmers. Till now in India no high oil variety/hybrid is available. Hence, the thrust is on the development of high yielding Single Cross Hybrids of specialty corn meeting international standards in quality parameters. Keeping all this in mind, DMR is involved in developing desirable maize germplasm for specialized purposes which would augment the breeding program of the entire country.

It is derived from Tempx Trop (HO) QPM-B-B-B-57-B-B (exotic germplasm) after 7-8 years of inbreeding

grown on deep loam and well drained soils but have the capacity to retain good soil moisture.

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20. DMRHO 57 (IC0589137; INGR11027), a Maize (*Zea mays*) Germplasm, with High Oil Line (6.34%)

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It is derived from Tempx Trop (HO) QPM-B-B-B-57-B-B (exotic germplasm) after 7-8 years of inbreeding

following by ear-to-row selection at Directorate of Maize Research, Indian Agricultural Research Institute, Pusa campus, New Delhi.

DMRHO-57 is late maturing, medium stature plant type with medium long cob. This line flowers in 57-60 days under Delhi conditions. This line is rich in oil content (6.34%). Based on the two year data the oil content of DMRHO 57 was higher by 5.67% and 5.31% over the two previously registered high oil inbred lines HKI-(T) and HKI-6, respectively. It has dense tassel branches and is a good pollen shedder. The anthocyanin colouration of both anthers and silk are present. The grain row arrangement is irregular and the anthocyanin colour of glume is white. It has very attractive yellow flint grains.

21. DMRE-9 (IC0589141; INGR11028), a Maize (*Zea mays*) Germplasm, as an Inbred Line as Source of Resistance to Pink Borer, *Sesamia inferans*

JC Shekhar, P Kumar, R Sai Kumar, J Kaul, S Rakshit, S Dass and SK Vasal
Directorate of Maize Research, Pusa Campus, New Delhi-110012
(E-mail: kauljyoti1@yahoo.co.in)

A late maturing line derived from WNZPBTL 3 after 7-8 years of inbreeding following by ear-to-row selection at Directorate of Maize Research, Indian Agricultural Research Institute, Pusa campus, New Delhi.

DMRE-9 is medium stature plant type with medium size cob. The line is late maturing and flowers in 57-62 days under Delhi conditions. The four year data with respect to pink borer reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM 300. The mean leaf injury for Pink borer in DMRE-9 ranged from 2.5 to 3.2 with a mean of 2.72. Thus can be utilized as a source of stable resistance against the above mentioned insect for development of insect free hybrids. It has sparse tassel branches and is a good pollen shedder. The grain row arrangement is straight and the anthocyanin colour of glume is purple. The anthocyanin colouration of both anthers and silk are present.

22. DMRE-57 (IC0589142; INGR11029), a Maize (*Zea mays*) Germplasm, as an Extra-early Line as Source of Resistance to Pink Borer, *Sesamia inferans*

JC Shekhar, P Kumar, R Sai Kumar, J Kaul, S Rakshit, S Dass and SK Vasal
Directorate of Maize Research, Pusa Campus, New Delhi-110012
(E-mail: kauljyoti1@yahoo.co.in)

An early maturing line derived from WNZPBTL-6 after 7-8 years of inbreeding following by ear-to-row selection at Directorate of Maize Research, Indian Agricultural Research Institute, Pusa campus, New Delhi.

DMRE-57 is medium stature plant type with medium size cob. This is an extra-early line (flowers in 43-45 days) with dense tassel branches and is a good pollen shedder. The four year data with respect to pink borer reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM 300. The mean leaf injury for Pink borer in DMRE-57 ranged from 3.0 to 3.5 with a mean of 3.17. Thus, can be utilized as a source of stable resistance against the above mentioned insect for development of insect free hybrids. The grain row arrangement is straight and the anthocyanin colour of glume is white. The anthocyanin colouration of both anthers and silk are absent.

following by ear-to-row selection at Directorate of Maize Research, Indian Agricultural Research Institute, Pusa campus, New Delhi.

DMRHO-57 is late maturing, medium stature plant type with medium long cob. This line flowers in 57-60 days under Delhi conditions. This line is rich in oil content (6.34%). Based on the two year data the oil content of DMRHO 57 was higher by 5.67% and 5.31% over the two previously registered high oil inbred lines HKI-(T) and HKI-6, respectively. It has dense tassel branches and is a good pollen shedder. The anthocyanin colouration of both anthers and silk are present. The grain row arrangement is irregular and the anthocyanin colour of glume is white. It has very attractive yellow flint grains.

21. DMRE-9 (IC0589141; INGR11028), a Maize (*Zea mays*) Germplasm, as an Inbred Line as Source of Resistance to Pink Borer, *Sesamia inferans*

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(E-mail: kauljyoti1@yahoo.co.in)

A late maturing line derived from WNZPBTL 3 after 7-8 years of inbreeding following by ear-to-row selection at Directorate of Maize Research, Indian Agricultural Research Institute, Pusa campus, New Delhi.

DMRE-9 is medium stature plant type with medium size cob. The line is late maturing and flowers in 57-62 days under Delhi conditions. The four year data with respect to pink borer reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM 300. The mean leaf injury for Pink borer in DMRE-9 ranged from 2.5 to 3.2 with a mean of 2.72. Thus can be utilized as a source of stable resistance against the above mentioned insect for development of insect free hybrids. It has sparse tassel branches and is a good pollen shedder. The grain row arrangement is straight and the anthocyanin colour of glume is purple. The anthocyanin colouration of both anthers and silk are present.

22. DMRE-57 (IC0589142; INGR11029), a Maize (*Zea mays*) Germplasm, as an Extra-early Line as Source of Resistance to Pink Borer, *Sesamia inferans*

JC Shekhar, P Kumar, R Sai Kumar, J Kaul, S Rakshit, S Dass and SK Vasal
Directorate of Maize Research, Pusa Campus, New Delhi-110012
(E-mail: kauljyoti1@yahoo.co.in)

An early maturing line derived from WNZPBTL-6 after 7-8 years of inbreeding following by ear-to-row selection at Directorate of Maize Research, Indian Agricultural Research Institute, Pusa campus, New Delhi.

DMRE-57 is medium stature plant type with medium size cob. This is an extra-early line (flowers in 43-45 days) with dense tassel branches and is a good pollen shedder. The four year data with respect to pink borer reaction revealed that line has shown consistently very high level of resistance against the susceptible check CM 300. The mean leaf injury for Pink borer in DMRE-57 ranged from 3.0 to 3.5 with a mean of 3.17. Thus, can be utilized as a source of stable resistance against the above mentioned insect for development of insect free hybrids. The grain row arrangement is straight and the anthocyanin colour of glume is white. The anthocyanin colouration of both anthers and silk are absent.

23. DPcl-10 (IC0589143; INGR11030), a Maize (*Zea mays*) Germplasm, a Popcorn Line with High Poppiness

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(E-mail: kauljyoti1@yahoo.co.in)

A late maturing line derived from WINPOP-8 after 7-8 years of inbreeding following by ear-to-row selection at Directorate of Maize Research, Indian Agricultural Research Institute, Pusa campus, New Delhi.

DPcl-10 is short stature plant type with long cob. It has sparse tassel branches and a good pollen shedder which is a merit of good pollinator. This line is late maturing and flowers in 56-58 days under Delhi conditions. The anthocyanin colouration of both anthers and silk are present. The grain row arrangement is straight and the anthocyanin colour of glume is white. It has attractive yellow round grains with 1000 kernel weight (gm) in the range of 100-150 and the mean as 139.6. DPcl-10 is a popcorn line and shows 100% poppiness.

Pink borer is a pest that infests maize during *rabi* season. With the development of late maturing Single Cross Hybrids, winter maize is gaining significant importance in India; the area under the winter maize is on the increase. Hence, pink borer tolerant germplasm is urgently sought.

24. BSBS-151 (IC0383192; INGR11031), a Dolichos bean (*Lablab purpureus*) Germplasm, with resistance to aphids (*Aphis craccivora*) and Anthracnose (*Colletotrichum lindemuthianum*)

SR Pandravada, B Sarath Babu, K Anitha, SK Chakrabarty, N Sivaraj, V Kamala, N Sunil and KS Varaprasad
National Bureau of Plant Genetic Resources, Regional Station, Rajendranagar, Hyderabad-500030, Andhra Pradesh
(E-mail: pandravadasr@yahoo.com)

Dolichos bean/ hyacinth bean/ lablab bean extensively cultivated in the tribal areas as well as in the plains of india is a popular vegetable which is a source of dietary protein. The main biotic constraints to increased production and productivity of dolichos bean are anthracnose (Rajesha, 2009) and aphids (Rekha and Mallapur, 2007), the incidence of which result in severe losses to both yield and quality of the pods and are major constraints in dolichos bean production.

Dolichos bean germplasm and field screening

Considering the importance of these two serious biotic constraints and the significance of identification of sources of resistance, 100 accessions of dolichos bean germplasm originated from South East Coastal India were screened in an augmented block design with RND-1 as a check variety in the Kharif season of 2003-04 and 2004-05 at NBPGR Reg. Station, Rajendranagar, Hyderabad. The weekly data on incidence of aphids and anthracnose manifestation was recorded on the germplasm.

Screening against aphids

The reaction of the genotypes based on the severity of aphid incidence was assessed by a visual rating on 0 - 9 scale with 15 genotypes recording nil incidence and the check variety RND-1 found to be highly susceptible with 7 and 9 ratings respectively during 2003-04 and 2004-05. Accession IC383192 was one among the 15 promising accessions with no aphid incidence considering the screening results for both the years.

Screening against anthracnose

The reaction of the genotypes based on the severity of anthracnose incidence was assessed by visual rating on 0-5 scale with 6 and 4 genotypes recording nil incidence and the check variety RND-1 found to be highly susceptible with 4 and 2 ratings respectively during 2003-04 and 2004-05. Accession IC383192 was one among the nine accessions promising with either 0 or 1 rating considering the screening results for both the years.

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Multiple resistance

Out of the germplasm screened, the genotype IC383192 was one of the two promising accessions showing consistent reaction with nil incidence to aphids during the both the seasons and also showing 0 and 1 rating scales against anthracnose during 2003-04 and 2004-05 respectively. This genotype, a Dolichos bean (*Lablab purpureus* (L.) Sweet var. *typicus*) assumes importance in view of it's resistance to anthracnose and aphids and also having impressive qualitative and quantitative traits.

About the dolichos bean accession IC383192

This particular germplasm accession originated from Chattisgarh was characterized by vigorous plant type, mid early flowering, high fresh pod (10 fresh pod weight- 92.2 g) and 100 seed weight (45.9 g) and attractive bold seed. The genotype IC383192 identified as resistant to aphids and anthracnose through field screening was purified and multiplied from single plant selection. This source is ideal for utilization in the crossing programmes for incorporation of resistance into desirable backgrounds for developing resistant varieties. The finding gains all the more significance in view of lack of stable resistance sources against these two serious pests in a single genotype.

References

Sarath Babu B, K Anitha, SR Pandravada, SK Chakrabarty, N Sivaraj, N Sunil and RDVJ Prasada Rao (2005) Reaction of *Lablab purpureus* germplasm from peninsular India to *Colletotrichum lindemuthianum* and *Aphis craccivora*. *J. Mycol. Plant Pathol.* **34:** 888-890.

Rajesha (2009) Studies on anthracnose of dolichos bean caused by *Colletotrichum lindemuthianum* (Sacc. And Magn.) Scrib.). http://www.lablab.org/ html/ diseases-managment.

Rekha S and CP Mallapur (2007) Abundance of seasonability of sucking pests of dolichos bean. *Karnataka J. Agric. Sci*. **20:** 397-398.

25. Ankur Goldy (IC0586943; INGR11032), a Dolichos Bean (*Lablab purpureus*) Germplasm, for Bushy Plant Type

SS Alkari and LP Aurangabadkar

Ankur Seeds Pvt. Ltd., 27, New Cotton Market Layout, Opposite MSRTC Bus Station, Nagpur-440018, Maharashtra (E-mail: sonalisa_alkari@yahoo.co.in)

Dolichos bean, *Lablab purpureus* belongs to the family Fabaceae and is the most ancient crop among cultivated plants. Dolichos bean is prominently in-determinate /viny in habit and requires support/stacking, which increase the cost of cultivation for farmers.

Ankur Goldy is indigenously developed by Research Department, Ankur Seeds Pvt. Ltd, at Ankur research farm Kinhi, by Varietal Improvement Program. Breeding objective for development of this variety is to develop determinate, bushy, early, high yielding variety which does not require stacking/support. ARDL-12 is an indeterminate / viny female parent and Konkan Bhushan (ARDL-2) is a dwarf / determinate male parent used in this varietal improvement program. Breeding method employed was Hybridization followed by Pedigree selection.

Morpho-agronomic characteristics

Characterization of Ankur Goldy was done as per the botanical characterisation done by GKVK, Bangalore and AVRDC for Indian beans. The detailed description is submitted herewith under Table 2.

Cultivation practices

For rainy season sowing can be done in June-July where as for *rabi* September-October is the suitable time. The

Table 1. Ankur Goldy performance on important traits for yield and yield components

Rep	Ger. %	Days to 50 % flower	Days to pod		Pod		No. of inflore-scence/ plant	No. of pods/ inflore-sence	No. of pods/ plant	Yield/ plant (gm)	Yield / acre (qt)
			Formation	Maturity	Length (cm)	Breadth (cm)					
I	95	43	57	64	11.1	6.4	24	2	43	179	16.6
II	92	43	57	65	11.1	6.2	33	1	44	231	24.9
III	91	45	57	65	10.4	5.8	28	1	35	201	21.7
M	93	44	57	65	10.9	6.1	28	1	41	204	21.1

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Table 2. Characters of Ankur Goldy [Dolichos beans]

Morphological characters of Ankur Goldy			Economical characters of Ankur Goldy		
S.No.	Character	Type	S.No.	Character	Type
1	Emerging cotyledon colour	green	1	No. of flower buds/raceme	40-45
2	Hypocotyl colour	green	2	No. of racemes per plant	8-10
3	steam pigmentation	Extensive	3	Racemes length in cm	30-35
4	Vein colour	green	4	Peduncle length in cms	1-1.5
5	Leaf anthocyanin	present	5	No. of nodes/raceme	10-12
6	Leaf colour	Pale green	6	No. of buds/node	3-5
7	Leaf hairiness	Moderately pubescent	7	Days to 50% flowering	38-40
8	Leaf length(CM)	8	8	Pod length (cm)	12-15
9	Leaf width(CM)	7	9	Pod width (cm)	3-3.2
10	Leaf let length(cm)	15	10	Pod thickness (cm)	0.4
11	Leaf shape	Round	11	Pod constriction	Slightly constricted
12	Leaf persistence	Intermediate	12	No. of pods/plant	30-35
13	Growth habit	semi determinate	13	No. of locules/pod	6-7
14	Primary branches	12-14	14	No. of seeds per pod	4-5
15	Secondary branches	9-10	15	Plant height in cms.	70-80
16	Branch orientation	Perpendicular to main steam	16	Green pod yield/plant	260-265 gm
17	Flower bud length (CM)	1.6 cm	17	Seed length(fresh)	1-1.5 cm
18	Flower bud width (CM)	0.5	18	Seed width(fresh)	0.8-1 cm
19	Flower bud colour	light yellow	19	Seed thickness(fresh)	0.3cm
20	Standard petal colour	white	20	Seed shape(fresh)	Flat
21	wing petal colour	white	21	100 seed weight (g) fresh	80-85
22	Raceme position	Intermediate	22	Pod coat thickness in cm(fresh)	0.4
23	Pod curvature	slightly curved	23	Seed coat thickness(fresh)	0.3 cm
			24	Seed colour dry	Brown
			25	Seed length(dry)	1 cm
			26	Seed width	0.7 cm
			27	Seed thickness(dry)	0.3 cm
			28	Seed shape(dry)	ovate
			29	100 seed weight (g) dry	40-45

crop should be planted at a spacing of 60x30 cm in medium soil and 60x45 cm in heavy soils. 24-30 kg seed is sufficient for one hectare plantation. Application of 60:60:60 kg NPK per hectare is recommended. The attack of lepidopterous and dipterous pod borers are of considerable importance can be controlled by use of systematic insecticides like oxydemanton-methyl, dimethoate or emidacloprid. Occurrence of anthracnose can be noticed on leaf and pods in humid season.

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26. RH 0116 (IC0584669; INGR11033), an Indian Mustard *(Brassica juncea)* Germplasm, with Tolerance to Salinity (10 ds/m) at Seedling Stage

D Singh, ML Chhabra, NK Thakur, N Chandra and A Singh
Choudhary Charan Singh Haryana Agricultural University, Hisar-125004, Haryana
(E-mail:oilseeds@hau.ernet.in)

A line of Indian mustard having tolerance to salinity at 10 ds/m. It is also thermo tolerant at seedling stage as its 50% mortality takes more than 3hr when exposed at 45± 1º C under lab. conditions.

27. Kachahalli Jack Fruit (IC0566526; INGR11034), a Jack Fruit (*Artocarpus heterophyllus*) Germplasm, with Pink Colour Pulp/Flakes, Excellent Taste and aroma, Less Cellulose Content

K Narayana Gowda, K Narasimhaiah, Doddahanumaiah, S Shyamalamma, SV Suresha, KN Srinivasappa, Babu RM Ray, DS Ashwathanarayana and MS Gangadhara
University of Agricultural Sciences, Gandhi Krishi Vignana Kendra, Bangalore-560065, Karnataka
(E-mail: knarayanagowda@yahoo.co.in)

The fruit of this tree have excellent taste. The tree produces around 250-300 fruits per year and each fruit weights around 45-50 kgs. On an average the fruits weighing 10 kgs may contain 25-30 bulbs and the one weighing 40-50 kgs may contain 350-500 bulbs. The bulb colour is deep pink. It has less aril and even the arils are tasty. The fruiting season starts from March to April and fruits are available up to August. There is lot of demand for this fruit and the farmer is getting 20,000 to 30,000 rupees per year.

28. DPO-14 (IC0586947; INGR11035), an Isabgol (*Plantago ovata*) Germplasm, with Early Maturing (80-85 days) and High Harvest Index (>22%)

P Manivel and R Saravanan
Directorate of Medicinal and Aromatic Plant Research, Anand-387301, Gujarat
(E-mail:manivelp@yahoo.com)

Isabgol is wonderful bulking fibre for constipation besides it is used for treatment of diarrhea, constipation and hemorrhoids. India is the sole exporter of this crop in the world market and earns considerable foreign exchange every year. It is being cultivated in arid and semi-arid regions of Gujarat, Rajasthan and parts of Madhya Pradesh as rainfed *rabi* crop (November to March) with supplementary irrigations and harvested at 110-120 days after sowing. Downy mildew is the major disease usually its occurrence starts during January (approximately 60 days after sowing) and progress to severe level during February (during peak flowering and seed formation stage) depending on the weather factor and micro climates and considerably reduce the yield. In such situation, the presently developed early maturing mutant DPO-14 may be the best alternative as it may escape from the disease as it mature before the disease occurrence or severe progress. Further, as this mutant is having higher harvest index and uniform maturity and it may be a good source parent for development of high yielding and early maturing isabgol varieties.

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29. UHFVAL-1 (IC0584665; INGR11036), an Indian Valerian/Mushkbala (*Valeriana jatamansi*) Germplasm, with High Valeportriates Content (approx. 4%)

R Raina, RC Rana and YP Sharma

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Valeriana jatamansi (Valerianaceae), widely distributed in sub-temperate Himalayas (Anonymous, 1976), is valued for its use both in traditional and modern medicines. Traditionally it is used for treating hysterical fits, hypochondriasis, nervous unrest, emotional troubles, epilepsy, asthma, leprosy, cholera and skin disease (Kirtikar and Basu, 1975; Anonymous, 1976; Husain, 1993). According to Wagner *et al.* (1980) and Grusla *et al.* (1986), most of the therapeutical properties like sedative and tranquilizing effect are due to the presence of a group of compounds known as valepotriates that are present in its rootstock. Essential oil mostly present in its roots is used in flavouring tobacco, honey etc and also in perfumery (Anonymous, 1976).

Rootstock of this species is being massively wild extracted and in the absence of any cultivation activity, the species is under stress. Need is increasingly being felt to introduce the species into the farming activity which shall not only conserve its natural stock but also provide assured supply to the users. However, such initiative shall necessitate identifying high yielding strains both in terms of active content and biomass.

During the course of extensive studies on this species, UHFVAL-1 (IC0584665; INGR11036) strain was isolated and multiplied (with about 4 per cent valepotriates' content) under AINRP M&APs centre at Dr. Y.S. Parmar University of Horticulture & Forestry Nauni, Solan.

Morpho-agronomical characters

Plants of Valeriana jatamansi are perennial and gynodioecious (female and bisexual flowers born on separate plants) (Raina & Srivastava 1992). Chemotype UHFVAL-1 (IC0584665; INGR11036) has been found to be superior in terms of valepotriates' content (about 4 %) present in its rootstock. The phenomenon of gynodioecism present in this species bestows an advantage as female flowered plant can be directly used as female parent in any hybridization programme without the need of emasculation which otherwise would have been difficult in this species as the floral size is very small. Pollination studies conducted here have revealed that the species is both cross and self compatible producing fertile seeds.

Associated characters and cultivation practices

The species can be grown on hill slopes as an understory as well as open cultivated. However biomass yield has been found to be higher under open cultivation conditions. It can be propagated both by seeds as well as by rhizome splits. Commercial production of biomass is attained after two years. On an average about 1000 kg/ha of dry rootstock can be obtained after two years of plantation. Rootstock yields valepotriates' and roots contain essential oil (1.8 %).

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