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Recent International Policy Developments for Plant Genetic Resources

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The plant genetic resources are very vital for the growth of agriculture in all countries of the world. All countries depend on genetic diversity from other countries which calls for international cooperation and open exchange of genetic resources The International Treaty on Plant Genetic Resources for Food and Agriculture is a step forward in this direction. The Treaty eases access to plant genetic resources and information and provides legal instrument for fair sharing of the benefits arising from these genetic resources The paper highlights the details of standard material transfer agreement, multi-year plan of work, extending the use and the training and technical assistance needed for effective implementation of the Treaty. The experience of CGIAR Centres in distributing and acquiring material under the standard material transfer agreement during the initial period of the new agreement has also been enumerated

Key Words: Material transfer agreement, International treaty, Convention on Biological Diversity, Multilateral system, Access and benefit sharing, Plant genetic resources

Introduction

The coming into force of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), on 29 June 2004, represented a crucial step in the fight against hunger and poverty. No country is self-sufficient in plant genetic resources; all depend on genetic diversity in crops from other countries and regions, which implies that international cooperation and open exchange of genetic resources are essential for food security. The Treaty eases access to plant genetic resources and information, and at its first meeting in June 2006, the Governing Body took another important step by implementing, for the first time, the fair sharing of benefits arising from the use of these resources through the Standard Material Transfer Agreement (SMTA) – the legal instrument that governs exchange of material and information under the Treaty. But this is just the beginning.

Standard Material Transfer Agreement

The Standard Material Transfer Agreement is a uniform contract that is simple to operate and will encourage widespread use. It will also ensure the sharing of benefits associated with the use of plant genetic resources. Its adoption was a clear signal that all parties were ready to rebuild an atmosphere of trust and collaboration that is bound to be good for the future of agriculture, especially in developing countries. The Treaty creates a multilateral system that enables access to plant genetic resources and also establishes benefit-sharing based on royalties levied on commercial products that use material obtained through the multilateral system. The SMTA sets out the terms that govern access and benefit sharing and will accompany all transfers of genetic materials. One major achievement in the adoption of the SMTA concerns the definition of a product: any variety that incorporates material from the multilateral system. Previous drafts had spoken of genetic thresholds and specific economically valuable traits, both difficult to assess. The simplified definition makes it easier to use the SMTA and will avoid problems of interpretation. The definition also broadens the scope of products that will trigger a payment, and because of that and its simplicity, the SMTA should encourage widespread use of the multilateral system. The royalty payment was set at 1.1% of sales. It is mandatory if the product is not available for further breeding and research. Payments are voluntary if the products are not restricted and are available for further use. The funds will be devoted to conservation efforts, mainly in developing countries.

The first meeting of the Governing Body also recognized the Global Crop Diversity Trust as an essential element of the International Treaty's funding strategy. This reaffirms the Trust's unique global mandate, and such strong endorsement from the international community will help the Trust to ensure the conservation and availability of plant genetic resources for the benefit of agriculture everywhere.

Multi-Year Plan of Work

The following year, in June 2007, the Commission on Genetic Resources for Food and Agriculture adopted a strong commitment to examine the specific needs of the

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agricultural sector with regard to access to genetic resources and the fair and equitable sharing of the benefits derived from their use. The Commission negotiated the International Treaty; with those out of the way, it had space to consider new work. After some discussion and good support from member countries, the Commission adopted a multi-year plan of work that covers all aspects of agriculture: plants, animals, forestry, fisheries, insects and microbes.

The Commission will address all genetic resources for food and agriculture, and it is absolutely appropriate that it examines all the components not in isolation but with a cross-sectoral approach. The multi-year plan of work adopts just such an approach and lays out the Commission's work for the next five sessions, ten years.

Before the International Treaty, the only international legal instrument regulating access and benefit-sharing for genetic resources was the Convention on Biological Diversity (CBD), which established a system that generally operates through bilateral agreements. Many commentators felt that this model was not appropriate for agriculture, which may have suffered as a result. The Treaty's multilateral system of access and benefit sharing, by recreating an innovative form of commons, establishes an alternative system for certain important plant genetic resources for food and agriculture.

The Commission's multi-year plan of work offers a chance to examine still other mechanisms for access and benefit sharing that may go beyond both the CBD and the International Treaty, taking into consideration the special needs of agriculture and the particularities of each sector's genetic resources. Furthermore, a deeper examination of access and benefit sharing systems on a cross-sectoral basis for food and agriculture could be good news for the use of biodiversity to improve agricultural resilience and productivity. The Commission's decision may represent the moment when the pendulum began to swing back in favour of agricultural research and how it can help poor people .

Extending the Use of the SMTA

Following the Commission's decision to consider all aspects of agriculture, the Governing Body of the Treaty, at its second meeting in November 2007, took several more decisions that will help the world community to fight poverty and hunger. One of the most important decisions was to extend the range of crops that the Consultative Group on International Agricultural Research (CGIAR) centres will distribute under the Standard Material Transfer Agreement. The SMTA, which CGIAR centres have been using since 1 January 2007, now covers plant genetic resources for food and agriculture that are not on Annex 1 of the Treaty, but that are nevertheless important to countless small farmers in the developing world and that are conserved in the CGIAR collections. It thus effectively brings those species within the scope of the multilateral system of the International Treaty.

The CGIAR collections are among the largest in the world, containing more than 650,000 samples of crops vital for food security, including species of globally important staples such as wheat, rice and maize. The collections are home to crop wild relatives and traditional varieties, valuable resources for helping farmers and breeders develop new varieties that are able to withstand the effects of climate change.

Extending the scope of the SMTA is a major step that bodes well for the future of the Treaty and the multilateral system, because distributing crop diversity under the SMTA ensures that material and information remain freely available and subject to the benefit sharing provisions of the Treaty.

Delegates took the decision following a report prepared by the CGIAR System-wide Genetic Resources Programme (SGRP) that described the CGIAR centres' experiences in distributing material under the SMTA. The centres distributed 97, 669 samples of crops to farmers and breeders around the world within the first seven months of using the agreement (Table 1). In the same period, they received 3,988 samples of new genetic material from collections around the world to safeguard in-trust for the global community.

A look at figures from 2004, the most recent year for which data are available, underlines the significance of the report. In the whole of 2004, the CGIAR centres sent out 90,504 samples and received 5033 new accessions. The figures for the first seven months of 2007 thus represent a clear increase for distributions. The report further showed that the CGIAR centres were distributing a high proportion of improved lines that breeders are releasing for further work and assessment by others, which is vitally important for the further development of crop varieties. Using the SMTA to do this ties the material and any products derived from it to the access and benefit sharing system of the Treaty and means that these lines will always be available for others to make use of.

Table 1. Experience of the CGIAR Centres in distributing and acquiring material under the SMTA during the first seven months of the new agreement

Centre	Acquisitions	Transfers normal PGRFA	Transfers PGRFA under development	Total transfers
Bioversity	36	85		85
CIAT	0			747
CIMMYT	1,890[1]	5,585	20,957	26,542
CIP	23[2]	1,324	63	1,387
ICARDA	0	6,554	[3]	6,554
ICRAF	No Annex 1 material			
ICRISAT	0	1,178	15,662	16,840
IITA	0			5,423
ILRI	0			406
IRRI	2,039	23,484	12,166	35,650
WARDA	0			4,035
TOTAL	3, 988	38,210	48,848	97,669

1 Samples developed by CIMMYT's breeding programmes and acquired by the genebank
2 SMTA not yet signed
3 14,442 samples were transferred using the old Material Transfer Agreement, since the material was not designated material in the in-trust collection. ICARDA will now be using the SMTA for transfers of improved material.

Following the report, delegates to the Governing Body approved the centres' proposal to use the SMTA for distributing material that falls outside the crops listed in Annex 1 of the International Treaty. In practice, footnotes will be included in the SMTA for those provisions that refer to Annex 1 materials or the Multilateral System, indicating that these should not be interpreted as precluding the use of the SMTA for transfers of non-Annex 1 materials. The issue will be reviewed by the Governing Body at its next session and Bioversity is leading an effort to develop guidelines that will help the centres implement this decision.

Training and Technical Assistance Needed

Although the centres' experiences with distributing material under the SMTA were mostly positive, the report also identified areas where the operation of the system could be eased. One of the most important areas was the need to train potential users about the Treaty. One centre commented in compiling its data for the report that there was an almost universal lack of awareness and understanding, with frequent requests for specific information or for training courses. In this regard, the Governing Body welcomed news of a Joint Programme being set up by Bioversity International and the Food and Agriculture Organization of the United Nations (FAO) to provide technical assistance to developing countries to help them implement the Treaty and its Multilateral System.

The session also approved requests from the International Cocoa Genebank of Trinidad and Tobago and the Secretariat of the Pacific Community to enter into agreements with the Governing Body, placing their collections within the purview of the Treaty.

Conclusion

Overall, the meeting held in November 2007 was a great success, and the prospects for ease of access to plant genetic resources and information, and for the equitable sharing of benefits derived from their use, look good. The number of countries that have ratified the Treaty has increased from 104 to 116 in just over a year. Positive messages were also heard from the United States (US) regarding the process of their ratification. The US has not signed the Convention on Biological Diversity; if it were to ratify the Treaty this would send a strong signal to other countries that have not yet ratified. The centres of the CGIAR have embraced the Treaty and are putting it to work. Perhaps the one negative note to be sounded in all this is that as of the second meeting of the Governing Body, no country had reported substantive progress in implementing the Treaty's provisions. Thus, while one can be optimistic, one also needs to exercise a certain caution. The need for the principles and practices enshrined within the International Treaty go well beyond the activities of the CGIAR centres and must include the global community as a whole. With more awareness, more training, and especially more political will among the many countries that have ratified it, the Treaty will really come into its own as an international instrument to improve agriculture for those who need it most.

Agroecological Patterns of Diversity in Pearl Millet [*Pennisetum glaucum* (L.) R. Br.] Germplasm from India

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India is the largest pearl millet growing country with diverse climate. Agroecological patterns of diversity for important agronomic traits was assessed in 5,197 pearl millet germplasm accessions originating in India and conserved at Rajendra S. Paroda Genebank at ICRISAT. Agroecological region 10, mostly covering Malwa and Bundelkhand regions, which accounted for maximum overall diversity with less representation in genebank (135 accessions), can be explored for additional diversity in the collection. Mean values and the frequency distribution suggest further exploration in agroecological region 3 for tall plant height, region 5 for short height, region 6 for high panicle exsertion and large seeds, region 8 for high number of productive tillers, region 10 for long panicles, region 11 for thick panicles, region 12 for late flowering and high tillering and region 14 for early flowering. Observed relationship between the climate of agroecological regions of India and the performance of pearl millet germplasm implies that the environmental factors such as rainfall, number of rainy days, temperature, soils and daily sunshine period are the important determinants of variation patterns.

Key Words: Agroecological region, Climatic zone, Geographical, Variation

Introduction

Pearl millet is one of the hardiest crops and its adaptation to a wide range of adverse environments makes it an important cereal in many countries of arid and semi-arid regions of Asia and Africa. India is the largest pearl millet growing country (10 million ha) contributing to 42 per cent production in the world (Bhatnagar, 2002). India, owing to its size, topography, and geographical position is characterized by extremely varied agroclimatic conditions on both seasonal and regional basis indicating wide genetic base in the crop germplasm. Information on climate at germplasm collection sites and the patterns of diversity distribution is very important for effective planning of future germplasm collection, conservation (Allard, 1970; Marshal and Brown, 1975) and its enhanced utilization in crop improvement programmes (Annicchiarico *et al.*, 1995; Hayward and Breese, 1993; Moreno-Gonzalez and Cubero, 1993). The availability of climatic and ecological databases and the new tools of Geographic Information System (GIS) in recent years have opened up new avenues for understanding and prediction of patterns of genetic diversity in natural populations. The Rajendra S. Paroda Genebank at ICRISAT holds the world's largest collection of 21,594 accessions of pearl millet germplasm, including 750 accessions of wild relatives from 50 countries. India is the major contributor with 6,647 accessions from a wide range of agroecological regions. In the present study, using the available passport information and characterization data of the accessions and the tools of GIS, we assessed the patterns of diversity for eight important agronomic characters of cultivated pearl millet germplasm collected in different agroecological regions of India.

Materials and Methods

The experimental material consists of 5,197 landraces of pearl millet germplasm originating from India and having information on geographic coordinates of collection site. The accessions were characterized in batches of 500-1000 at ICRISAT farm, Patancheru (17°25'N latitude, 78°00'E longitude and 545 m asl) in alfisols, during rainy season (June–November) from 1974 through 2006. Each accession was sown in two, 4 m long rows with spacing of 75 cm between rows and 10 cm between plants. Life saving irrigation was provided. Fertilizers were applied at the rate of 100 kg ha^{-1} N and 40 kg ha^{-1} P_2O_5. Rainy season at Patancheru is characterized by long (13.9 hrs. in June to 12.4 hrs. in November) and warm (minimum temperature: 21.8°C; maximum temperature: 30.9°C) days. The mean daily sunshine hours ranged from 4.1 in July to 8.3 in November with a mean of 6.0 during the crop growth. Data of eight important agronomic traits, days to 50% flowering, plant height, number of total and productive tillers, panicle exertion, length and thickness and 1000-seed weight were recorded using the Descriptors for Pearl millet (IBPGR and ICRISAT, 1993).

The delineation of the agroecological regions (20) of India developed by National Bureau of Soil Survey

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and Land Use Planning, Indian Council of Agricultural Research (ICAR), Nagpur, India was used in the present study (Sehgal *et al.*, 1992). Climatic zone is defined in terms of major climate variables that affect crop growth and is thus suitable for a certain range of crops and cultivars (FAO, 1983). Agroecological region is an area of the earth's surface characterized by distinct ecological responses to macroclimate as expressed by soils, vegetation, fauna and aquatic systems. Therefore, the agroecological region is the land unit carved out of climatic zones. The agroecological regions are more homogeneous both in terms of cropping patterns and climate and thus provide a better basis for studying crop responses to climatic variations (Carter and Konijn, 1988). Each climatic zone is divided in to 3-9 smaller agroecological regions depending on the rainfall, temperature, soils, vegetation, length of growing period, etc. Division of the Indian climatic zones has resulted in three agroecological regions (1, 2 and 3) in the arid zone, five regions (4, 5, 6, 7 and 8) in the semi-arid zone, nine regions (9, 10, 11, 12, 13, 14, 15, 16 and 17) in the sub-humid zone and three regions (18, 19 and 20) in the coastal zone (Fig. 1).

Geographic coordinates were retrieved to fill the gaps for accessions having location information using Microsoft Encarta[R], an electronic atlas (MS Encarta[R] Interactive World Atlas, 2000) and the accuracy of coordinates was checked by mapping all accessions on to a political map of India. The information on mean minimum and maximum temperature and rainfall for each collection site was retrieved using DIVA-GIS software (Hijmans *et al.*, 2005a, b). ArcView[R]-GIS was used to overlay the collection sites of all accessions along with characterization data on to the map of agroecological regions in India (Fig. 1). These two maps were spatially joined to separate the accessions from each agroecological region along with the characterization data. Data for selected traits of accessions from individual climatic zones and agroecological regions were analyzed for basic statistics using GENSTAT 6.1. Means, variances and diversity index (H') for all traits, climatic zones and agroecological regions within each zone were estimated and compared (Keuls, 1952; Newman, 1939; Levene, 1960; Shannon and Weaver, 1949). Frequency distribution of accessions within each extreme group/modality of different characters was estimated to identify the trait specific germplasm in each climatic zone and in different agroecological regions and discussed in light of available information on climatic factors at the collection sites.

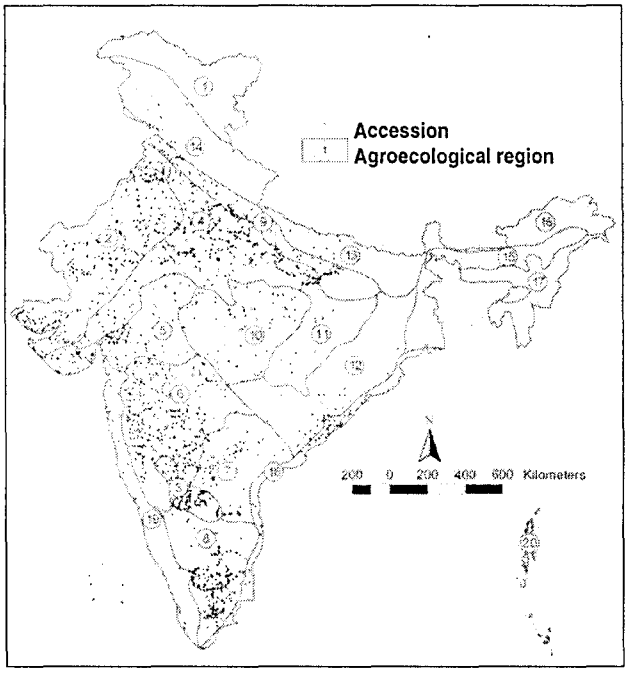

Fig. 1: Map of India, showing twenty agroecological regions (1-20) and the pearl millet germplasm collection sites (circles)

Results and Discussion

Important characteristics of all climatic zones and agroecological regions of India along with the number of pearl millet germplasm accessions collected in each region are presented in Table 1. Semi-arid zone with 3,298 accessions (63.5%) followed by arid zone with 1,070 accessions (20.6%) are the major source of pearl millet germplasm. Among the agroecological regions, region 4 with 1,118 accessions (21.5%) and region 6 with 1,036 accessions (19.9%) are the major source of pearl millet germplasm. On the other hand, regions 11, 13, and 14 were under represented with <50 accessions and regions 1,15,16,17 and 20, which had very little pearl millet area are not represented in the collection (Fig. 1).

Newman-Keuls test of significance for mean values indicated significant differences between climatic zones and agroecological regions within each climatic zone (Table 2). Mean values indicated arid zone as the major source of early flowering and short statured pearl millet with significantly low mean values. Arid and semi-arid zones with highest means for 1000-seed weight differed significantly from sub-humid and coastal zones. Significant differences were found among the zones for total tiller number and pearl millet from coastal zone being the highest producer of total as well as productive tillers.

Table 1. Characteristics of climatic zones and agroecological regions of India and the number of accessions collected in each region

Climatic zone	Agro ecological region*	No. of accessions	Rainfall mm	Potential evapotrans-piration (mm)	Water deficit (mm)	Mean elevation (m)	Major soil type	Length of growing period (days)	Physiography
Arid	2	905	<300	1500-2000	1500-1800	190.9	Desert and saline	<90	Western plain and Kachchha peninsula
	3	165	400-500	1800-1900	1500-1800	536.6	Red and black	<90	Deccan plateau including Bellary, SW parts of Bijapur and Raichur of Karnataka and Ananthapur of A.P.
Semi-arid	4	1118	500-800	1400-1900	700-1000	227.2	Alluvium derived	90-150	Northern plains, central highlands including parts of Gujarat plains
	5	401	500-1000	1600-2000	800-1200	290.1	Medium and deep black	90-150	Central highlands (Malwa), Gujarat plains and Kathiawar Peninsula
	6	1036	600-1000	1600-1800	800-1000	503.1	Shallow and medium black	90-150	Deccan plateau including central and western parts of Maharashtra, northern parts of Karnataka and western parts of A.P.
	7	164	600-1000	1600-1700	700-800	283.5	Red and black	90-150	Deccan plateau (Telangana) and Eastern Ghats
	8	579	600-1000	1300-1600	400-700	465.8	Red loamy	90-150	Eastern ghats (Tamil Nadu uplands) and Deccan plateau (Karnataka)
Sub-humid	9	274	1000-1200	1400-1800	500-700	169.3	Alluvium derived	150-180	Northern plain (parts of Indogangetic plains and plains of W. Himalayas)
	10	135	1000-1500	1300-1500	500-700	440.3	Black and red	150-180 (210)	Central highlands (Malwa and Bundelkhand)
	11	45	1200-1600	1400-1500	500-700	419.2	Red and yellow	150-180	Eastern plateau (Chattisgarh region)
	12	85	1000-1600	1400-1700	500-700	330.9	Red and lateritic	150-180 (210)	Eastern plateau and Eastern Ghats
	13	18	1400-1600	1300-1500	400-500	78.2	Alluvium derived	180-210	Eastern plain
	14	24	1600-2000	800-1300	300-500	2738.0	Brown forest and podzolic	180-210	Western Himalayas
Coastal	18	178	00-1600	1200-1900	400-1000	31.2	Alluvium derived	90- (>210)	Eastern and coastal plain
	19	70	2000-3200	1400-1600	300-400	307.9	Red, lateritic and alluvium	>210	Western Ghats and coastal plain

* There were no collections from regions 1, 15, 16, 17 and 20 and hence not represented

As expected, accessions from coastal zone produced smallest seeds. Across the agroecological regions, Newman-Keuls test of significance for mean values indicated that region 2 and 5 for short height (<190 cm) and 1000-seed weight (=>7.7 g); region 3 for late flowering (77.4 days), tall (316.4 cm), and thick panicles (23.4 mm); region 6 for high panicle exsertion (8.6 cm), thickness (23.2 mm) and 1000-seed weight (8.09 g); region 7 for thick panicles (23.3 mm) and 1000-seed weight (7.8 g); region 8 for high total tiller number (4.4); region 10 for long panicles (24.8 cm); region 12 for late flowering (78.4 days), and high tillering (4.6); region 14 for early flowering (49.5 days), short height (185.4 cm) and long panicles (25.2 cm) and region 18 for high total (4.6) as well as productive (3.0) tiller number, as the most promising sources (Table 2).

Variances were heterogeneous ($p=<0.01$ to 0.001) for all traits in all climatic zones (Table 3). Similarly, variances were heterogeneous for all traits except total tillers among agroecological regions of arid zone; for all traits in regions of semi-arid zone; for days to 50% flowering, total tillers, productive tillers and 1000-seed weight in regions of sub-humid zone; and for days to 50% flowering, panicle exsertion and length in coastal zone (Table 3). Among agroecological regions, region 5 for panicle length; region 8 for plant height, total and

Table 2. Mean values for different characters in pearl millet germplasm from different climatic zones and agroecological regions within each zone of India, evaluated at ICRISAT, Patancheru, India

Climatic zone/ Agroecologocial region*	No. of accessions	Days to 50% flowering	Plant height (cm)	Total tillers (no.)	Productive tillers (no.)	Panicle exsertion (cm)	Panicle length (cm)	Panicle thickness (mm)	1000-seed weight (g)
Arid	1070	57.6c[1]	208.2b	3.4b	2.7b	6.8a	22.9a	21.4b	7.6a
2	905	54.0b	188.5b	3.4a	2.7a	6.7b	23.1a	21.1b	7.7a
3	165	77.4a	316.4a	3.3a	2.5a	7.9a	22.0b	23.4a	7.1b
Semi-arid	3298	60.2b	219.5a	3.2c	2.4c	6.7a	22.3a	22.0a	7.5a
4	1118	57.7b	221.4c	2.8b	2.3b	5.0c	24.5a	21.9b	7.6c
5	401	53.2c	183.1e	2.9b	2.3b	5.5c	23.3b	21.9b	7.9ba
6	1036	58.5b	201.9d	2.9b	2.1b	8.6a	19.1c	23.2a	8.0a
7	164	59.6c	242.0b	3.2b	2.3b	7.2b	22.9b	23.3a	7.8bc
8	579	73.1a	266.3a	4.4a	3.1a	7.5b	22.8b	19.8c	5.8d
Sub-humid	581	64.9a	226.2a	2.9d	2.3c	5.1b	23.0a	22.0a	7.2b
9	274	61.7b	230.6a	2.7b	2.3b	4.5bc	22.7ba	22.7a	7.6a
10	135	65.8b	233.8a	2.5b	2.1b	6.4ba	24.8a	22.2a	7.5a
11	45	66.3b	236.6a	2.5b	2.1b	5.3bc	23.1ba	22.2a	7.5a
12	85	78.4a	208.3b	4.6a	3.4a	4.4bc	20.7b	19.7b	4.9b
13	18	60.1b	216.1ba	2.4b	1.7b	3.3c	21.4b	22.8a	6.9a
14	24	49.5c	185.4c	2.3b	1.7b	8.1a	25.2a	21.5a	7.5a
Coastal	248	65.5a	222.0a	4.2a	2.9a	6.5a	22.3a	21.1b	6.1c
18	178	67.9a	218.1b	4.6a	3.0a	6.2b	21.7b	20.4b	5.8b
19	70	59.5b	231.9a	3.4b	2.6a	7.3a	23.6a	22.7a	7.0a

1=Means tested by Newman-Keuls test (same letters indicate non-significant and different letters indicate significant results at p=0.05)
* There were no collections from regions 1, 15, 16, 17 and 20 and hence not represented

Table 3. Variances for different characters in pearl millet germplasm from different climatic zones and agroecological regions of India, evaluated at ICRISAT, Patancheru, India

Climatic zone/ Agroecological region*	No. of accessions	Variance/ F value/ Pr>F	Days to 50% flowering	Plant height (cm)	Total tillers (no.)	Productive tillers (no.)	Panicle exertion (cm)	Panicle length (cm)	Panicle thickness (mm)	1000-seed weight (g)
Arid	1070	Variance	120.6	3540	3.1	1.5	15.4	25.1	12.9	1.7
2	905	Variance	42.2	1342	3.3	1.6	16.1	26	13.1	1.7
3	165	Variance	89.3	1740	1.8	1	10	19.3	7.1	1.2
		F value	32.08	5.01	3.42	4.57	5.46	2.38	17.65	2
		Pr>F[1]	<.001	0.025	0.065	0.033	0.020	0.012	<.001	0.016
Semi-arid	3298	Variance	181.6	3338	4	1.7	20	27.8	11	2.3
4	1118	Variance	60.2	1773	1.9	0.8	15.4	26.1	8.3	1.2
5	401	Variance	57.2	2112	2	1	14.5	32.5	12.3	1.2
6	1036	Variance	138.6	3123	1.6	0.8	22	18	7.5	1.8
7	164	Variance	103.1	1790	2.4	0.7	15.4	16.8	6.9	1.2
8	579	Variance	385.1	4240	12.6	5.4	16.2	18.9	14.7	2.7
		F value	244.61	42.94	24.21	53.18	7.09	14.69	24.71	39.84
		Pr>F	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001
Sub-humid	581	Variance	224.6	1580	3	1.4	18.1	23.2	11.4	2.3
9	274	Variance	68.8	1421	2.4	1.1	17.2	21.2	9.4	1.3
10	135	Variance	141	1363	0.9	0.8	17.3	30.2	11.2	1.1
11	45	Variance	79.3	1233	2.7	0.6	16.4	19.9	11.8	0.8
12	85	Variance	750.9	1961	6.1	2.7	18.7	13.4	14.3	3.4
13	18	Variance	71.3	1618	0.5	0.2	22.4	8.6	5.7	0.8
14	24	Variance	12.4	539	1.6	0.5	7.2	17.1	5.7	0.6
		F value	151.38	1.97	3.86	5.07	0.72	1.85	2.2	9.72
		Pr>F	<.001	0.081	0.002	0.001	0.607	0.101	0.528	<.001
Coastal	248	Variance	424.7	2250	9.4	2.7	14.3	18.8	11.4	3
18	178	Variance	469.7	2081	11.1	2.8	16.9	17.2	10.8	2.6
19	70	Variance	264.5	2579	4	2.4	7.2	20.6	9.5	2.8
		F value	7.16	0.76	0.68	0.03	4.62	0.78	0.39	0.14
		Pr>F	0.008	0.385	0.409	0.871	0.033	0.038	0.532	0.707
Over all zones		F value	45.15	26.55	4.28	1.98	6.63	4.5	3.16	9.01
		Pr>F	<.001	<.001	0.005	0.012	0.002	0.004	0.024	<.001

1=Variance homogeneity tested by Levene's test at p=0.05
* There were no collections from regions 1, 15, 16, 17 and 20 and hence not represented

productive tiller number and panicle thickness; region 12 for days to 50% flowering and 1000-seed weight and region 13 for panicle exertion showed the maximum variance.

The Shannon-Weaver diversity index (H') was calculated to assess the phenotypic diversity for all characters in different climatic zones and agroecological regions (Table 4). Across the climatic zones, highly diverse accessions were found in region 2 for days to 50% flowering; region 3 for productive tillers and 1000-seed weight; region 4 for panicle exsertion, panicle length, and thickness and 1000-seed weight; region 5 for panicle length; region 6 for total tiller number; region 8 for days to 50% flowering and 1000-seed weight; region 12 for panicle length and region 18 for plant height. Mean diversity index over all characters indicate accessions from region 4 (H'=0.68±0.019) and region 10 (H'=0.68±0.005) as highly diverse (Table 4). The high overall diversity in these two regions may be attributed to the alluvium derived soils of northern plains and central highlands and red and black soils of central highlands coupled with highly varied mean monthly minimum (27.5°C in June to 13.2°C in November) and maximum (39.4°C in June to 29.2°C in November) temperature in region 4 and mean monthly minimum (26°C in June to 13.9°C in November) and maximum (37.5°C in June to 28.8°C in November) temperature in region 10. Region 4 is well represented in the collection with 1,118 accessions. Region 10, which also accounted for maximum overall diversity with less representation in genebank (only 135 accessions), needs to be explored for additional diversity to augment world collection of pearl millet.

Frequency distribution for different trait extremes of all characters under study indicated arid zone as the promising source for early flowering, short height and large seeds; semi-arid zone for thick panicles, high panicle exsertion; sub-humid zone for tall and long panicles. Reflecting the higher length of growing period (90 to >210 days), high frequency of accessions from coastal zone was late flowering and produced high total as well as productive tillers (Table 5). Irrespective of climatic zone, frequency distribution indicated that agroecological region 3 was promising for tall plant height, region 5 for short plant height, region 6 for high panicle exsertion and large seeds; region 8 for more productive tillers; region 10 for long panicles; region 11 for thick panicles; region 12 for

Table 4. Shannon-Weaver diversity index (H') for different characters of pearl millet germplasm from different climatic zones and agroecological regions of India, evaluated at ICRISAT, Patancheru, India

Climatic zone/ Agroecological region*	Days to 50% flowering	Plant height (cm)	Total Tillers (no.)	Productive tillers (no.)	Panicle exsertion (cm)	Panicle length (cm)	Panicle thickness (mm)	1000-seed weight (g)	Mean
Arid	0.62	0.66	0.64	0.67	0.66	0.67	0.69	0.64	0.66 ± 0.008
2	0.69	0.7	0.65	0.68	0.66	0.64	0.68	0.63	0.67 ± 0.009
3	0.59	0.69	0.64	0.71	0.61	0.63	0.69	0.71	0.66 ± 0.017
Regional mean	0.64±0.050	0.70±0.005	0.65±0.005	0.70±0.015	0.64±0.025	0.64±0.005	0.69±0.005	0.67±0.040	0.66 ± 0.005
Semi-arid	0.59	0.68	0.51	0.57	0.69	0.7	0.67	0.69	0.64 ± 0.025
4	0.68	0.67	0.56	0.66	0.72	0.7	0.73	0.71	0.68 ± 0.019
5	0.55	0.68	0.63	0.68	0.67	0.7	0.69	0.69	0.66 ± 0.017
6	0.65	0.64	0.69	0.68	0.66	0.66	0.7	0.69	0.67 ± 0.007
7	0.67	0.67	0.57	0.65	0.62	0.62	0.71	0.69	0.65 ± 0.016
8	0.69	0.68	0.42	0.43	0.67	0.69	0.69	0.71	0.62 ± 0.043
Regional mean	0.65±0.025	0.67±0.007	0.57±0.049	0.62±0.048	0.67±0.016	0.67±0.015	0.70±0.007	0.70±0.005	0.66 ± 0.010
Sub-humid	0.65	0.69	0.56	0.62	0.68	0.69	0.69	0.67	0.66 ± 0.016
9	0.68	0.66	0.55	0.60	0.71	0.67	0.69	0.69	0.66 ± 0.019
10	0.67	0.7	0.66	0.69	0.68	0.67	0.66	0.69	0.68 ± 0.005
11	0.52	0.67	0.36	0.68	0.69	0.67	0.61	0.65	0.61 ± 0.040
12	0.66	0.69	0.62	0.65	0.64	0.7	0.68	0.67	0.66 ± 0.009
13	0.56	0.54	0.62	0.63	0.64	0.64	0.58	0.68	0.61 ± 0.016
14	0.59	0.69	0.62	0.53	0.63	0.62	0.71	0.62	0.63 ± 0.020
Regional mean	0.61±0.027	0.66±0.024	0.57±0.045	0.63±0.024	0.67±0.013	0.66±0.011	0.66±0.020	0.67±0.011	0.64 ± 0.012
Coastal	0.5	0.68	0.5	0.56	0.61	0.66	0.7	0.68	0 61 + 0.029
18	0.55	0.71	0.45	0.54	0.64	0.66	0.71	0.69	0.62 ± 0.034
19	0.39	0.63	0.62	0.61	0.65	0.68	0.66	0.68	0.62 ± 0.033
Regional mean	0.47±0.080	0.67±0.040	0.54±0.085	0.58±0.035	0.65±0.005	0.67±0.010	0.69±0.025	0.69±0.005	0.62 ± 0.000
Regional grand mean	0.61±0.022	0.67±0.011	0.58±0.025	0.63±0.020	0.66±0.008	0.66±0.007	0.68+0.010	0.68±0.007	0.65 ± 0.033

* There were no collections from regions 1, 15, 16, 17 and 20 and hence not represented

Table 5. Frequency distribution (%) for different trait extremes of each character in pearl millet germplasm from different climatic zones and agroecological regions of India, evaluated at ICRISAT, Patancheru, India

Climatic zone/ Agroecological region*	Days to 50% flowering		Plant height (cm)		Total tillers (no.)		Productive tillers (no.)		Panicle exertion (cm		Panicle length (cm)		Panicle thickness (mm)		1000-seed weight (g)	
	Early (<45)	Late (>80)	Short (<125)	Tall (>250)	Low (<2)	High (>7)	Low (<2)	High (>7)	Poor (< 0)	Good (>12)	Small (<15)	Long (>30)	Thin (<15)	Thick (>30)	Small (<5)	Large (>10)
Arid	5.05	7.01	4.67	17.01	22.06	4.21	37.57	0.56	5.23	5.14	4.21	5.51	2.43	0.65	1.87	2.80
2	5.97	0.22	5.52	3.20	23.20	4.64	37.46	0.66	5.75	5.08	3.76	6.30	2.76	0.66	1.66	3.20
3	0.00	44.24	0.00	92.73	15.76	1.82	38.18	0.00	2.42	5.45	6.67	1.21	0.61	0.61	3.03	0.61
Semi-arid	3.70	8.82	4.40	24.08	25.17	2.97	46.88	1.30	7.82	8.46	9.25	4.34	2.79	0.70	7.34	1.97
4	1.79	0.27	4.11	24.51	25.49	1.25	42.58	0.09	12.61	2.06	2.95	7.78	0.72	0.27	0.81	0.89
5	2.99	0.75	15.96	5.99	31.92	0.75	49.38	0.25	7.48	2.00	5.74	7.23	0.75	1.50	0.25	2.99
6	7.72	5.69	3.28	14.09	29.05	0.58	54.63	0.00	4.73	18.63	22.39	0.48	0.10	0.87	2.03	3.38
7	3.05	4.88	0.00	35.98	16.46	3.05	44.51	0.00	4.88	3.66	2.44	1.83	1.22	0.61	2.44	3.05
8	0.86	37.65	0.17	50.26	15.37	12.09	40.24	7.08	5.18	8.46	2.25	3.28	13.47	0.69	35.75	0.52
Sub-humid	2.75	10.15	0.86	31.33	35.80	3.27	51.46	0.86	12.22	2.41	2.41	5.68	2.75	0.52	8.95	1.03
9	0.73	0.36	0.73	36.13	37.59	2.55	55.47	0.36	13.87	2.19	1.09	3.65	1.46	0.36	0.36	1.09
10	2.96	13.33	0.74	36.30	41.48	0.00	55.56	0.00	10.37	3.70	4.44	13.33	0.00	0.74	1.48	0.74
11	2.22	2.22	0.00	33.33	46.67	2.22	53.33	0.00	13.33	2.22	0.00	6.67	0.00	2.22	0.00	0.00
12	7.06	45.88	1.18	16.47	9.41	12.94	18.82	4.71	10.59	1.18	5.88	1.18	14.12	0.00	57.65	2.35
13	0.00	0.00	5.56	27.78	33.33	0.00	72.22	0.00	22.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00
14	12.50	0.00	0.00	0.00	58.33	0.00	79.17	0.00	0.00	4.17	0.00	4.17	0.00	0.00	0.00	0.00
Coastal	3.63	22.98	1.61	18.95	12.50	7.66	29.84	2.02	5.24	2.82	5.24	1.61	6.05	0.00	29.03	0.81
18	4.49	25.28	2.25	19.10	8.43	8.99	26.40	1.69	6.74	2.81	5.62	1.69	7.87	0.00	35.39	0.00
19	1.43	17.14	0.00	18.57	22.86	4.29	38.57	2.86	1.43	2.86	4.29	1.43	1.43	0.00	12.86	2.86

* There were no collections from regions 1, 15, 16, 17 and 20 and hence not represented

late flowering, high tillering, and region 14 for early flowering (Table 5).

Frequency distribution and mean values for different agroecological regions indicated unequal diversity distribution of pearl millet for different traits. Region 14, located at higher elevations (2738 m asl) followed by region 2 with typical arid climate are the most promising sources for early flowering. Being a short day crop, pearl millet adapted to higher sunshine (8.6 hours/day) and lowest minimum (16.1°C) and maximum (28.3°C) temperature in region 14 flowered early when evaluated under relatively low sunshine (6.0 hours/day) at Patancheru conditions showing their sensitivity to photoperiod (Fig. 2) (Arnold, 1959; Ferere, 1984; Bidinger and Rai, 1989). None of the accessions from region 14 flowered late. Region 2 with typical hot arid climate with lowest mean annual rainfall of <300 mm and lowest mean number of rainy days (3 days), highest mean minimum and maximum temperature during June (27.4°C and 39.0°C) and July (26.4°C and 35.0°C) at collection sites and desert sandy soils, which holds low water and causes mild water stress conditions had lowest length of growing period (Fig. 2, Table 1) (Sehgal *et al.*, 1992). The pearl millet adapted to such conditions is expected to flower early and grows to a short height. Angus and Monur (1977) reported that mild water stress hastened anthesis in wheat, while severe stress delayed anthesis. Mahalakshmi *et al.* (1987) reported reduced plant height and increased tiller number due to water stress during early stages and stem elongation period. Interestingly, all early flowering, short height and high productive tillering accessions of arid zone are from region 2, where mild moisture stress is common (Fig. 2).

On the other hand, agroecological region 12 followed by region 3, receiving erratic rainfall and having red, lateritic soils, which cause severe water stress conditions in early stages of crop growth, are the good source of late flowering accessions, which produced more tillers having small and thin panicles (Angus and Monur, 1977; Lahiri and Kumar, 1966; Mahalakshmi and Bidinger, 1985). Increased tillering results in the reduced panicle and seed size primarily due to the reduced availability of current photosynthates for seed filling (Mahalakshmi and Subramanian, 1985). Deviation from the expected length of growing period in region 3, the smallest region with very different climate from that of other regions may be attributed mainly to the erratic rainfall (5 days per month), which is more common in Southern India than in Northern India (Fig. 2) (Harinarayana, 1987; Mahalakshmi and Bidinger, 1986). Furthermore, continuous rainy days and amount of rainfall plays important role in deciding the length of growing period in any region (Gadgil *et al.*,

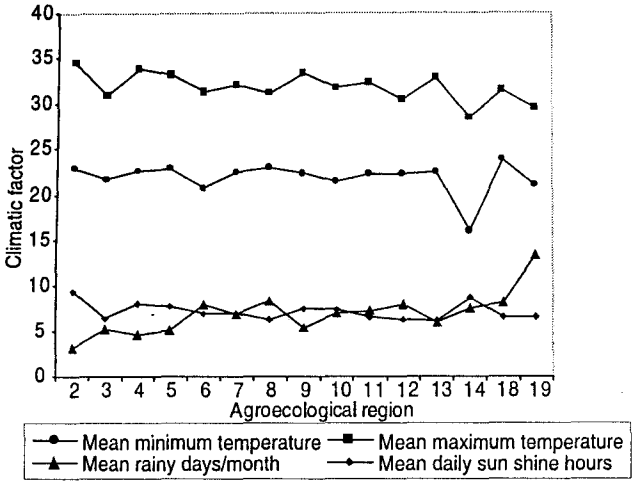

Fig. 2: Monthly mean minimum and maximum temperature, rainy days per month and daily sunshine hours at the collection sites of pearl millet germplasm accessions during crop season (June to November)

1988; World Water and Climate Atlas October, 2000). Sensitivity of the accessions, particularly to the photoperiod also contributed to late flowering in pearl millet from these two regions. When compared to the accessions from all other types of soils, red and black soils and mixture of these two soils resulted in high frequency (56%) of tall accessions (Table 5). Pearl millet adapted to such soil conditions in region 3, where red and black soils are predominant, resulted in high frequency (92.7%) of tall accessions (>250 cm).

Probably high total rainfall, high mean rainy days per month (about 8 days/month), coastal climate and red and lateritic soils in region 12 and red loamy soils in region 8 have resulted in high tillering (Fig. 2) (Fussel *et al.*, 1980; Harinarayana, 1987). High rainfall and fertile soils of the region 10 and 11 resulted in high frequency of accessions with long and thick panicles, respectively. Probably due to salinity in some areas and intermittent dry spells causing stress conditions during stem elongation, the highest frequency (15.96%) of short stature accessions was in region 5 (Mahalakshmi and Bidinger, 1985; Mahalakshmi *et al.*, 1987; Sehgal *et al.*, 1992). Region 6 with black soils and optimum temperature at panicle development stage resulted in more accessions with highly exserted panicles with large seeds (Fussel *et al.*, 1980; Ong and Monteith, 1985; Sehgal *et al.*, 1992).

In general, the results indicated that the pearl millet from southern and eastern parts of India was good source for late flowering, tall, high tillering, and small panicles with smaller seeds; whereas the pearl millet accessions from northern and western parts of India was good source for early flowering, short height and large seeds. Results illustrated a closer relation between the climate of agroecological regions and the performance of pearl millet germplasm for different characters, implying that the environmental factors such as rainfall, temperature, daily sunshine hours and soils are the important determinants of variation patterns of pearl millet in different climatic zones and agroecological regions suggesting the need to record sufficient data on agrometeorological variables, in particular, rainfall, temperature, daily sunshine hours and soil type at collection sites (Reddy *et al.*, 2004). Studies in different crops have shown that a careful investigation of climatic variables can lead to the identification of germplasm with useful and predictable attributes (Rick, 1973; Klebesadel and Helm, 1986). Therefore, the assessment of diversity patterns in relation to the crop ecology of more homogeneous and smaller agroecological regions revealed patterns of diversity in a better way (Carter and Konijn, 1988; Sehgal *et al.*, 1992). Natural selection pressure for adaptation to different climatic and agroecological conditions coupled with farmer's selection for cultivation of a specific type of material in adverse conditions in some areas might have accounted for the observed patterns of diversity.

Since, the pattern of diversity for each character varied in different climatic zones and agroecological regions within each climatic zone, collection missions could be effectively planned for trait-specific pearl millet germplasm. Using the diversity patterns in different agroecological regions, cost effective collection missions could be prioritized to explore high diversity regions, under-collected and threatened areas for materials of interest. Though the evaluation data used in the present study are preliminary in nature, and recorded over years, these data reflect the differences in the genetic makeup of the accessions in terms of clear patterns of diversity. Further, such studies help in identifying suitable sites for regeneration of trait-specific germplasm sets and introduction of appropriate pearl millet into different regions and emphasize similar studies on germplasm collections from different countries.

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A Quantitative Analysis of Genetic Erosion in the Genus *Momordica* L. in South Peninsular India

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The experience of germplasm collecting over a decade has shown that wild species of *Momordica* are subjected to varied types of threats affecting their survival in India, especially in Peninsular South India. A numerical model was used for quantifying threat of genetic erosion, with the total score indicative of the magnitude of threat. The studies revealed a grave threat for *M. dioica* in its entire range and *M. sahyadrica* in the Western Ghats of Kerala. Overall, *M. charantia* var. *muricata* faces a medium level of threat across its geographic range. Habitat loss and fragmentation brought about by population pressure and developmental activities, poor distribution and low population density of *Momordica* species coupled with inadequate *in situ* conservation efforts, and acculturation of the forest dwelling communities are the major factors attributed to their heightened threat status affecting their long-term survival in the wild.

Key Words: *Momordica* L., Quantitative Analysis, Genetic Erosion, Conservation, South India

Introduction

The genus *Momordica* L. offers wild and cultivated vegetables of high nutritional value. Six species occur in India and among them, three species, *viz.*, *M. sahyadrica* Joseph and Antony, *M. dioica* Roxb. and *M. charantia* L. var. *muricata* (Willd.) Chakrav. occur in South India (de Wilde and Duyfjes 2002; Joseph *et al.*, 2006, Joseph and Antony, 2007a,b). Except the cultivated bitter gourd (*M. charantia* L. var. *charantia*), other species occur in the wild state and are gathered by tribal communities as vegetables. This genus has a very rich ethnobotanical history with linguistic, religious, cultural and socioeconomic ramifications across its geographic range, with implications in its sustainable utilization and conservation (Joseph and Antony, 2007b). However, personal experience of germplasm collecting over a decade has revealed that these wild species are subjected to varied types of threats, affecting their survival in India especially in Southern Western Ghats and Peninsular India.

Red lists of endangered taxa have become an important and reliable tool in conservation planning when it is based on precise and scientifically sound data as in the case of developed countries in the West. As Ibisch *et al.* (2002) have stated, in the case of tropical species, the assessment of the threat status and assignment of the appropriate threat category is primarily and often exclusively based on restricted distribution The only reference to threatened status of *Momordica* is given in IUCN Red Data Book (IUCN, 1997) where *Momodica subangulata* Blume. from Wynad (Kerala) and South Canara (Karnataka) is accorded 'threatened-indeterminate status'. In fact, the species referred to as *M. subangulata* from Wynad might be *M. sahyadrica* (Joseph and Antony, 2007a), as true *M. subangulata* do not occur in Kerala (Joseph, 2005). Also, there are a few other reports expressing apprehensions of species as being 'endemic', 'endangered' or 'nearing extinction' in India (Dwivedi, 1999; Jha and Ujawane, 2002). However, these reports are primarily based on bibliographic compilations and not supported by authentic fieldwork. As the available data is highly scattered and incomplete, extensive fieldwork needs to be undertaken in order to have an objective assessment of the threat of genetic erosion of *Momordica* species.

Materials and Methods

Study Sites

An extensive ecogeographical survey was conducted during September-November, 2004 across the south Peninsular India, covering all the major areas of distribution. This region comprises agro-climatically diverse areas, namely, southern part of hot-humid Western Ghats (one of the mega diversity hotspots and highly vulnerable to anthropogenic disturbances) and drier peninsular Deccan Plateau. Observations were recorded from 42 sites spread over the states of Kerala, Karnataka, Goa and Tamil Nadu. (Fig. 1 and Table 2). The locations

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include diverse habitats like partially opened forest fragments and tribal settlements, protected areas, riverbanks, cultivated areas and commercial plantations, thus representing the entire ecogeographic range of the target species.

Methodology

An indirect method of quantifying genetic erosion, originally proposed by Guarino 1995 and subsequently refined by de Oliveira and Martins (2002) and Anete Keiša *et al.* (2007), was used with modifications incorporated to suit the actual field conditions pertinent to the taxa (Table 1). This model is based on assigning numerical values for various biological, environmental and socioeconomic risk factors, with the total score indicative of the magnitude of threat. The numerical values were entered in the data sheets at the collection sites itself, giving due attention to each factor.

Data Analysis

The threat of genetic erosion faced by a population in a particular site was obtained by the sum of scores attributed to each of the 16 factors. The threat due to a single factor was calculated as the sum of the scores of that factor in all the 42 sites. As the emphasis was more at the species level rather than geographical jurisdiction, the sites were further grouped under the three species. The magnitude of threat in each species is therefore reflected in the average score in that particular group.

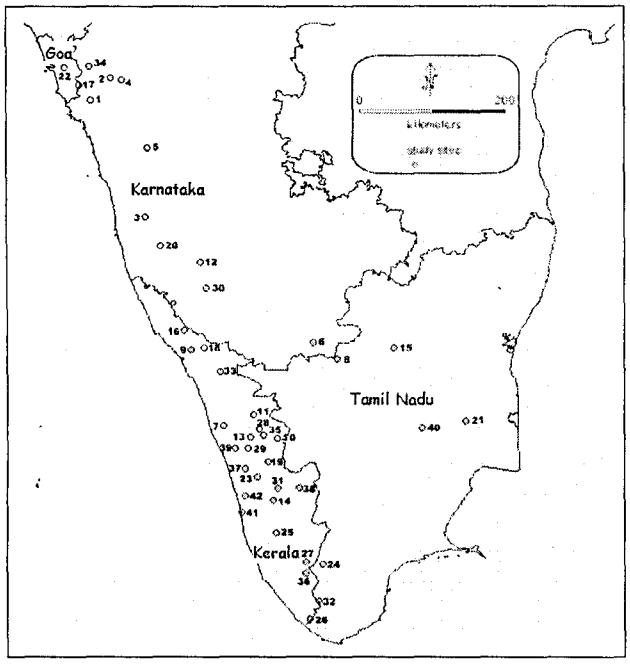

Fig. 1: Map of South India showing the study sites (Refer Table 2 for details of the sites)

Results

Threat Scores and its Spatial Pattern

Table 2 presents the sum of scores attributed to the 16 factors of risk for each of the 42 study sites. In order to clarify the comparison among threat levels faced by each study area, an arbitrary value of 1.0 was attributed to threat faced by least endangered area (KAS1 with the score of 10) and computed again the threat faced by the other sites relative to this value. The 42 sites were assigned ranks in descending order with the lowest rank (1) indicating the most threatened site. The studies showed that populations growing in each of the 42 sites that were evaluated were not subjected to same level of threat. The cumulative threat score showed a high degree of variation from the lowest score of 10.0 (KAS1) to 124.9 (KED8 and KED10) with the most threatened sites showing a 12.5-fold increase over the least threatened locality. Among the 14 most endangered sites, 10 were from Kerala (Table 2). Similarly, eight of the least threatened sites fall within the state of Karnataka and the remaining six are in Kerala, most of them falling within the jurisdiction of protected areas.

Threat at Species Level

Each of the three species is also subjected to varying levels of threat. Mean threat in *M. dioica* was 84.8 (average score from 14 sites ranging from 29.8 to 124.9) followed by *M. charantia* var. *muricata* with 64.8 (26.5-111.6) and *M. sahyadrica* with 57.7 (10.0-104.1). If the 42 study sites are divided into three groups based on cumulative threat score (most, least and medium threatened), 7 out of 14 locations in *M. dioica* (50%), 5 out of 17 (29.6%) in *M. sahyadrica* and only 2 out of 11 (18.1%) in *M. charantia* var. *muricata* fall in the most threatened group. Conversely, 7 out of 14 in *M. dioica*, 12 out of 17 in *M. sahyadrica* and 9 out of 11 in *M. charantia* var. *muricata* come under either least threatened or medium threatened group.

Threat Factors

Relative contribution of each of the 16 factors of risk to the total threat of genetic erosion is presented in Table 3. The data showed a high degree of variation among the contribution of a given factor to the cumulative threat. The three most important factors were F8, F12 and F13 (distance to major population centre, taxon distribution, and extent of wild habitat of target species within study area), contributing nearly one-third to the total threat in all the three species. Least important factors were F6 and

Table 1. Checklist used for quantifying the threat of genetic erosion (adapted from Guarino, 1995; de Oliveira and Martins, 2002)

	Factor	Score
F1	Clearing of land for agriculture/forestry plantations	
	High in the immediate vicinity	10.0
	Nearby locality (5-10 Km radius)	5.0
	Not likely to occur	0
F2	Clearing of land/land conversion for big housing projects & tourism industry (over the last 20 years)	
	Increasing drastically	10.0
	Increasing marginally	5.0
	Static or non-existent	0
F3	Habitat loss due to natural calamities (landslides, riverbank erosion, floods, drought and wildfire)	
	Highly prone	10.0
	Medium	5.0
	Low or not likely to occur	0
F4	Habitat loss due to invasive alien species/weeds/cover crops	
	Extensive	10.0
	Moderate	5.0
	Not existent	0
F5	Agricultural pressure on wild habitats	
	Large-scale cultivation within habitat margins	10.0
	Subsistence cultivation areas within habitat margins	7.5
	Land suitable for cultivation, cultivated areas within 3 kms of habitat margins	5.0
	Land suitable for cultivation, cultivated areas within 3-10 kms of habitat margins	2.5
	Land unsuitable for cultivation	0
F6	Weeding practices in Plantation forestry	
	Herbicide application	10.0
	Sickle weeding of entire area	6.6
	Selective weeding in patches	3.3
	No weeding	0
F7	Extent of use of wild habitat of target species	
	Industrial exploitation	10
	Exploitation by surrounding populations	6.6
	Gathering by small local communities	3.3
	Completely protected	0
F8	Distance to major population centre	
	<20 km	10.0
	20-50 km	5.0
	>50 km	0
F9	Human population growth rate per year	
	>3%	10
	1-3%	5
	<1%	0
	5.0	
F10	Distance to developmental projects	
	<20 km	10.0
	20-50 km	5.0
	>50 km	0
F11	Acculturation of indigenous tribes, changes in economic base, livelihood options and change in food habit	
	Not dependant on wild food plants	10.0
	Losing interest	
	Highly dependant on food plants enabling protection and seed distribution	0
	B. Species specific	
F12	Taxon distribution	
	Rare	10.0
	Locally Known	5.0
	Widespread or abundant	0
F13	Extent of wild habitat of target species within study area	
	Very restricted ((<5%)	10.0
	Restricted (5-15%)	6.6
	15-50%	3.3
	Extensive (>50%)	0
F14	Conservation status of target species	
	Species not known to occur in any protected area	10.0
	Species known to occur in a protected area, but protection status poor or unknown	5.0
	Species known to occur in a protected area, and protection status good	0
F15	Extent of use of target species (harvesting of fruits leading to seed depletion)	
	Destructive (whole plant)	10.0
	Extensive (insufficient for healthy natural regeneration)	6.6
	Marginal (sustainable, but endangering in the long run)	3.3
	Protected or not used	0
F16	Harvesting of tubers for medicinal use	
	Highly destructive (>50% harvested every year)	10
	Extensive (<50% harvested every year)	6.6
	Marginal (sustainable, but endangering in the long run)	3.3
	Protected or non-existent	0

Table 2. Study sites with cumulative threat score and ranking

S.No.	Site Code	Study Site	Provenance	Total Score	Ranking relative to least score		Level of threat
					Threat	Sites	
1	KAS1	Anaci	Karnataka/Uttar Kannad	10	1.0	31	Least threatened
2	KAS2	Dandeli	Karnataka/Uttar Kannad	16.6	1.7	30	
3	KAS3	Kudremukh	Karnataka/Daksin Kannad	20	2.0	29	
4	KAM1	Haliyal	Karnataka/Uttar Kannad	26.5	2.7	28	
5	KAS4	Soraba	Karnataka/Shimoga	27.4	2.7	28	
6	KAD2	Biligirirangan	Karnataka/Kodagu	29.8	3.0	29	
7	KES2	Chimmony	Kerala/Thrissur	33.3	3.3	28	
8	KAD1	Kolli Hills	Karnataka/Salem	49.8	5.0	27	
9	KES6	Aralam	Kerala/Kannur	49.9	5.0	27	
10	KEM4	Nelliampathy	Kerala/Palakkad	50.7	5.1	26	
11	KEM2	Mannarkad	Kerala/Palakkad	52.3	5.2	25	
12	KAS6	Sakleshpura	Karnataka/Hassan	53.2	5.3	24	
13	KEM3	Mayannur	Kerala/Thrissur	54	5.4	23	
14	KEM1	Illithode	Kerala/Iddukki	58.5	5.8	22	
15	TNM1	Sevaroi Hills	Tamil Nadu/Salem	57.3	5.7	21	Medium level of threat
16	KES7	Kannavam	Kerala/Kannur	59	5.9	20	
17	GAS1	Vilyan forest	Goa/South Goa	62.3	6.2	19	
18	KES3	Chandanathod	Kerala/Kannur	63.2	6.3	18	
19	KES4	Malakkapara	Kerala/Palakkad	63.2	6.3	18	
20	KAS5	Chikmagalur	Karnataka/Chikmagalur	63.2	6.3	18	
21	TND2	Melavarampatti	Tamil Nadu/Tirunelveli	66.5	6.7	17	
22	GAM1	Sanguem forest	Goa/North Goa	69	6.9	16	
23	KED2	Malayatur	Kerala/Ernakulam	71.5	7.2	15	
24	TND1	Kadayanellur	Tamil Nadu/Tirunelveli	71.5	7.2	15	
25	KEM5	Ponthenpuzha	Kerala/Kottayam	73.2	7.3	14	
26	KEM7	Amboori	Kerala/Thiruvanathapuram	76.5	7.7	13	
27	KED4	Achenkovil	Kerala/Kollam	79.9	8.0	12	
28	KED7	Thonikadavu	Kerala/Thrissur	82.4	8.2	11	
29	KES5	Kuthiran	Kerala/Thrissur	84	8.4	10	Most threatened
30	KAM2	Kushalnagara	Karnataka/Kodagu	85.7	8.6	9	
31	KED1	Neriamangalam	Kerala/Iddukki	87.3	8.7	8	
32	TNS1	Manchola	Tamil Nadu/Kanyakumari	89.8	9.0	7	
33	KES8	Tamarassery	Kerala/Kozhikode	89.9	9.0	7	
34	KAS7	Castlerock	Karnataka/Uttar Kannad	91.6	9.2	6	
35	KED9	Malamalamukku	Kerala/Palakkad	92.4	9.2	6	
36	KED3	Aryankavu	Kerala/Kollam	95.6	9.6	5	
37	KED5	Chalakudi	Kerala/Thrissur	104.1	10.4	4	
38	KES1	Pallivasal	Kerala/Iddukki	104.1	10.4	4	
39	KED6	Viyyur	Kerala/Thrissur	106.6	10.7	3	
40	TNM2	Trichi fort area	T. Nadu/Tiruchirappalli	111.6	11.2	2	
41	KED8	Chertala	Kerala/Alapuzha	124.9	12.5	1	
42	KED10	Tripunithura	Kerala/Ernakulam	124.9	12.5	1	

F16 (weeding practices in plantation forestry and harvesting of tubers for medicinal use). Factor F16 (harvesting of tubers for medicinal use) is of considerable importance to *M. dioica*, though of no significance to the other two species. Similarly, some factors like F4 (habitat loss due to invasive alien species/weeds/cover crops) are of great importance in a given geographical sub area (for example in Kerala forests), whereas of no significance in rest of the study area. Overall, there is a very similar pattern in all the three species.

Discussion

Methodology, Threat Scores, Spatial Pattern of Threat and Factors

Though the danger of genetic erosion or loss of biodiversity have long been recognized, practical means of assessing the loss, identifying factors likely to cause loss and how loss might be countered is poorly defined (Arunachlam, 1999; Anete Keiša *et al.*, 2007). Several approaches have been employed to estimate the degree

Table 3. Contribution of each factor towards total threat (species wise)

Factor	Contribution to threat (%) at species level		
	M. dioica	*M. sahyadrica*	*M. charantia* var. *muricata*
F1	7.16	8.67	7.71
F2	5.90	4.59	4.21
F3	2.53	6.12	3.50
F4	4.63	1.02	2.80
F5	6.95	9.94	9.81
F6	1.39	3.71	5.55
F7	6.98	4.38	7.42
F8	10.11	10.71	11.92
F9	2.95	2.04	2.80
F10	7.16	6.12	4.91
F11	5.90	4.08	4.91
F12	13.77	10.95	10.51
F13	10.36	7.78	10.22
F14	8.67	5.90	7.71
F15	7.51	8.08	6.01
F16	3.64	0.34	0.00

of genetic erosion that a particular taxon faces in a certain region over a given time. Maxted and Guarino (2006) have given an exhaustive account of various direct and indirect methods presently available for genetic erosion assessment. Though, ideally the magnitude of genetic erosion could be assessed directly using a molecular genetic approach, an indirect estimation of threat of genetic erosion may be the better practical option especially for wild and previously poorly studied plant species (Anete Keiša *et al.*, 2007).

The numerical scoring method of Guarino (1995) assumes significance as a practical means of indirect assessment of genetic erosion. de Oliveira and Martins (2002) have demonstrated the usefulness of this method in assessing the threat of genetic erosion faced by the wild medicinal plant 'ipecac' in the rain forests of southeastern Brazil. Anete Keiša *et al.* (2007), with their case study of wild *Vicia* spp. in Syria, have empirically tested the objectivity and efficiency of this method in detecting spatial and temporal patterns of threat distribution. They, however, caution that the practical application of an indirect genetic erosion threat assessment requires good prior knowledge of the target species, populations and territory.

The present checklist was very carefully designed, adding a few factors of prime importance and deleting some parameters perceived to be irrelevant for the target species and study areas. Factors 1-4 were included to assess the extent of habitat loss and fragmentation, whereas factors F5-F11 are aimed at elucidating the probable reasons for the same. Besides, the species-specific factors (F12-F16) give an estimate of the distribution, extent of habitat presently available, present conservation status and utilization of the specific taxon.

Habitat loss coupled with fragmentation, poor distribution and low population density of the taxon are the major reasons attributed to the high threat levels. The very limited extent of the habitat of the target taxon within the study area (F13) and extensive use of the wild habitat of target species for other purposes (F6) are perhaps true direct indicators of the present situation. Pressure for forestland (for agriculture and developmental activities) is enormous and bound to increase further as indicated by the high density of population, proximity to major population centres (F8) and developmental activities (F10). Acculturation of forest dwelling communities (F11), who have been the traditional custodians of forest biodiversity, is one factor that should not be lost sight of. In more progressed and urbanized tribal societies in Kerala, the knowledge and interest in crop husbandry and culinary preparations of wild *Momordica* are fast eroding, which will have an irreversible impact on its conservation. The consumption pattern has changed drastically as the younger generation depends heavily on store bought food (Joseph and Antony, 2007b).

The *in situ* conservation efforts (F14) have been largely unsatisfactory, not withstanding that *M. sahyadrica* has been well represented in the protected areas in the Western Ghats of Karnataka (which largely contributed towards its lesser threat status). It has been well maintained in some of the coffee plantations in Hassan and Shimoga areas of Karnataka, an excellent working model of an *in situ/on-farm* conservation, which can be adopted in other cropping systems and extended to more

areas. Unfortunately, it is not the case with the other two species. Efforts at the *ex situ* conservation front has been equally disappointing, taking in to the fact the present genebank collections are very negligible and they do not represent the available diversity. Besides, exploration and collection efforts are not concentrated on the most vulnerable taxa and areas.

All the taxa are facing comparatively higher levels of threat in the geographical area of Kerala when compared to the neighbouring states. All the sites in the 'most threatened category' were mostly wastelands in the suburban areas, forest edges with high influx of tourists, or highly disturbed riverbanks. All the sites coming within protected areas fall under least threatened category, implying adequate protection levels afforded in areas within their jurisdiction. However, they are still susceptible to threats like invasive weeds (F4) as in the Kerala forests (KED1, KED3, KED10 and KEM1), though not observed in the neighbouring Karnataka forests so far.

Threat at Species Level

M. dioica, even though figured to have wider distribution in the Indian subcontinent as per herbarium survey (data not shown), has a very restricted distribution and poor frequency in Kerala. It occupies partial shades of well-drained low elevation forests or undisturbed riverbanks and partially opened woodlands. With urbanization and unprecedented growth of tourism industry, privately owned woodlands are being increasingly developed for commercial activities. A few plants have been spotted in the coastal lowlands of Ernakulam, Alapuzha, Kottayam, Thrissur and Palakkad districts where human population density is one of the highest in the World. Like *M. sahyadrica*, this taxon is also subject to habitat loss (but more severely due to invasive weeds). In the four forest spots, *i.e.*, Achenkovil and Aryankavu in Quilon District, Malayatoor in Ernakulam District and Neriyamangalam in Iddukki District, *Mikania* was found to be spreading alrmingly. Destructive harvest of tubers for medicinal preparations is also rampant.

Repeat collecting visits to given areas some years apart are invaluable sources of information on genetic erosion (Guarino, 1995). At Tripunithura (KED10) in Ernakulam District, the bearing female vines (spotted during September, 2001) or any of the seedlings could not be located during subsequent visits, where the introduced cover crop *Mucuna pruriens* (L) DC has covered the entire floor. At Viyyur (KED6) in Thrissur, (where around 68 individual plants were spotted in August 2001), by 2004 the population has dwindled alarmingly and an invasive cover crop, *Mimosa diplotricha* C. Wright (=*Mimosa invisa* C. Mart.) was found to be spreading rapidly preventing seedling emergence. There is no domestication attempt and this taxon has inherent problems associated with seed dormancy, dioecy and pollination and dispersal syndrome. Less than 100 mature individuals only could be located in Kerala. By virtue of its very restricted distribution in a narrow range, population pressure on the habitat and market demand leading to destructive harvest of tuber, the species is in an endangered state and needs immediate attention.

The field studies indicate *M. sahyadrica* to be out of danger in Karnataka because of the healthy populations in the various protected areas (KAS1, KAS2 and KAS3) and because of the patronage it avails in coffee estates (KAS6 and KAS5). Being a high value vegetable with many of the taboos associated with use of tubers as planting material, self-sown plants (female and few pollenizors) are well taken care of in coffee estates (Joseph and Antony 2007b). Medicinal uses are restricted to few tribes only, where fortunately, there is good population of this species and they cultivate it as a vegetable. Hence, destructive collection of tubers would not lead to endangerment. The most threatened site was KAS7 (Castle rock), a highly open forest fragment subjected to high influx of tourist activity throughout the year.

However, in the Kerala forest, it is subjected to severe threat especially from invasive weeds such as *Mikania micrantha* Kunth. and *Lantana camara* L. *Mikania* covers the entire forest floor and smothers emerging seedlings, thus preventing regeneration of seedlings and tuber sprouts. Having preference to well drained ridges and slopes of forest openings, it is also vulnerable to landslides, flash floods, and invasion of cover crops. On a conservative estimate, less than 500 plants only could be spotted throughout Kerala, out of which about 100 in a small area in Olakara range of Peechi Forest Division (type locality). Hence, the taxon is highly vulnerable in this part of the distribution range and needs protection and rehabilitation.

M. charantia var. *muricata* is by far the most well distributed species occurring throughout the range of Western Ghats. Its population is sporadic and less dense in Kerala forests whereas in Goa and Karnataka forests especially in Uttar Kannada, it has dense population. Maximum density is seen near tribal homesteads probably

because of the role of man in inadvertent distribution of seeds of wild gathered fruits. Overall, this species faces a medium level of threat across its geographic range. However, the study delineates a picture of two extremes ranging from good protection expected to be afforded by a Wildlife sanctuary (KAM1, Haliyal) to the extreme threat being faced at one of the most vulnerable locations (TNM2, Trichi fort area). The rest of the sites spread across the states of Kerala, Karnataka, Tamil Nadu and Goa face intermediate levels of threat.

Conclusions

As Guarino (1995) pointed out, studies at regional levels are very important as the data on specific areas, populations and species coming out of these studies can be integrated at the national level to estimate the danger to a country's biodiversity as a whole. Collection priorities and conservation strategies are formulated based on the importance of the germplasm (utility) and more importantly the extent and prospect of genetic erosion. Studies conducted in this group of taxa revealed the threat of genetic erosion to a great extent in *M. dioica* in its entire range and *M. sahyadrica* in the Western Ghats of Kerala. *M. charantia* var. *muricata* faces a medium level of threat across its geographic range. The situation demands expeditious development and implementation of appropriate strategies for *in situ* and *ex situ* (including *on-farm*) conservation of these taxa.

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Methods of Constructing Core Set Using Agro-morphological Traits in Foxtail Millet [*Setaria italica* (L.) Beauv]

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The two different methods were employed to construct core sets of foxtail millet germplasm using data on geographical distribution and agro-morphological traits and the variation generated for different traits in core sets developed by two methods was compared with the entire collection. First method was grouping the accessions under distinct morphological traits followed by clustering and Principal Component Analysis which resulted in C_1 having 156 accessions; second was by using a software called Power Core which yielded C_2 consisting of 78 accessions. In both the core sets formed, maximum accessions were from Asian continent. Newman-Keuls test for means inferred that both the core sets were true representatives of entire collection. Similarly, Levene's test for homogeneity of variances revealed non-significant differences between entire set, C_1 and C_2. The range for the traits studied in both C_1 and C_2 were almost similar to the range of the traits in the entire collection. Likewise, the chi-square test for frequency distribution analysis for different morphological traits indicated that the variation available in the entire collection was preserved in both the core sets. The Shannon-Weaver diversity indices of 11 quantitative and 12 qualitative traits of entire collection, C_1 and C_2 indicated the presence of diversity of entire collection in the core sets.

Key Words: Core set, Diversity index, PowerCore, Foxtail millet

Introduction

Foxtail millet [*Setaria italica* (L.) Beauv] is one of the oldest crops cultivated for food grain and fodder. It is an indispensable crop of rainfed areas in semi-arid regions of India. It can withstand severe moisture stress and can adjust to wide range of soil conditions. China is considered to be the native home of foxtail millet. The nearest relative of *Setaria italica* is *S. viridis* and both have same genomic constitution. It is presumed that the cultivated species was most probably derived from *S. viridis* in china and later spread to Africa, Europe and Asia in pre-historic times.

The foxtail millet collection exceeding 1,400 accessions assembled and maintained at Project Co-ordinating Unit (Small Millets), All India Coordinated Small Millets Improvement Project (AICSMIP), Bangalore represents good diversity from various regions within and outside the country. The size of the large germplasm collection is an obstacle to their evaluation and exploitation. Their utilization in breeding programme could be increased if more information is available on the amount and kind of variation present in these collections. However, in most cases, the resources needed to characterize these accessions phenotypically and genotypically are meagre and unavailable.

The management and use of large germplasm collection could be enhanced if a limited number of genetically diverse accessions within the collection are selected as core collection (Frankel, 1984) and given priority to evaluation and hybridization (Brown, 1989). Core collection which is a subset of entire collection should include the maximum genetic variation contained in the entire collection with a minimum repetitiveness. There are different methods proposed for constructing core set and also for evaluating representatives of core set. But how many of these methods meet the goals of core set depends on the species, the composition of the collection and the type of characters of interest.

In the present study, two different methods of core formation *i.e.*, one by grouping accessions under distinct morphological traits followed by clustering and Principal Component Analysis and another by using PowerCore software were followed to develop core sets using entire collection of foxtail millet. The amount and the kind of variation generated for quantitative and qualitative traits in core sets developed by two methods were compared with the entire collection.

Materials and Methods

a) Evaluation of Entire Germplasm

A total of 1,478 accessions of foxtail millet maintained at National Active Germplasm Site (NAGS), Project Co-ordinating Unit (Small Millets), Bangalore were evaluated at the main research station, Gandhi Krishi Vigyana Kendra, Bangalore, over years from 2002 to 2006. The

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accessions were grown in a single row of 3 m length with a spacing of 22.5 cm between rows and 10 cm between plants within a row. Data on 25 descriptors were recorded following the procedures given in descriptors of foxtail millet (Anon., 1985).

Observations were recorded on five competitive plants in each accession and averaged for eleven quantitative traits, namely, days to 50 per cent flowering, plant height (cm), number of basal tillers, flag leaf length (cm), flag leaf width (cm), peduncle length (cm), ear length (cm), panicle exertion, days to maturity, grain yield per plant (g) and 1000-grain weight (g) and for twelve qualitative traits *i.e.* plant pigmentation at flowering, blade pubescence, sheath pubescence, senescence, inflorescence shape, inflorescence compactness, grain color, grain shape and apical sterility in panicle.

b) Formation and Evaluation of Core Set

Method 1: Data on 11 quantitative and 12 qualitative traits were used to form Core Set 1 based on scores of Principal Component Analysis and is designated as C_1. In this method, initial grouping of accessions was done using distinct morphological traits, *viz.,* plant pigmentation, grain colour, grain shape and inflorescence shape. The groups thus formed were further subjected to clustering analysis using SYSTAT 9 package. Clusters having large number of accessions were further subjected to Principal Component Analysis (PCA) using package SPLUS 2000. Using PCA scores, 156 accessions (10%) were selected for inclusion in C_1.

Method 2: A software called PowerCore (v.1.0) developed by Genetic Resources Division, Rural Development Administration, Republic of Korea, was used to form Core Set 2 of 78 accessions using both quantitative and qualitative traits of entire collection and designated as C_2. This new method is used for the establishment of core and allele mining sets by the Advanced M (Maximization) Strategy implemented through a Modified Heuristic Algorithm. It minimizes the loss of useful alleles and effectively selects accessions with highest diversity reducing the repeated alleles.

c) Comparison of Entire and Core Sets

The accessions in the entire collection, C_1 and C_2 were classified according to their place of origin and their percentages were calculated and compared. The quantitative data were subjected to statistical analysis to estimate mean, range, coefficient of variability and variance and the same were compared to determine whether the core sets formed represents the entire collection for the variability present.

The mean data of entire collection and two sets of core were compared using Newman-Keuls procedure (Newman, 1939; Keuls 1952). Levene's test was used to test the homogeneity of variances of the entire collection and two sets of core (Levene, 1960).

The ratio of different sub descriptors of qualitative trait of entire collection, C_1 and C_2 were compared using chi-square test (χ^2). The Shannon- Weaver diversity index (H') (Shannon and Weaver, 1949) of the entire collection and core sets which gives the measures of diversity was estimated for all the traits studied.

Results and Discussion

The accessions of entire collection of foxtail millet showed considerable variability for all the traits studied. The PCA scores of entire collection yielded 156 accessions which were included in C_1. This C_1 constituted around 10.55 per cent of the entire collection. Similarly, using power core statistical package, C_2 was formed which comprised of 78 accessions and constituted around 5.27 per cent of the entire collection. The accessions of entire collection, C_1 and C_2 were grouped based on geographical distribution and their percentages are presented in Table 1.

The distribution of different accessions of foxtail millet were first classified under different continents and then into countries and states. Among the continents, maximum share to entire collection were from Asia (1,392) followed by USA (39), Africa (9) and Europe (3). In Asian continent, major share was from India (1,363) followed by China (25), Bangladesh (3) and Pakistan (1). Among the different states of India, Uttar Pradesh (553) contributed more followed by Andhra Pradesh (164) and Karnataka (145). In the entire collection, 197 accessions were from unknown regions of India and 35 accessions were from unknown countries.

With respect to C_1, Asia (144) had the maximum number of accessions followed by USA (6) and Europe (1). Within Asian continent, India (140) again contributed more number of accessions. Among states of India, Uttar Pradesh contributed 64 accessions followed by Andhra Pradesh (14), Karnataka (10) and 29 accessions from unknown region of India.

Only Asian continent contributed to the C_2. Source of remaining one accession was unknown. Among the countries of Asia, India (70) ranked first whereas among

Table 1. Number and percentage of accessions contributed to entire collection (E) core 1 (C_1) and core 2 (C_2) from different continents and states within India in foxtail millet

Continent		Countries/States	E		C_1		C_2	
I. Asia	1.	India						
	a	Andhra Pradesh	164	11.10	14	8.97	5	6.41
	b	Bengal	25	1.69	-	-	-	-
	c	Bihar	57	3.86	5	3.21	5	6.41
	d	Chattisgarh	10	0.68	1	0.64	-	-
	e	Gujarat	11	0.74	-	-	-	-
	f	Himachal Pradesh	8	0.54	-	-	-	-
	g	Jammu and Kashmir	12	0.81	2	1.28	1	1.28
	h	Karnataka	145	9.81	10	6.41	6	7.69
	i	Kerala	7	0.47	1	0.64	-	-
	j	Madhya Pradesh	34	2.30	4	2.56	-	-
	k	Maharashtra	28	1.89	3	1.92	3	3.85
	l	NEFA	13	0.88	1	0.64	1	1.28
	m	Orissa	11	0.75	1	0.64	-	-
	n	Punjab	10	0.68	-	-	-	-
	o	Rajasthan	2	0.14	-	-	-	-
	p	Tamil Nadu	76	5.14	5	3.21	4	5.13
	q	Uttar Pradesh	553	37.42	64	41.03	31	39.74
	r	Unknown (India)	197	13.33	29	18.59	14	17.95
		Total (India)	1363	92.23	140	89.74	70	89.74
	2	China	25	1.69	3	1.92	6	7.69
	3	Pakistan	1	0.07	-	-	-	-
	4	Bangladesh	3	0.20	1	0.64	1	1.28
		Total (Asia)	1392	94.19	144	92.30	77	98.71
II. Europe								
	1	USSR	2	0.14	-	-	-	-
	2	Turkey	1	0.07	-	-	-	-
		Total (Europe)	3	0.21	-	-	-	-
III. N. America								
	1	USA	39	2.64	6	3.85	-	-
		Total (America)	39	2.64	6	3.85	-	-
IV. Africa								
	1	Ethiopia	4	0.27	-	-	-	-
	2	Kenya	5	0.34	1	0.64	-	-
		Total (Africa)	9	0.61	1	0.64	-	-
V. Unknown source			35	2.37	5	3.21	1	1.28
		Grand total	1478		156		78	

states, Uttar Pradesh had 31 accessions followed by Karnataka (6), Andhra Pradesh (5) and source of one accession was not known. Thus, the number of accessions present in C_1 and C_2 represented adequately with the number of accessions present in the entire collection. However, entries of C_1 corresponded more with the entries of entire collection than the C_2.

Mean, range, variance and co-efficient of variability of eleven quantitative traits of entire collection, C_1 and C_2 are presented in Table 2. The difference between the means of entire collection and C_1 were non significant for all the eleven traits considered for forming core set. The difference was also non significant for all the traits except plant height in C_2. The homogeneity test for variances between entire collection and C_1 was non significant for all the traits. It was also non significant for all the traits between entire collection and C_2. The range for the traits studied in both C_1 and C_2 were almost similar to the range of the traits in the entire collection. From these variability characteristics, it is evident that two cores formed from two different methods, *viz.*, PCA scores and power core was adequate representative of the entire collection.

In all the three sets (entire, C_1 and C_2), scores were recorded for different sub descriptors of 12 qualitative traits and are presented in Table 3. In order to test whether the ratio of sub descriptors of qualitative traits of core sets formed were in accordance with the ratio of entire collections, chi-square (χ^2) test was done. The χ^2 values for both C_1 and C_2 were non significant indicating that both the methods were successful in forming cores that are true representative of entire collection.

Shannon-Weaver diversity index (H') which indicates the presence of genetic diversity for an individual trait

Table 2. Comparison of mean, range, variance and co-efficient of variability for the quantitative traits in the entire collection and core sets of foxtail millet

S.No.	Characters	Range			Mean			Difference	
		E	C_1	C_2	E	C_1	C_2	C_1	C_2
1.	Days to 50% flowering	33-69	33-69	33-69	49.242	49.391	48.372	NS	NS
2.	Plant height (cm)	52.20-184.00	95.20-184.00	52.20-180.00	142.430	142.858	132.180	NS	*
3.	Number of basal tillers	1.00-12.20	1.00-12.20	1.00-12.00	3.915	3.737	3.908	NS	NS
4.	Flag leaf length (cm)	16.00-47.50	16.00-47.50	17.00-47.50	27.683	28.182	29.114	NS	NS
5.	Flag leaf width (cm)	0.78-4.40	0.85-3.50	0.85-4.40	1.512	1.534	1.597	NS	NS
6.	Peduncle length (cm)	13.40-56.50	13.80-56.50	15.25-56.50	28.055	28.126	29.858	NS	NS
7.	Ear length (cm)	3.60-24.50	3.80-24.50	3.60-23.80	14.766	15.068	15.025	NS	NS
8.	Panicle exertion	1.50-29.00	1.50-29.00	2.70-29.00	13.315	13.135	14.060	NS	NS
9.	Days to maturity	72-110	72-110	72-110	90.800	91.083	89.244	NS	NS
10.	Grain yield per plant (g)	2.10-23.80	2.80-20.00	2.10-23.80	9.751	10.238	10.014	NS	NS
11.	1000-grain weight (g)	1.90-4.00	2.00-4.00	2.00-3.90	3.069	3.034	2.999	NS	NS

Table 2. Contd.

S.No.	Characters	Variance			Difference		CV (%)		
		E	C_1	C_2	C_1	C_2	E	C_1	C_2
1.	Days to 50% flowering	13.926	24.046	35.276	NS	NS	7.578	9.928	12.279
2.	Plant height (cm)	195.518	197.378	701.881	NS	NS	10.379	9.834	20.043
3.	Number of basal tillers	2.009	3.008	5.225	NS	NS	36.204	46.410	58.491
4.	Flag leaf length (cm)	30.401	44.970	51.114	NS	NS	19.917	23.795	24.557
5.	Flag leaf width (cm)	0.078	0.103	0.355	NS	NS	18.471	20.922	35.110
6.	Peduncle length (cm)	19.711	33.055	62.864	NS	NS	15.825	20.441	26.555
7.	Ear length (cm)	5.973	9.915	10.970	NS	NS	16.551	20.897	22.044
8.	Panicle exertion	11.016	17.704	24.649	NS	NS	24.927	32.034	35.311
9.	Days to maturity	45.274	50.296	68.524	NS	NS	7.410	7.786	9.276
10.	Grain yield per plant (g)	15.212	16.884	18.786	NS	NS	39.999	40.135	43.282
11.	1000-grain weight (g)	0.133	0.150	0.192	NS	NS	11.883	12.765	14.611

NS-Non Significant at P=0.05

was estimated for all the 23 traits in the three sets (entire, C_1 and C_2) (Table 4). The comparison between average H' values of 11 quantitative and 12 qualitative traits of entire collection and C_1; entire collection and C_2 indicated the presence of diversity of entire collection in both C_1 and C_2. Thus, the diversity of entire collection was well captured in both the cores, representing the entire collection. But when the Shannon-weaver Index of both the cores was compared, the diversity pattern showed that for each of the qualitative variables except for three, the diversity index was higher for C_2 (PowerCore) compared to C_1 obtained from PCA scoring method indicating the preciseness of power core. This might be accounted for the decrease in the redundancy of the alleles in the accessions of the core set formed using Powercore which resulted in decreased sample size (5%) compared to PCA scoring method (10%).

Comparing the two core forming techniques, PCA score method aims at improving the percentage of sampled diversity without modifying the relative intensity of the selection (10%) as proposed by Brown (1989). In contrast, this technique does not consider the qualitative traits which symbolize principally the phylogenetic diversity. On the other hand, PowerCore has many advantages over the PCA technique. Firstly, PowerCore takes into account the uniqueness in the value of an accession for each character including qualitative traits during the filling of the diversity cells and retains all classes in the core collection. Secondly, increase in number of classes leads to more accessions being selected to fill in the range thus giving more weight or capturing more diversity in the particular character.

A sampling method to obtain a core set should maximize the diversity in the core set thus by reducing the repetitiveness of the identical genotypes. The frequencies of the rare classes should increase with reduction in most represented classes. The core sets thus extracted can be used to widen the genetic base of their breeding population by identifying new yield promoting and other desirable alleles. Core sampling also helps in

Table 3. Descriptors, descriptor states, score code and phenotypic proportions in entire collection (E) and core sets (C_1 and C_2) of foxtail millet

S.No.	Descriptor	Descriptor state	Score code	E	C_1	C_2	χ^2	
							C_1	C_2
1	Plant pigmentation	Non-pigmented	0	1292	139	64	NS	NS
	at flowering	Pigmented	1	186	17	14		
2	Blade pubescence	Essentially glabrous	1	1469	153	77	NS	NS
		Medium pubescent	5	7	2	1		
		Strongly pubescent	9	180	17	10		
3	Sheath pubescence	Essentially glabrous	1	154	17	8	NS	NS
		Medium pubescent	5	1144	122	60		
		Strongly pubescent	9	180	17	10		
4	Senescence	Actively growing	1	160	27	11	NS	NS
		Dead	9	1318	129	67		
5	Inflorescence lobes	Absent	0	250	28	16	NS	NS
		Short	3	979	90	43		
		Long	7	244	36	18		
		Large and thick	9	5	2	1		
6	Inflorescence bristles	Absent	0	27	4	4	NS	NS
		Very short	1	146	18	10		
		Short	3	289	28	17		
		Medium	5	496	51	22		
		Long	7	508	52	23		
		Carrying a spikelet	9	12	3	2		
7	Lobe compactness	Loose	3	27	5	4	NS	NS
		Medium	5	173	16	12		
		Compact	7	1000	104	47		
		Spongy	9	276	31	15		
8	Inflorescence shape	Cylindrical	1	1378	143	70	NS	NS
		Pyramidal	2	99	13	8		
		Obovate	3	1	0	0		
9	Inflorescence compactness	Loose	3	208	24	11	NS	NS
		Medium	5	508	51	25		
		Compact	7	341	31	20		
		Spongy	9	421	50	22		
10	Fruit colour	Red	1	52	6	7	NS	NS
		Black	2	22	2	2		
		White	3	1018	113	51		
		Yellow	4	386	35	18		
11	Grain shape	Oval	1	1310	136	64	NS	NS
		Elliptical	2	168	20	14		
12	Apical sterility in panicle	Absent	0	708	78	46	NS	NS
		Present	1	770	78	32		

NS- Non Significant at P=0.05

defining a specific characteristics in which portion of the entire collection is likely to be found. The two methods used to construct foxtail core sets were found to preserve the variation of the entire collection as shown by their non significant differences thereby representing the total diversity of the entire collection. These core sets can be extensively examined for all economically important traits. The data generated will provide the information on genetic variability in foxtail millet. This core set developed should be revised periodically as additional accessions and information becomes available.

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Table 4. Shannon-Weaver diversity index (H') for 11 quantitative and 14 qualitative characters in the entire collection (E) and core sets (C_1 and C_2) of foxtail millet

S.No.	Character	Shannon–Weaver Index		
	Quantitative character	E	C_1	C_2
1	Days to 50% flowering	2.092	2.321	2.453
2	Plant height (cm)	2.132	2.100	2.660
3	Number of basal tillers	2.293	2.371	2.496
4	Flag leaf length (cm)	2.615	2.721	2.802
5	Flag leaf width (cm)	1.712	1.782	2.254
6	Peduncle length (cm)	2.071	2.198	2.497
7	Ear length (cm)	2.254	2.416	2.495
8	Panicle exertion	2.263	2.416	2.606
9	Days to maturity	2.195	2.139	2.430
10	Grain yield per plant (g)	2.635	2.627	2.652
11	1000 grain weight (g)	2.614	2.590	2.717
	Mean ± SE	2.261 ± 0.08	2.335 ± 0.08	2.551 ± 0.04
	Qualitative character			
1	Plant pigmentation at flowering	0.378	0.344	0.470
2	Blade pubescence	0.040	0.355	0.270
3	Sheath pubescence	0.690	0.675	0.699
4	Senescence	0.343	0.461	0.407
5	Inflorescence lobes	0.890	1.020	1.068
6	Inflorescence bristles	1.393	1.577	1.608
7	Lobe compactness	0.906	0.935	1.063
8	Inflorescence shape	0.251	0.287	0.555
9	Inflorescence compactness	1.339	1.339	1.347
10	Fruit colour	0.885	0.890	1.264
11	Grain shape	0.465	0.474	0.623
12	Apical sterility in panicle	0.692	0.693	0.677
	Mean ± SE	0.689 ± 0.12	0.754 ± 0.11	0.837 ± 0.12
	Overall mean ± SE	1.48 ± 0.78	1.55 ± 0.79	1.70 ± 0.85

PowerCore (v. 1.0) software and his guidance in forming core.

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Kheep (*Leptadenia pyrotechnica*): Potential Rangeland Shrub of Western Rajasthan, India

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Kheep (*Leptadenia pyrotechnica* [Forsk.] Decne) is a widely distributed shrub in western Rajasthan, India. Having xerophytic characters, it is well adapted to harsh edapho-climatic conditions of hot arid region. It is one of most important fibre yielding plants of Thar Desert. It is also traditionally used as food, medicine and thatching purpose by the desert dwellers. As a drought hardy shrub, it plays an important role in arid ecosystem as a greening vegetation in the time of less and erratic rainfall. This paper presents the state of available information on ethnic uses, potential and future research needs of the species.

Key Words: Hot arid regions of India, Fibre, *Leptadenia pyrotechnica*, Kheep, Sand dune, Western Rajasthan

Harsh climatic conditions such as low and erratic rainfall, high evapotranspiration demand, extreme temperature, high wind velocity coupled with poor fertility and water holding capacity of soil resulted in sparse vegetation in hot arid western Rajasthan.The physiognomic aspect of the desert is poor, scanty, xerophytic vegetation, widely dispersed, leaving large barren land. Indian arid zone has 682 species (Bhandari, 1990) of which only 48 species are shrubs. Though, shrubs are less in number of species, they are ecologically most successful biotypes and have maximum share with respect to vegetation cover in the desert environment (Singh *et al.*, 2008). The species like Bordi [*Ziziphus nummularia* (Burm.f.) Wt.], Bawli [*Acacia jacquemontii* Benth.], Lana [*Haloxylon salicornicum* (Moq.) Bunge ex Boiss.], Phog [*Calligonum polygonoides* L.], Kheep [*Leptadenia pyrotechnica* (Forsk.) Decne.], Kair [*Capparis decidua* (Forsk.) Edgew.], Anni [*Clerodendrum phlomidis* L.f.], Aak [*Calotropis procera* (Ait.) R.Br.], Sinia (*Crotalaria burhia* Buch.-Ham.) are the important arid zone shrubs. The halophyte shrubs, *viz.*, Khara lana [*Haloxylon recurvum* (Moq.) Bunge ex Boiss], Lani [*Salsola barysoma* (Roem. and Schult.) Dandy], Luni [*Suaeda fruticosa* (L.) Forsk.], etc. are also the important species of the saline soils in hot arid region.

Leptadenia pyrotechnica (Forsk.) Decne (Family: Asclepiadaceae) locally known as Kheep is one of the important shrubs of natural vegetation of western Rajasthan. It is an erect, much branched, often leafless shrub with watery sap, up to 1.5 m high, sometimes attains a height of 3 m (in protected sites). It occurs on deep, sandy and soils having gravely subsoil in arid region. Natural stands of Kheep (*L. pyrotechnica*) trap the moving sand particles resulting in formation of sand hummocks. In many places, the dunes and interdunal plains are usually barren except for some *L. pyrotechnica,* along with Bui (*Areva pseudotomentosa*) and Sinia (*Crotalaria burhia*). Together with, another Asclepiadaceae species, *Sarcostemma acidum* (Roxb.) Voigt, *L. pyrotechnica* forms a degradation stage of *Calligonum polygonoides* (Mehor-Homji, 1977).

L. pyrotechnica is widely distributed in India, Pakistan, Iran, Israel, Arabia and northern and Sub-Sahalian Africa (Ali, 1983). In India, it is a typical species found on sandy soil throughout western Rajasthan. Being possessing xerophytic characters *L. pyrotechnica* is well adapted to harsh arid conditions of western Rajasthan. Studies on *L. pyrotechnica* in the Egyptian desert shown that it possesses highly effective mechanisms of drought resistance (Migahid *et. al.*, 1972). It has been found to have roots extending to a depth of 11.5 m with lateral extensions to 10 m (Batanouny and Abdel Wahab, 1973).

In the wake of degradation of natural resources and risk associated with arable crops, there is an urgent need of harnessing the potential of this underutilized shrub, which has multiple uses.

Materials and Methods

The information regarding ethnic uses of *L. pyrotechnica* was collected from the Bikaner, Jaisalmer, Churu, Hanumangerh and Sriganganagar districts of North-western Rajasthan during survey attempted to collect the germplasm of arid rangeland shrubs during year 2001-2003. The information was collected from inhabitants of above mentioned districts of hot arid region through

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personal interview method. In the present paper, an attempt has been made to pool up the information collected from survey with available information from the diffused literature.

Ethnic Importance

The *L. pyrotechnica* caters various needs of inhabitants of arid region (Table 1). The detailed information regarding its ethnic uses is as under.

Food: The unripe pods known as '*Khipoli*' are used as vegetable by local inhabitants of western Rajasthan and are supposed to be delicious and nutritious. In arid parts of Gujarat (India), its tuberous roots are consumed as vegetable (Tikka and Jaimini, 2005; Vyas, 2005). The leaves and tender shoots of another species *L. reticulata* (Retz.) Wt. & Arn. is also used in some parts of India as a vegetable, especially during times of scarcity. Its follicles (fruits) known as '*Shinguti*' or '*Dodhi*' are also sometimes used.

Fodder: Kheep is browsed by camel and goats in times of drought. Young branches are used as fodder during scarcity period. It is described as one of the important fodder for horses, cattle and camel in the *Sind Gazetteer* (Watt, 1989-93). Inhabitants of surveyed region opined that if Kheep is much browsed by the camel and goats it adversely affect their reproduction in the upcoming years. They also informed that it adversely affected the semen formation in camels and creates reproductive problems in she camel. Skin problem in goat and camel is reported after over browsing of Kheep.

Fibre: Kheep is recognized as one of the important fibre yielding plants since ancient times in the arid region. It is traditionally used for making cordage and ropes. These ropes are used for fastening the firewood bundles. Ropes for *charpoys* (cots) are also prepared, particularly because the green watery latex (juice) present in the stem prevents it fibre from decomposing (Bhandari, 2005). Being fairly resistant against rotting, its rope are used to draw water from wells, particularly in Sindh Provenance of Pakistan, where it frequently blend with fibre of *Periploca aphylla* Decene (Watt, 1889-93).

Medicine: Local inhabitants of arid region from centuries use Kheep as an antihistaminic and expectorant. Bed prepared from its green branches is used to cure fever and sometime sheet of branches is used to cover body to reduce high temperature. In the villages, its juice is used to melt or remove the spines from the body part. Plant juice is mixed with sugar and crushed wheat, and then tied on the affected body part to take out the thorn (Bhandari, 2005). Plant paste is applied over the paralyzed portion of the body for relief. It is applied in paste form to cure boils and blisters. Plant sap is used to cure eczema and skin diseases by Garsia tribe (Singh and Pandey, 1998) in Rajasthan. Kumar *et al.* (2005) reported detailed ethno-medicinal uses for abortion, antidote, typhoid, arthritis, rheumatism, flatulence, tumour and skin irritation in western Rajasthan. Oil extracted from it, known as "*Kubjprasarni* oil" is used in bones disorders and stone cases. As a veterinary herbal, stem decoction is given to cattle after delivery to facilitate the expulsion of 'Jair' (placenta) and also given to cattle for removing fatigue (Takhar, 2004; Bhandari, 2005). Stem is boiled and given orally to sheep to maintain smooth movement of joints (Takhar, 2004).

Table 1. Common uses of *L. pyrotechnica* in arid region

Ethnic Importance	Item/form	References
Food	Unripe pods and roots as vegetable	Tikka and Jaimini, 2005; Vyas, 2005
Fodder	Young/tender shoots	
Fibre	Branches for making cordage and ropes	Bhandari, 2005
Medicine	Plant sap, decoction	Kumar *et al.*, 2005, Takhar, 2004
Fuel wood	Dried stem and roots	–
Biofence	Row of plants on field boundary	
Other uses	Thatching material, brooms	–

Fuel wood : With diminishing availability of common fuel wood species like Phog (*Calligonum polygonoides*) and Khejri (*Prosopis cineraria*) in western Rajasthan, local people started to use Kheep as fuel wood. It is fulfilling the need of fuel wood in the area where the quality wood either not available or costly. It is also much used in *Bhattis* (furnace) for preparing *Mava* (condensed milk) from the milk as substitute wood of Phog (*C. polygonoides*). The local inhabitants of the region were with the impression that large amount of smoke produced during burning of its wood is harmful to human health and caused problems like headache, giddiness and eye problems.

Biofence: Kheep is also used as biofence around the field boundaries. It is supposed to check the soil erosion and also the protection from stray animals. However, its adverse effects on the adjoining rows of crop plants are also reported by some of the farmers. They believe that rain water falling through the Kheep plants adversely

affects the soil quality and thereby crop production. It needs detailed scientific study in this direction.

***Social and religious aspect*:** Dried Branches are used in funeral ceremony for making the *Sidhi* (ladder) for carrying the dead body.

***Other uses*:** Since long, Kheep is extensively used for thatching purpose. In western Rajasthan, it is used for making sidewalls of huts and animal sheds in rural areas. Serving dishes are made for keeping cooked vegetable and other things (Kumar *et al.*, 2005). Brooms are also made from its stems. Camel carts carrying the loads of *L. pyrotechnica* branches are a common feature in the area, which fulfill the local demand for thatching and other purposes.

Exploitation Potential

Fibre: There is growing awareness of utilizing the newer plant resources all over the world for a variety of products. Utilization of indigenous shrubs that constitute a major part of woody vegetation is important to livelihood of the people of arid region. Many such species offer considerable scope for the extraction and use of fibre for cordage, ropes and handicrafts (Singh *et al.*, 2005). Its production potential can be very well utilized in small-scale cottage industries in the area.

Various researchers have dealt quality aspect of *L. pyrotechnica* fibre from India and Pakistan (Jamil, 1970, Jamil *et al.*, 1971; Manavalan *et al.*, 1979; Mojumdar *et al.*, 2001). Jamil (1970) have opined that Kheep fibre is better than most of the bast fibres and can be ranked along with flax and ramie in quality. Mojumdar *et al.*, (2001) reported that owing to high a-cellulose and low lignin contents along with favourable length/breadth ratio of its fibre make it suitable for use in blending with cotton or polyester fibres to produce blended textiles yarns and in pulp and paper industries. Laghari (1983) reported that its fibre accepts silk dyes, but not dyes suitable for cotton or wool. Further, he has been able to prepare ropes, carpets and similar items by spinning the thread on the indigenous handloom. It has also been suggested that Kheep fibre – wool industries may be established on a large scale for this purpose.

During the survey of Northwestern Rajasthan by the authors, it was observed that for making ropes, the branches are spread on the roads before extracting the fibre. This method also vogue in Pakistan (Laghari, 1983) as tyred motor vehicles run over them, thus simulating the stress to which they are subjected when spread on sandy tracts to provide traction for vehicles. Ali (1986) mentioned that this method in separation of fibres has yet to be examined and tried commercially.

Food/green vegetable: The unripe fruits locally known as '*Khipoli*' reported to be rich in nutrients. It contains about 23.18 per cent fibre, 9.83 per cent carbohydrate and 3.13 per cent protein with energy value of 68.4 kcal/ 100 g. It is also fairly good source of minerals e.g., phosphorus, potassium, calcium, sodium, iron and vitamin C having 317 mg, 226 mg, 156 mg, 125 mg, 3.48 mg and 39 mg per 100 g, respectively (Goyal and Choudhary, 2005). They found that Kheep could be used as cheap and readily available ingredient for the diet in the arid region. Thus, nutritionally it is well balanced in term of major and micronutrients and can be included in food basket of local inhabitants having low purchasing power.

Raw material for pharmaceuticals: Effectiveness of alcoholic stem and flower of Kheep against typhoid fever caused by *Salmonella typhi* was reported by Gehlot and Bohra (2000). Furthermore, the presence of various phenolic compounds and alkaloids in *L. pyrotechnica*, adds new dimensions to its pharmaceutical values. A new pentacyclic triterpenoid, named leptadenol, was isolated from a hexane extract of *L. pyrotechnica* collected from Dumba Goth, near Karachi in Pakistan (Noor *et al.*, 1993). Manavalan and Mithal (1980) confirmed presence of triterpenoids, taraxerol and fernenol and b-sitosterol in *L. pyrotechnica.* Resemblance of *L. pyrotechnica* acid phosphatase with human prostatic acid phosphomonoesterase was reported by Dhawan and Singh (1976b). They also reported presence of amino acids (and lysine, arginine, alanine, threonine, methionine, isoleucine and 2-dipeptides) and sugar (raffinose, sucrose, glucose and fructose) in it (Dhawan and Singh, 1976 a). Thus, the use of *L. pyrotechnica* to cure various diseases and disorders in vogue since long back, and there is an urgent need to unfolding the secrets of its medicinal values through modern scientific tools to expand its uses further.

Fodder resource during drought: Sporadic evidences are available about its use as fodder for livestock particularly for camels. Chemical analysis of *L. pyrotechnica* attempted by Dhir *et al.* (1984) and Sharma *et al.* (1984) revealed that it is comparable to other shrubs and trees of arid western Rajasthan with respect to macro and micronutrients contents (Table 2). Abdalla *et al.* (1995) from United Arab Emirates reported 6.94 per cent crude protein content with gross energy of 4.89 kcal/g DM in it. Venkatesh *et al.* (1971) and Venkatesh and Singh (1973)

reported maximum ascorbic acid content 123 mg per 100 g green leaves of Kheep during winter months followed by rainy season (63 mg/ 100 g) and summer (36 mg per 100 g) season. Chromatographic analysis revealed the presence of raffinose and fructose (Dhawan and Singh, 1976a). Detailed investigations are required to evaluate its fodder value and validate the belief of its adverse effect for anti-quality factors in camel and goats.

Material of sand dune stabilization: Shrubs have a key role in resisting soil erosion due to their wider adaptability and ability to withstand biotic pressure, *L. pyrotechnica* showed high potential local raw material using in the checkerboard or parallel hedges as micro wind breaks to halt the movement of sand prior to planting work in sand dune stabilization programme. It has an important role in initial colonization of the bare dunes when its material is used in the checkerboard. The intact ripe fruits with its branches germinate in favorable condition, provide good protection against wind erosion and establish well in adverse conditions. On sand dunes it also does well with indigenous perennial grasses like *Panicum turgidum*. It is one of the potential species used for desert control in Mauritania (Hadjej *et al.*, 1991). In Abu Dhabi, forest areas are being extensively interplanted with fodder shrubs such as *Atriplex, Calligonum comosum* and *Leptadenia pyrotechnica* by the Forest and Agriculture Departments (Khan, 1982).

Suitability as biofence in agricultural fields: As inhabitants believe that the Kheep plants adversely affect the soil quality and thereby crop production. It needs detailed scientific study in this direction. Root and shoot extracts of *L. pytotechnica* exhibit negative effect on germination of arid shrub *Phog* (*Calligonum polygonoides*) and *Sewan* grass (*Lasiurus scindicus*) (Gautam and Bishnoi, 1991).

Conclusions

Western Rajasthan represents a range of diversity in native shrubs, which occur on a wide range of habitats. Some of these species like *L. pyrotechnica* grow in extreme desert conditions and survive in harsh climatic. The diverse material of this indigenous shrub offer a good scope in arid ecosystem to exploit the fiber potential and medicinal value of this shrub along with other ethnic uses. It can supply the raw material even in the times of drought and low rainfall condition. The wastelands and other marginal lands can be utilized for planting this species. This will be particularly useful on those areas where this species make the dominant cover even in times of drought. There is an urgent need to collect and evaluate the diverse germplasm of *L. pyrotechnica* from its natural distribution cover in the hot arid region. Suitable genotypes for different purposes like food, fodder, fibre, and medicinal value can be identified with multidisciplinary team of research organizations.

Table 2. Elements in *Leptadenia pyrotechnica* (Kheep)

Nutrient	Content	Reference
Phosphorus	0.140 %	Dhir *et al.*, 1984
Calcium	2.72 %	do
Magnesium	0.56 mg/100 g	do
Potassium	1.36 %	do
Sodium	0.077 mg/100 g	do
Zinc	22 ppm	Sharma *et al.*, 1984
Manganese	80 ppm	do
Copper	15.5 ppm	do
Iron	131	do

Future Thrust

- Germplasm collection, evaluation and characterization from arid region;
- Standardizing the propagation technique and agro techniques;
- Introduction of suitable genotypes in wasteland development programme and integration in various Alternate Land Use Systems (ALUS) in farming system perspective;
- Designing cost effective technology to extract its fibre and identifying use on commercial scale;
- Identification and characterization of secondary metabolites of pharmaceutical significance;
- Evaluating for anti-quality factors and exploring the possibilities of its use as livestock fodder during drought and scarcity period.

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Durability of Packing Systems for Cost Effective Conservation of Germplasm

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Germplasm is generally conserved in genebanks wherein temperature and relative humidity are adjusted according to term of storage. At Directorate of Wheat Research, Karnal, more than 10,000 wheat accessions are conserved under medium-term storage facility. However, it proved to be a costly affair. As an alternative to cut costs, 7,691 accessions were stored in a room under cold dry conditions at 3,000 m above sea level at Dalang Maidan, Lahaul and Spiti, Himachal Pradesh (HP), India. Three types of packing, namely, cloth bags (A), water proof paper bags (B) and water proof aluminium bags (C) were used for storing. In order to observe the effects and durability of the packing system on viability of seeds stored under these conditions, germinability of a sample comprising of 29 accessions was recorded every year. The difference in germination under two conditions after eight years of storage was non-significant indicating that conservation costs can be reduced by storing material under natural cold dry conditions. Besides, the stability parameters revealed that genotypes C 306, CPAN 3004, GW 173, HD 2009, HD 2285 and HP 1744 were stable in germination and therefore, these genotypes can be stored in any of the packing systems, the most economical and convenient being packing A.

Key Words: Conservation, Cost effective, Genebank, Germplasm, Packing systems, Stability, *Triticum aestivum*

Introduction

The commercialization of agriculture, area development projects and other related activities have led to shrinking of diversity in genetic resources. To save the biodiversity from unforeseen disasters and extinction and to ensure its availability for future, it is conserved using both *in situ* and *ex situ* means. *Ex situ* conservation of plants involves three methods, namely, field genebanks, seed banks and *in vivo* storage. Of these, seed banks are the most efficient and effective method of conservation for orthodox seed. It is an effective and compact method of storage. The seeds are placed in packets and stored in medium-term storage facilities (maintained at 0 to 5°C temperature and 15-20% relative humidity) as active collections. Most of the material is also kept in long-term storage facilities (held at colder temperatures, –20°C to –18 °C). The seed samples are expected to remain viable for 20-30 years in medium-term storage and for up to 100 years in long-term storage depending upon the species, the initial seed quality and specificity of storage environment and general state of infrastructure (such as electricity supplies), etc. (Koo *et al.*, 2002).

However, conserving germplasm in genebanks at low temperature and at low moisture regime is a reasonably costly affair, which includes labour, buildings, equipments, electricity supply, power back up, their maintenance and other operational costs (Pardey *et al.*, 2001). According to a study (Koo *et al.*, 2003), the cost for conserving and distributing the genetic material held in CGIAR genebanks is US $5.7 million per year while to provide these genebank services to all future generations may cost US $149 million. With heavy competition for funding among the world's research institutions, genebanks generally have not fared well (Duvick, 1995; McFerson *et al.*, 1996). Due to lack of funds, equipment malfunction and unreliable power supply, seed genebanks in developing countries often have a hard time fulfilling their mandate to conserve plant genetic resources for future use. Therefore, in order to cut cost, alternative conservation strategy has to be explored.

At Directorate of Wheat Research (DWR), Karnal, wheat germplasm is conserved in medium-term storage facilities where temperature is maintained at 4 ± 1 °C temperature and 23% relative humidity in water proof aluminium packets. Before storage, the seed moisture content is reduced to 9–10%. One set of the germplasm is stored under cold dry natural conditions at DWR Regional Station, Dalang Maidan, Lahaul and Spiti (HP). The station is situated at an altitude of 3,000 m above sea level, where the average maximum temperature remains around 15°C during summers and up to –22 °C during winters. At this station, the germplasm is stored in a room using three types of packings; (i) cloth bags (A), (ii) water proof paper bags (B) and (iii) water proof aluminium bags (C). Presently, about 10,339 accesssions comprising of *T. aestivum, T. dicoccum, T. durum* and *Triticale* are conserved in the module at DWR. Of these, 7,691 accessions are also stored at alternative place,

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Dalang Maidan. In order to determine the economical efficiency of conservation under natural conditions and durability of packing system for storage over eight years period under cold dry conditions, these accessions were evaluated for their germination percentage from 1999 to 2006 and the results are discussed in this paper.

Materials and Methods

Of the 90 accessions stored under natural cold dry conditions in 1998, twenty nine were randomly selected and were evaluated for their germination percentage. With the addition of new accessions every year, the total number of accessions stored at Dalang Maidan has risen to 7,691. However, these twenty nine accessions were evaluated for their germination percentage every year from 1999 to 2006. Four replications of each accession of twenty five seeds from each type of packing were germinated on moist filter paper in petri dishes. The experiment was laid out in completely randomized block design (CRD) with four replications under lab conditions at DWR, Karnal, during November every year. The same accessions from Karnal genebank were evaluated once during 2006 after eight years of conservation. The data on germination percentage was recorded and analyzed following the design of experiment. Packing system in which genotypes' germination remained consistent and did not change over eight years was considered durable. The data were subjected to combined analysis of variance as per Eberhart and Russel (1966) Model considering packing and storage duration as environments, separately.

Results and Discussion

The analysis revealed significant differences over different years and accessions stored under natural conditions at Dalang Maidan, Lahaul and Spiti location. The average germination decreased marginally from 97.7% in 1999 to 88.0% in 2006. However, the germination percentage under medium-term storage facility for 8 years was 100% irrespective of the accessions investigated. The type of packing used for storage also influenced the germination pattern. It was statistically significant for seeds stored in different packings. Germination percentage for cloth bags (packing A) and aluminium packing (C) as well as cloth bags and waterproof paper bags was significantly different for all the years. However, the difference in water proof paper bags and aluminium packing was non-significant initially for 5 years (1999-2003) but was significant thereafter (Table 1). The average germination was recorded the least (90%) in cloth bags followed by that in water proof paper bags (93%) and the maximum in water proof aluminium bags (95%). Over the years, the decline in germination percentage was from 96 to 82% in cloth bags, from 98 to 88% in water proof paper bags and from 99 to 94% in water proof aluminium bags.

The analysis of variance (Table 2a) revealed that genotypes and environments were significant ($p = 0.01$) in all the packing systems indicating differences among the genotypes and environments (storage duration). However, genotype x storage duration interaction was significant ($p = 0.01$) in packing system A and C indicating that germination behaviour of genotypes was inconsistent with duration. Packing system B did not exhibit genotype x storage duration interaction, revealing that genotypic response to germination pattern for eight years period was consistent. The variance due to storage duration (L) and genotype x storage duration (L) when tested against pooled deviation mean square was found significant ($p = 0.01$). Similarly, pooled deviation when tested against pooled error was also found significant ($p = 0.01$) indicating that both linear and non-linear components of variance contributed to genotype and storage duration (environment) interaction.

Considering the packing system as environments, the germination percentage data were separately analysed over different durations of storage. The results of analysis (Table 2b) revealed that genotypes were found to be significant ($p = 0.01$) after one, three, four, six and seven years of storage duration, while environments (packing) showed significance in all storage durations. The genotype x packing interaction component of variance,

Table 1. Mean germination[s] (%) of accessions stored under natural conditions

Year	Duration of storage (years)	Packing A	Packing B	Packing C	CD
1999	1	96.2	97.7	98.8	2.354
2000	2	92.5	95.6	95.3	2.227
2001	3	94.1	96.0	96.7	2.307
2002	4	90.9	94.4	94.8	2.350
2003	5	87.3	92.3	91.4	2.556
2004	6	87.6	91.1	93.8	2.395
2005	7	86.1	89.8	95.0	2.421
2006	8	82.1	87.6	94.3	2.544

Table 2(a). ANOVA for genotype x storage duration interaction for germination of wheat genotypes in three packings

Source	d.f.	Packing A	Packing B	Packing C
Genotype (G)	28	**	**	**
Storage Duration (S)	7	**	**	**
G x S	196	**	ns	**
S + (G* S)	203	ns	ns	ns
S (L)	1	**	**	**
G x S (L)	28	**	**	**
Pooled Deviation	174	**	**	**

** = indicate mean squares significance at 1% level,
NS = mean squares non-significant

Table 2(b). ANOVA for genotype x packing interaction for germination of wheat genotypes in eight storage duration

Source	d.f.	Storage duration (years)@							
		1 (1999)	2 (2000)	3 (2001)	4 (2002)	5 (2003)	6 (2004)	7 (2005)	8 (2006)
Genotype (G)	28	**	*	**	**	*	**	**	*
Packing (P)	2	**	**	**	**	**	**	**	**
G X P	56	**	ns	**	ns	ns	ns	ns	ns
P + (G* P)	58	**	**	**	**	**	**	**	**
P (L)	1	**	ns	ns	*	*	ns	**	ns
G x P (L)	28	ns	ns	ns	ns	ns	ns	ns	ns
Pooled Deviation	29	**	**	**	**	**	**	ns	**

*, ** = indicate mean squares significance at 5% and 1% level,
NS = mean squares non-significant,
@ parenthesis indicate year of germination test.

however, was significant only in two cases *i.e.* after one and three years of storage duration, revealing that genotypes and packing interacted. This indicated that germination of the stored genotypes in different packings remained consistent over different storage durations. The components of environment (packing) (linear) were observed to be significant in all durations of storage. The G x E (linear) interaction, however, was significant for one, four, five and seven year durations. Pooled deviation when tested against pooled error was found to be significant in all storage durations except for seven year duration.

Mean performance of genotypes stored in different packing systems (Table 1) from 1999 to 2006 varied from 82.1% (in A packing 2006) to 98.8% (in C packing 1999). In general, germination percentage was the highest in packing C from 1 to 8 years of storage followed by packing B. But, statistically both were at par. Germination percentage in packing A from 1999 to 2006 was significantly low. Based on overall mean performance of germination and interaction of genotypes with duration of storage, packing system B was found to be superior over A and C packing. Non-significant G x E interaction in case of B packing revealed that germination pattern of all genotypes was consistent and predictable under different durations of storage.

When germination pattern of genotype was analyzed after different durations of storage over three packing systems, it was observed that genotypes interacted with the packing systems only after one and three years of storage duration. In remaining cases, the germination pattern was consistent and predictable. This showed that packing system based on overall mean performance of different genotypes could be adjudged superior or inferior. This further confirmed that packing system B, which did not exhibit genotype x storage duration interaction and showed statistically better germination pattern was superior over the two other systems of packing. The packing system B (water proof paper bag) was also economical and convenient for storage than packing system C (water proof aluminium bags) and hence, was found to be durable.

The germplasm storage in genebanks involves maintenance of low temperature and low relative humidity. At Dalang Maidan, the climatic conditions are cold and dry, which support the survival of germplasm. It is evident from high germination percentage observed during the present study. However, there was reduction in germination over eight years, 15% in case of cloth bags, 10% in water proof paper bags and 5% in water proof aluminium bags. This is attributed to packing type. The non-water resistant packing *i.e.* cloth bags had maximum

reduction whereas the difference in reduction in germination in water proof packings was non-significant.

On examining the individual genotypic response, in different packings and for different storage durations, it was observed that the highest (100%) germination was recorded in ten genotypes in packing A, eight in B and two in C after one year of storage, one genotype each in B and C packing after two years storage. Eight genotypes in packing C and four each in packing A and B recorded 100% germination after three years storage duration. In general, some of the genotypes in packing C recorded up to 98% germination after 4 to 8 years of storage duration.

According to Eberhart and Russel (1966) model, regression coefficient (bi) equal or near to one coupled with zero squared deviation from linear regression (s^2d) indicated average stability. When this is associated with higher genotypic mean value than the population mean, genotypes were categorized having general adaptability and when associated with lower mean value, genotypes were termed poorly adapted to all environments. Based on this, the stability parameters i.e. regression coefficient (bi) and squared deviation from linear regression (s^2d) in packing A and C revealed that genotypes C 306, CPAN 3004, GW 173, HD 2009, HD 2285, HP 1731, HP 1744 and HI 977 were found to be stable in performance. This emphasized that considering the economics of three different packing systems, these genotypes could be stored in cheapest and easiest packing. Genotypic response to different storage durations over three packing systems revealed that GW 173, HD2009 and HD 2285 genotypes recorded consistent germination pattern for all eight durations of storage, while C 306, CPAN 3004 and HP 1744 for seven, GW 190, HD 2329 and HI 977 for six, HP 1731 and HUW 206 for five and HP 1633 and HUW 234 for four durations. These results suggested that the genotypes showing consistent behaviour for 7-8 durations were suitable for medium-term storage in any of the packing systems, possibly the most economical and convenient one *i.e.* packing A, cloth bags than water proof paper bags and water proof aluminium bags. It is further recommended that the longevity of these genotypes could be prolonged under long-term storage and their germination may be tested after 2-3 years period instead of every year.

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Wide Hybridization between *Hirschfeldia incana* L. (Lagreze Fossat) and *Brassica carinata* Braun: Towards Development of New Genetic Resource

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A wide hybrid between *Hirschfeldia incana*, (which shows shattering resistance and can accumulate thallium) and *Brassica carinata* was produced through sequential culture of ovary and ovule. Hybridity of F_1 progeny was confirmed through morphological studies.

Key Words: *Hirschfeldia incana*, *Brassica carinata*, Wide hybrid, Genetic resource

Introduction

Improvement of brassicas through breeding necessitates to search for newer genetic resources which can be used to transfer desirable traits to crop brassicas. The wild relatives of crop brassicas in tribe *Brassiceae* are potential sources of genes responsible for biotic and abiotic stresses (Warwick, 1993; Chopra *et al.*, 1996). Wide hybridization followed by repeated backcrossing, allows distantly related genomes to come together that eventually lead to introgression of desirable genes into the cultivars (Rao *et al.*, 1996; Chrungu *et al.*, 1999; Banga *et al.*, 2003; Chandra *et al.*, 2004). Therefore, production of wide hybrids is the first step for brassica improvement programmes. However, a major bottleneck in production of wide hybrids is operation of pre and/or post-fertilization barriers (Inomata, 1992; Shivanna, 1996). Embryo rescue methods have been successfully used in several crosses to overcome the latter (Inomata, 1992; Diederichsen and Sacristan, 1994; Vyas *et al.*, 1995; Rao *et al.*, 1996).

Hirschfeldia incana is a late flowering shrub with pubescent stem and leaves and fruits of this species are shattering resistant. The floral parts of the shrub accumulate thallium and therefore its role in phyto-remediation is being explored (Madejon *et al.*, 2005). The present communication reports intergeneric hybridization between *H. incana* and *Brassica carinata* through embryo rescue technique, towards broadening the narrow genetic base of crop brassicas.

Materials and Methods

The seeds of all the species used in the present investigation were obtained from National Research Centre for Plant Biotechnology, Indian Agricultural Research Institute, New Delhi. Plants of *H. incana* (2n=14) and *B. carinata* (2n=34, BBCC) were grown under field conditions in the Botanical Garden of the Department of Botany, University of Delhi.

Flower buds of the female parent (*H. incana*) were emasculated a day prior to anthesis and bagged. They were pollinated the next day by pollen from the male parent and were subsequently rebagged. Some of the pollinated pistils were used for studies on pollen germination and pollen tube growth using the aniline blue fluorescence technique (Shivanna and Rangaswamy, 1992). Rest of the pollinated pistils were left on the plant until drying or fruit maturity or used for embryo rescue methods in the form of ovary, ovule and sequential culture on MS medium (Murashige and Skoog, 1962) supplemented with casein hydrolysate (500 mg l^{-1}). For ovary and sequential cultures, ovaries were excised 4-6 days after pollination (DAP) and surface sterilized in 0.1% $HgCl_2$ prior to culturing. For ovule culture, ovaries were excised 15-18 DAP, surface-sterilized and ovules were excised under aseptic conditions and cultured. For sequential culture, the cultured ovaries were removed from culture medium ten days after the initiation of culture; enlarged ovules were then dissected out and re-cultured on fresh medium. Cross efficiency (Sacristan and Gerdemann, 1994) was calculated using the formula:

$$\textit{Cross efficiency} = \frac{\textit{Number of hybrids obtained}}{\textit{Number of pollinated pistils}}$$

The hybrid seedlings and BC_1 progeny were multiplied *in vitro* through culture of shoot tips and single

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node segments and then rooted on MS medium supplemented with 0.2 mgl^{-1} benzylaminopurine (BAP) (Nanda Kumar and Shivanna, 1991) and 0.2 mgl^{-1} naphthalene acetic acid/indole butyric acid, respectively. *In vitro* raised plantlets were hardened and transferred to earthen pots filled with garden soil. For meiotic studies flower buds were fixed in Carnoy's fixative (ethanol: chloroform: acetic acid, 6:3:1) for 24 h. Anthers were squashed in 1% acetocarmine.

Results and Discussion

Aniline blue fluorescence studies demonstrated that *H. incana* is a self-incompatible species. Reciprocal intergeneric crosses were attempted to study the crossability barriers and to produce hybrids. Pollen of *B. carinata* germinated profusely on the stigma of *H. incana* and pollen tubes were traced up to the ovary or ovules. No pollen germination was observed on the stigma of *B. carinata* when *H. incana* was used as the male parent. Table 1 shows the results of field pollinations, embryo rescue techniques and their efficacy. Sixteen hybrid seedlings could be obtained through sequential culture of ovary and ovule.

Morphology of the F_1 hybrid plants was mostly intermediate between the parents (Table 2). The height and branching pattern of the hybrids were closer to the male parent. The flowers borne by the F_1 hybrids appeared normal but the anthers were flaccid and papery with mauve tip and were indehiscent. There were no pollen grains in the anthers. The anther squashes of young bubs showed a mass of cells, which did not differentiate, into microspore mother cells.

Aniline blue fluorescence studies revealed absence of pre-fertilization barriers in the crosses where *H. incana* was used as the female parent. Reciprocal crosses showed strong pre-fertilization barriers. Such unilateral incompatibility (*i.e.* cross is successful only in one direction) has been reported in many other crosses (Batra *et al.*, 1990; Gundimeda *et al.*, 1992; Shivanna, 1996). Absence of seed set through field pollinations even in crosses in which pre-fertilization barriers were absent, indicated the presence of post- fertilization barriers. To circumvent these barriers, embryo rescue techniques (ovary, ovule and sequential cultures) were attempted. However, only sequential culture of ovary and ovule proved successful in realizing the hybrids. Better efficiency of sequential culture over ovary and ovule culture in production of intergeneric hybrids in Brassiceae has been reported earlier (Agnihotri *et al.*, 1990; Batra *et al.*, 1990; Gundimeda *et al.*, 1992; Vyas *et al.*, 1995). F_1 hybrids could be confirmed through morphological studies. Cytological studies could not be done because of absence of microspore mother cells from the anthers. However, BC_1 progeny (using *B. carinata* as pollen parent) from F_1 hybrids could be obtained through sequential culture.

It has been shown that chromosome triplication exists across the tribe *Brassiceae* (Lysak *et al.*, 2005). This

Table 1. Efficacy of field pollinations and embryo rescue in hybrid production

Observations	Number	Cross efficiency
Field pollinations		0%
Pistils pollinated	63	
Hybrid seeds obtained	0	
Ovary culture		0%
Pistils cultured	68	
Hybrid seedlings obtained	0	
Ovule culture		0%
Pistils cultured	51	
Ovules cultured	132	
Hybrid seedlings obtained	0	
Sequential culture		30.1%
Pistils cultured	53	
Ovules cultured	204	
Hybrid seedlings obtained	16	

Table 2. Comparative account of morphological characters of parents (*H. incana* and *B. carinata*) and F_1 hybrid

S. No.	Morphological character	*H. incana*	F_1 hybrid	*B. carinata*
1	Plant height (cm)	83.8	151.0	160.3
2	Internode length (cm)	8.3	11.2	15.0
3	Average no. of primary branches	5	11.1	12.4
4	Days to flower	125-130	110-115	95-100
5	Duration of flowering	70-75	65-70	60-65
6	Petal length (mm)	7.0	10.0	13.0
7	Petal color	Light yellow	Light yellow	Yellow
8	Sepal length (mm)	4.0	5.0	7.0
9	Anther length at anthesis (mm)	1.5	2.0	3.0
10	Condition of anther at anthesis	Turgid	Flaccid	Turgid
11	Pistil length (mm)	3.5	6.0	7.0
12	No. of ovules/ovary	14.2	15.3	18.6

implies that homeologous regions are present in genomes of different genera within *Brassiceae*. Therefore, intergeneric hybrids can show allosyndesis between genomes of wild relatives and the cultivars. Such allosyndesis in wide hybrids results in new genetic recombinations and thus can be utilized as a new genetic resource for *Brassica* improvement programmes.

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Electrophoretic Characterization of *Cajanus cajan* x *C. cajanifolius* Hybrids

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Electrophoretic analysis of seed protein of nine F_4 progenies of three interspecific hybrids and their parents was carried out to study the variability in protein band expression. In all, 23 protein bands were identified ranging with molecular weight of 98 to 16 kD. Of these, three protein bands of 95.0, 71.5 and 60.0 kD were unique to *Cajanus cajan*, while four bands of 77.5, 67.5, 29.5 and 22.5 kD were specific to hybrids only. On the other hand *C. cajanifolius* has no unique protein band. Parents showed variability in protein band expression ranging from 7 in ICPL 84023 to 9 in UPAS 120 and *Cajanus cajanifolius*. The inter-progeny differences were observed for number, length and intensity of polypeptide bands of the protein. The similarity index of hybrids with *Cajanus cajanifolius* ranged from 35.29 to 66.66%. In general, bands at 87.5, 74.0, 46.0 and 34.5 kD were common in parents as well as hybrids.

Key Words: *Cajanus cajan*, *Cajanus cajanifolius*, Electrophoresis, Interspecific hybrids, Pigeonpea, Seed protein

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an important grain legume crop in the semi-arid tropics and contains about 24% protein in seeds. Breeding tools employed for genetic improvement in this crop are limited to selection and intervarietal hybridization. Conventional intervarietal hybridization has not met with much success in developing high seed protein cultivars. Seed size and quality are important attributes in pigeonpea.

It is imperative to introduce alien variation by transferring desirable protein trait from wild species into cultivated ones. *C. cajanifolius* (Haines) Van der Maesen, the putative progenitor of pigeonpea, can be used as a potential donor for genes conferring high protein (Panigrahi *et al.*, 2001). These genes could be effectively introgressed into pigeonpea genotypes by interpecific hybridization. Seed protein markers have been effectively employed for varietal differentiation in several crop plants (Mohanty *et al.*, 2001). Electrophoretic banding patterns of seed proteins helps in differentiating similarities and differences between genotypes and hybrids derived among them. For most seeds, except cereals, storage proteins are predominantly globulins (Krishna and Bhatia, 1985). The mature seed provides a stable and convenient system for biochemical analysis to establish relationship in parents and hybrids. *C. cajanifolius*, a wild species of pigeonpea, has specific features such as high seed protein content, mechanical resistance to pod borer and high pod set, etc. Of the techniques available, analysis of seed protein using electrophoresis is widely used because of their reliability, rapidity and cost effectiveness. Gel electrophoresis of seed protein act as a function of genotypic fingerprinting for distinguishing plant varieties and allied aspects. Since genetic differences are reflected in shifts of seeds protein patterns, the present study was undertaken on biochemical characterization of seed storage protein in order to assess variation for seed protein in F_4 populations of *C. cajan* x *C. cajanifolius* by using sodium dodecyl sulphate-polyacrylamide slab gel electrophoresis (SDS-PAGE).

Materials and Methods

Nine F_3 progenies of three interspecific hybrids derived from hybridization of three cultivated lines, *viz.*, Pant A 134, UPAS 120 and ICPL 84023 with *C. cajanifolius* were raised in Randomized Complete Block Design with three replications at Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar during *Kharif* 2003-04. The F_4 seeds obtained in hybrid population were grouped in three seed types, *viz.*, cultivated, intermediate and wild types on the basis of seed shape appearance. Protein separation in duplicate sets was carried out by polyacrylamide slab gel electrophoresis (SDS-PAGE) according to standard method of (Laemmli, 1970) using 12% acrylamide separating gel with a top layer of 6% acrylamide stacking gel. The protein sample of 10-12 µl was loaded on slab gel wells. Initially the electrophoresis was conducted at 10 mA at normal room temperature and than raised to 30 mA sometime after the dye front crossed the stacking and separating gel interface. The run was

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continued till the tracking dye front migrated upto about 1-1.5 cm from the bottom of the separating gel. The staining was done overnight in Coomassie Brilliant blue solution. Then the gel was destained by repeatedly washing with methanol: acetic acid: water (50:70:880, V/V/V, respectively). The prepared electrophoregrams was photographed by gel documentation. The protein bands were numbered from cathode end and their relative mobilities were calculated. The degree of electrophoretic similarity was calculated by pair wise comparison of the parents and hybrids. Similarity Index (SI) was worked out as per the following method suggested by Mishra *et al.* (1996):

$$SI = \frac{\text{Number of similar bands in a sample}}{\text{Total number of bands for the two samples}} \times 100$$

Results and Discussion

The relative mobility (Rm) values for various seed protein bands of inter-specific hybrids of *C. cajan* x *C. cajanifolius* ranged from 0.02 to 0.75, suggesting a wide range of variability in protein band expression (Table 1). In all, 23 protein bands of different Rm values were identified on the basis of electrophoretic mobility. Nine protein bands (98.0, 92.5, 87.5, 80.0, 74.0, 57.5, 46.0, 34.5, 23.0 kD) were observed in *C. cajanifolius* (Table 1). Among *C. cajan* genotypes, Pant A 134 depicted 9 bands followed by 8 in UPAS 120 and 7 in ICPL 84023. The similarities in polypeptide bands at 95.0, 87.5, 71.5 and 60.0 kD were noted in cultivated parents, *viz.*, Pant A 134, UPAS 120 and ICPL 84023, whereas bands at 34.5 and 26.0 kD were present only in two out of three female parents. One band of 87.5 kD was common in all the three cultivated lines as well as in *C. cajanifolius* which might be due to genetic relationship among them. Few polypeptide bands characterizing *C. cajanifolius* were also seen in the hybrids, *viz.*, Pant A 134 x *C. cajanifolius* (87.5, 80.0, 74.0, 57.5, 46.0, 34.5 and 26.0 kD), UPAS 120 X *C. cajanifolius* (98.0, 92.5, 87.5, 74.5, 46.0 and 34.5 kD) and ICPL 84023 x *C. cajanifolius* (98.0, 92.5, 87.5, 74.5, 46.0, 34.5 and 23.0 kD). It was interesting to note that one band (87.5 kD) was common in all the three cultivated parents, wild parent as well as in hybrids [Pant A 134 x *C. cajanifolius* (C), Pant A 134 x *C. cajanifolius* (W), UPAS 120 x *C. cajanifolius* (W), ICPL 84023 x *C. cajanifolius* (C) and ICPL 84023 x *C. cajanifolius* (I) and ICPL 84023 x *C. cajanifolius* (W)] and this might be due to genetic relationship among them. Bands of 46.0 kD was present in the UPAS 120, *C. cajanifolius* as well as in hybrids Pant A 134 x *C. cajanifolius* (I and W), UPAS 120 x *C. cajanifolius* (I), ICPL 84023 x *C.*

Table 1. Electrophoretic protein banding patterns of parents and interspecific hybrids of *C. cajan* x *C. cajanifolius* derived from SDS-PAGE of seed protein

Band No.	Rm Value	Mol. wt. kD	Pant A 134	UPAS 120	ICPL 84023	*C. cajanifolius*	Pant A 134 x *C. cajanifolius*			UPAS 120 x *C. cajanifolius*			ICPL 84023 x *C. cajanifolius*		
							C	I	W	C	I	W	C	I	W
1	0.02	98.0	-	+	-	+	-	-		-	+	-	+	-	-
2	0.04	95.0	+	+	+	-	-	-	-	-	-	-	-	-	-
3	0.05	92.5	-	-	-	+	-	-	-	+	+	+	+	-	-
4	0.08	87.5	+	+	+	+	+	-	+	-	-	+	+	+	+
5	0.11	80.0	-	-	-	+	+	-	-	-	-	-	-	-	-
6	0.12	77.5	-	-	-	-	-	-	-	-	-	+	+	+	-
7	0.14	74.0	-	-	-	+	+	+	+	-	-	-	-	+	+
8	0.15	71.5	+	+	+	-	-	-	-	-	-	-	-	-	-
9	0.17	67.0	-	-	-	-	-	-	-	-	-	+	-	-	-
10	0.20	60.0	+	+	+	-	-	-	-	-	-	-	-	-	-
11	0.21	57.5	-	-	-	+	-	-	+	-	-	-	-	-	-
12	0.25	51.0	-	-	-	-	+	-	-	-		-	-	-	-
13	0.28	46.0	-	+	-	+	-	+	+	-	+	-	-	+	-
14	0.30	44.0	-	-	+	-	+	-	-	-	-	-	+	+	+
15	0.34	39.0	+	-	-	-	-	-	-	-	-	+	-	-	-
16	0.39	34.5	+	+	-	+	+	-	+	+	+	+	-	+	-
17	0.41	33.0	+	-	-	-	-	+	+	-	-	-	+	-	-
18	0.44	31.5	-	-	+	-	-	+	+	-	-	-	-	+	-
19	0.48	29.5	-	-	-	-	-	-	-	-	-	+	-	-	-
20	0.55	26.0	+	+	-	-	+	+	+	-	-	+	-	-	-
21	0.61	23.0	-	-	+	+	-	+	+	-	-	-	+	+	+
22	0.62	22.5	-	-	-	-	-	+	-	-	-	-	-	-	-
23	0.75	16.0	+	-	-	-	-	+	-	-	-	-	-	-	-

C: cultivated, I: intermediate and W: wild

cajanifolius (I). Similarly, the band of 34.5 kD was also present in the Pant A 134 , UPAS 120, *C. cajanifolius* as well as in six hybrids, namely, Pant A 134 x *C. cajanifolius* (C and W), UPAS 120 x *C. cajanifolius* (C, I and W) and ICPL 84023 x *C. cajanifolius* (I). There was homogeneity of bands at 95.0, 71.5 and 60.0 kD among cultivated parents (Pant A 134, UPAS 120 and ICPL 84023). However, these bands were absent in the *C. cajanifolius* as well as from all the nine hybrids. Similarly, four polypeptide bands were expressed only in the two pigeonpea varieties and lacked expression in *C. cajanifolius* and the two putative hybrids (Panigrahi *et al.*, 2001). Deletion or mutation of structural genes coding for the polypeptides or their regulatory loci results in inhibition of transcription or translation of polypeptides leading to the lack of expression of the concerned polypeptides (Brown *et al.*, 1981).

Highest similarity index with wild parent, *C. cajanifolius* (Table 2) was seen in wild type seeds of hybrids Pant A 134 x *C. cajanifolius* (66.66%) followed

Table 2. Qualitative and quantitative differences among progenies of interspecific hybrids of *C. cajan* x *C. scarabaeoides*

Genotype	Qualitative differences		Quantitative differences				SI with *C. cajanifolius* (%)	SI with cultivated parents (%)
	Total no. of bands	Specific band number	Thick	Medium	Thin	Faint		
Pant A 134 x *C. cajanifolius*								
Male parent	9	98.0 (0.02), 92.5 (0.05), 57.5 (0.21), 46.0 (0.28), 23.0 (0.61)	1	0	0	8	-	-
Cultivated type seed	7	51.0 (0.25), 44.0 (0.30), 26.0 (0.55)	1	2	1	3	50.00	37.50
Male parent	9	98.0(0.02), 92.5 (0.05), 87.5 (0.08), 80.0 (0.11), 57.5 (0.21), 34.5 (0.39)	1	0	0	8	-	-
Intermediate type seed	8	33.0 (0.41), 31.5 (0.44), 26.0 (0.55), 22.5 (0.62), 16.0 (0.75)	1	1	4	2	35.29	35.29
Male parent	9	98.0 (0.02), 92.5 (0.05), 80.0 (0.11)	1	0	0	8	-	-
Wild type seed	9	33.0 (0.41), 31.5 (0.44), 26.0 (0.55)	2	1	2	4	66.66	44.44
UPAS 120 x *C. cajanifolius*								
Male parent	9	98.0 (0.02), 87.5 (0.08), 80.0 (0.11), 74.0 (0.14), 57.5 (0.21), 46.0 (0.28), 23.0 (0.61)	1	0	0	8	-	-
Cultivated type seed	2	Nil	0	1	0	1	36.36	20.00
Male parent	9	87.5 (0.08), 80.0 (0.11), 74.0 (0.14)), 57.5 (0.21), 23.0 (0.61)	1	0	0	8	-	-
Intermediate type seed	4	Nil	1	1	0	2	61.53	50.00
Male parent	9	98.0 (0.02), 80.0 (0.11), 74.0 (0.14), 57.5 (0.21), 46.0 (0.28), 23.0 (0.61)	1	0	0	8	-	-
Wild type seed	8	77.5 (0.12), 67.0 (0.17), 39.0 (0.34), 29.5 (0.48), 26.0 (0.55)	2	3	1	2	35.29	37.50
ICPL 84023 x *C. cajanifolius*								
Male parent	9	80.0 (0.11), 74.0 (0.14), 57.5 (0.21), 46.0 (0.28), 34.5 (0.39)	1	0	0	8	-	-
Cultivated type seed	7	77.5 (0.12), 44.0 (0.30), 33.0 (0.41)	2	0	2	3	50.00	42.85
Male parent	9	98.0 (0.02), 92.5 (0.05), 80.0 (0.11), 57.5 (0.21)	1	0	0	8	-	-
Intermediate type seed	8	77.5 (0.12), 44.0 (0.30), 31.5 (0.44)	0	1	1	6	58.82	53.33
Male parent	9	98.0 (0.02), 92.5 (0.05), 80.0 (0.11), 57.5 (0.21), 46.0 (0.28), 34.5 (0.39)	1	0	0	8	-	-
Wild type seed	4	44.0 (0.30)	0	1	0	3	46.15	54.54

Figures in parenthesis are Rm values; SI = Similarity Index; Male parent = *C. cajanifolius*

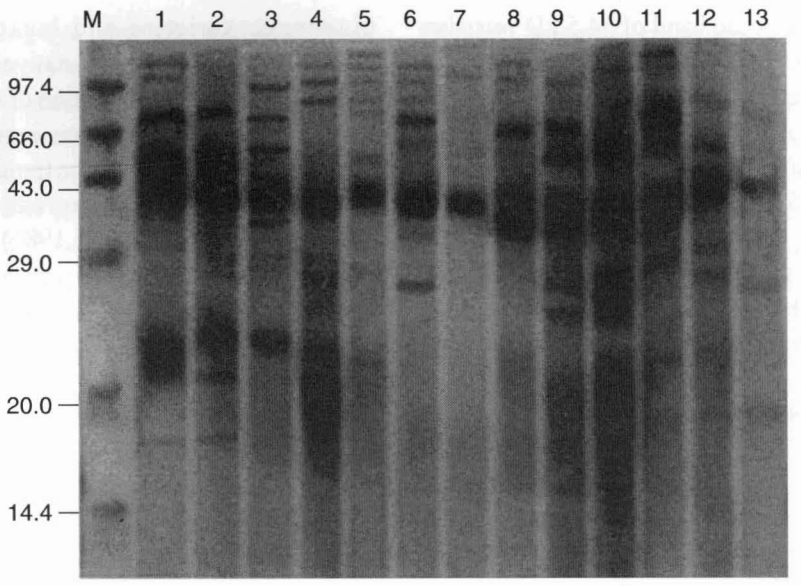

Fig. 1: Electrophoregram or polypeptide banding patterns of three genotypes of *Cajanus cajan*, nine interspecific hybrids and *C. cajanifolius* derived from SDS-PAGE of seed protein; Pant A 134 (Lane 1), UPAS 120 (Lane 2), ICPL 84023 (Lane 3), *C. cajanifolius* (Lane 4), Pant A 134 X *C. cajanifolius* (C) (Lane 5), Pant A 134 X *C. cajanifolius* (I) (Lane 6), Pant A 134 X *C. cajanifolius* (W) (Lane 7), UPAS 120 X *C. cajanifolius* (C) (Lane 8), UPAS 120 X *C. cajanifolius* (I) (Lane 9), UPAS 120 X *C. cajanifolius* (W) (Lane 10), ICPL 84023 X *C. cajanifolius* (C) (Lane 11), ICPL 84023 X *C. cajanifolius* (I) (Lane 12), ICPL 84023 X *C. cajanifolius* (W) (Lane 13)

by intermediate type seed of UPAS 120 x *C. cajanifolius* (61.53%) and ICPL 84023 x *C. cajanifolius* (58.82). High order of similarity with respect to cultivated parent was seen in wild type (54.54-37.50 %) in all the three hybrids. Cultivated seed type of two hybrids (ICPL 84023 x *C. cajanifolius* and Pant A 134 x *C. cajanifolius)* also shared fairly good similarity index, 42.85 and 37.50%, respectively with their respective cultivated parents. Gangwar and Bajpai (2007) also noted the similarity index of hybrids with *C. scarabaeoides* ranged from 33.33 to 75.75%. All types of protein band intensity were observed (Fig. 1). Maximum 9 bands were noted in wild seed types of hybrid derived with Pant A 134 followed by 8 bands in intermediate and wild seed types of all the three crosses.

The hybrids had protein bands of both high as well as low molecular weight ranging from 98.0 to 16 kD. Similarly, Naik and Kole (2001) observed bands from 17.4 to 75 kD in mungbean. Panigrahi *et al.* (2001) also noted polypeptide bands with Rm values ranging from 0.248 to 0.634 in five genotypes including two pigeonpea cultivars, C. *cajanifolius* and their two putative hybrids. Singh *et al.* (1992) and Roy *et al.* (2001) also noted differences in band mobility, width and intensity in legumes. Proteins being the direct gene products reflect the genomic composition of lines accurately to some extent and, therefore, are ideal for genotypes distinctiveness.

In all, 23 protein bands observed in the F_4 populations of *C. cajan* x *C. cajanifolius* hybrids seem to be very informative and useful in deriving qualitative and quantitative differences in various protein fractions. It was noted that a protein band of 87.5 kD was universally present in hybrid progenies as well as in parents indicating that the genes controlling expression of these protein bands appeared to behave as a single block. The observed differences in protein band intensity in cultivated, intermediate and wild type seeds could be utilized in identification of high protein rich progenies from successive generations. Such types of close relationships and/ or minor variations were also observed in chickpea (Kharkwal, 1999). The results also substantiated the conclusion that the interspecific hybridization is important for creating wide variability for seed protein in genus *Cajanus*. The present study is preliminary on interspecific hybrids of *C. cajan* x *C. cajanifolius* and further study of seed protein fractions would be required in advance generations of the hybrids.

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Genetic Variability and Correlation Studies on Germplasm of Yellow Sarson [*B. rapa* (L.) var. *yellow sarson*] for Seed Yield and its Component Traits

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Genetic variability and correlation in sixty three indigenously collected germplasm accessions of yellow sarson were evaluated for seed yield and its components traits. Analysis of variance for seed yield and its related components showed that there was significant variability among accessions. The maximum PCV was observed in seed yield per plant followed by seeds per siliqua. High heritability coupled with high genetic advance were observed for plant height, seeds per siliqua, 1000-seed weight, seed yield per plant and harvest index. The seed yield per plant was positively and significantly correlated with main shoot length, siliquae on main shoot, primary branches per plant, oil content, 1000-seed weight, harvest index and days to maturity. The accessions IC361512, IC342762 and IC334290 were identified as useful genotypes for various traits.

Key Words: Rapeseed-mustard, Accessions, Genetic Variability, Heritability, Correlation

Introduction

Rapeseed-mustard is an important group of crop plants with great economic value world wide. *Brassica juncea* (Indian mustard) and *B. rapa* are the important oilseed crops in India. The *B. rapa* is divided into three ecotypes, *viz.*, toria, brown sarson and yellow sarson which are grown in India. Of these three ecotypes, yellow sarson is self compatible in breeding behavior and is one of the most important members among them. Yellow sarson is mainly grown in Assam, Bihar, Uttar Pradesh, Sikkim, Meghalaya and West Bengal, (Misra, 2008). It occupies an important position due to the presence of high oil content (up to 45%), high seed yield and early maturity (around 100 days) as compared to Indian mustard (130-150 days), furthermore, it's yellow seed coat colour has preference over brown seed colour. The oil is mainly used for edible purposes and in addition to this, the yellow sarson is most preferred choice as leafy vegetables among the entire cultivated oilseed brassicas in India (Chatterjee, 1992).

The improvement for yield and other traits not only depends on the amount of variability present in the breeding materials for the required traits but also on proper evaluation and further, utilization in the breeding programmes (Kumar *et al.*, 2004; Kumar and Misra, 2007). The present study was undertaken to find out variability for 15 agro-morphological traits in the yellow sarson germplasm. The estimation of extent and nature of variability in the germplasm accessions for yield and other economic traits is the pre-requisite for breeding programme. The effectiveness of selection for seed yield depends upon both, the genetic variability present in the population and the degree of association that exists between seed yield and its components traits. Therefore, the present investigation was undertaken to estimate the magnitude of genetic variability and correlation in the diverse germplasm of yellow sarson and selection of superior genotypes.

Materials and Methods

Sixty three accessions of yellow sarson (*B. rapa* L. var. *yellow sarson*) were evaluated during *rabi* season 2006-07 in an augmented complete block design with four checks (NDYS 2, Pusa gold, Ragani and YST 151) at the National Research Centre on Rapeseed–Mustard, Bharatpur, Rajasthan. These indigenously collected accessions of yellow sarson were acquired from National Bureau of Plant Genetic Resources, New Delhi (India). The collections were made in various exploration trips in the states of Bihar, Chattisgarh, Jharkand, Uttar Pradesh and West Bengal. Each genotype was sown in paired rows of 3 m length with 30 x 10 cm spacing. Recommended standard agronomic package of practices and plant protection measures were adopted. Randomly tagged five plants were selected at appropriate growth stage to record observations on morphological traits, namely, initiation of flowering, 50% flowering, maturity, plant height, primary branches and secondary branches per plant, main shoot length, siliquae on main shoot, siliqua length, and seeds per siliqua. Post-harvest observations include seed yield per plant, 1000-seed weight, harvest index and quality traits such as oil and protein content. The mean values of five plants for each character were considered for computation, except for days to flower initiation, 50%

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flowering and days to maturity (which was recorded on whole plot basis). 1000-seeds were counted by electronic seed counter (Contador, Germany) and weighed by electronic balance. Further, oil and protein content were analyzed by Near Infrared Reflectance Spectroscopy, (Dickey-John, Instalab 600). The mean data were subjected to analysis of variance, the data analyzed by using software Statistical Package for Augmented Design (SPAD) of IASRI, New Delhi. Phenotypic (PCV) and genotypic coefficient of variance (GCV) were calculated using formula suggested by Burton (1952), heritability (h^2) in broad sense and expected genetic advance as per cent of mean at 5% intensity of selection differential were calculated for each character as suggested by Johnson *et al.* (1955) and correlation coefficients were calculated according to the procedure of Singh and Chaudhary (1977).

Results and Discussion

Analysis of variance (Table 1) for seed yield and its related components showed that there was significant variability among accessions for initial flowering, 50% flowering, plant height, primary and secondary branches per plant, main shoot length, siliquae on main shoot, seeds per siliqua, 1000-seed weight, siliqua length, harvest index, oil content and seed yield per plant, suggesting that the material has adequate variability to support the breeding programme for improving the seed yield. The blocks show the intermingling relationship of significant and non-significant for the traits indicating lack of homogeneity among the blocks. The check versus genotype interaction showed highly significant for initial flowering, plant height, siliqua on main shoot and seeds per siliqua. This indicates difference between check as a group and genotype as another group.

The range, mean, genotypic and phenotypic coefficient of variation (GCV and PCV), heritability in broad sense and genetic advance expressed as percentage of mean value for different characters are presented in Table 2. The PCV was greater than GCV for all the characters indicating the influence of the environment in the expression of these traits. The maximum PCV was observed in seed yield per plant (44.8%) and followed by seeds per siliqua (25.2%), secondary branches per plant (24.8%) and harvest index (23.9%). The PCV varied from 2.9% (oil content) to 44.8% (seed yield per plant). The maximum GCV was found in seed yield per plant (35.0%) followed by harvest index (20.2%), seeds per siliqua (19.9%) and siliquae on main shoot (16.9%). The rest of the characters showed low PCV and GCV. High PCV and GCV for seed yield per plant, secondary branches per plant, seed per siliqua and harvest index were reported in oilseed brassicas (Mondal and Khajuria, 2000; Sikarwal *et al.*, 2000; Mahala *et al.*, 2003; Meena *et al.*, 2006)

Heritability is important selection parameter, since it is estimated from additive genetic variance, it plays important role in the selection of genotypes (Nadarajan and Gunasekaran, 2005). High heritability (broad sense value >60) values were observed for initial flowering, 50% flowering, plant height, siliqua length, harvest index, 1000-seed weight, seeds per siliqua and seed yield per plant. High genetic advance is another parameter to access the expected improvement in a character by hybridization and selection. High values for genetic advance were recorded for plant height, siliquae on main shoot, seeds

Table 1. Analysis of variance for different agro-morphological traits in yellow sarson

S.No.	Characters	Mean sum of square due to			
		Blocks	Checks	Entries	Checks vs entries
	Degree of freedom	4	3	68	1
1	Initial flowering (days)	29.1	149.4*	39.3**	128.9*
2	50% flowering (days)	41.3	132.9*	31.0**	57.1
3	Plant height (cm)	9995.4**	563.7	309.5**	4556.7**
4	Primary branches per plant	0.25	10.9*	1.1*	14.5
5	Secondary branches per plant	0.33	0.31	0.56*	3.9
6	Main shoot length (cm)	9.7	163.4	44.6*	2.0
7	Siliquae on main shoot	18.1	11.4	28.0**	103.6*
8	Siliqua length (cm)	0.08	0.78*	0.22**	2.2
9	Seeds per siliqua	29.2	102.1	57.1**	381.6*
10	1000-seed weight (g)	1.1*	1.27*	0.39**	1.2
11	Harvest index (%)	54.8*	69.7	32.6**	37.2
12	Maturity (days)	452.6*	28.8	58.0	29.3
13	Protein content (%)	0.18	0.83	0.4	4.7
14	Oil content (%)	2.41	1.9	1.5**	13.5
15	Seed yield per plant (g)	2.3	11.5	16.7**	4.0

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

Table 2. Mean, range, genotypic and phenotypic coefficient of variation, heritability and genetic advance for different traits in yellow sarson

Characters	Mean	Range	GCV %	PCV %	Broad sense heritability (%)	Genetic advance (%)
Initial flowering (days)	47.0	35.0-53.0	11.1	13.3	69.7	19.2
50% flowering (days)	53.7	33.0-64.0	8.6	10.4	68.1	14.5
Plant height (cm)	100.3	69.4-152.3	14.0	17.5	64.1	23.2
Primary branches per plant	4.5	2.6-6.8	15.0	23.3	41.8	20.0
Secondary branches per plant	3.0	1.9-5.6	15.5	24.8	39.3	20.1
Main shoot length (cm)	44.5	36.9-72.2	10.2	15.0	46.2	14.3
Siliquae on main shoot	24.0	18.3-45.3	16.9	22.0	58.6	26.6
Siliqua length (cm)	3.8	2.8-4.9	10.1	12.2	68.2	17.2
Seeds per siliqua	29.6	15.9-45.9	19.9	25.5	60.8	32.0
1000-seed weight (g)	3.2	8.9-31.5	15.5	19.7	61.5	25.0
Harvest index (%)	23.9	8.2-32.6	20.2	23.9	71.8	35.3
Maturity (days)	117.0	102.0-135.0	4.2	6.5	42.4	5.7
Protein content (%)	20.1	17.9-22.9	2.4	3.1	57.5	3.7
Oil content (%)	42.7	39.6-45.6	2.2	2.9	58.7	3.5
Seed yield per plant (g)	9.1	5.3-25.3	35.0	44.8	61.1	56.3

per siliqua, 1000-seed weight, seed yield per plant and harvest index. In the present study, high heritability coupled with high genetic advance was observed for plant height, seeds per siliqua, 1000-seed weight, seed yield per plant and harvest index. Similar trends have also been reported by various other workers in *Brassica* spp. (Uddin *et al.*, 1995; Pant and Singh, 2001; Pandey and Singh, 2002; Mahala *et al.*, 2003).

Correlation estimates between seed yield and other morphological traits are useful in selection of desirable plant type in designing an effective breeding programme. Seed yield is a complex phenomenon which is encompassing the interactions between many yield contributing traits. Therefore, selection should be based on these traits and their correlation with seed yield (Grafius, 1964). The correlation coefficients with seed yield *vis-a-vis* other yield contributing traits and their all possible interrelationships are given in Table 3. The seed yield per plant was positively and significantly correlated with main shoot length, siliquae on main shoot, primary branches per plant, oil content, 1000-seed weight, harvest index and days to maturity, while remaining characters observed non-significant correlations except for two characters in seeds per siliqua and protein content, which showed negative but significant correlations with this trait. Seeds per siliqua showed positive and significant correlations with initiation of flowering, 50% flowering and siliqua length. There was significant positive correlations of harvest index with 1000-seed weight and oil content. Similarly, significant positive correlation was recorded in siliquae on main shoot with main shoot length and plant height; oil content with 1000-seed weight; plant

Table 3. Estimates of phenotypic correlation coefficient in different traits in yellow sarson

Characters	#IF	FF	PH	PB	SB	MSL	SMS	SL	SPS	SW	PC	OC	HI	DM
FF	0.866**													
PH	0.297*	0.325**												
PB	-0.004	-0.064	0.404**											
SB	0.021	0.037	0.244*	0.456**										
MSL	0.136	0.124	0.302**	0.148	0.099									
SMS	0.117	0.117	0.388**	0.128	0.189	0.683**								
SL	0.017	0.080	0.272*	-0.049	-0.074	-0.102	-0.047							
SPS	0.407**	0.428**	0.026	-0.132	-0.130	-0.201	-0.199	0.282*						
SW	-0.163	-0.177	-0.618**	-0.373**	-0.227	0.153	-0.021	-0.139	-0.143					
PC	0.085	0.086	0.192	0.015	0.198	-0.005	0.154	-0.271*	0.150	-0.290*				
OC	-0.135	-0.111	-0.547**	-0.260*	-0.278*	-0.021	-0.186	0.076	-0.184	0.676**	-0.606**			
HI	-0.142	-0.141	-0.275*	0.104	0.110	0.223	0.150	-0.014	-0.202	0.496**	-0.287*	0.632**		
DM	-0.174	-0.180	-0.665**	-0.360**	-0.199	0.266*	0.089	-0.290*	-0.288*	0.830**	-0.302**	0.609**	0.493**	
SYP	0.061	0.057	0.097	0.267*	0.166	0.514**	0.379**	0.006	-0.327**	0.308**	-0.329**	0.376**	0.610**	0.315**

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

#IF: Initiation of flowering, FF: 50% flowering, PB: Primary branches per plant, SB: Secondary branches per plant, MSL: Main shoot length, PH: Plant height, SMS: Siliquae on main shoot, DM: Maturity duration, SL: Siliqua length, SYP: Seed yield per plant (g), SPS: Seeds per siliqua, HI: Harvest index, SW: Seed weight, PC: Protein content and OC: Oil content

Table 4. Promising accessions of yellow sarson

Characters	Promising Accessions
Initial flowering (days)	< 47: IC331817, IC342766, IC361510, IC361512
50% flowering (days)	< 53: IC331817, IC334291
Plant height (cm)	> 118: IC447818, IC447822, IC520757, IC521379
Primary branches per plant	> 5.4: IC361512, IC447818, IC520748, IC520749
Secondary branches per plant	> 3.5: IC355391, IC355397, IC361512, IC520748
Main shoot length (cm)	> 50.5: IC334290, IC336456, IC342762, IC342768
Siliquae on main shoot	> 28.0: IC336456, IC342760, IC342762, IC361506
Siliqua length (cm)	> 4.1: IC342766, IC355365, IC520755, IC520771
Seeds per siliqua	> 39.0: IC447740, IC447824, IC520748
1000-seed weight (g)	> 3.04: IC355412, IC355368, IC355382, IC361508
Seed yield per plant (g)	> 17.7: IC336456, IC355419, IC520771
Harvest index (%)	> 25.1: IC334200, IC334290, IC355365, IC361512
Oil content (%)	> 42.7: IC342283, IC355307, IC355312, IC355368, IC355378, IC355382

height with initiation of flowering and 50% flowering; siliqua length with plant height and primary branches per plant with plant height. Hence, selection for the higher values of these traits will be desirable for increase seed yield. The associations between the yield related attributes reveal the mutual relationship between two or more characters; therefore, it is an important parameter for taking a decision regarding the selection and its further utilization in improvement in the crop. This is in conformant of some of the earlier reports on *Brassica* (Yadav *et al.*, 2001; Kumar *et al.*, 2001; Patel and Patel, 2005; Misra *et al.*, 2007a, b).

Promising donors were identified for various seed yield contributing traits which are to be useful donors in the variety development programme. Accession IC361512 was identified as a useful donor for early flowering, high harvest index, more number in primary branches and secondary branches per plant (Table 4). The accessions IC342762 and IC334290 were recorded for more number of siliquae on main shoot and long main shoot length. IC355382 accession had high oil content and 1000-seed weight, and IC520748 showed more seeds per siliqua and primary branches per plant. Besides this accession IC355365 had long siliqua and high harvest index and IC447818 recorded for short plant height and high number of primary branches per plant. The highest seed yield per plant (21.9 g), 1000-seed weight (5.1 g) and number of seeds per siliqua (48.9) were recorded in accessions IC336456, IC361508 and IC447740, respectively.

On the basis of different variability parameters and correlation, the present investigation revealed that there is an adequate variability for siliquae on main shoot, main shoot length, 1000-seed weight, seeds per siliqua and harvest index in the indigenously collected germplasm of *Brassica rapa* var. *yellow sarson*. The promising accessions can be used directly for hybridization and other breeding strategy related to genetic enhancement of yellow sarson. It may be concluded that characters such as seeds per siliqua, siliquae on main shoot, oil content, harvest index, 1000-seed weight and seed yield per plant will help in improving the seed yield directly and indirectly. Therefore, these characters should be considered for seed yield improvement in yellow sarson breeding programmes.

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Characterization of Ahu Rices of Assam for Quality Traits

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A study on characterization of Ahu rices of Assam for quality traits showed wide variability with respect to 12 quality traits and grain yield amongst 147 entries. Coefficient of variation was observed highest for alkali digestion value which was followed by grain yield and water uptake number. Observation on physical grain quality and cooking quality attributes revealed that Ahu varieties were mostly of long bold grain type with poor alkali digestion (high gelatinisation temperature) value, low volume expansion, water uptake and kernel elongation. These varieties, thus, differs in quality from the rices normally preferred by consumers. A few varieties, on the other hand, exhibited desirable values for individual quality traits. However, the desirable physical grain quality attributes were observed to be associated with undesirable cooking qualities and vice versa. Kernel elongation exhibited positive and significant association with grain yield. Basantbahar, identified as the best superfine-grained variety had very poor cooking quality, while another variety Betguti I having highest kernel elongation and volume expansion exhibited very poor physical grain quality. Breeding effort for breaking these undesirable associations is necessary to improve qualities of Ahu rices of Assam.

Key Words: Ahu rice, Characterization, Quality traits

Introduction

Traditional photoinsensitive early maturing rice varieties of Assam grown during Feb-March to June-July as either dry broadcast or transplanted are popularly known as Ahu rices. Attempts for evaluation of this group of rice germplasm have been very much limited. Although earlier workers evaluated some of the varieties in this group with respect to yield and yield components (Das *et al.*, 1981), drought tolerance and grain dormancy (Kalita *et al.*, 1990; Kalita and Baruah, 1993) and pigmentation pattern (Sarma *et al.*, 2003) the varieties have not been evaluated for quality traits. It is generally accepted that Ahu rices are not only poor in yield but also low in quality as compared to normal winter rices for which, these traditional varieties have suffered from gradual extinction from cultivation. It is the general practice that Ahu rices are used after parboiling to enhance consumer acceptability. It is, therefore, important to carry out complete characterization of Ahu rice germplasm with respect to yield, quality and other morpho-agronomic and adaptive traits. As a part of this, the present report entails evaluation of a set of 147 Ahu varieties for important quality traits.

Materials and Methods

The materials for the present investigation comprised of 147 Ahu rice genotypes of Assam procured from the Regional Rice Research Station, Titabar, Assam and B.N. College of Agriculture, Biswanath Chariali, Assam. The genotypes were grown in three row plots of two meter length with a spacing of 15 x 20 cm during wet season, 2001. Observation on 12 traits related with quality, *viz.*, grain length (GL), grain breadth (GB), grain length-breadth ratio (L:Bg), kernel length (KL), kernel breadth (KB), kernel length-breadth ratio (L:Bk), kernel elongation ratio (KR), breadth-wise expansion of kernel (BE), water uptake number (WU), volume expansion (VE), alkali digestion value (AD) and chalkiness of endosperm (CH) along with grain yield /plant (GY) were recorded following standard evaluation system (IRRI, 1996). Modification of scale was made wherever standard system was not satisfied. Variability parameters, *viz.*, mean, range, standard deviation, coefficient of variation, skewness and kurtosis were calculated for each of the quality traits under study following Panse and Sukhatme (1989). Frequencies of genotypes in different classes were worked out and represented in column diagram. Varieties were further classified into five grain shapes, *viz.*, long slender (>6.0 mm length, >3.9 L:B), long bold (>6.0 mm length, <3.0 L:B), short slender (<6.0 mm length, >3.0 L:B), medium slender (4.5-6.0 mm length, 2.5-3.0 L:B) and short bold (<5.0 mm length, < 2.5 L:B) and four kernel shapes, *viz.*, slender (>3.0 L:B), medium (2.1-3.0 L:B), bold (1.1-2.0 L:B) and round (<1.1 L:B). Simple linear

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correlation coefficients amongst different quality traits and grain yield were estimated.

Results and Discussion

A wide range of variation was observed for grain quality attributes along with grain yield plant^{-1} in the Ahu rice genotypes under study (Table 1). Considerable range of variation was observed for all the traits under study indicating wide spectrum of variation in Ahu rice germ plasm for various traits under study. Highest coefficient of variation (CV) was observed for alkali digestion value (55.37%) followed by grain yield plant^{-1} (32.36%) and water uptake number (21.89%). Among the traits under study, lowest variation was exhibited by kernel elongation ratio (8.55%). Based on the coefficient of variation, it could be visualized that among the grain quality traits, alkali digestion value, volume expansion, water uptake number and length breadth ratio of grain and kernel were most likely to contribute to the diversity in Ahu rices. Considerable diversity in Ahu rices with respect to grain yield was earlier reported by Das *et al.* (1981) and Baruah *et al.* (1994). Their observation revealed that panicle weight and panicle number/plant reasonably accounted for the yield variation in Ahu rices.

Frequency distribution against different classes for all the traits under study are presented in Fig.1. Observations on grain and kernel shape and size as revealed from length, breadth and length: breadth ratios, indicated that most of the entries had long bold grains and medium kernel. Forty two varieties had long slender grains, while slender kernel was observed only in 8 entries. Siddiq (1982) observed that kernel length 7 mm or above and breadth less than 2 mm were highly remunerative in international trade. Among the Ahu rice varieties under study, only one variety, Basantbahar, satisfied this norm. Pericarp colour is also a important feature of physical quality of rice kernel determining market acceptance. In the same set of genotypes, Sarma *et al.* (2003) reported that most of the Ahu varieties had pigmentation in pericarp, intensity varying from light brown to red and, thus, differed from rices normally preferred by consumers. Frequency distribution of chalkiness of endosperm showed that majority of the varieties had none to small (<10%) chalky areas in the endosperm, while the others had medium to large chalky areas. Chalkiness is an important consideration for breeding quality rice (Jennings *et al.*, 1979). The consumer preference goes in favour of a clear endosperm against the chalky types and pays a premium price for it.

Cooking quality in rice is normally determined by water uptake, volume expansion and kernel elongation which are primarily influenced by amylose content and alkali digestion value (Tomar and Nanda, 1982). In the present study, water uptake ranged from 187.3 to 458.1, volume expansion from 2.13 to 5.1 and kernel elongation from 1.23 to 2.12. Moreover, breadth-wise expansion is also another important cooking quality criterion. Thinner the cooked kernel, better is the demand (Sarkar *et al.*, 1994). Breadth-wise expansion ranged from 1.08 to 2.38, majority of the varieties being in the lower range for the trait. Relative frequencies against different classes for these traits revealed that Ahu rices are mostly poor in alkali digestion, volume expansion and kernel elongation. Consumer preference in a large part of India is for rice, which is non-sticky but soft after cooking. Low alkali digestion value indicates high gelatinisation temperature (GT), which is not common in Indian rices (Bhattacharya *et al.*, 1980). Contrary to this, Ahu rices as observed in the present study are mostly of high GT type. In the study of Bhattacharya *et al.* (1980), the varieties from Assam belonged to normal winter rice group. Two of the exceptions were the varieties CH 63 from Assam and NC 324 from West Bengal, having very high GT (Low AD). Interestingly, the variety CH 63 which is a Chinese

Table 1. Variability parameters for grain quality traits and grain yield in Ahu rices

	GL(mm)	GB (m)	L:Bg	KL (mm)	KB (mm)	ER	L:Bk	VE	WU (ml)	BE	AD	CH	GY (g)
Range:													
Min	4.92	1.99	1.67	3.25	1.62	1.23	1.33	2.13	187.33	1.08	1.00	8.10	6.23
Max.	9.06	3.55	4.46	7.85	3.24	2.12	4.35	5.10	458.10	2.35	7.00	25.30	27.48
Mean	6.94	2.58	2.76	5.54	2.37	1.52	2.39	3.59	309.96	1.52	2.98	14.56	14.32
Variance	0.65	0.14	0.31	0.47	0.11	0.02	0.22	0.61	4599.36	0.05	2.74	11.41	21.48
Standard deviation	0.80	0.37	0.56	0.69	0.33	0.13	0.47	0.78	67.82	0.23	1.65	3.38	4.63
CV(%)	0.12	0.14	0.20	0.12	0.14	0.09	0.20	0.22	0.22	0.15	0.56	0.23	0.32
Sem (±)	0.07	0.03	0.05	0.06	0.03	0.01	0.04	0.07	5.71	0.02	0.14	0.28	0.39
Skewness	-0.10	0.04	0.67	0.44	0.47	0.78	1.14	0.48	0.12	0.78	1.30	0.60	0.66
Kurtosis	-0.06	-1.25	0.09	1.22	-0.66	2.25	3.00	-0.51	-1.07	0.75	0.18	0.69	-0.14

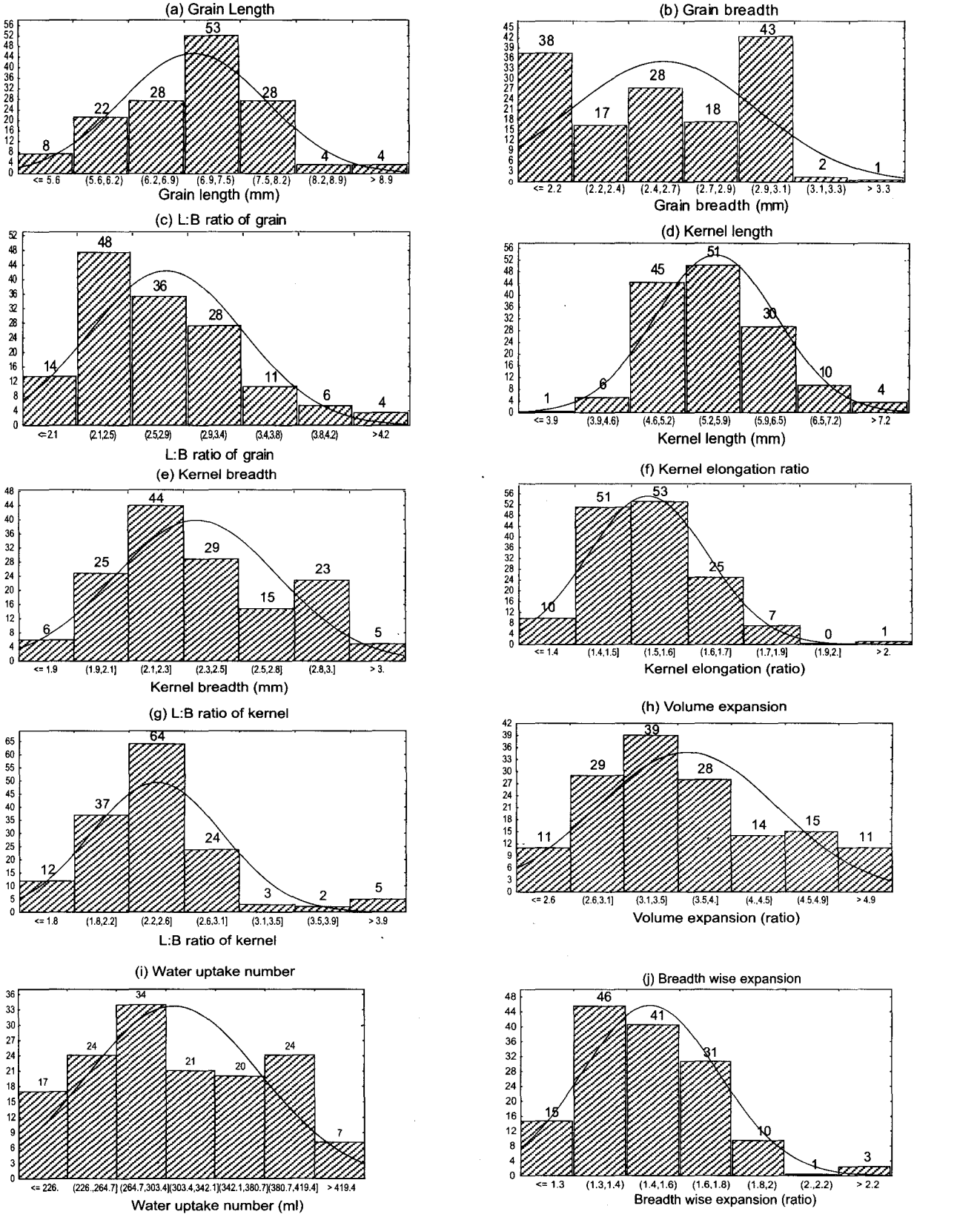

Fig. 1: Frequency distribution for various traits in Ahu rices (a) Grain length, (b) Grain breadth, (c) L:B ratio of grain, (d) kernel length, (e) Kernel breadth, (f) Kernel elongation ratio, (g) L:B ratio of kernel, (h) Volume expansion

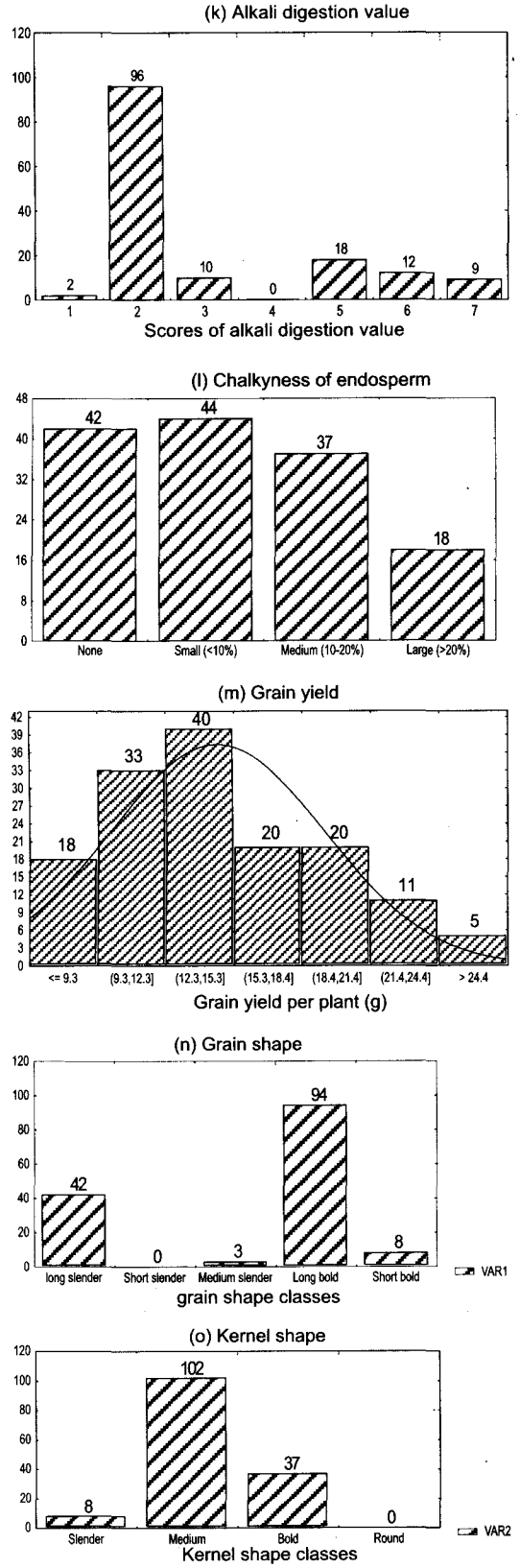

Fig. 1 (Contd.): (i) Water uptake number, (j) Breadth wise expansion, (k) Alkali digestion value, (l) Chalkiness of endosperm, (m) Grain yield, (n) Grain shape, and (o) Kernel shape

introduction is presently one of the popular Ahu varieties of Assam and was also included in the present study; exhibited very low (2.0) alkali digestion. This gives a clear indication that the Ahu rices are quite different than the other groups of Assam rice varieties in terms of quality.

A few varieties were identified excellent for individual quality features. Highest kernel elongation and volume expansion was exhibited by Betguti I, which is a short bold- seeded variety having very low alkali digestion value. Basantabahar was identified as the best superfine grain-type variety which exhibited highest L:Bg L:Bk and lowest grain breadth. However, cooking quality of this variety was observed to be poor associated with low kernel elongation and high breadth wise expansion. A number of varieties were observed having desirable alkali digestion value and non-chalky endosperm. However, no one of them was observed to possess other desirable attributes as well. Grain yield plant^{-1} was observed along with the quality traits. Significant variability was observed for this trait as well ranging from 6.23 to 24.48 g plant^{-1}. However, a large number of varieties were poor yielders. The best three Ahu rice varieties identified for grain yield plant^{-1} were Padumoni II, Ikra II and Khoijoi. An insight into the quality of these three varieties indicated that the first two varieties were very poor in alkali digestion value, kernel elongation, and volume expansion and water uptake number in comparison to the third one. The variety Khoijoi, however, had intermediate alkali digestion value and also comparatively higher values for volume expansion, water uptake and kernel elongation. All of them had long bold grains with red pericarp.

Correlation studies (Table 2) revealed that GL and KL was positively and significantly correlated with L:Bg, L:Bk, AD and CH. Kernel length, on the other hand, was negatively correlated with kernel elongation. This indicated that long grained varieties tended to have high AD values and high degree of endosperm chalkiness along with poor kernel elongation. Highly significant correlation of the length-breadth ratio of grain and kernel were observed with VE, BE, AD and CH. Thus, it was realized that the desirable physical quality was associated with many of the undesirable cooking qualities like higher grain chalkiness, lower gelatinisation temperature, higher breadth-wise expansion and poor kernel elongation. Kernel elongation, volume expansion and water uptake were observed to be significantly and positively correlated with each other. Tomar and Nanda (1982) also reported similar result with regard to these traits. Grain yield

Table 2. Correlation matrix for 12 quality traits and grain yield in Ahu rices

	GB	L:Bg	KL	KB	ER	L:Bk	VE	WU	BE	AD	CH	GY
GL	-0.17*	0.72**	0.52**	-0.24**	-0.02	0.52**	0.15	0.08	0.16	0.22	0.28**	0.09
GB		-0.79**	-0.18*	0.39**	0.21*	-0.41**	-0.14	-0.18*	-0.26**	-0.12	-0.13	0.10
L:Bg			0.46**	-0.43**	-0.14	0.63*	0.19*	0.17*	0.28**	0.24	0.27**	-0.01
KL				-0.12	-0.20*	0.74**	-0.26**	-0.27**	0.03	0.18	0.17*	0.07
KB					-0.06	-0.73**	-0.55**	-0.48**	-0.58**	-0.14	-0.09	0.05
ER						-0.07	0.41**	0.34**	0.07	-0.08	0.01	0.17*
L:Bk							0.20*	0.14	0.40**	0.23	0.18*	0.03
VE								0.84**	0.68**	0.22	0.19*	0.02
WU									0.60**	0.09	0.14	-0.03
BE										0.13	0.11	0.01
AD											0.80*	0.10
CH												0.16

* Significant at P= 0.05, **Significant at P=0.01

exhibited significant positive correlation with kernel elongation but did not show significant relationship with any other quality traits under study.

From the above results, it appeared that the Ahu rices in general do not confer the generally acceptable quality norm of Indian rices with respect to the major quality attributes. Inhabitants of the native region might have adapted with the rice type, developing their own system of use and processing. In order to improve the grain quality of Ahu rices, crossing programme may be undertaken to bring different desirable traits distributed in the varieties in a common background. Consideration of the grain yield and related traits along with the quality parameters would be beneficial in formulating breeding programmes for improving Ahu rices for yield and quality together. Many undesirable associations between the physical quality traits and cooking quality attributes would limit direct selection of varieties for simultaneous improvement of multiple traits. Therefore, it would be necessary to undertake breeding programme to break these undesirable linkages for bringing about improvement in Ahu rices in terms of quality attributes.

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Seed-borne Pathogens Intercepted in Germplasm Introduced in India During 2005-06

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Quarantine processing of 1,48,917 samples of seeds and other planting material of various agri-horticultural crops imported during 2005-2006 resulted in the interception of 34 fungi and one bacterium. These interceptions included pathogens of quarantine significance, *viz.*, *Peronospora manshurica*, a fungus not known to occur in India; *Tilletia foetida* and *Botrytis cinerea* with a limited geographical distribution in the country; *Drechslera maydis* and *Phoma lingam* which are known to possess physiological races; *Colletotrichum dematium*, *Drechslera sorokiniana*, *Fusarium moniliforme*, *F. solani* and *Macrophomina phaseolina*, with wide host range and other pathogens reported to cause significant economic losses e.g. *Alternaria brassicicola*, *A. sesame*, *A. padwickii*, *A. radicina*, *Verticillium albo-atrum* and *Xanthomonas campestris* pv. *campestris*, etc. Economic significance of pathogens intercepted is discussed and the need to conduct a thorough and critical seed health testing during quarantine processing for safer introduction of planting material is emphasized.

Key Words: Germplasm, Quarantine, Interception, Pathogens

Introduction

International exchange of germplasm has played an important role in the crop improvement programme world over. Since a large number of pathogens are known to be seed-borne/ transmitted, there is always an inadvertent risk of introducing new pathogens or their more virulent strains along with introduced planting material. National Bureau of Plant Genetic Resources (NBPGR), New Delhi is the nodal agency for exchange (import/export) and undertaking quarantine clearance of germplasm meant for research use by public as well as private sector. Every year > 60,000 samples of various agri-horticultural crops and their wild relatives are processed for quarantine clearance. During quarantine processing a large number of pathogens have been intercepted (Khetarpal *et al.*, 2001) including pathogens which are not reported from India such as *Peronospora manshurica* (Naum.) Syd. (Agarwal *et al.*, 2006a); *Uromyces betae* Kickx (Agarwal *et al.*, 2006b); *Fusarium nivale* (Fr.) Ces. (Dev *et al.*, 1989); and a new fungus, *Drechslera pluriseptata* sp. nov. (Khetarpal *et al.*, 1984). In this paper, 35 pathogens intercepted in germplasm and trial material introduced during 2005-2006 are reported and economic significance of major ones is discussed.

Materials and Methods

During 2005-06, a total of 348 consignments comprising of 1,48,917 samples (43,017 germplasm and 1,05,900 samples of international trial material) of various agri-horticultural crops and their wild relatives from 47 countries were received for quarantine processing. It comprised of 314 consignments (1,47,620 samples) of true seeds and 34 consignments (1,297 samples) of vegetative propagules such as rooted plants, bud wood cuttings, tubers and *in vitro* plantlets of > 50 crop species. The highest number of consignments were received from USA (87) followed by the Philippines (51), Mexico (48), Taiwan (31), Australia (18), Thailand (14) and Syria (7) and remaining 92 from the other 40 countries. Wheat with 62,743 samples (61 consignments) constituted the largest import followed by rice with 49,867 samples (59 consignments) and maize with 11,133 samples (51 consignments).

All the samples were tested as per standard seed testing procedures (ISTA, 1968). Samples were first subjected to dry examination under stereo-binocular microscope for bacterial/fungal symptoms like discoloration, pigmented, deformed and abnormal seeds, presence of infected seeds or fungal fructification, mycelium or spores on the surface of seeds or planting material. Seed samples coated with microbial cultures and/or suspected to carry traces of externally-borne spores were subjected to washing test by mechanical stirring seeds in small quantity of distilled water. Apparently unhealthy looking seeds and small portions from planting material showing pigmentation or abnormal growth were

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subjected to incubation test by placing them on moist blotter discs in plastic petri plates. Number of seeds tested varied from 10- 400 depending on the size of the sample being tested. The plates were incubated for 7 days at 20 ± 1°C under alternate cycles of light and darkness and were examined on eighth day under stereo-binocular microscope for the associated pathogens. The pathogens were identified on the basis of bacterial/fungal growth and colony characters. Wherever required, slides were prepared and examined for spore/conidial characters for identification of pathogen up to species level. Infected samples were decontaminated/disinfected by suitable physical or chemical treatment.

Eight thousand nine hundred and forty four (8,944) chemically treated samples of international trials of wheat (6,391), barley (2,240) and triticale (313) were grown in post-entry quarantine nursery (PEQN), NBPGR, New Delhi, for detection of seed-borne diseases.

Samples of various crops found infected/ contaminated and pathogens detected during dry examination, incubation test and PEQN along with their source/country, total number of samples received, samples found infected and per cent samples infected are listed in Table 1.

Results and Discussion

During visual examination under stereo-binocular microscope, downy mildew fungus of soybean, *P. manshurica* was detected as a crust of oospores on seed surface. Examination of decant from washing test also revealed oospores of the fungus. *P. manshurica* was intercepted in nine samples from Taiwan (6) and USA (3). As per the Plant Quarantine (Regulation of Import into India) Order (2003), for any import of soybean seeds for sowing purposes an additional declaration is required in the Phytosanitary Certificate issued by the exporting country, certifying the consignment to be free from this fungus. *P. manshurica* is not yet reported from India, however, it has been repeatedly intercepted on soybean seeds from several countries including Malaysia and Indonesia where the disease is not officially recorded (Agarwal *et al.*, 2006a). Oospores are reported to retain viability up to eight years in soil and a large number of physiological races are reported in *P. manshurica* (Marcinkowska, 1991; Li *et al.*, 1992; Hartman *et al.*, 1999). Total yield losses due to soybean downy mildew in Argentina, Canada, China, Italy and USA were estimated to be 3,87,900 metric tonns (Wrather *et al.*, 1997). *P. manshurica* was observed in France in 1974 (Signoret *et al.*, 1975) indicating the possibility of its spread into new areas. In view of this, fungus being a quarantine pest for India, its interception is of high quarantine significance. All the infected samples were rejected and incinerated.

Tilletia foetida (Wallr.) Liro, the causal agent of common bunt or hill bunt of wheat with smooth walled uredospores was intercepted in one sample of *Triticum* sp. from USA. In India, the disease is restricted only to Delhi, Himachal Pradesh, Jammu and Kashmir, and Punjab. In the past, *T. foetida* was frequently intercepted in wheat imported from 15 countries (Dev *et al.*, 2005). Common bunt is an important disease in many wheat growing areas of the world. The ustilospores can survive for several years on contaminated seed and in the soil and the unfavorable odour affects the market value of wheat. More than 50% crop losses were reported in the crop raised from untreated seeds in Turkey (CABI, 2006) and in Australia average potential loss due to bunt was estimated up to 361 million Australian dollars (Brennan and Murray, 1988). Teliospores of *Puccinia helianthi* the causal organism of rust were detected in 25 samples of sunflower from USA (9), Egypt (5) and France (11) in washing test.

During blotter test, *Alternaria brassicae* (Berk) Sacc., the causal fungus of grey leaf spot in brassicas was intercepted in one sample out of the two samples of *Crambe abyssinica* received from UK. *A. brassicae* causes pre- and post-emergence damping off of seedlings resulting in yield losses. Yield losses up to 70 per cent were reported from various parts of the world (CABI, 2006). *Alternaria brassicicola* (schw.) Wilts., the causal agent of black spot, was intercepted in 44 samples of *Brassica* spp. from Australia (16), Canada (25), China (1) and the Netherlands (2) and one sample each of *C. abyssinia* from UK, *Capsicum* sp. from Russia and *Citrullus lanatus* from China. Though *A. brassicicola* has a wide host range (CABI, 2006) and is known to be seed-borne in 10 crops (Richardson, 1990), it is detected on seeds of *Capsicum* and *C. lanatus* for the first time and this is the first report of the fungus being seed-borne on these two crops. During last 25 years, this fungus was repeatedly intercepted on species of *Brassica* and *Allium* (Agarwal *et al.*, 2004). Black spot is regarded as a major disease in brassicas in the Netherlands and other European countries. Infected seeds recorded reduction in germination and seedling vigor, and yield losses of up to 70 per cent have been reported (CABI, 2006). *Alternaria*

Table 1. Seed-borne pathogens intercepted in germplasm introduced in India during 2005-06

Fungi/bacterium intercepted	Crop	Country/ Source	No. of samples	
			Processed	Found infected
Alternaria brassicae[3]	*Crambe abyssinica*	UK	2	1
A. brassicicola[3]	*Brassica juncea*	Australia	10	7
		Canada	400	25
	B. napus	Australia	21	9
	B. oleracea	China	5	1
		Netherlands	392	2
	Capsicum sp.	Russia	9	1
	Citrullus lanatus	China	26	1
	C. abyssinica	UK	2	1
A. lini[3]	*Linum* spp.	Russia	4	2
A. padwickii[3]	*Oryza sativa*	Philippines	49,701	122
A. radicina[3]	*Daucus carota*	China	3	3
	Capsicum spp.	Taiwan	295	1
Botrytis cinerea[3]	*B. juncea*	Germany	8	1
		Canada	400	1
	Carthamus tinctorious	Germany	18	2
	Helianthus annuus	France	350	3
	Hordeum vulgare	Sweden	20	1
Cephalosporium sp[3]	*Beta vulgaris*	USA	12	2
	Capsicum spp.	Taiwan	295	1
	Lycopersicon esculentum	Taiwan	218	1
	O. sativa	Philippines	49,701	3
	Sorghum bicolor	USA	36	3
	Vigna radiata	Taiwan	36	1
	Zea mays	Thailand	1,927	7
Ceratocystis sp.[3]	*C. abyssinica*	UK	2	1
Colletotrichum dematium[3]	*Cicer arietinum*	Syria	3,624	1
	C. abyssinica	UK	2	1
	Glycine max	Taiwan	278	5
		USA	5	1
	Gossypium sp.	USA	1,903	1
	H. annuus	USA	32	5
	L. esculentum	Taiwan	218	2
Curvularia lunata[3]	*O. sativa*	Philippines	49,701	69
	S. bicolor	USA	36	1
Drechslera avenae[3]	*H. vulgare*	Australia	129	1
D. cynodontis[3]	*Capsicum* spp.	Taiwan	295	1
D. maydis[3]	*Z. mays*	Thailand	1,927	4
		Philippines	125	1
D. oryzae[3]	*O. sativa*	Bangladesh	3	1
		Philippines	49,701	15
D. sorokiniana[3]	*B. juncea*	Canada	400	1
	Capsicum sp.	China	34	1
	L. esculentum	Taiwan	218	1
	Poa pratensis	USA	27	1
	Triticum spp.	Belgium	5	1
		USA	1,860	16
		Mexico	64,528	4
		Nepal	5,220	9
D. sorghicola[3]	*Z. mays*	Philippines	125	1
Fusarium culmorum[3]	*H. vulgare*	Australia	129	1
F. dimerum[3]	*O. sativa*	Philippines	49,701	18
F. equiseti[3]	*Capsicum* spp.	Taiwan	295	1
	H. annuus	France	350	1
		USA	32	1
F. moniliforme[3]	*Beta vulgaris*	France	8	1
		USA	12	3
	Capsicum spp.	China	34	1
		Taiwan	295	8
	Citrullus lanatus	China	26	1

Contd.

Table 1 Contd.

Fungi/bacterium intercepted	Crop	Country/ Source	No. of samples	
			Processed	Found infected
	C. abyssinica	UK	2	1
	G. max	Taiwan	278	7
	Gossypium spp.	USA	1,903	10
	H. annuus	France	350	3
	H. vulgare	Australia	129	2
		Sweden	20	1
	L. esculentum	Taiwan	218	3
	O. sativa	Philippines	49,701	104
	Perilla frutescens	USA	19	5
	S. bicolor	USA	36	5
	Triticum spp.	USA	1860	12
		Mexico	64,528	2
	V. radiata	Sri Lanka	3	1
		Taiwan	36	4
	Z. mays	Thailand	1,927	41
		USA	459	28
		Philippines	125	1
F. semitectum[3]	*B. vulgaris*	USA	5	3
	Gossypium spp.	USA	1,903	16
	O. sativa	Philippines	49,701	43
	Triticum sp.	Mexico	64,528	1
	Z. mays	Thailand	1,927	2
F. solani[3]	*C. tinctorious*	Germany	18	1
	C. arietinum	Syria	3,624	1
	Gossypium spp.	USA	1,903	1
	L. esculentum	Taiwan	218	1
	O. sativa	Philippines	49,701	2
Macrophomina phaseolina[3]	*G. max*	Taiwan	278	2
		USA	5	2
Nigrospora oryzae[3]	*Triticum* sp.	Belgium	5	1
Peronospora manshurica[1,2]	*G. max*	Taiwan	278	6
		USA	5	3
Phoma lingam[3]	*B. juncea*	Canada	400	3
Phoma sp.[3]	*Capsicum* spp.	Taiwan	295	1
	H. vulgare	Australia	129	1
	O. sativa	Philippines	49,701	90
	P. frutescens	USA	19	1
	P. pratensis	USA	27	1
	V. unguiculata	Columbia	6	1
Puccinia helianthi[2]	*H. annuus*	USA	32	9
		Egypt	10	5
		France	350	11
Rhizoctonia bataticola[3]	*O. sativa*	Philippines	49,701	8
R. solani[3]	*B. vulgaris*	USA	5	4
	Papaver dubium	Denmark	6	2
Tilletia foetida[1,2]	*Triticum* spp.	USA	1,860	1
Ustilago nuda[4]	*H. vulgare*	Mexico	2,240	5
Ustilago segetum var. tritici[4]	*Triticum* spp.	Mexico	6,391	2
Verticillium albo-atrum[3]	*Capsicum* spp.	Taiwan	295	1
	Carica papaya	Cuba	2	1
	H. annuus	France	350	4
	O. sativa	Philippines	49,701	1
	Solanum melongena	Taiwan	22	1
Xanthomonas campestris pv. *campestris*[3]	*B. juncea*	Canada	400	6
		USA	4	1
		Germany	8	2
	B. napus	Germany	42	5

Pathogen detected during: 1-dry examination; 2-washing test; 3–incubation test; 4-PEQN

linicola Groves and Skolko, the causal organism of seedling blight in flax was intercepted in two out of 4 samples of linseed received from Russia. *A. linicola* is regarded as an important pathogen in most flax growing areas, and can seriously decrease emergence when infected seed is sown (Mercer *et al.*, 1991).

Alternaria padwickii (Ganguly) M.B. Ellis, the causal agent of stack burn disease of rice was intercepted in 122 samples of paddy from the Philippines. Grain discoloration, caused by this fungus alone or in combination with other fungi, can reduce the market value of the crop (Saini, 1985). *Alternaria radicina* Meier, Drechsler & Eddy, the black rot fungus of carrots has a wide host range and known to be seed-borne in 10 crops. The fungus was intercepted in *Daucus carota* from China (3) and *Capsicum annuum* from Taiwan (1). There is no report of *A. radicina* infecting *Capsicum* and hence this is a new host record for the fungus. Besides, the fungus is not reported to occur in Taiwan and the information regarding the origin of the accession found infected is not available i.e. whether originated from Taiwan or collected by AVRDC, Taiwan from other source. The fungus is known to cause considerable damage in the storage resulting in reduction of seed quality and germination. A distinction is made by some authorities between the eastern and western races of the cultivated carrot, where a greater degree of resistance is known to occur in the western race (CABI, 2006).

Botrytis cinerea Pers. Fr, the grey mould fungus was intercepted in *Brassica juncea* from Canada and Germany (one each), *Carthamus tinctorius* from Germany (2), *Helianthus annuus* from France (3) and *Hordeum vulgare* from Sweden (1). Due to the wide host range, *B. cinerea* is considered a constant threat to agricultural crops (CABI, 2006). The fungus is also known to be seed-borne in 56 crops (Richardson, 1990). Though considered a common saprophyte world wide, in India it was reported to cause heavy losses in chickpea in the states of Bihar, Haryana, Himachal Pradesh, Madhya Pradesh, Punjab and Tamil Nadu (Laha and Grewal, 1983). It causes yield losses in the field and during post harvest storage and transport. Economic losses of more than 50 per cent may occur in many crops, depending on the prevailing environmental conditions and intensive use of fungicides is needed to control grey mould.

Colletotrichum dematium (Pers.) Grove, the causal organism of dieback or anthracnose, has a wide host range. The fungus was intercepted in seven samples, one sample each of *Cicer arietinum*, *Crambe abyssinica* and *Gossypium* sp. from Syria, USA, and UK, respectively and five samples each of *Glycine max* and *H. annuus* from Taiwan and USA. Awasthi and Bhargawa (2000) reported a significant reduction in chickpea production in India due to *C. dematium*.

Curvularia lunata (Wakker) Boedjin was intercepted in 70 samples of paddy from the Philippines (69) and sorghum from the USA (1). Grain mould caused by a complex of *C. lunata* and other fungi like *Fusarium moniliformae* and *Phoma sorghina* has been classified as a high priority disease of sorghum in East Africa, Venezuela and the USA (Hulluka *et al.*, 1992; Teyssandier, 1992; Frederiksen and Duncan, 1992).

Drechslera avenae (Eidam) Sharif, the causal agent of leaf spot or pre-emergence damping off was intercepted in one sample of barley from Australia. The disease is most damaging when cool wet conditions prevail during the early seedling stage and depending on the cultivar and climatic conditions, about 14 per cent yield losses are reported (Kunovski and Breshkov, 1981).

Drechslera maydis (Nisikado and Miyabe) Subram. and Jain, the maydis leaf blight fungus was detected in three samples of maize from Thailand and the Philippines. The fungus possess three races, including a devastating race, Race-T that caused the great epidemic of 1970 in USA due to a large scale planting of cytoplasmic male sterile lines. Earlier, Ram Nath *et al.* (1973) had intercepted Race T of the fungus in sorghum seed from USA. Introduction of exotic and more virulent strains along with the introduced germplasm can pose a serious threat to the indigenous maize cultivars.

Drechslera oryzae (Breda de Haan) Subram. and Jain [= *Cochliobolus miyabeanus* (Ito & Kurib.) Drechsler ex Dastur], brown leaf spot fungus of rice was detected in 16 samples from the Philippines and Bangladesh. Brown spot is a common disease of rice worldwide and can cause considerable yield losses. The disease was the main cause of the Great Bengal Famine of 1942 in India and crop losses during the epidemic year ranged from 50 to 90 % (Padmanabhan, 1973).

Drechslera sorokiniana (Sacc.) Subram. and Jain [teleomorph- *Cochliobolus sativus* (Ito & Kurib) Drechsler ex. Dastur], the causal agent of leaf blight/ seedling blight is the most important foliar pathogen on many crops throughout the world, particularly on wheat and barley. The fungus was intercepted in 33 samples including 29 samples of wheat from Belgium, Mexico,

Nepal and USA and one sample each of *B. juncea* from Canada, *Capsicum* sp. from China, *Lycopersicon esculentum* from Taiwan and *Poa pratensis* from USA. Yield losses up to 19 per cent are reported (CABI, 2006). In past, the fungus was intercepted on various crops (Khetarpal *et al.*, 2001) and on *Triticum* spp. alone from 23 countries (Dev *et al.*, 2005). The fungus has many physiological races and geographically remote populations are reported to differ in virulence (Levitin *et al.*, 1985) hence, its interception from various countries is significant from quarantine point of view.

Fusarium moniliforme Sheldon [teleomorph-*Gibberella fujikuroi* (Sawda) Ito] the causal organism of bakanae disease of rice and maize stalk rot was intercepted in 245 samples of 15 crop species from 11 countries. The interception of *F. moniliformae* in five samples out of total 19 samples of *Perilla frutescens,* an under utilized crop introduced from USA is very significant from quarantine point of view. The fungus is reported to infect a large number of crops of economic significance and can survive up to 26 months in infected grains. A variation in virulence is reported in the fungus (CABI, 2006). Yield losses due to bakanae disease ranges from 20-50 per cent in Japan and 15 per cent losses are reported from eastern districts of Uttar Pradesh in India (Ou, 1985).

Fusarium solani (Mart.) Sacc., [teleomorph-Nectria haematococa (Wollenw.) Gerlach], the causal agent of wilt, blight and collar and root rots in a large number of crops was intercepted in one sample each of chickpea, cotton, safflower, tomato from Syria, the USA, Germany and Taiwan, respectively, and two samples of rice from Philippines. Though known to be seed-borne in cotton, in this laboratory, the fungus was intercepted on this host for the first time. During last 25 years, *F. solani* was intercepted in 93 crop species including 65 crop species where the fungus was not known to be seed-borne earlier (Agarwal *et al.*, 2005). *F. solani* causes substantial economic losses in various crops worldwide. Foot-rot syndrome in legumes has been reported as a major limiting factor to crop production causing substantial yield losses in pea and bean crops in Europe and North America. Sudden death syndrome of soybean, an important disease in the southern USA is now becoming more prevalent and severe in northern states also (Scherm and Yang, 1996). Lima and Lopes (1998) reported different levels of aggressiveness between isolates of *F. solani* that attack potato in Brazil. Recent molecular studies also revealed high levels of diversity within the fungus (CABI, 2006).

Macrophomina phaseolina (Tassi) Goid (synonym *Rhizoctonia bataticola* (Taubenh.) Butler), the causal agent of charcoal rot was intercepted in two samples of *G. max* from Taiwan. Charcoal rot is an economically important disease in a large number of crops throughout the world. During last 25 years the fungus was intercepted on several crops from many countries (Khetarpal *et al.*, 2001). Seed infection reduces germination and the pathogen retains viability for 15 months in seeds at room temperature. Significant yield losses are reported in chickpea, groundnut, sunflower, sorghum and soybean (CABI, 2006).

Phoma lingam (Tode) Desm. [teleomorph-*Leptosphaeria maculans* (Desm.) Ces. and De Not], the causal organism of black leg or stem canker of crucifers was intercepted in *B. juncea* from Canada. *P. lingam* is one of the most important pathogens of brassicas and yield losses up to 90 per cent have been reported from Australia, America and Europe (CABI, 2006). The fungus is known to be highly variable and two strains termed as virulent (group A) and avirulent (group B) are being reported which are further known to possess genetically distinct sub-groups (Taylor *et al.*, 1991). Recent studies have revealed that the population structure of the fungus varies in different regions of the world; A-group isolates predominate in Australia, B-group isolates predominate in China and eastern Europe, and isolates are evenly distributed between the two strains in western Europe and North America (West *et al.*, 2002).

Rhizoctonia solani Kuhn was intercepted in 4 out of 5 samples of *Beta vulgaris* from USA and 2 out of 6 samples of *Papaver dubium* from Denmark. It is a pathogen with a worldwide distribution and infects a large number of crops. Yield and economic losses caused by the fungus have not been determined in the majority of crops and environments.

Verticillium albo-atrum Reinke and Berthold, the causal agent of Verticillium-wilt is limited to cool, temperate regions of the world and in India the fungus is mainly present in Karnataka, Rajasthan, Tamil Nadu and Uttar Pradesh (CABI, 2006). The fungus can infect numerous economically important plant species and is seed-borne in 15 crops (Richardson, 1990). Infected planting material is the primary source of introducing the pathogen into disease-free areas. *V. albo-atrum* is known to possess a number of physiological strains and its potential to evolve more virulent strains is the major constrain in the breeding plants for resistance. The fungus

was detected in *Capsicum* sp. and *Solanum melongena* (Taiwan), *Carica papaya* (Cuba), *H. annuus* (France) and *Oryza sativa* (the Philippines). *V. albo-atrum* is considered of high economic importance and reported to cause significant losses in hops and lucerne crops in UK and the USA, respectively (CABI, 2006). In addition to these fungi, *Cephalosporium* spp., *Ceratocystis* sp., *Drechslera sorghicola*, *Fusarium culmorum*, *F. dimerum*, *F. semitectum*, and *Phoma* spp. were detected on a large number of crops from various countries.

Xanthomonas campestris pv. *campestris* (Pammel) Dowson, the causal agent of bacterial black rot of crucifers was intercepted in 14 samples of *Brassica* spp. from Canada, Germany and USA. In the past, *X. campestris* pv. *campestris* the was intercepted on brassicas from several countries (Singh *et al.*, 2006). The bacterium is widely distributed throughout the world and can survive in seeds for more than three years. Infected seeds are the primary source of dissemination and more than six virulent strains of the bacterium are known to occur (CABI, 2006). The disease causes severe losses in production and is of great concern in most of the brassica growing regions of the world.

Chemically treated seeds of wheat, barley and triticale grown in PEQN revealed the detection of loose smut caused by *Ustilago segetum* (Pers.) var. *tritici* Jensen in two entries of wheat and covered smut caused by *U. nuda* (Pers.) Legerh. in five entries of barley from International Maize and Wheat Improvement Centre (CIMMYT), Mexico. Infected plants in the field were uprooted and incinerated.

In all, 754 samples of various crops were found to be infected/ contaminated with 35 pathogens. Out of these, 745 samples were disinfected/decontaminated using various salvaging techniques such as mechanical separation (for bunted seeds), ethyl alcohol wash (for samples with bunt and rust spores), hot-water treatment (for samples infected with species of *Alternaria*, *Colletotrichum*, *P. lingam*, *Rhizoctonia* and *X. campestris* pv. *campestris*, etc.) and pesticidal seed treatment/ dip for seeds/ planting material infected with species of *Drechslera*, *Fusarium*, etc.). Nine samples of soybean infected with the downy mildew infection were rejected and incinerated.

It was observed that out of total 865 infection incidences detected in 754 samples (0.05% of the total import), from 23 countries, the highest infection percentage was observed in the samples from the Philippines (55.26%) followed by the USA (16.72%), Thailand (6.24%), Taiwan (5.54%), Canada (4.16%), Australia (2.42%), Germany (2.32%) and rest of the countries (8.50%). Other samples including vegetative propagules and *in vitro* planting material were found to be free from any pathogen. Nine samples amounting to 1.19% of the total infected samples (0.01% of the total import) were rejected and rest were made disease-free and released to the indenters.

Interception of 35 pathogens in 754 samples of various crops from 23 countries is very significant from quarantine point of view as introduction of even a low incidence of seed-borne exotic pathogens or their more virulent strains along with planting material can pose a threat to the indigenous crops. Quarantine thus has a significant role in protecting agriculture from avoidable damage caused by such introductions and in regulating the safe introduction of plant genetic resources.

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SHORT COMMUNICATION

Estimation of Genetic Divergence in Apricot (*Prunus armeniaca* L.)

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Genetic divergence was assessed in 30 apricot collected from various parts of Kashmir Valley on the basis of eight characters. The genotypes were grouped into four clusters on the basis of relative magnitude of D^2 values using Tochers method. Cluster I was the largest with 22 genotypes followed by cluster II consisting of four genotypes. Inter-cluster D value was maximum between cluster III (1621.03) and cluster II (83.41). Crossing between genotypes having high genetic distance should be used in hybridization. Mean yield/ tree, fruit weight, fruit length, fruit diameter and stone weight was found maximum in cluster III.

Key Words: *Prunus armeniaca*, Cluster, Divergence, Apricot, Genotypes, Mahalanobis

Apricot cultivation is an important source of income to the tribal people as they sell the sun dried apricots, their kernel and oil extracted from the kernel which contains 40-46% oil in Leh division of Kashmir. Table type apricot mainly grown in Kashmir Valley, due to tendency of growing high value crop (apple) with long shelf life, its plantation is shrinking and old plantations are being replaced. The Kashmir Valley witnesses lot of genetic variability in apricot with regard to shape, size, and yield as well as morpho-physiological attributes. Viewing above facts in mind, an exploration in genetic diversity region was conducted in order to conserve quality landraces for subsequent breeding programme. In exploration programme, some promising selections collected for the genebank were APS-8, most attractive having 51 kg/tree yields, 91 g fruit weight, symmetrical, yellow skin, TSS 133.5%; APS-9 yields 47.7 kg/tree, fruit weight 76.5 g, medium TSS, APS-3 also high yielder, fruit weight 58.4 g/fruit, TSS 15.5%, sweet kernel; APS-29, APS-25 and APS-30 yield 25 to 30 kg/tree, fruit weight 22-25 g/fruit, sweet kernelled with TSS 11 to 13%.

Understanding of the variability, grouping as well as appropriate scale is quite imperative. The information about the extent of genetic divergence is critical for the improvement of any crop in order to have high heterotic and desirable segregants (George, 1976; Valsakumari *et al.*, 1985). Selection of genetically diverse parents will enable the expansion of genetic base and development of superior types. Hence, an effort was made to estimate the magnitude of genetic divergence in apricot genotypes to identify genetically divergent parent which can be utilized in hybridization programme.

A survey for collection and evaluation of apricot genotypes were carried in Srinagar, Budgam, Baramulla, Anantnag, Pulwama and Doda districts of Jammu and Kashmir. At the time of maturity, fruit samples of 30 to 40 in numbers were collected randomly in three replications for recording observations on fruit weight, fruit length, fruit diameter, acidity, total soluble solids, total sugar and stone weight. The fruit yield was recorded per tree basis at the end of harvesting.

The Mahalanobis D^2 statistics was used to estimate the genetic divergence among the genotypes as suggested by Rao (1952), Chaudhary and Singh (1975) and George (1976). All the genotypes were grouped into clusters according to Tocher's method as described by Rao (1952).

The assessment of genetic divergence among the genotypes showed the presence of appreciable amount of divergence. The genotypes were grouped into four clusters (Table 1). Cluster I was the largest with as many as 22 genotypes, cluster II had four genotypes, while as cluster III and Cluster IV consisted two genotypes each. Zaffer *et al.* (2004) also observed similar genetic divergence among various genotypes of apricot in Kargil region. The grouping of genotypes of different geographical locations into one cluster may be due to presence of some common genes controlling the most important characters or through modifying effect of micro and macro environment affecting genetic diversity like adoption, selection procedure and environmental conditions. The grouping of genotypes into 4 clusters reveals that cultivars growing in different pockets of Kashmir division had no tendency to group together in cluster which may be the result of diverse agro-ecological

Table 1. Distribution of 30 apricot genotypes into clusters

Cluster Number	No. of Genotypes	Genotype(s)/ Accession number
I	22	APS-24, APS-1, APS-13, APS-12, APS-19, APS-18, APS-17, APS-22, APS-3, APS-14, APS-7, APS-16, APS-2, APS-23, APS-15, APS-4, APS-27, APS-21, APS-10, APS-28, APS-5, APS-24
II	04	APS-3, APS-25, APS-29, APS-30
III	02	APS-8, APS-9
IV	02	APS-1, APS-6

Table 2. Intra-cluster (diagonal) and inter-cluster distances among grouped apricot clusters

Cluster Number	I	II	III	IV
I	244.91 (15.65)	274.12 (16.56)	1095.49 (33.10)	471.98 (21.86)
II		83.41 (9.43)	1621.03 (40.26)	668.88 (25.86)
III			398.96 (19.97)	1007.19 (31.74)
IV			0.00	0.00

▪ Parenthesis: D value, Outside parenthesis: D^2

conditions in the area of adoption. Another feature that genotypes from same location were placed in separate cluster indicating wide diversity among genotypes from same place. These findings are in general agreement with Prasad *et al.* (1993, 2001).

The intra and inter-cluster D^2 values among the four clusters are presented in the Table 2. The cluster III had the maximum intra-cluster distance 398.96 followed by cluster I with a distance of 244.91. The inter-cluster distance was the maximum between cluster III (1621.03) and II (83.41) followed by cluster III (398.96) with cluster IV (1007.19) on the other hand minimum distance (244.91) was recorded between cluster I and cluster II (274.12) indicating minimal diversity between these clusters. Genotypes belonging to the clusters separated by the high genetic distance should be used in hybridization to obtain a wide spectrum of variation among the progenies *i.e.* cluster III APS-8 and APS-9 and cluster II APS-3, APS-25, APS-29 and APS-30 as such the inter-cluster distance was registered the highest. It is advisable to make crosses between genotypes selected from the cluster with high mean performance to get desirable transgressive segregates (Dwivedi and Mitra, 1996).

The existence of diversity among the genotypes was also assessed by the amount of variation in cluster means for different characters (Table 3). Average yield per tree (49.50 kg), fruit weight (63.75 g), fruit length (5.90 cm), fruit diameter (5.13 cm) and stone weight (4.35 g) was found maximum in cluster III followed by cluster IV exhibited fruit weight, fruit length and fruit diameter. Total sugar was found superior in cluster IV (15.70° brix). Mean fruit yield/tree, fruit weight, fruit length, diameter, total sugar and stone weight was found the lowest in cluster II. As far as acidity was concerned, cluster II exhibited the maximum acidity (0.68%). Thus, by involving the genotypes of outstanding mean performance from these cluster as potential parents in crosses, hybrids with high yield and quality can be developed. Sardana *et al.* (1997) observed that cluster means represented an interesting picture of the nature of existing diversity among the material under study.

The per cent contribution of each character in grouping the genotypes was worked out and presented in Table 3. Total 435 D^2 values were obtained and based on these D^2 values, per cent contributions of different characters towards divergence were obtained. Stone weight ranked first *i.e.* 143 times with a maximum contribution of 32.64 per cent followed by fruit length 100 times (22.10%) contribution. These characters can be given greater importance in selection of potential parents for hybridization. De *et al.* (1988) proposed that

Table 3. Mean values for different characters of 4 clusters in apricot

Traits	Clusters				Per cent contribution towards divergence	Number of times appearing as first in the ranks
	I	II	III	IV		
Average yield/ tree	34.14	25.00	49.50	32.67	8.30	36
Fruit wt. (g)	33.40	26.87	63.75	53.07	8.51	37
Fruit length (cm)	4.00	3.70	5.90	4.51	22.98	100
Fruit diameter (cm)	4.30	3.00	5.13	4.60	0.00	0
Acidity (%)	0.42	0.68	0.07	0.15	0.92	4
T.S.S. (° Brix)	14.02	12.30	11.93	13.50	4.60	20
Total sugars (%)	10.50	9.30	10.90	15.70	22.10	96
Stone wt. (g)	2.43	1.37	4.35	2.00	32.64	142

traits contributing the maximum towards the D^2 values need to be given greater emphasis for deciding on the cluster to be chosen for the purpose of further selection and choice of parents for hybridization.

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SHORT COMMUNICATION

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

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

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

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

Ten parents of linseed having diverse geographical origin, *viz.*, Shubhra (Mukta x K2), Garima (T-126 x Neelum), Shekhar (Laxmi-27 x Ec1387), Janaki (New River x LC-216), J-23 (EC 9882 x Heera), T 397 (T 491 x T-1193-1), Gaurav (Selection 3 x EC-152), Belinca (Exotic Collection, Netherlands), Rasmi (Gaurav x Janaki), Nagarkot (New River x LC-216) were crossed in all possible combinations excluding reciprocals at Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, during *rabi* 2002. The 45 F_1s, 45 F_2s and 10 parents were sown in a randomized block design with three replications having 10 m^2 plot size. Each plot had 6 rows of 5 m length with row to row distance of 30 cm. The observations were recorded for 13 traits, *viz.*, days to flower, plant height (cm), technical plant height (cm), days to maturity, stem diameter (mm), number of capsules per plant, number of tillers per plant, seed yield per plant (g), oil content (%), fibre lengths (cm), fibre strength (g/tax), fibre fineness (tax) and fibre yield per plot (kg). Components of genetic variation were worked out by following the approach of Hayman (1958).

The estimates of six genetic parameters, *viz.*, $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{F}$, $\hat{h}^2$ and $\hat{E}$ along with their related statistics (Comstock and Robinson, 1948) are presented in Table 1. The mean value of the degree of dominance $(\hat{H}_1/\hat{D})^{0.5}$ indicated over dominance for eight traits, *viz.*, stem diameter, number of capsules per plant, number of tillers per plant, seed yield per plant, oil content, fibre length, fibre strength and fibre fineness in both F_1 and F_2 generations whereas, days to flower (50%), plant height, technical plant height, days to maturity and fibre yield per plot were found over dominance in F_2 generation only. Days to maturity and fibre yield per plot expressed partial dominance in the F_1 generation and significant $\hat{h}^2$ for the characters also confirmed the importance of dominance gene action. Similar findings were in agreement to Swarnkar *et al.* (2005) and Polonetskaya *et al.* (2002) for plant height, days to flower, number of capsules per plant and number of tillers per plant. The proportion of genes with positive and negative effect $(\hat{H}_2/4\hat{H}_1)$ was lesser compared to the theoretical value (0.25) in both F_1 and F_2 generations for all the characters, indicating that the positive and negative alleles were distributed in a considerable symmetrical manner across the parents.

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

Table 1. Estimates of genetic parameters $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{F}$, $\hat{h}^2$, $\hat{E}$ and related statistics for 13 characters in 10x10 diallel cross of linseed

Genetic parameters and related statistics	Days to 50% flowering		Plant height		Technical plant height		Days to maturity		Stem diameter	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
$\hat{D}$	91.22 ±5.70	91.01** ±6.67	326.95** ±14.71	326.30** ±19.83	245.30** ±8.62	245.12** ±10.59	77.64** ±5.33	77.77** ±3.67	0.09 ±-0.11	0.09 ±0.06
$\hat{F}$	22.32 ±13.15	71.34* ±30.78	21.83 ±33.94	124.43 ±91.50	40.88* ±19.90	103.74* ±48.86	12.79 ±12.30	51.87** ±16.94	-0.12 ±0.26	0.32 ±0.29
$\hat{H}_1$	66.70** ±12.13	295.93** ±56.80	168.95** ±31.31	737.07** ±168.83	149.90** ±18.36	379.14** ±90.15	47.60** ±11.35	162.29** ±31.25	1.18** ±0.24	2.28** ±0.53
$\hat{H}_2$	51.31** ±10.31	247.05** ±48.27	134.39** ±26.61	542.07** ±143.49	126.38** ±15.60	327.18** ±76.61	35.61** ±9.65	115.22** ±26.56	0.98** ±0.20	1.83** ±0.45
$\hat{h}^2$	2.05 ±6.90	40.81** ±8.08	1.30 ±17.81	64.72* ±24.01	33.37** ±10.44	37.15** ±12.82	0.46 ±6.46	22.17** ±4.44	0.28* ±0.14	0.09 ±0.08
$\hat{E}$	1.10 ±1.72	1.31 ±2.01	1.62 ±4.43	2.27 ±5.98	1.83 ±2.60	2.01 ±3.19	0.50 ±1.61	0.37 ±1.11	0.03 ±0.03	0.03 ±0.02
$(\hat{H}_1/\hat{D})^{0.5}$	0.85	1.80	0.72	1.50	0.78	1.24	0.78	1.44	3.56	4.92
$(\hat{H}_2/4\hat{H}_1)$	0.19	0.21	0.20	0.18	0.21	0.22	0.19	0.18	0.21	0.21
$[(4\hat{D}\hat{H}_1)^{0.5} + F/ (4\hat{D}\hat{H}_1)^{0.5} - F]$	1.34	1.56	1.10	1.29	1.24	1.41	1.24	1.60	0.69	2.04
$\hat{h}^2/\hat{H}_2$	0.04	0.17	0.01	0.12	0.26	0.11	0.01	0.19	0.28	0.05
r	-0.45	0.87	-0.88	-0.08	-0.14	-0.20	0.75	0.70	-0.30	0.58

Table 1 contd.

Genetic parameters and related statistics	No. of capsules/ plant		No. of tillers/ plant		Seed yield/plant		Oil content		Fibre length	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
$\hat{D}$	504.26** ±53.87	503.52** ±47.85	0.38 ±0.20	0.38 ±0.24	0.92** ±0.14	0.93** ±0.09	1.53 ±0.94	1.54 ±0.74	33.76** ±5.41	33.74** ±2.02
$\hat{F}$	493.22** ±124.29	1083.73** ±220.81	0.76 ±0.46	1.29 ±1.10	0.57 ±0.31	0.60 ±0.39	0.55 ±2.18	0.76 ±3.43	-30.04* ±12.49	-53.13** ±9.34
$\hat{H}_1$	718.52** ±114.67	2228.89** ±407.41	1.82** ±0.42	7.78** ±2.04	1.45** ±0.29	4.70** ±0.73	11.84** ±2.01	32.18** ±6.33	55.01** ±11.52	184.04** ±17.23
$\hat{H}_2$	513.71** ±97.45	1583.36** ±346.25	1.24** ±0.36	5.96** ±1.73	1.20** ±0.25	3.65** ±0.62	11.38** ±1.71	28.38** ±5.38	39.33** ±9.79	127.07** ±14.64
$\hat{h}^2$	1.17 ±65.23	-0.76 ±57.94	0.49 ±0.24	0.34 ±0.29	1.52** ±0.17	0.90** ±0.10	1.97 ±1.14	0.74 ±0.90	18.23** ±6.55	19.67** ±2.45
$\hat{E}$	4.43 ±16.24	5.16 ±14.43	0.10 ±0.06	0.10 ±0.07	0.05 ±0.04	0.03 ±0.03	0.08 ±0.28	0.07 ±0.22	0.69 ±1.63	0.71 ±0.61
$(\hat{H}_1/\hat{D})^{0.5}$	1.19	2.10	2.18	4.52	1.26	2.24	2.78	4.56	1.28	2.34
$(\hat{H}_2/4\hat{H}_1)$	0.18	0.17	0.17	0.19	0.21	0.19	0.24	0.22	0.18	0.17
$[(4\hat{D}\hat{H}_1)^{0.5} + F/ (4\hat{D}\hat{H}_1)^{0.5} - F]$	2.39	3.09	2.68	2.20	1.66	1.34	1.14	1.11	0.48	0.50
$\hat{h}^2/\hat{H}_2$	0.002	0.00	0.39	0.06	1.26	0.25	0.17	0.03	0.46	0.15
r	0.59	0.48	0.15	-0.42	-0.51	0.79	-0.41	-0.72	-0.40	-0.09

Table 1 contd.

Genetic parameters and related statistics	Fibre strength		Fibre fineness		Fibre yield/ plot	
	F_1	F_2	F_1	F_2	F_1	F_2
$\hat{D}$	6.18** ± 1.99	6.22** ± 1.09**	0.42** ±0.07	0.41** ± 0.04	0.31**± 0.02	0.31** ±0.01
$\hat{F}$	-5.76 ± 4.59	-9.13 ± 5.04	0.20 ± 0.17	0.22 ± 0.17	0.02 ± 0.04	0.17* ± 0.06
$\hat{H}_1$	36.08** ± 4.23	78.23** ± 9.31	0.57** ± 0.16	1.15**± 0.32	0.17** ± 0.04	0.57** ± 0.11
$\hat{H}_2$	28.14** ± 3.60	62.95** ± 7.91	0.50** ± 0.13	1.09** ± 0.27	0.14** ± 0.03	0.41** ± 0.09
$\hat{h}^2$	56.37** ± 2.41	19.32** ± 1.32	0.80** ± 0.09	0.07 ± 0.05	0.00 ±0.02	0.01 ± 0.02
$\hat{E}$	0.81 ± 0.60	0.76** ± 0.33	0.00 ± 0.02	0.01 ± 0.01	0.01 ± 0.01	0.01 ± 0.00
$(\hat{H}_1/\hat{D})^{0.5}$	2.42	3.55	1.17	1.66	0.75	1.35
$(\hat{H}_2/4\hat{H}_1)$	0.20	0.20	0.22	0.24	0.19	0.18
$[(4\hat{D}\hat{H}_1)^{0.5} + F/$ $(4\hat{D}\hat{H}_1)^{0.5} - F]$	0.68	0.66	1.53	1.38	1.08	1.50
$\hat{h}^2/\hat{H}_2$	2.00	0.31	0.17	0.07	0.00	0.01
r	-0.76	-0.65	-0.44	-0.21	-0.08	0.33

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

The estimated ratio of $(\hat{h}^2/\hat{H}_2)$ was less than unity for most of the characters in F_1 and F_2 generations except seed yield per plant in the F_1 generation. The characters having lesser value than unity indicated that at least one major gene was controlling their inheritance while the characters displaying values higher than unity were governed by more than one major gene. The coefficient of correlation (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) was negative for most of the characters in both F_1 and F_2 generations. However, it was positive for days to maturity and number of capsules per plant. In F_1 generation, number of tillers per plant and in F_2 generation days to flower, stem diameter, seed yield per plant and fibre yield per plot showed positive "r" values. The positive value of "r" indicated that negative genes were dominant for most of the traits. On the contrary, negative values showed that positive genes were mostly dominant for expression of these traits. The presence of preponderance of non additive genetic variation for majority of characters may be exploited in breeding programme of linseed.

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SHORT COMMUNICATION

Evaluation of Mungbean Germplasm for Genetic Diversity

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Key Words: Genetic diversity, Euclidean distances, Mungbean

Mungbean is one of the most important grain legume crops. It ranks third in total production amongst the pulses grown in the country after chickpea and pigeon pea. It is estimated that India's population will touch nearly 1.35 billion marks by 2020 AD and will require 30.3 million tonnes of pulses as against the present production of 12-14 million tonnes (Tiwari, 2004). Clearly a quantum jump is required in the total production of pulses to increase the per capita availability and to meet the challenges of increasing population. Conventional strategies for increasing the production of pulses include development and utilization of improved plant varieties, production technologies and plant protection procedures, which are expected to reduce the existing gap in production and requirement of pulses. The genetic reconstruction of plant type is required for developing high yielding varieties by improving yield component characters. The available germplasm serves as the most valuable natural reservoir for providing the desirable plant attributes for obtaining the high yielding crop varieties (Hawkes, 1981). The present study was conducted with an objective to select divergent parents for further use in improvement of mungbean.

The experiment was conducted during *kharif*, 2003 and 2004 at Crop Research Farm of Department of Genetics and Plant Breeding, Allahabad Agricultural Institute (Deemed University), Allahabad, comprising 132 mungbean genotypes. The experiment was laid in randomized complete block design in three replications of plot size 1x1 m^2 with 30 cm and 10 cm inter and intra-row spacing, respectively. Observations were recorded on 10 morphological characters, *viz.*, plant height (cm), number of primary branches, number of clusters $plant^{-1}$, number of pods $cluster^{-1}$, number of pods $plant^{-1}$, number of seeds pod^{-1}, pod length (cm), days to maturity, 100-seed weight (g) and seed yield $plant^{-1}$(g) on five randomly selected plants of each genotype. Recommended cultural practices and plant protection measures were followed to raise a healthy crop. The pooled data were subjected to multivariate analysis as suggested by Mahalanobis (1936) and genotypes were grouped into different clusters based on Euclidean distances by non- hierarchical cluster analysis (Spark, 1973).

The pooled analysis of variance showed a wide range of variation and significant differences for all 10 characters (Table 1). In the present study, 132 genotypes were grouped into 10 clusters. Cluster IV comprised 28 genotypes, evolving the largest cluster, followed by cluster I with 26 genotypes while, cluster VII emerged as mono genotypic and constituting only one genotype *i.e.* EC398889. Distribution of genotypes into different clusters, suggested the presence of substantial genetic divergence among the germplasm and indicated that this material may serve as good source for selecting the diverse parents for hybridization programme, aimed at isolating desirable recombinants for seed yield as well as other characters (Raje and Rao, 2001). The grouping of genotypes originating from different eco-geographical regions into one cluster could be attributed to frequent exchange of breeding material and operation of similar forces of natural and artificial selection resulting in perpetuation, adaptation and stabilization of similar genotypes (Murty and Arunachalam, 1966). The perusal of clustering pattern of the genotypes clearly revealed the lack of relationship between geographic distribution and genetic diversity as the distribution of accessions into various clusters was fairly random (Loganathan *et al.*, 2001; Reddy *et al.*, 2004). Therefore, selection of parents for hybridization should be based on genetic diversity rather than geographic distribution.

The intra and inter-cluster average distances among 10 clusters were variable (Table 2). The maximum intra-cluster distance (D^2) was registered for cluster V (6.631) followed by cluster X (4.924) and cluster IX (4.343). Inter-cluster distance (D^2) was found the maximum between clusters VIII and IX (148.645) followed by

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Table 1. Distribution of 132 mungbean genotypes into different clusters

S. No	Cluster No.	Number of genotypes	Genotypes included
1	I	26	EC30400, EC393407, LM-497, K-1310, EC399223, V-4512, V-2815, K-1284, V-3957, ML-613, KM-2194, K-92-200, TARM-1, LLR-2, PUSA-103, NARP-280, BHUM-93-34, PUSA-9531, AKM-8802, PUSA-9132, MARP-280, AKM-9241, PM-9001, LM-407, LLR-3, LLR-4
2	II	14	IPRM-90, UPM-83-1, OUM-11-5, ML-5, SONAMUNG, ML-131, PUSABAISAKHI, PS-16, AKM-9243, PANT MUNG-1, AKM-9601, T-1, CO-9, LGG-478
3	III	15	OBGG-11, V-2070, MUM-1-1, K-1460-1, NP-28, WGG-37, T-44, OBGG-52, MGG-47, PUSA-105, TARM-2, V-2015, MH-90-1, MGG-295, LM-23
4	IV	28	SAMRAT, ML-390, ML-583, PDM-1, HUM-10, PS-10, ML-406, JYOTI, HUM-1, PDM-54, PUSA-9072, SUJATA, DPM-90-1, SABARMATI, HUM-8, LGG-420, PDM-89-226, MGG-347, MH-309, LGG-460, PDM-11, PDM-84-139, ML-803, HUM-7, LGG-410, HUM-14, PUSA-102, NM-1
5	V	13	WGG-2, KM-2197, PUSA-9871, PUSA-108, PDM-139, LM-1119, V-3561, KM-2192, LM-490, V-4589, K-2192, K-1284, LM-387
6	VI	4	EC398888, MSO-9, PUSA BOLD-2, MSO-8
7	VII	12	PUSA-9332, ML-955, ML-405, MUM-2, BHU-MGP-17, HUM-2, BDYR-MUM-2-1, OBGG-40, LLR-1, K-851, K-1310, DMG-1098-1
8	VIII	1	EC398889
9	IX	9	LGG-470, MP-28, PUSA-9071, PDM-84-143, NARENDRA M-1, PIMS-11/ 99, V-1133, DMG-1103, VC-3944
10	X	10	V-557, ML-287, ML-588, K-1084, ML-575, LGG-499, LGG-477, Lam M-2, LGG-491, LGG-476

Table 2. Intra (diagonal) and inter-cluster average distances (D^2) for 10 characters in mungbean

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X
	3.415	10.511	5.272	4.661	7.5076	17.758	8.827	132.803	6.791	8.745
I	**(1.848)**	(3.242)	(2.296)	(2.159)	(2.740)	(4.214)	(2.971)	(11.524)	(2.606)	(2.957)
II		**3.787**	17.181	8.341	18.473	19.625	27.552	134.885	13.786	11.042
		(1.946)	(4.145)	(2.888)	(4.298)	(4.430)	(5.249)	(11.614)	(3.713)	(3.323)
III			**3.516**	7.393	15.140	28.665	4.439	143.976	6.401	21.372
			(1.875)	(2.719)	(3.891)	(5.354)	(2.107)	(11.999)	(2.530)	(4.623)
IV				**3.003**	12.440	13.119	13.742	118.657	10.170	9.967
				(1.733)	(3.527)	(3.622)	(3.707)	(10.893)	(3.189)	(3.157)
V					**6.631**	31.349	16.728	138.086	7.209	10.036
					(2.575)	(5.599)	(4.090)	(11.751)	(2.684)	(3.168)
VI						**3.119**	37.259	99.341	34.751	14.846
						(1.766)	(6.104)	(9.967)	(5.895)	(3.853)
VII							**3.870**	145.010	13.542	31.776
							(1.967)	(12.042)	(3.681)	(5.637)
VIII								**0.000**	148.645	129.368
								(0.000)	(12.192)	(11.374)
IX									**4.343**	14.585
									(25.084)	(3.819)
X										**4.924**
										(2.219)

D^2 values are represented in parentheses

clusters VII and VIII (145.010). Clusters with maximum inter-cluster distance were found to be highly divergent groups. Hence, inter cluster distance must be taken into consideration while selecting the parents for hybridization programme.

Mean performance of different clusters revealed wide range of differences (Table 3). Cluster II included genotypes having the highest number of pods cluster^{-1} and number of pods plant^{-1} and cluster IV had early maturing genotypes which may serve as a suitable source for incorporation of earliness into other genotypes, cluster VI comprised genotypes with long pods, high 100-seed weight and seed yield plant^{-1}. However, cluster VII was characterized with dwarf plants.

Table 3. Mean values of 10 clusters for 10 characters in 132 mungbean genotypes

Cluster No./ Characters	Plant height (cm)	No. of primary branches/plant	No. of clusters/ plant	No. of pods/ cluster	No. of pods/ plant	No. of seeds/ pod	Pod length (cm)	Days to maturity	100-seed weight (g)	Seed yield/ plant (g)
I	47.04	3.50	15.36	2.78	38.72	10.14	6.64	82.55	3.49	9.68
II	53.74	3.40	14.07	5.36	53.24	11.05	7.11	79.93	3.91	13.49
III	41.64	2.64	12.02	3.07	31.73	7.91	6.08	75.47	3.41	9.38
IV	50.80	3.63	14.58	3.30	39.83	10.31	6.83	68.38	3.54	12.88
V	39.56	4.64	23.05	2.92	49.54	8.79	5.53	82.18	4.48	10.01
VI	59.42	3.92	16.58	2.83	37.67	11.25	10.73	72.75	4.88	14.72
VII	31.14	3.64	10.11	2.79	21.11	8.25	5.80	76.67	3.39	6.04
VIII	69.67	5.33	12.33	2.33	24.00	11.33	9.90	58.00	2.63	13.80
IX	43.37	3.96	14.59	3.74	43.63	7.19	5.11	82.22	3.46	11.30
X	65.53	4.20	21.87	3.00	54.73	10.03	7.24	83.03	3.66	13.84

Since choice of appropriate parents plays a vital role in hybridization programme, best performing genotypes from distant clusters like VII, VIII and IX should be selected. Progenies of genetically diverse parents are likely to produce a broad spectrum of variability in segregating generations which will facilitate the isolation of transgressive segregants and recombinants for improvement of mungbean crop.

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SHORT COMMUNICATION

Ovipositional Preference of Mustard Sawfly, *Athalia proxima* Klug on some *Brassica* Germplasm and Varieties*

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Fifteen varieties/germplasm accessions of rapeseed mustard were evaluated for ovipositional preference by mustard sawfly. The experiment was conducted in earthen pots, under nylon net during two consecutive years 2004-05 and 2005-06. RK 2010, RK 2015, Kanti, Urvasi, RK 2011 and RK 2004 were less preferred by gravid female sawfly to lay eggs on them, while RK 2006, Rohini, RK 2013, Basanti, Kesari and Varuna were most preferred for egg laying. Reduced egg hatchability was observed on the variety RK 2011, RK 2010, RK 2004, Kanti, RK 2014, RK 2015, PR 4001 and Urvasi.

Key Words: Ovipositional preference, Mustard sawfly, *Brassica*, Germplasm

Mustard sawfly, *Athalia proxima* Klug is a serious pest of rapeseed mustard crop at seedling stage and it causes about 25 per cent reduction in yield (Sachan, 1990). Seedlings are very sensitive stage and very less time is available to manage this pest. It is best to use preventive measures such as use of resistant variety to overcome this pest problem. The presence of secondary plant substances such as glycosides in mustard are known to govern preference in host plant. Some biophysical characters of host plant are also responsible for this phenomenon (Painter, 1951).

The experiments were conducted during two consecutive years (2004-05 and 2005-06) under nylon net. For this purpose, well manured soil filled earthen pots were used. Seeds of all 15 varieties/germplasm (Table 1, 2) were sown on 25th October in three replication and the pots were arranged in three groups fallowed by covered with separate nylon net measuring 180×100×110 cm (length×width×height). Five pairs of adult sawfly were released daily in each replication block from the time two true leaf stage is attained and repeated every 5 days. Number of egg layings on all five plants of each replication was counted with the help of 20X hand lens. After seven days, all emerging larvae were counted consequently damage done by them were recorded weekly. The data so collected were analyzed in completely randomized design and t-test was used to compare the effect of biophysical characters on per cent egg layings.

Screening of various germplasm accessions/varieties of mustard under net house conditions indicated that RK 2010, RK 2015, Kanti, Urvasi, RK 2011 and RK 2004 were at par and significantly less preferred by gravid female sawfly to lay eggs on them, which registered 7.67, 8.00, 9.00, 10.33, 10.33 and 12.00 eggs/5 plants during 2004-05, respectively and 8.00, 8.00, 8.67, 11.67, 12.33 and 8.67 egg/5 plant during 2005-06, respectively. RK 2006, Rohini, RK 2013, Basanti, Kesari and Varuna were most preferred by female sawfly on which 23.33 to 19.67 eggs/5 plants and 25.00 to 19.33 eggs/5 plants were laid during 2004-05 and 2005-06, respectively. Egg hatchability of sawfly was significantly reduced on RK 2011, RK 2010, RK 2004, Kanti, RK 2014, RK 2015, PR 4001 and Urvasi which registered 75.46, 77.21, 76.26, 77.78, 78.15, 79.31, 79.40 and 80.58 per cent egg hatching during 2004-05, respectively and 78.93, 78.69, 79.95, 81.25, 79.61, 79.73, 82.80 and 82.00 per cent egg hatching during 2005-06, respectively. Whereas, RK 2006, Varuna, Maya and RK 2003 were most suited for egg hatchability which recorded 97.00 to 94.17 and 95.88 to 92.27 per cent during 2004-05 and 2005-06, respectively. After that the significantly reduced population of sawfly larvae was observed on RK 2010, RK 2015, Kanti, Urvashi, RK 2004, RK 2011, RK 2014 and RK 2003 and it varied from 4.52 to 7.67 and 5.00 to 8.00 larvae/5 plants during 2004-05 and 2005-06, respectively, whereas higher population was registered on RK 2006, Rohini, RK 2013, Basanti and RK 2001 which was varied from 14.67 to 11.00 and 15.00 to 11.00 larvae/ 5 plants during 2004-05 and 2005-06, respectively.

Sachan and Sumati (1985) and Sachan and Ujagir (1989) reported that mustard cultivar Varuna had more eggs than other cultivars which is in agreement with

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Table 1. Ovipositional preference of *A. proxima* on different germplasm/varieties of *Brassica* under net house condition during 2004-05

Entries	Number of eggs/5 plants		Percent hatchability		Number of larvae/5 plants		Leaf surface
RK 2001	19.33	(4.45)	83.98	(66.41)*	11.00	(3.32)	Hairy
RK 2002	16.67	(4.12)	94.17	(76.03)	8.33	(2.97)	,,
RK 2003	12.33	(3.53)	95.10	(77.21)	7.67	(2.81)	,,
RK 2004	12.00	(3.49)	76.26	(60.84)	7.00	(2.72)	,,
RK 2005	17.00	(4.16)	84.29	(66.65)	8.67	(3.02)	,,
RK 2006	23.33	(4.86)	97.00	(80.06)	14.67	(3.85)	,,
RK 2007	18.00	(4.29)	83.36	(65.93)	9.33	(3.09)	,,
RK 2008	17.00	(4.16)	86.29	(68.27)	9.00	(3.01)	,,
RK 2009	19.00	(4.38)	87.14	(68.99)	10.00	(3.17)	,,
RK 2010	7.67	(2.84)	77.21	(61.49)	4.52	(2.24)	,,
RK 2011	10.33	(3.26)	75.46	(60.28)	6.67	(2.66)	,,
RK 2012	13.67	(3.73)	85.52	(65.29)	8.00	(2.86)	,,
RK 2013	22.67	(4.80)	92.56	(74.17)	11.33	(3.38)	Smooth
RK 2014	11.33	(3.40)	78.15	(62.13)	7.00	(2.72)	,,
RK 2015	8.00	(2.88)	79.31	(62.94)	5.31	(2.41)	,,
Basanti	21.33	(4.66)	89.77	(71.35)	11.33	(3.38)	,,
Kanti	9.00	(3.01)	77.78	(61.88)	6.05	(2.56)	Hairy
Kesari	21.00	(4.59)	90.32	(71.87)	14.33	(3.81)	,,
Maya	14.00	(3.77)	95.57	(77.85)	8.00	(2.86)	,,
PR 4001	19.67	(4.48)	79.40	(63.01)	10.67	(3.27)	,,
Rohini	27.33	(5.26)	79.96	(63.41)	13.00	(3.61)	,,
Vaibhav	16.67	(4.12)	89.21	(70.82)	8.33	(2.96)	,,
Vardan	13.00	(3.65)	81.50	(64.53)	7.67	(2.81)	,,
Varuna	19.67	(4.48)	96.81	(79.71)	10.33	(3.25)	,,
Urvasi	10.33	(3.25)	80.58	(63.85)	6.67	(2.66)	,,
SE m ±	–	0.23	–	1.47	–	0.21	–
CD at 5%	–	0.66	–	4.16	–	0.60	–

Figures in parentheses are square root and arc sin* transformation value

Table 2. Ovipositional preference of *A. proxima* on different germplasm/varieties of *Brassica* under net house condition during 2005-06

Entries	Number of eggs/5 plants		Percent hatchability		Number of larvae/5 plants		Leaf surface
RK 2001	20.00	(4.52)	84.48	(66.80)*	11.00	(3.38)	Hairy
RK 2002	16.00	(4.03)	89.32	(70.93)	9.33	(3.06)	,,
RK 2003	12.67	(3.60)	92.27	(73.86)	8.00	(2.86)	,,
RK 2004	8.67	(3.02)	79.95	(63.40)	6.33	(2.60)	,,
RK 2005	15.67	(4.00)	84.39	(66.73)	9.00	(3.03)	,,
RK 2006	25.00	(5.02)	95.88	(78.29)	15.00	(3.92)	,,
RK 2007	16.67	(4.12)	87.50	(69.30)	9.00	(3.03)	,,
RK 2008	16.67	(4.12)	84.29	(66.65)	9.33	(3.06)	,,
RK 2009	17.00	(4.16)	84.54	(66.85)	9.67	(3.14)	,,
RK 2010	8.00	(2.89)	78.69	(62.51)	5.00	(2.30)	,,
RK 2011	12.33	(3.55)	78.93	(62.68)	7.33	(2.76)	,,
RK 2012	13.67	(3.73)	87.78	(69.54)	9.00	(3.03)	,,
RK 2013	23.00	(4.84)	89.42	(70.82)	11.67	(3.46)	Smooth
RK 2014	12.67	(3.58)	79.73	(63.16)	6.67	(2.66)	,,
RK 2015	8.00	(2.88)	89.42	(63.24)	5.33	(2.38)	,,
Basanti	21.33	(4.66)	81.25	(71.02)	11.33	(3.43)	,,
Kanti	8.67	(3.02)	88.35	(64.34)	6.33	(2.55)	Hairy
Kesari	20.00	(4.50)	88.35	(70.04)	10.33	(3.27)	,,
Maya	15.00	(3.91)	92.31	(73.90)	8.67	(3.02)	,,
PR 4001	18.00	(4.29)	82.20	(65.05)	10.00	(3.18)	,,
Rohini	24.67	(4.50)	84.04	(66.45)	13.67	(3.75)	,,
Vaibhav	13.00	(3.64)	89.77	(71.35)	8.33	(2.94)	,,
Vardan	13.00	(3.65)	83.98	(66.41)	8.00	(2.86)	,,
Varuna	19.33	(4.42)	93.98	(75.06)	10.33	(3.25)	,,
Urvasi	11.67	(3.46)	82.00	(64.90)	6.67	(2.65)	,,
SE m ±	–	0.26	–	1.33	–	0.22	–
CD at 5%	–	0.73	–	3.78	–	0.62	–

Figures in parentheses are square root and arc sin* transformation value

present finding. No statistical difference was found between smooth and hairy leaves for either ovipositional preference, egg hatchability or larval feeding. It is concluded from the present findings that RK 2010, RK 2015, Kanti, Urvasi, RK 2011 and RK 2004 were not only less preferred by female for oviposition but per cent egg hatchability and larval population were also reduced. These genotypes may be used in future breeding programmes to develop mustard sawfly resistant varieties.

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SHORT COMMUNICATION

Evaluation of High Fibre Strength Strains of the American Cotton (*G. hirsutum* L.) Suitable for High Speed Spinning

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Cotton plays important role in Indian economy and provides principal raw material for Indian textile industry. Until late nineties fiber length was considered major fibre quality parameter. However, during nineties genetic improvement of fibre strength became top priority with the adoption of high speed rotor/open-end spinning by the textile industry. Six strains of *G. hirsutum* L., namely, P 56-2, P 56-4, P 56-6, C4-9-2-1-1, C4-9-2-2 and P 4515-1 were therefore evaluated for fibre strength and other important quality and economic traits at Indian Agricultural Research Institute, New Delhi during *kharif*-2003 and *kharif*-2004. Two strains, namely, P56-4 and P 56-6 showed high fibre strength of 28.1 g/tex and 27.3 g/tex, respectively. This is significant in the light of the fact that most of varieties released in North Zone have fibre strength ranging from 18 g/tex to 20 g/tex. These strains also showed desirable fibre length, micronaire value, uniformity and maturity and were found suitable for rotor/open-end spinning.

Key Words: American cotton, Fibre strength, Ginning percentage, Lint index, Genetic improvement

Cotton is an important commercial crop and plays a vital role in our economy. It provides principal raw material for Indian textile industry. Until late nineties, the genetic improvement for fibre quality was mainly confined to improvement of fibre length. A large number of improved varieties and hybrids were thus developed in different staple length categories from medium staple to extra long staple. These varieties were suitable for conventional ring spinning system. However, as part of modernization, the textile industry has adopted high speed rotor/open- end spinning system. This modern rotor/open-end spinning system require cotton cultivars with high fibre strength. Consequently genetic improvement of fibre strength has become the most important fibre quality trait, followed by fibre length, fibre fineness and maturity. The present investigation was therefore undertaken to identify/develop promising strains having high fibre strength.

Six American cotton (*G. hirsutum* L.) genotypes, namely, P 56-2, P 56-4, P 56-6, C4-9-2-1-1, C4-9-2-2 and P 4515-1 were evaluated against the local check Pusa 8-6 at the research farm of the Indian Agricultural Research Institute, New Delhi during *kharif* (rainy season) 2003 and 2004 in complete randomized block design with 3 replications. The inter-row and intra-row spacing was kept at 75 cm and 30 cm, respectively. Each genotype was grown in 5 row plots having row length of 4.2 m. Data were recorded on important characters like number of monopodial and sympodial branches per plant, plant height (cm), number of bolls per plant, boll weight (g), seed index (g), lint index (g) and ginning out-turn (%), lint yield (kg/ha) and seed cotton yield (kg/ha). Lint samples of 100 g from each entry were sent to Central Institute for Research on Cotton Technology (CIRCOT), Mumbai, for evaluation of the fibre quality. Data were subjected to statistical analysis and the parameters like mean, range, standard deviation and coefficient of variation were estimated using the procedure suggested by Johnson *et al.* (1955).

Data on seed cotton yield and important yield components during two years period 2003 and 2004 along with the mean for two years is given in the Table 1. Likewise, data on important fibre quality traits is given in Table 2. Strain C4-9212 showed the highest mean seed cotton yield of 1430 kg/ha as compared to 1175 kg/ha of the check Pusa 8-6. This was followed by strains C4-9211 and P 56-2 with seed cotton yield of 1314 kg/ha and 1246 kg/ha, respectively. Likewise, strain C4-9212 also showed highest lint yield of 456 kg/ha in comparison to 384 kg/ha of the check. Higher lint yield of 437 kg/ha in comparison to that of the check Pusa 8-6 was also observed in the strain C4-9211. The highest ginning percentage of 33.5% was observed in C4-9211. All other strains showed low ginning out turn ranging from 29.6% in P 56-4 to 32.6% in C4-9212. In comparison the check Pusa 8-6 showed 32.8% ginning out turn. Boll weight, an important yield component, ranged from 3.3 g to 4.5 g against 3.7 g of the check Pusa 8-6.

Table 1. Seed cotton yield and other important traits of promising strains during 2003 and 2004 at IARI, New Delhi

Strains	Seed Cotton Yield (Kg/ha)			Lint Yield (Kg/ha)			Ginning Outturn (%)			Boll Weight (g)		
	2003	2004	Mean	2003	2004	Mean	2003	2003	Mean	2003	2004	Mean
P 56-2	700	1791	1246	223	549	386	32	30.8	31.4	3.2	3.4	3.3
P 56-4	406	1586	996	121	463	292	30	29.2	29.6	3.5	3.8	3.7
P 56-6	730	1247	988	230	376	303	32	30.2	31.1	3.4	3.7	3.6
C 4-9211	708	1920	1314	239	634	437	34	33.1	33.5	3.9	3.9	3.9
C 4-9212	619	2242	1430	213	698	456	34	31.2	32.6	3.6	4.1	3.9
P 4515-1	558	1636	1097	181	498	339	32	30.5	31.2	4.5	4.4	4.5
P 8-6 (LC)	745	1604	1175	246	523	384	33	32.6	32.8	3.9	3.5	3.7

Table 2. Fibre quality traits of promising starins during 2003 and 2004 at IARI, New Delhi

Strains	2.5 Span length (mm)			Micronaire Value			Fibre Strength (g/tex)		
	2003	2004	Mean	2003	2004	Mean	2003	2003	Mean
P 56-2	26.7	26.2	26.5	4.4	4.6	4.5	24.3	22.6	23.5
P 56-4	28.6	28.5	28.6	3.7	3.8	3.8	29.4	26.7	28.1
P 56-6	27.4	27.3	27.3	4.2	4.4	4.3	29.2	25.3	27.3
C 4-9211	27.2	25.7	26.4	4.3	4.8	4.6	25.4	24.2	24.8
C 4-9212	26.8	27.0	26.9	4.4	4.5	4.5	25.3	23.7	24.5
P 4515-1	28.0	28.1	28.1	4.4	4.4	4.4	26.0	21.8	23.9
P 8-6 (LC)	28.0	26.3	27.2	4.7	4.7	4.7	24.2	24.3	24.3

Table 2 Contd.

Strains	Fibre Uniformity(%)			Elongation (%)			Short Fibre Content (%)		
	2003	2004	Mean	2003	2004	Mean	2003	2003	Mean
P 56-2	50.6	52.7	51.6	5.4	4.7	5.1	10.1	12.1	11.1
P 56-4	51.6	53.0	52.3	6.1	4.7	5.4	6.8	8.0	7.4
P 56-6	52.2	54.0	53.1	5.8	4.8	5.3	9.9	11.3	10.6
C 4-9211	50.5	53.0	51.7	5.7	4.8	5.3	9.8	12.0	10.9
C 4-9212	52.7	51.3	52.0	5.9	4.7	5.3	10.2	11.9	11.1
P 4515-1	51.0	48.7	49.9	5.2	4.1	4.7	8.5	9.0	8.8
P 8-6 (LC)	52.1	52.7	52.4	5.5	4.8	5.2	7.8	11.7	9.8

The performance of different genotypes for fibre quality traits, namely, 2.5% span length, fibre uniformity, fibre fineness (micronaire value), fibre strength, elongation and short fibre content (%) during the two year period is summarized in Table 2. Fibre length in terms of 2.5% span length ranged from 26.4 mm in C4-9211 to 28.6 mm in P 56-4. Genotypes P 4515-1 (28.1 mm) and P 56-6 (27.3 mm) also showed better fibre length as compared to the check P 8-6 (27.2 mm). All the genotypes showed very good fibre uniformity ranging from 49.9% in P 4515-1 to 53.1% in P 56-6. Likewise, micronaire value for fibre fineness ranged from 3.8 in P 56-4 to 4.7 in Pusa 8-6 and were thus within the desired range for the medium staple cottons.

Fibre strength which is now the number one priority in cotton breeding programme for genetic improvement of fibre quality, ranged from 23.5 g/tex in P 56-2 to 28.1 g/tex in P 56-4 on the basis of mean of two years (2003 and 2004). Two strains, namely, P56-4 (28.1 g/tex) and P 56-6 (27.3 g/tex) showed high fibre strength of 28.1 g/tex and 27.3 g/tex, respectively. The ratio of fibre strength to that of fibre length in respect of these 2 strains was found to be 0.98 and 1.00, respectively, which was very close to 1.0 and hence the most desired combination of fibre length and fibre strength. Breaking elongation of all the genotypes including check ranged from 4.7% to 5.5% and short fibre content (SFC) ranged from 7.4% in P 56-4 to 11.1% in C4-9212 and was thus relatively low.

It is thus evident that 3 genotypes, *viz.*, C4-9211, C4-9212 and P 56-2 showed higher seed cotton yield and lint yield over the check variety Pusa 8-6. Genotypes C4-9212 and C4-9211 in fact ranked number 1 and number 2, respectively, with regard to seed cotton and lint yield also showed relatively good ginning out turn and boll weight. Besides good performance for seed cotton yield and other traits, these 2 strains also showed good fibre strength of 24.5 g/tex and 24.8 g/tex, respectively, and desirable micronaire value and fibre uniformity. On the other hand,

two strains *i.e.* P 56-4 and P 56-6 were found promising for most of the fibre quality traits in general and fibre strength in particular. The mean fibre strength observed in P 56-4 and P 56-6 was 28.1 g/ tex and 27.3 g/tex, respectively. These strains also showed most acceptable ratio of fibre strength to fibre length which was 0.98 and a perfect 1.0, respectively. However their ginning percentage was very low at 29.6% and 31.1%, respectively. Meredith Jr. (1984) and Tang-Bing *et al.* (1996) also reported low ginning percentage in high fibre strength genotypes. Nonetheless, the fibre strength of the strains P 56-4 and P 56-6 was very superior as compared to most of varieties released in North Zone for most of which it ranged from 18 g/ tex to 20 g/ tex. It is thus needless to say that the fibre quality of the strains P 56-4 and P 56-6 is suitable for the high speed and very efficient rotor spinning. It is therefore suggested that these strains could be used as sources for genetic improvement of fibre strength, in addition to their use as one of the parents for development of hybrids with high fibre strength.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XVI[th] meeting held on 14[th] May 2007 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 50 germplasm lines out of the 121 proposals considered.

1. FLW20 (IC548327; INGR07001), a Wheat (*Triticum aestivum*) Germplasm with Amber Grain and Pyramided Rust Resistance Genes, *Sr* 24 and *Sr25*

Dibendu Datta, RN Brahma, M Prashar and SC Bhardwaj
Directorate of Wheat Research, Regional Station, Flowerdale, Shimla, Himachal Pradesh

FLW20 (INGR No.07001, IC548327) was derived from the cross between PBW343 and *TcLr19* and FLW6 at Directorate of Wheat Research, Regional Station, Flowerdale. This stock is completely resistant to brown rust and black rust and moderately resistant to yellow rust. It carries rust resistance genes, *Lr9+Lr19+Lr24+Lr26+Sr24+Sr25+Sr31+Yr9+Yr27*. This stock has amber seed with test weight 38.5 g, average plant height is 88 cm and matured in about 119 days. This stock has good agronomic characteristics with good yield potential.

2. VL858 (IC546940; INGR07002), a Wheat (*Triticum aestivum*) Germplasm with Excellent Chapati Quality

Lakshmikant, V Mahajan, HS Gupta, BD Pandey, SK Pant and RK Gupta
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora-263601, Uttarakhand

VL 858, was developed through pedigree selection from a cross OPATA/RAYON/KAUZ at Vivekananda Parvatiya Krishi Anusandhan Sansthan (ICAR), Almora. It has excellent chapatti quality (8.11 on 0 to 10 scale) under irrigated to very good (7.83 on 0 to 10 scale) under rainfed conditions. In addition, it possesses high hectolitre weight (79.15 and 80.43 kg/hl), high carotene (4.6 to 4.1), iron (33.0 & 36.6), zinc (3.5 & 24.0) and manganese (57.4 & 29.7) ppm under rainfed and irrigated conditions, respectively. It is spring wheat, having intermediate growth habit and green coleoptile's colour. Its average plant height is 95-100 cm. It takes on an average 160-170 days to maturity. It has dull white colour ears with amber coloured grain, ovoid shape and 38-39 gm thousand grain weights. It has been tested in All India Coordinated yield evaluation trails of Northern Hills Zone from 2002-03 to 2004-05 and gave grain yield of 28.0 and 45.3 q/ha under rainfed and irrigated conditions, respectively (ACRP Report 2004). In addition it possesses high degree of field resistance to yellow and brown rust diseases. VL 858 is well adapted to Northern Hills Zone conditions and the recommended package of practices has been found suitable for it.

References

All India Coordinated Wheat and Barley Improvement Project (2003-04) *Quality* **Vol. IV** pp 110, 112 and Research Highlights.

All India Coordinated Wheat and Barley Improvement Project (2003-04) *Quality* **Vol. IV** pp 134, 135 and Research Highlights.

* *As Communicated by Drs. AK Singh, Anjali Kak and Veena Gupta, Germplasm Conservation Division, NBPGR*

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3. VL 824 (IC549923 INGR07003), a Wheat (*Triticum aestivum*) Germplasm for Powdery Mildew Resistance

Lakshmikant, HS Gupta, SK Pant, BP Singh, AK Sharma and GS Bankoti
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora-263601, Uttarakhand

VL 824, resistant to powdery mildew was developed through pedigree selection from a cross Laj 3302/Turaco/ /Turaco at Vivekananda Parvatiya Krishi Anusandhan Sansthan (ICAR), Almora. It is a spring wheat, having intermediate growth habit and green coleoptile colour. Its average plant height is 97 cm. It takes on an average 160-162 days to maturity. It has white coloured ears with amber coloured grain, ovoid shape and 41 gm thousand grain weight. It has been tested in All India Coordinated yield evaluation trials of Northern Hills Zone from 2000 to 2002 and yielded grain yield of 19.96 q/ha under rainfed conditions. In addition, it possesses high degree of field resistance to yellow and brown rust diseases. VL 828 is well adapted to Northern Hills Zone conditions and the recommended package of practices has been found suitable for it.

Reference

Singh PP, AK Sharma, S Nagrajan, J Kumar, MS Sachan, Jag Shoran, VC Sinha, LB Goel, SK Nayar, M Parashar, A Singh, KD Singh, AN Tewari, J Kumar, KP Singh, SK Pant, Ashwani Kumar, SK Rana, BK Sharma, D Singh, and RN Bhahma (2005). Powdery mildew resistance genotypes in wheat and *Triticale Indian Phytopathology* **58(1):** 124.

4. FKW 4 (IC549915 INGR07004), a Wheat (*Triticum aestivum*) Germplasm Incorporating Resistance Gene(s) for Brown Rust Races from Tetraploid Durum Wheat

BS Tyagi, Jag Shoran, SC Bhardwaj, SK Singh and G Singh
Directorate of Wheat Research, Karnal-132001, Haryana

Efforts are on to achieve economic and ecological sustainable wheat production in the country without compromising on yield levels. To strengthen the Indian wheat-breeding programme, Directorate of Wheat Research, Karnal initiated the pre-breeding work to create new genetic variability. Initially, the emphasis was laid on certain inherent limitations, such as susceptibility to rust diseases and seed shrivelling. The cytogenetic stock FKW 4 was derived from the cross between durum variety DWR 1006 and the most popular *aestivum* variety PBW 343. The morpho-agronomic traits (high grain weight, tiller number and good plant type) and leaf rust resistance is stable and inherited steadily from F_4 to the latest generation (F_8). The F_{1s} between FKW4 and PBW 343 were healthy, indicating thereby that the novel resistance genes and bold grain traits from this stock can easily be transferred to bread wheat. Morphology of this stock is different from bread and durum wheat. This stock is completely resistant to all races of leaf rust. It has amber seed, average plant height is 124 cm with good number of tillers along with very high thousand grain weight (60g), protein content (>13%) and matured in about 125 days.

Table1. Seedling Resistance Test and field resistance of FKW 4 at multi-location to virulent pathotypes of brown, black and yellow rusts

Pedigree	Brown Rust							Black Rust			
	SRT					Field data		SRT		Field data	
	77-2	77-5	77-7	77-8	104-2	W-04	K-05	40	40-1	W-04	K-05
AGRA LOCAL	3+	3+	3+	3+	3+	80S	60S	3+	3+	60S	0
PBW343	0;	3+	3+	3+	3+	5MR	30S	2-	2-	15MR	0
WH542	0;	3+	3+	3+	3+	60S	60S	2-	2-	15MR	0
DWR1006	;	;	;	;	;	R	R	2-	2-	R	R
FKW4	;	;	;1-	;	;1-	R	R	2-	2-	R	0

R=Resistance; Immune=0; MR=Moderately resistant; Resistant=,,;1-, 2, 2-; S=Susceptible; Moderately susceptible =2+; 0= Free from rust; Susceptible =3,3+

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4. FKW 4 (IC549915 INGR07004), a Wheat (*Triticum aestivum*) Germplasm Incorporating Resistance Gene(s) for Brown Rust Races from Tetraploid Durum Wheat

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AGRA LOCAL	3+	3+	3+	3+	3+	80S	60S	3+	3+	60S	0
PBW343	0;	3+	3+	3+	3+	5MR	30S	2-	2-	15MR	0
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DWR1006	;	;	;	;	;	R	R	2-	2-	R	R
FKW4	;	;	;1-	;	;1-	R	R	2-	2-	R	0

R=Resistance; Immune=0; MR=Moderately resistant; Resistant=,,;1-, 2, 2-; S=Susceptible; Moderately susceptible =2+; 0= Free from rust; Susceptible =3,3+

Resistance genes were postulated on the basis of differential host-pathogen interaction. The leaf rust resistance pattern of cultivated durum wheat varieties is different from that of *Triticum aestivum*. The infection type matrix of resistant durum wheat viz. DWR 1006 is distinct from known leaf rust resistance genes and hence likely to carry novel resistance genes. DWR 1006 was crossed with PBW 343 to transfer novel resistance with unknown genes into good agronomic base of bread wheat variety. The derived BCF_8 lines showing resistance to all races of leaf rust were selected.

Developing Multiple Rust Resistance Lines in Wheat (*Triticum aestivum*) by Bringing Genes from Different Sources

Dibendu Dutta, M Prashar and SC Bhardwaj
Directorate of Wheat Research, Karnal-132001, Haryana

5. FLW 24 (IC549926; INGR07005), a wheat (*Triticum aestivum*) germplasm resistance to brown and black rusts and predominant pathotypes of yellow rust

FLW24 (INGR No.0762, IC549926), was derived from the cross between PBW343 and Tc*Lr19*. This stock is completely resistant to brown rust and black rust and moderately resistant to yellow rust. It carries the rust resistance genes, *Lr19+Lr26 +Sr31+Yr9+Yr27*. This stock has white seed with test weight of 39.1 gm, average plant height is 88cm and matured in about 119 days. Yield per meter row was at par with PBW343.

6. FLW25 (IC549927; INGR07006), a wheat (*Triticum aestivum*) germplasm as a diverse source for resistance to brown rust.

FLW25 (INGR No.0763, IC549927), was derived from the cross between PBW343 and *Lr28* (CS2D2M3/8). This stock is completely resistant to brown rust and black rust and moderately resistant to yellow rust. It carries the rust resistance genes, *Lr9+Lr19+Lr24+; r26+Sr24+Sr25+ Sr31+Yr9+Yr27*. This stock has white seed with test weight 38.9 gm, average plant height is 85 cm and matured in about 118 days. Yield per meter row was at par with PBW343.

7. FLW26 (IC549928; INGR07007), wheat (*Triticum aestivum*) germplasm, another source for brown rust resistance.

FLW26 (INGR No.0764, IC549928), was derived from the cross between PBW343 and *Lr42* (KS91WGRC11). This stock is completely resistant to brown rust and black rust and moderately resistant to yellow rust. It carries rust resistance genes, *Lr26, Lr42, Sr31, Yr9* and *Yr27*. This stock has white seed with test weight 38.4 gm, average plant height is 88 cm and matured in about 119 days. Yield per meter row was less than PBW343.

8. FLW27 (IC549929; INGR07008), a wheat (*Triticum aestivum*) germplasm, another source for brown rust resistance.

FLW27 (INGR No.0765, IC549929), was derived from the cross between PBW343 and *Lr45*(Tc*4/ST-1). This stock is resistant to brown and black rusts and moderately resistant to yellow rust. It carries rust resistance genes, *Lr26, Lr44, Sr31, Yr9* and *Yr27*. This stock has red seed with test weight 39.1gm, average plant height is 90 cm and matured in about 120 days. Yield per meter row was less than PBW343.

Resistance genes were postulated on the basis of differential host-pathogen interaction. The leaf rust resistance pattern of cultivated durum wheat varieties is different from that of *Triticum aestivum*. The infection type matrix of resistant durum wheat viz. DWR 1006 is distinct from known leaf rust resistance genes and hence likely to carry novel resistance genes. DWR 1006 was crossed with PBW 343 to transfer novel resistance with unknown genes into good agronomic base of bread wheat variety. The derived BCF_8 lines showing resistance to all races of leaf rust were selected.

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8. FLW27 (IC549929; INGR07008), a wheat (*Triticum aestivum*) germplasm, another source for brown rust resistance.

FLW27 (INGR No.0765, IC549929), was derived from the cross between PBW343 and *Lr45*(Tc*4/ST-1). This stock is resistant to brown and black rusts and moderately resistant to yellow rust. It carries rust resistance genes, *Lr26, Lr44, Sr31, Yr9* and *Yr27*. This stock has red seed with test weight 39.1gm, average plant height is 90 cm and matured in about 120 days. Yield per meter row was less than PBW343.

Development of Wheat (*Triticum aestivum*) Germplasm with Diverse and New Resistant Source Against Stripe Rust Pathotype 46S119

Sanjay Kumar, Dharam Pal, DK Bhatnagar and Rashmi Bhatnagar
Indian Agricultural Research Institute, Regional Station, Tutikandi, Shimla

9. WBM1587 (IC549931; INGR07009)

WBM1587 is selected from cross MILAN/SHA 7 and was found resistant against pathotype 46S119, the most virulent pathotype of stripe rust (*Puccinia striiformis* Westend) in India. It gives 'fleck' (;) score at seedling and '0' score in adult stage. The resistance in this germplasm is controlled by two dominant complimentary genes and it differs from resistance of PBW343 which is controlled by a recessive gene. WBM 1587 mature in 142 days under northern hills condition with average plant height of 108 cm. Ear is clavate shape and grains are bold ovate. This germplasm can be used widely in generating diverse resistant wheat materials with major objective of stripe rust resistance.

10. WBM 1591 (IC549932; INGR070010)

WBM 1591 is selected from cross PYN/BAU//MILAN and was found resistant against pathotype 46S119, the most virulent pathotype of stripe rust (*Puccinia striiformis* Westend). It gives fleck (;) score at seedling and '0' score in adult stage against pathotype 46S119. The resistance in this germplasm is controlled by two dominant complimentary genes and it differs from resistance of PBW343 which is controlled by a recessive gene. WBM 1591 mature in 160 days under northern hills condition with average plant height of 100 cm. Ear is tapering in shape and grains are medium bold with oblong shape. It can be used widely in generating diverse resistant wheat materials with major objective of stripe rust resistance.

Conservation of CMS Lines of Paddy Having Different Cytoplasmic Sources

UB Apte[1], Dilip S Sawant[2], BB Jadhav[3] and VN Shetye[1]
[1] *Agricultural Research Station, Shirgaon, Ratnagiri-415629 (MS)*
[2] *Regional Agricultural Research Station, Karjat, Raigad-410201 (MS)*
[3] *Dr. B. S. Konkan Krishi Vidyapeeth, Dapoli, Ratnagiri-415712 (MS)*

At present a few CMS lines of paddy having wild abortive (WA), Borotype (BT) and Gambica (GAM) etc. cytoplasmic sources have been identified for commercial use in hybrid rice development (Yuan and Virmani, 1988; Virmani *et al.* 1996). Therefore, it was imperative that diversified CMS lines should be evolved to avoid danger of epidemics. Most of the CMS lines of paddy used in India for evolving the rice hybrids are of exotic origin. Therefore, it was essential to evaluate CMS lines of indigenous origin with diversified cytoplasmic sources which will perform stably in Indian climatic conditions and in severe incidence of pest and diseases. Therefore, the hybridization programme (Backcross breeding) was under taken at Agricultural Research Station, Shirgaon, Ratnagiri (MS) with a view to evolve CMS lines of paddy invloving different cytoplasmic sources. For the backcross breeding programme the seed material of different CMS lines of different sources were collected from International Rice Research Institute, Philippines and Panvel-2, Sona and Indrayani varieties were used as donor (Male parent) in F_1 and subsequent generations. This led to development of a number of CMS lines. Of these, RTN - 2A, RTN – 3A, RTN – 4A, RTN – 5A, RTN –6A, RTN –11A, RTN – 12A, RTN –13A, RTN – 14A, RTN – 17A and RTN – 18A based on good agronomic features, such as mid-late duration, long slender grain, good panicle exsertion, out crossing rate and stigma exsertion were found significantly superior, suitable for registration. Salient features of each of these lines in addition to cytoplasmic sterility are described below-

11. RTN 2A (IC548328 INGR07011), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

12. RTN 3A (IC548329 INGR07012), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

13. RTN 4A (IC548330 INGR07013), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

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WBM1587 is selected from cross MILAN/SHA 7 and was found resistant against pathotype 46S119, the most virulent pathotype of stripe rust (*Puccinia striiformis* Westend) in India. It gives 'fleck' (;) score at seedling and '0' score in adult stage. The resistance in this germplasm is controlled by two dominant complimentary genes and it differs from resistance of PBW343 which is controlled by a recessive gene. WBM 1587 mature in 142 days under northern hills condition with average plant height of 108 cm. Ear is clavate shape and grains are bold ovate. This germplasm can be used widely in generating diverse resistant wheat materials with major objective of stripe rust resistance.

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At present a few CMS lines of paddy having wild abortive (WA), Borotype (BT) and Gambica (GAM) etc. cytoplasmic sources have been identified for commercial use in hybrid rice development (Yuan and Virmani, 1988; Virmani *et al.* 1996). Therefore, it was imperative that diversified CMS lines should be evolved to avoid danger of epidemics. Most of the CMS lines of paddy used in India for evolving the rice hybrids are of exotic origin. Therefore, it was essential to evaluate CMS lines of indigenous origin with diversified cytoplasmic sources which will perform stably in Indian climatic conditions and in severe incidence of pest and diseases. Therefore, the hybridization programme (Backcross breeding) was under taken at Agricultural Research Station, Shirgaon, Ratnagiri (MS) with a view to evolve CMS lines of paddy invloving different cytoplasmic sources. For the backcross breeding programme the seed material of different CMS lines of different sources were collected from International Rice Research Institute, Philippines and Panvel-2, Sona and Indrayani varieties were used as donor (Male parent) in F_1 and subsequent generations. This led to development of a number of CMS lines. Of these, RTN - 2A, RTN – 3A, RTN – 4A, RTN – 5A, RTN –6A, RTN –11A, RTN – 12A, RTN –13A, RTN – 14A, RTN – 17A and RTN – 18A based on good agronomic features, such as mid-late duration, long slender grain, good panicle exsertion, out crossing rate and stigma exsertion were found significantly superior, suitable for registration. Salient features of each of these lines in addition to cytoplasmic sterility are described below-

11. RTN 2A (IC548328 INGR07011), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

12. RTN 3A (IC548329 INGR07012), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

13. RTN 4A (IC548330 INGR07013), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

14. RTN 5A (IC548331 INGR07014), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

15. RTN 6A (IC548332 INGR07015), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

16. RTN 11A (IC548333 INGR07016), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

17. RTN 12A (IC548334 INGR07017) a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

18. RTN 13A (IC548335 INGR07018), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

19. RTN 14A (IC548336 INGR07019), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

20. RTN 17A (IC548337 INGR07020) a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

21. RTN 18A (IC548338 INGR07021), a rice (*Oryza sativa*) germplasm with male sterility in mid late duration, long slender grain, good panicle and stigma exsertion.

The performance of these CMS lines of paddy under multi-location trials is given in Table 1. The CMS lines RTN-4A, RTN-5A, RTN-13A and RTN-14A were found to be stable performance in all India CMS evaluation Nursery Trial during *kharif* 2005 season at seven locations. All these above mentioned CMS lines of paddy are of indigenous origin with some of them are having diversified cytoplasmic source. Hence, these CMS lines of paddy will be useful in production of rice hybrids with indigenous genetic background and different cytoplasmic sources.

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Virmani SS, BC Viraktamath, CL Casal, RS Toledo, MT Lopez and JO Manato (1996) *Hybrid Rice Breeding Manual* IRRI, Philippines.

Yuan LP and SS Virmani (1998) Status of hybrid rice research and development in hybrid rice, IRRI, Philippines, pp. 7-24.

Table 1. All India Multi- locational performance of CMS lines of paddy during Kharif 2005 season (Mean data of 7 locations)

CMS Line	Pedigree		DFF		HT		TN		PL		TS		PE%	SE%	SS%	HGW
	Cross	Cytoplasmic Source	A	B	A	B	A	B	A	B	A	B	A	A	A	B
RTN-2A	IR 54755A/ Panvel-2	Assam rice collection (ARC)	104	102	73	79	10.1	10.4	24.3	23.7	200	228	78	47	28	1 . 9
RTN-3A	IR 68885A/ Panvel-2	Induced by gamma irradiation of IR 62829 B	104	102	70	81	10.3	9.9	24.8	23.4	189	190	80	45	25	1.9
RTN-4A	IR 58025A/ Panvel-2	Wild rice with abortive pollen	104	102	71	78	9.9	10.2	25.1	24.4	166	177	80	48	23	1.9
RTN-5A	D 297A/ Panvel-2	Dissi	104	100	71	81	8.9	11.2	25.2	24.6	160	186	79	48	19	2.0
RTN-6A	G 46 A/ Panvel-2	Gambiaca	105	102	73	79	9.4	9.5	24.3	23.9	201	183	80	41	23	2.1
RTN -11A	IR 54755A/ Sona	Assam rice collection (ARC)	103	101	71	77	9.6	11.2	24.0	23.9	197	190	80	43	28	2.0
RTN-12A	IR 68885A/ Sona	Induced by gamma irradiation of IR 62829 B	104	102	72	81	9.9	10.1	25.2	24.4	158	192	78	44	27	1.9
RTN-13A	G 46 A/Sona	Gambiaca	104	102	71	82	10.9	11.6	24.8	23.6	194	218	81	47	34	2.0
RTN-14A	IR 58025A/ Sona	Wild rice with abortive pollen	105	101	72	79	9.2	9.1	23.2	23.7	178	175	78	48	34	2.0
RTN-17A	D 297A/ Indrayani	Dissi	104	101	83	91	9.4	10.1	24.3	24.1	163	168	76	39	23	2.2
RTN-18A	G 46 A/ Indrayani	Gambiaca	104	101	79	92	10.1	11.3	23.1	23.0	167	177	81	47	28	2.2
Checks																
IR 58025A			101	99	74	82	11.0	11.5	23.7	23.9	170	181	79	58	33	2.0
IR 68885A			91	88	72	84	12.2	12.1	23.7	22.7	131	138	81	51	25	2.3
IR 68888A			88	85	72	83	11.2	11.5	24.0	23.2	137	148	81	50	24	2.3

Locations – Jabalpur, Faizabad, Karjat, Pant Nagar, Coimbatore, Ratnagiri and Hyderabad.
A – CMS line, B – Maintainer line.; DFF – Days to 50% flowering, HT – plant height (cm), TN – Tiller number, PL – Panicle length (cm), TS – Total spike lets/panicle, PE – Panicle exsertion (%), SE – Stigma exsertion (%), SS – Seed set (%), HGW – 100 grain weight (g)

22. Pusa 1401 (IC548339; INGR07022), a Basmati rice (*Oryza sativa*) Germplasm with Better Grain, Cooking, Higher Elongation Ratio and Free from Grain Chalkiness

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Pusa 1401 is developed through hybridization between Pusa Basmati-1/ Pusa 1121-92-8-2-7-1 followed by pedigree method of selection. Pusa1401 (IET 18005) has been identified with superior quality Basmati variety than the traditional Basmati variety "Taraori Basmati" (DRR, Annual Progress Report 2004 Vol I, Varietal Improvement, pp 1.283). It has been found better than the most popular traditional basmati "Taraori Basmati" in grain, cooking, eating quality and grain yield (34%). It is semi-dwarf (85 cm) and will not lodge like traditional tall Basmati varieties. Its cooked rice appearance, fluffiness, kernel length after cooking (16.07mm) with least breadth-wise swelling and pleasant aroma is attractive to catch the consumers' attention in the International and domestic market. In the panel tests conducted over three years it was found better in comparison to Taraori Basmati and Pusa Basmati-1 in overall acceptability.

Table 1. Panel Test Scores of Pusa 1401 (IET-18005) in AVT-2 BT, DRR, 2002-04

Characters/ Entry	Pusa 1401			PB1			Taraori Basmati	
Year	2002	2003	2004	2002	2003	2004	2002	2003
Appearance	4.25	4.5	4.8	4.1	3.42	4.5	4	4
Cohesiveness	4	3.9	4.3	3.66	4.27	3.91	4.75	3.67
Taste	3.5	3.3	3.5	3.17	2.92	3.33	3.25	3
Aroma	4	3.9	3.8	4	3.33	3.66	4.25	3.33
Elongation	3.6	3.25	3.7	3.1	2.4	3.2	2.5	2.7
OA	3.98	3.84	4.06	3.66	3.25	3.87	3.59	2.87

Overall acceptability (OA):4.0-4.9 Excellent, 3.0-3.9 Good, 2.0-2.9 Acceptable

Reference

Directorate of Rice Research (DRR) (2002-04) *All India Coordinated Rice Improvement Programme. Annual Reports* (2002-04).

23. BM 68 (Bindli Mutant 68) (IC548340; INGR07023), a Rice (*Oryza sativa*) Germplasm with Resistance to Rice Tungro Virus Disease

VP Singh, AK Singh, SS Atwal, T Mohapatra, FR Niazi, J Singh and RP Pant
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Rice Tungro disease is a serious constraint in rice productivity in South and South East Asian countries. Affected plants have profuse tillering, stunted growth and yellowing of leaves. Tungro disease is caused by two morphologically distinct strains. One is rice tungro spherical virus (RTSV, RNA virus) and rice tungro bacillus virus (RTBV, DNA virus). BM 68 is semi dwarf (85 cm) induced mutant from traditional tall aromatic rice Bindli. It is highly resistant for both of the virus forms of the Tungro Virus (Table 1). It has stiff stem, dark green leaves, semi erect leaf orientation, long panicle, complete panicle exertion, occasional awning, and highly aromatic short bold kernels. Purple pigmentation in apiculi and awns is a distinct character. It has intermediate amylose content (22.5%) and intermediate gelatinization temperature (alkali spreading value 5).

Table 1. Detection of tungro viruses in rice cultivars by Immunosorbent Electron Microscopy (ISEM) (adapted from Niazi *et al.*, 2004)

Cultivars inoculated with RTV 3 strains containing spherical and bacillus viruses	Visual Symptoms	Detection of viruses by ISEM	
		RTSV	RTBV
Crossa	Moderate	–	+
Nakera	Moderate	–	+
BJ–1	Moderate	–	+
Pankaj	Mild	+	–
Pusa Basmati–1	Severe	+	+
Pusa–169	Severe	+	+
IRGC–100139	Severe	+	+
Chenga	Severe	+	+
ARC–11554	No Symptoms	+	+
Bindli Mutant–66	No Symptoms	–	–
Bindli Mutant–68	No Symptoms	–	–
Pankhari–203	No Symptoms	–	–
TN 1	Severe	+	+

Reference

Niazi FR, Jasvir Singh and RP Pant (2004) Differential suseptability of rice cultivars to rice tungro spherical and bacilliform viruses. *Indian Phytopathology* **57(4):** 507-508.

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24. UPR 2870-98-125 (IC553263; INGR070024), a Rice (*Oryza sativa*) Germplasm with New Plant Type

SC Mani, MP Pandey, H Singh, JPS Malik, Surendra Singh and S Singh
Govind Ballabh Pant University of Agriculture and Technology, Pantnagar

IC 553263 (UPR 2870-98-125) has been developed by pedigree method of breeding following hybridization between BG 132 and UPRI 95-141 at Govind Ballabh Pant University of Agriculture & Technology, Pantnagar . It is the first *indica* rice variety developed on the concept of New Plant Type for higher yield potential and synchronized tillering. Mean yield of IC 553263 (UPR 2870-98-125) based on 10 trials over three years in two zones was 7665 kg/ha (with a range from 4054 to 11111 kg/ha), compared to Jaya, the national check with 5917 kg/ha. The plants are semi-dwarf (92 cm) with good tillering capacity. The panicles are compact, well exerted and tip-awned. The colour of apiculus is green. UPR 2870-97-125 flowers in 100 days with seed to seed duration of 130 to 135 days. UPR 2870-98-125 is resistant to leaf blast, moderately resistant to bacterial blight and sheath rot diseases. It gives very high milling (73.3%) and head rice (52.4%) recovery, better kernel length and L/B ratio. The alkali spreading score is intermediate (5.00) and desirable as compared to Jaya (6.75). Important morphological and quality characters are given in Table 1.

Table 1. Important morphological characters of IC 553263 (UPR 2870-98-125)

S.No.	Morphological characters	Description
1.	Plant height	92 cm
2.	Number of tillers / plant	10-12
3.	Flowering duration	100 days
4.	Awning	Tip awned
5.	1000-grain weight	26.29 g
6.	Kernel length	6.28 mm
7.	Kernel breadth	2.22 mm
8.	L/B ratio	2.83
9.	Milling recovery	73.35 %
10.	Head rice recovery	52.45 %

25. SC7-2-1-261 (IC549903; INGR07025), a Maize (*Zea mays*) Germplasm Source of Resistance to Maydis Leaf Blight

RC Sharma, SN Rai, RD Singh[1], RM Gadag[2] and S Rakshit[3]
[1] *Division of Plant Pathology, Indian Agricultural Research Institute, New Delhi-110012*
[2] *Division of Genetics, IARI, New Delhi-110012*
[3] *Directorate of Maize Research, Pusa Campus, New Delhi-110012*

Maydis leaf blight (MLB) incited by *Bipolaris maydis* (= *Cochliobolus heterostrophus*) is a major and economically important disease of maize (*Zea mays* L.). A total of 17 elite inbred lines including two resistant checks, CM 104 and CM 105 (2) and one susceptible check CM 119, received from Maize Breeding Unit of Division of Genetics and Directorate of Maize Research, were evaluated against MLB under artificial field inoculations during 1999, 2000 and 2001 at IARI, New Delhi. The disease reactions were assessed on 1-5 scale (1). Among the 14 lines, 3 *viz.* SC-24-(92)-3-2-1-1, Suwan 1(S)C#-f-f and SC-7-2-1-2-6-1 were classified as highly resistant (<1.5 scale) (3). In this note, details of the line SC-7-2-1-2-6-1, as per DUS testing guidelines is presented. The inbred line (SC-7-2-1-2-6-1) was developed from an experimental single cross, through recycling procedure by the Maize Breeding Unit of IARI. The resistant plants were selfed for five generations followed by advancing of the specific selected genotype in each generation till homozygosity. Morphological features of the line are-

1. *Plant:* (a) length (up to flag leaf) – short and (b) ratio between height of insertion of upper ear to plant length – medium
2. *Leaf:* (a) angle between blade and stem (on leaf just above upper ear) - medium (25-75^0), (b) altitude of blade (on leaf just above upper ear) - curved, (c) anthocyanin colouration of sheath (in middle of plant) – absent and (d) width of blade (leaf of upper ear) - narrow
2. *Stem:* anthocyanin colouration of brace roots – present
3. *Tassel:* (a) time of anthesis (on middle third of main axis, 50% of plants) – late, (b) anthocyanin

24. UPR 2870-98-125 (IC553263; INGR070024), a Rice (*Oryza sativa*) Germplasm with New Plant Type

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1. *Plant:* (a) length (up to flag leaf) – short and (b) ratio between height of insertion of upper ear to plant length – medium
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2. *Stem:* anthocyanin colouration of brace roots – present
3. *Tassel:* (a) time of anthesis (on middle third of main axis, 50% of plants) – late, (b) anthocyanin

colouration at base of glume (in middle third of main axis) – present, (c) anthocyanin colouration of glumes excluding base (in middle third of main axis) – absent, (d) anthocyanin colouration of anthers (in middle third of main axis of fresh anthers) – absent, (e) density of spikelets (in middle third of main axis) – medium, (f) angle between main axis and lateral branches (in lower third tassel) – medium (25-750), (g) altitude of lateral branches (in lower third of tassel) – curved, (h) number of primary and lateral branches – absent, (i) length of main axis above lowest side branch – short and (j) length of main axis above upper side branch - short

4. *Ear:* (a) time of silk emergence (50% plants) – late, (b) anthocyanin colouration of silks – absent, (c) length of peduncle – short, (d) length without husk – medium, (e) diameter without husk (in middle) – small, (f) shape – conical, (g) number of rows of grains – many, (h) type of grain (in middle third of ear) – flint, (i) colour of top of grain – yellow and (j) anthocyanin colouration of shank of cob – white; Kernel – row arrangement – straight
5. *Grain:* (a) shape – toothed and (b) size (1000 grain weight) – 225.79g

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26. CRS-1 (IC549901; INGR07026), Sorghum (*Sorghum bicolor)* Germplasm with Better Drought Tolerant Mechanisms

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Rabi sorghum is grown over a total area of 5.6 million hectares mainly in the states of Maharashtra, Karnataka and Andhra Pradesh with average productivity of 634 kgs/ha. Despite low productivity, it continues to be an important component of dryland economy in these states with fairly consistent area over many years. The low yields are mainly due to various abiotic (drought, nutrients, temperature etc.) and biotic (shoot fly, charcoal rot etc.) stresses. When deep and medium black soils are not fully charged with water, severe drought causes late maturity (M35-1 and CSV 216 R) failing head emergence from boot. Hence, there is a need to develop drought resistant early maturity genotypes suitable for rainfed situations under medium to shallow soil depths.

CRS-1=Selection from Hegari land race from Hegari village, Bijapur district, based on the evaluation data from 2000-01 to 2004-05 under shallow soils in coordinated trials across locations gave significantly higher grain yields and harvest index and was evaluated for critical physiological traits associated with drought adaptation. Evaluation from 2000-01 to 2002-03 indicated that it matured 4 days earlier and showed significantly superior grain yield (21.7%) than M35-1 with better tolerance to shoot fly and charcoal rot (Table 1).

In *rabi* 2002-03 to 2003-04 in coordinated physiology trials CRS-1, was earliest for phenology (days to flowering) and it matured 4-5 days earlier than the popular land race M35-1 and by 8 days than check CSV 216R. SAPD readings were higher for CRS-1. It recorded 35% higher total chlorophyll than check. In both leaf N (%) and specific leaf nitrogen, CRS-1 showed 21% superiority over checks, and for harvest index, CRS 1 showed 34%

Table 1. Performance of CRS-1 (SPV-1537) in coordinated trials from 2000-01 to 2002-03

Varieties	Days to flower	Plant height (cm)	Days to mature	Grain yield (kg/ha)	Increase over (%)	SFDH (%)	CR (%)
CRS-1 (SPV-1537)	70.0	122.0	111.0	970.0	–	34.7	35.0
RSIG-262	73.0	144.0	113.0	941.0	3.08	33.7	32.5
Sel.3	69.0	142.0	108.0	602.0	61.1	54.3	27.4
M35-1	74.0	144.0	114.0	797.0	21.7	42.2	35.1
CSV-216R	80.0	151.0	120.0	763.0	27.1	25.2	37.9
CD at 5%	3.0	13.5	5.0	185.0	–	1.3	2.1
C.V.%	2.3	6.0	2.5	19.9	–	16.2	10.5

colouration at base of glume (in middle third of main axis) – present, (c) anthocyanin colouration of glumes excluding base (in middle third of main axis) – absent, (d) anthocyanin colouration of anthers (in middle third of main axis of fresh anthers) – absent, (e) density of spikelets (in middle third of main axis) – medium, (f) angle between main axis and lateral branches (in lower third tassel) – medium (25-750), (g) altitude of lateral branches (in lower third of tassel) – curved, (h) number of primary and lateral branches – absent, (i) length of main axis above lowest side branch – short and (j) length of main axis above upper side branch - short

4. *Ear:* (a) time of silk emergence (50% plants) – late, (b) anthocyanin colouration of silks – absent, (c) length of peduncle – short, (d) length without husk – medium, (e) diameter without husk (in middle) – small, (f) shape – conical, (g) number of rows of grains – many, (h) type of grain (in middle third of ear) – flint, (i) colour of top of grain – yellow and (j) anthocyanin colouration of shank of cob – white; Kernel – row arrangement – straight
5. *Grain:* (a) shape – toothed and (b) size (1000 grain weight) – 225.79g

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26. CRS-1 (IC549901; INGR07026), Sorghum (*Sorghum bicolor)* Germplasm with Better Drought Tolerant Mechanisms

Prabhaker, SS Rao, IK Das and MS Raut
National Research Centre for Sorghum, Hyderabad

Rabi sorghum is grown over a total area of 5.6 million hectares mainly in the states of Maharashtra, Karnataka and Andhra Pradesh with average productivity of 634 kgs/ha. Despite low productivity, it continues to be an important component of dryland economy in these states with fairly consistent area over many years. The low yields are mainly due to various abiotic (drought, nutrients, temperature etc.) and biotic (shoot fly, charcoal rot etc.) stresses. When deep and medium black soils are not fully charged with water, severe drought causes late maturity (M35-1 and CSV 216 R) failing head emergence from boot. Hence, there is a need to develop drought resistant early maturity genotypes suitable for rainfed situations under medium to shallow soil depths.

CRS-1=Selection from Hegari land race from Hegari village, Bijapur district, based on the evaluation data from 2000-01 to 2004-05 under shallow soils in coordinated trials across locations gave significantly higher grain yields and harvest index and was evaluated for critical physiological traits associated with drought adaptation. Evaluation from 2000-01 to 2002-03 indicated that it matured 4 days earlier and showed significantly superior grain yield (21.7%) than M35-1 with better tolerance to shoot fly and charcoal rot (Table 1).

In *rabi* 2002-03 to 2003-04 in coordinated physiology trials CRS-1, was earliest for phenology (days to flowering) and it matured 4-5 days earlier than the popular land race M35-1 and by 8 days than check CSV 216R. SAPD readings were higher for CRS-1. It recorded 35% higher total chlorophyll than check. In both leaf N (%) and specific leaf nitrogen, CRS-1 showed 21% superiority over checks, and for harvest index, CRS 1 showed 34%

Table 1. Performance of CRS-1 (SPV-1537) in coordinated trials from 2000-01 to 2002-03

Varieties	Days to flower	Plant height (cm)	Days to mature	Grain yield (kg/ha)	Increase over (%)	SFDH (%)	CR (%)
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M35-1	74.0	144.0	114.0	797.0	21.7	42.2	35.1
CSV-216R	80.0	151.0	120.0	763.0	27.1	25.2	37.9
CD at 5%	3.0	13.5	5.0	185.0	–	1.3	2.1
C.V.%	2.3	6.0	2.5	19.9	–	16.2	10.5

superiority over check. CRS-1 offers great scope for test as variety under receding soil moisture conditions of *rabi* or for use as donor in developing early maturing varieties with resistance to drought. It can also be grown directly under rainfed conditions in medium to shallow type of soils which constitutes about 50% of *rabi* sorghum area.

Reference

Prabhakar Rao SS, IK Das and MS Raut (2006) New early maturing elite line with drought tolerance. *Jowar Samchar* **Vol.2, No.1:** 4-6.

27. CGMS UPAS 120 A (IC548343; INGR07027), Pigeonpea (*Cajanus cajan*) Thermo-insensitive CMS, with Cytoplasm of *Cajanus scarabaeoides*

IP Singh and BB Singh
Indian Institute of Pulses Research, Kanpur

CGMS UPAS 120 A is an early maturing, stable and thermo-insensitive male sterile line developed in conversion programme, bringing male sterility into most popular and early maturing variety UPAS 120 following the backcross method at Indian Institute of Pulses Research, Kanpur. In this method UPAS 120 was used as recurrent (male) parent and GT 288A, a male sterile line developed from cross between *C. scarabaeoides* and GT 288 was used as female parent. F_1 was backcrossed with UPAS 120 and backcrossing was followed for 6 generations. In each backcross progeny only male sterile plants possessing plant type of UPAS 120 were selected. In BC_6 all plants were sterile and possessed plant type of UPAS 120.

This line is tolerant to *Fusarium* wilt and resistant to sterility mosaic disease. It may be used as female parent (male sterile 'A' line) for getting it crossed with desired male parent (restorer 'R' line) for development of CGMS based pigeonpea hybrids. The seed yield was optimum at a ratio of 6 female: 1 male on 4m row length with intra and inter row spacing of 15 cm and 60 cm, respectively in isolation of 300 m from another pigeonpea field.

Table 1. Important morphological characters of CGMS UPAS 120 A

Plant type	Indeterminate
Days to flower	82
Days to maturity	125
Plant height (cm)	131
Primary branches per plant	6.3
Pods per plant	180.25
Seeds per pod	3.4
Pod length (cm)	4.4
Test weight (g)	9.25
Flower colour	Yellow
Pod colour	Mixed (Green with black streaks)
Seed colour	Reddish yellow

28. APG248 (IC553269; INGR07028) a Urd bean (*Vigna mungo*) Induced Mutant with Brown Pod and Yellow Seed

AK Sharma[1], VP Singh, SS Malik[2], SA Kerkhi* and Vipin Kumar[1]
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221005

A urdbean (*Vigna mungo*) mutant with brown pod and yellow seed was developed at Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi through induced mutation. Four hundred pure, uniform, healthy and dry (9.5 % moisture) seeds of cultivar Pant Urd-30 were treated with ^{60}Co gamma rays (100, 200, 300 and 400 Gy doses), EMS (0.2, 0.4, 0.6 and 0.8%) and combination of gamma doses, *viz.*, 100, 200, 300 and 400 Gy with 0.2 per cent EMS during Summer, 2001. In M_2 generation, eight double mutations for seed and pod colour were observed in different frequencies in various treatments of EMS, gamma rays and combination of both. A brown colour pods with yellow rough seed mutant was identified and selected in the 200Gy+0.2 per cent combination dose of gamma rays and EMS. This mutant (Seed Mutant-2) has Brown pods, yellow rough seeds, tall and high yielding with higher (5.0g) 100 seed weight.

This mutant has lower infestation (%) of MYMV and CLS diseases in comparison of the parent (PU-30). Such mutations for different seed colour have been reported in other pulse crops *viz.*, arhar (Ali Kahn and Veeraswamy, 1974), soybean (Takagi and Hiraiwa, 1980) and mungbean (Singh, *et al.*, 1982). A single gene but the simultaneous

superiority over check. CRS-1 offers great scope for test as variety under receding soil moisture conditions of *rabi* or for use as donor in developing early maturing varieties with resistance to drought. It can also be grown directly under rainfed conditions in medium to shallow type of soils which constitutes about 50% of *rabi* sorghum area.

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This line is tolerant to *Fusarium* wilt and resistant to sterility mosaic disease. It may be used as female parent (male sterile 'A' line) for getting it crossed with desired male parent (restorer 'R' line) for development of CGMS based pigeonpea hybrids. The seed yield was optimum at a ratio of 6 female: 1 male on 4m row length with intra and inter row spacing of 15 cm and 60 cm, respectively in isolation of 300 m from another pigeonpea field.

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variations for yields and other morphological characters indicate a gross change or perhaps very closely related linked group of genes are controlling this trait (Saini *et al.*, 1974).

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Development Mutant in Sesame (*Sesamum indicum*)

GSS Murty

Nuclear Agriculture & Biotechnology Division, Bhabha Atomic Research Centre, Mumbai

29. N-129 (IC548341; INGR07029)

At seedling stage sesame (*Sesamum indicum* L.), competes poorly with the weeds due to its slow growth. Hence, it was suggested that early seedling vigor and elongated hypocotyl could be helpful in overcoming weed competition (Ashri, and Poetiary, 1981). Among several induced mutants isolated, a mutant N-129 was isolated in M_2 generation and designated later on as Tall Seedling mutant. It was obtained following 300 Gy gamma ray treatment to the seeds of cv. N62-32 developed by JNKVV, Jabalpur. N-129 is easily identifiable at 20 days after sowing (DAS) and even earlier from other sesame genotypes due to elongated hypocotyl length. At 20 DAS it was significantly taller (16.4 ± 0.5 cm) than its parent (5.4 ± 0.2 cm). The length of first internode in mutant was longer compared to parent (Murty and Joshua, 1986). Mutant has slightly less number of cells per unit length of stem than its parent. However, cell length is greater in mutant. Although mutant is tall in seedling stage it is equivalent to its parent in height at harvest. It is agronomically poor compared to the parent (Murty and Joshua, 1986).

In order to study the inheritance pattern of the induced mutant and to incorporate tall seedling trait, N-129 was crossed with the national check variety TC-25. Phenotypic and genotypic segregations in the F_2 and F_3 generations indicated that the tall seedling trait of mutant (*ts*) is inherited as monogenic recessive (Murty, 1988).

References

Ashri A and P Poetiray (1981) Sesame: Status and Improvement. *FAO Plant Production and Protection Paper,* (Rome 1980) **29:** pp 192.

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30. APG306 (IC553270; INGR07030)

In sesame (*Sesamum indicum* L.) among several induced mutants, a mutant N-29 with free corolla lobes was isolated in M_2 generation and designated as Polypetalous Corolla mutant. It was obtained following 16 Gy fast neutron treatment at APSARA reactor in the Bahbha Atomic Research Centre, Mumbai-400085 to the seeds of cv. N62-32, developed by JNKVV, Jabalpur. Due to free corolla lobes, it is different from normal sesame flower and wild relatives which are gamopetalous and have tubular obliquely campanulate corolla with four epipetalous, didynamous stamens (Joshi, 1961). N-29 mutant was similar to the parent N62-32 in vegetative characters. The chief distinguishing trait of the mutant is absence of tubular corolla making the petals free as in the case of polypetalous species and united only at the base, giving the false appearance of polypetalous corolla. In the absence of tubular corolla, the epipetalous stamens in mutant remain away from the stigma. These results in poor capsule set but facilitates cross pollination by insects like open flowers, compared to the parent and other wild type plants.

In order to understand the mutant trait, N-29 was crossed with its parent and cv. Phule Til-1, which have gamopetalous corolla. The F_1 hybrids showed tubular corolla indicating mutant trait is recessive. The observed segregations in the F_2 and F_3 generations for tubular and polypetalous corolla (*pc*) showed that polypetalous trait of N-29 monogenic recessive to the gamopetalous condition. This trait could be useful to develop hybrid seed under controlled conditions using honey bees.

References

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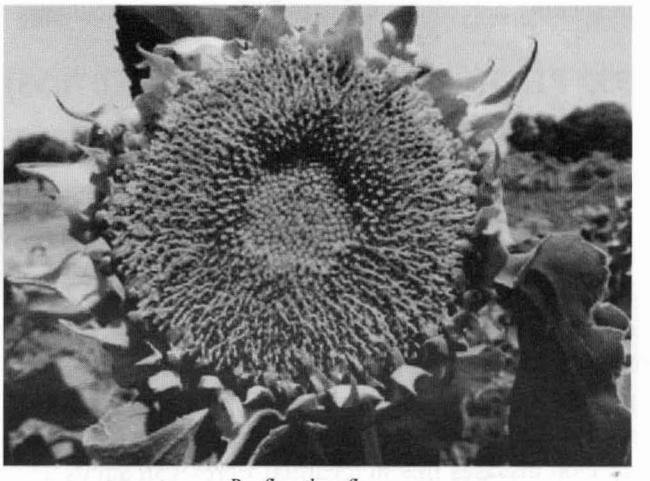
31. (IC548342; INGR07031) a Sunflower (*Helianthus annuus*) Mutant without Ray Florets

M Sujatha
Directorate of Oilseed Research, Hyderabad

The rayfloret-less variant IC548342 has been identified at the Directorate of Oilseeds Research in the interspecific hybrid population between cultivated sunflower (*H. annuus*) and *H. divaricatus* (a source of resistance to *Alternaria helianthi*). In the process of selection and generation advancement of material showing high levels of tolerance to *A. helianthi*, a novel flower variant devoid of ray florets was isolated in BC_2F_8 generation. The plants were late maturing, dwarf (plant height: 60 cm) with slender stems. Leaves and stems were smooth and non-pubescent. Leaves were thick and leathery with short petioles. The floral bracts were invariably pointed and the capitula were flat. The size of the flowers were normal (head diameter: 12.5 cm) and of the same size as that of flowers from sister lines with ray flowers. Such capitula can be called as homogamous, eradiate, eliguliflorous or discoid heads. Selfing and sister plant mating of this morphotype resulted in the development of a stable line bearing ligulate-less flowers. The outermost single layer had modified florets that were intermediate of the ray and disc florets. The corolla colour was yellow and similar to that of the ray florets but was tubular and hermaphrodite as that of the disc florets (Fig. 1). However, this modified



Rayfloretless flower

layer of florets had slightly longer tubular florets than the regular disc florets. Seeds are black with 100 seed weight of 5.2 g and an oil content of 33.0%. There were no significant differences in the oil content, plant maturity and seed filling frequency in these variants and the sister lines with petaled flowers. The plants possessed field tolerance to *A. helianthi.* These rayfloret-less sunflower plants are being maintained through sister plant mating.

32. TG 18A (IC553271; INGR07032) a Groundnut (*Arachis hypogaea*) Germplasm with Large Pod and Seed

Chandra Mouli and DM Kale*
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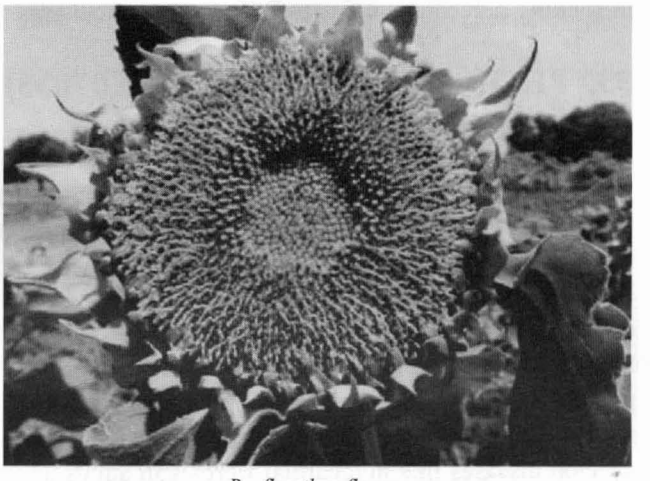
In groundnut (*Arachis hypogaea* L.), Spanish group (sub-sp. *fastigiata*) genotypes are bunch type with sequential flowering, early maturing and medium to small pods and non-dormant seeds. On the other hand, Virginia group (sub-sp. *hypogaea*) genotypes are bunch, spreading, semi-spreading or trailing type, profusely branching with alternate flowering and late maturing and large pods and seed dormancy. Spanish bunch combined with large pods were developed at Bhabha Atomic Research Centre, Mumbai by inter-mutant hybridization and irradiation of selected cultures. Among these a mutant designated Trombay Groundnut (TG) 18A was isolated after gamma ray treatment. TG-18A was induced by 200 Gy gamma rays of Virginia bunch culture, TG 18. It had Spanish bunch growth and branching habit with sequential flower pattern. Compared to parent, number of branches got reduced in TG 18A (8 + 17 Vs. 5 + 4). It had green foliage and plant height similar to TG 18. It matured earlier than parent due to its early flowering characteristics by eight and five days in both *kharif* and *rabi* season, respectively. Pegs and pods on the stem and branches were similar to other Spanish bunch variety and very distinct from parent. The size of pod and seed in TG 18A was similar to parent and about two times bigger than other Spanish bunch

31. (IC548342; INGR07031) a Sunflower (*Helianthus annuus*) Mutant without Ray Florets

M Sujatha
Directorate of Oilseed Research, Hyderabad

The rayfloret-less variant IC548342 has been identified at the Directorate of Oilseeds Research in the interspecific hybrid population between cultivated sunflower (*H. annuus*) and *H. divaricatus* (a source of resistance to *Alternaria helianthi*). In the process of selection and generation advancement of material showing high levels of tolerance to *A. helianthi*, a novel flower variant devoid of ray florets was isolated in BC_2F_8 generation. The plants were late maturing, dwarf (plant height: 60 cm) with slender stems. Leaves and stems were smooth and non-pubescent. Leaves were thick and leathery with short petioles. The floral bracts were invariably pointed and the capitula were flat. The size of the flowers were normal (head diameter: 12.5 cm) and of the same size as that of flowers from sister lines with ray flowers. Such capitula can be called as homogamous, eradiate, eliguliflorous or discoid heads. Selfing and sister plant mating of this morphotype resulted in the development of a stable line bearing ligulate-less flowers. The outermost single layer had modified florets that were intermediate of the ray and disc florets. The corolla colour was yellow and similar to that of the ray florets but was tubular and hermaphrodite as that of the disc florets (Fig. 1). However, this modified



Rayfloretless flower

layer of florets had slightly longer tubular florets than the regular disc florets. Seeds are black with 100 seed weight of 5.2 g and an oil content of 33.0%. There were no significant differences in the oil content, plant maturity and seed filling frequency in these variants and the sister lines with petaled flowers. The plants possessed field tolerance to *A. helianthi.* These rayfloret-less sunflower plants are being maintained through sister plant mating.

32. TG 18A (IC553271; INGR07032) a Groundnut (*Arachis hypogaea*) Germplasm with Large Pod and Seed

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In groundnut (*Arachis hypogaea* L.), Spanish group (sub-sp. *fastigiata*) genotypes are bunch type with sequential flowering, early maturing and medium to small pods and non-dormant seeds. On the other hand, Virginia group (sub-sp. *hypogaea*) genotypes are bunch, spreading, semi-spreading or trailing type, profusely branching with alternate flowering and late maturing and large pods and seed dormancy. Spanish bunch combined with large pods were developed at Bhabha Atomic Research Centre, Mumbai by inter-mutant hybridization and irradiation of selected cultures. Among these a mutant designated Trombay Groundnut (TG) 18A was isolated after gamma ray treatment. TG-18A was induced by 200 Gy gamma rays of Virginia bunch culture, TG 18. It had Spanish bunch growth and branching habit with sequential flower pattern. Compared to parent, number of branches got reduced in TG 18A (8 + 17 Vs. 5 + 4). It had green foliage and plant height similar to TG 18. It matured earlier than parent due to its early flowering characteristics by eight and five days in both *kharif* and *rabi* season, respectively. Pegs and pods on the stem and branches were similar to other Spanish bunch variety and very distinct from parent. The size of pod and seed in TG 18A was similar to parent and about two times bigger than other Spanish bunch

variety. The per cent distribution of three different grades of hundred seed weight from the sieve screening of the varieties indicated improved recovery of HPS (Hand Picked Selections) kernels in TG 18A.

TG 18A has 20 days seed dormancy. Kernel out turn of 75 per cent in TG 18A demonstrated an improvement in shelling percentage compared to large seed cultures. The induced sequential flowering habit in TG 18A was governed by duplicate pair of recessive genes.

Reference

Chandramouli and DM Kale (1982) Gamma-ray induced Spanish bunch mutant with large pod groundnut. *Oléagineux* **37(12):** 583-588.

33. PHOP-2-2 (IC553274; INGR07033), a Germplasm with High Oleic and Low Erucic Acid in *Brassica* rapa (toria)

JN Sachan, B Singh, SP Singh, DP Pant, AK Singh, R Kumar and D Singh
GB Pant University of Agriculture & Technology, Pantnagar, Uttarakhand

Rapeseed oil with high oleic acid ratio (18:1), and low erucic acid (<2%) is valuable for human nutrition. However, Indian rapeseed varieties contain only 10-20 per cent oleic acid in oil. Increase of oleic acid content in seed results from reduced erucic acid, which is likely to develop diseases like myocardial fibrosis in adults and lipidosis in children. Therefore, oil quality can be improved by developing varieties with reduced contents. Rapeseed oil with more than 80 per cent oleic acid represents not only improved edible oil, but also opens new possibilities for oleo-chemical uses. Laakso *et al.*, (1995) used selection for increasing the levels of oleic acid in spring turnip (*B. rapa*).

Recurrent selection for high oleic acid content in *B. rapa* exotic cv Parkland (oleic acid=36%) resulted in the development of high oleic (18:1) line PHOP-2-2. Initially 25 individual plants with high oleic acid content were selected from parkland and selfed by bud pollination/ bagging of individual plant. Identification of single plant with increased level of oleic acid (18:1) was the basis of further selection. The half-seed technique (Downey and Harvey, 1963) was used to screen the single plant progeny, followed by selfing and recurrent selection for high oleic content. Extraction and methynolysis of oil from whole seed and half seeds was carried out by modification of Hougen and Bado (1973) method. The fatty acid composition was expressed as per cent of total fatty acids. Instrument used for fatty acid analysis was HP 5890 series II with capillary column at 250°C, detector at 280°C and injector at 260°C. The increase in oleic acid was achieved with selfing in selected plants. The third selfed generation seed of high oleic plants derived through half-seed selection collected during 2002-03 showed a distinct fatty acid profile with oleic acid content up to 70.1% in Parkland (range 57.14 to 70.1%, mean = 60.70%). Oleic acid content in these half-seed derived plants (mean of two bulked seed samples) was almost similar to the corresponding half-seed, which indicated the stability of oleic acid content. The Table 1 presents Physio-morphological traits of PHOP-2-2 compared to checks.

Table 1. Physio-morphological traits of PHOP-2-2, evaluated during 2005-06

Characters/Genotype	PHOT-2-2	PT-303	T-9
Seed yield weight (g)	5.8	10.69	11.69
1000 seed weight (g)	3.38	4.94	5.10
Oil content (%)	38.47	39.20	38.47
Days to maturity (nos.)	108	95	92
Days to flowering (nos)	33	31	31
PH (CM)	107	124	102
LMS (CM)	47.22	51.20	42.10
Siliqua in main shoot (CM)	35	50	42
No. of PB	5	5	6
No. of SB	3	8	5
No. of silique/plant (no.)	184	190	150
No. of seeds/silique	14	15	12
Siliqua length	5.15	4.94	5.10
Colour of seed coat	Yellow	Brown	
Brown			

References

Laakso I, X Howinen and T Seppanen-Lasskso (1995). Modification of linolenic and a linolenic acid levels in spring turnip rape by long term selection. *Proceeding of 9th International Rapeseed Congress* D-2.

Downy RK and BL Harvey (1963) Method for breeding for oil quality in rape. *Canadian Journal of Plant Science,* **43:** 271-275.

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Sachan JN, Basudeo Singh, AK Singh, DP Pant and Rakesh Kumar (2004) Fatty acid profile in S3 lines selected for high oleic acid in toria (*Brassica rapa* var. *toria*). *Pantnagar Journal of Research* **2(1):** 20-21.

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34. POHT-2-8-11 (IC553275; INGR07034), a Low Linolenic Acid, *Brassica rapa* (toria)

JN Sachan, B Singh, SP Singh, D Singh and AK Singh
GB Pant University of Agriculture and Technology, Pantnagar

High linolenic acid in oil of rapeseed reduces stability, developing an undesirable odour during frying. Extensive efforts were carried out to develop nutritionally superior genotypes at Pantnagar center. Individual plants containing low linolenic acid, were selected from *Brassica rapa* exotic cv. Tobin with 11.90 per cent linolenic acid and Parkland with 10.20 per cent linolenic acid in oil. For selection, half seed technique of Downey and Harvey (1963) was adopted. Half seed selection was followed by selfing and recurrent selection for low linolenic acid content. Extraction and methodologies of oil from whole seed and half seeds was carried out by modification of Hougen and Bado (1973) method. The fatty acid composition was expressed as per cent of total fatty acids. Instrument used for fatty acid analysis was HP5890 Series II with capillary column at 250°C, detector at 280°C and injector at 260°C. The third selfed generation derived from half seed of low linolenic acid plants shows a distinct fatty acid profile and exhibited considerable decrease in linolenic acid in Tobin (range 3.03-5.43%, mean = 4.21%), with same decrease in Parkland (range=8.23-8.95%, mean = 8.60%) from the original parental materials, Tobin and Parkland. Fatty acid composition is an embryonic character, thus selfed seeds of Tobin and Parkland obtained after first selfing were analysed for fatty acid composition and the desired types were selected. PHOT-2-8-11, selected from Tobin, containing lowest linolenic acid i.e. 3.03 per cent, can be utilized in breeding for low linolenic acid. Table 1 presents Physio-morphological traits of PHOT-2-8-11 in comparison to checks.

Table 1. Physiomorphological traits of PHOT-2-8-11, evaluated during 2005-06

Characters/Genotype	PHOT-2-2	PT-303	T-9
Seed yield weight (g)	9.69	10.69	11.69
1000 seed weight (g)	3.65	4.94	5.10
Oil content (%)	38.69	39.20	38.47
Days to maturity (nos.)	110	95	92
Days to flowering (nos)	34	31	31
Plant height (CM)	124	124	102
Lateral Mean Spread (CM)	56.22	51.20	42.10
Siliqua in main shoot (CM)	44	50	42
No. of Primary branches	5	5	6
No. of Secondary branches	3	8	5
No. of silique/plant	184	190	150
No. of seeds/silique	14	15	12
Siliqua length	5.15	4.94	5.10
Colour of seed coat	Yellow	Brown	Brown

References

Downey RK and BL Harvey (1973) Method for breeding for oil quality in *Brassica rapa*. *Canadian Journal of Plant Sciences* **23:** 211-215.

Hougen FW and V Bodo (1973) Extraction and methynolysis for oil from whole or crushed rapeseed for fatty acid analysis. *J. Am. Oil Chem. Soc.* **44:** 104-111.

Sachan JN, Basudeo Singh, AK Singh, SP Singh and Sharad Pandey (2003) Development of low linolenic acid toria (*Brassica rapa*). *In. National Seminar on Advances in Genetics and Plant Breeding.* Impact of DNA Revolution, Oct., 30-31, 2003, USA, Dharwad.

35. CSPF-1 (IC549909; INGR07035) a Cotton Mutant (*Gossypium hirsutum* L.)

SL Ahuja [1], KN Gururajan[2], LS Dhayal[1], D Monga[1] and BM Khadi[3]
[1] *Central Institute for Cotton Research, Regional Station, Sirsa-125055, Haryana*
[2] *Central Institute for Cotton Research,Regional Station, Coimbatore (TN)-641003*
[3] *Central Institute for Cotton Research, Nagpur-440010*

CSPF-1 is a cotton (*Gossypium hirsutum* L.) with pink flower colour. The ability of cotton to tolerate duplication and deficiencies complicates the recovery of mutants from high energy radiation treatments (Kohel *et al.* 1970). Majority of cultivated upland cottons have petal colour varying from white, cream, light yellow, yellow or pale purple which often becomes pinkish or purplish with age. However, these colours are not uncommon in the so-called primitive cottons or race stocks. *G.hirsutum* cotton genotype with pink coloured flowers is relatively uncommon. CSPF-1 is a spontaneous mutant with pink petals, identified in a plant during 2003-04 crop seasons from the F_3 population of T-7 x LSC-5, involving both *G. hirsutum* cultivars (Flower of T-7 has cream petals, yellow anther and that of LSC-5 is cream petal segregating for anther colour cream or yellow). The mutant identified

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Table 1. Physiomorphological traits of PHOT-2-8-11, evaluated during 2005-06

Characters/Genotype	PHOT-2-2	PT-303	T-9
Seed yield weight (g)	9.69	10.69	11.69
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Oil content (%)	38.69	39.20	38.47
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Days to flowering (nos)	34	31	31
Plant height (CM)	124	124	102
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CSPF-1 is a cotton (*Gossypium hirsutum* L.) with pink flower colour. The ability of cotton to tolerate duplication and deficiencies complicates the recovery of mutants from high energy radiation treatments (Kohel *et al.* 1970). Majority of cultivated upland cottons have petal colour varying from white, cream, light yellow, yellow or pale purple which often becomes pinkish or purplish with age. However, these colours are not uncommon in the so-called primitive cottons or race stocks. *G.hirsutum* cotton genotype with pink coloured flowers is relatively uncommon. CSPF-1 is a spontaneous mutant with pink petals, identified in a plant during 2003-04 crop seasons from the F_3 population of T-7 x LSC-5, involving both *G. hirsutum* cultivars (Flower of T-7 has cream petals, yellow anther and that of LSC-5 is cream petal segregating for anther colour cream or yellow). The mutant identified

bred true to type. The mutant colour identified is governed by a dominant gene (as indicated in crosses of RS-2013 x CSPF-1 and CSPF-1x RS-2013), possess good fiber properties and agronomic attributes and therefore, can serve as morphological genetic marker in genetic mapping, varietal identification and in production of superior hybrids (Table 1).

Table 1. Distinctive morpho-agronomic features of pink flower mutant CSPF-1

Character	Normal F_3 Plant	Pink flower mutant
Plant height(cm)	125-135	140-150
Number of monopodial branches/plant	5-6	5-7
Number of sympodial branches/plant	13-15	15-17
Days to maturity	170	180
Bolls/plant	35-40	50-60
Boll weight (g)	2.97	3.0
Seed cotton yield/plant(g)	62-70	100-120
Ginning Out Turn(%)	33.3	35.3
Petal colour	Cream	Pink
Seed index (g)	7.50	8.1
2.5% span length (mm)	26.2	28.6
Uniformity ratio (%)	52.0	45.0
Micronaire value 10^{-6} g/in	4.6	3.9
Maturity coefficient (%)	78	75
Tenacity (g/tex) (3.2mm)	21.3	24.0

Reference

Kohel RJ, TR Richmond and. CF Lewis (1970) Texas marker-1 Description of a genetic standard for *Gossypium hirsutum* L. *Crop Sci.* **10:** 670-71.

36. CPF-1 (IC549924; INGR07036) a Cotton (*Gossypium hirsutum*) Mutant

SL Ahuja[1], LS Dhayal[1], BR Patil[2], MB Badodkar[2], D Monga[1] and BM Khadi[3]

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[2] *Dr. Punjab Rao Deshmukh Krishi Vidyapeeth, Krishi Nagar, Akola-444104*

[3] *Central Institute for Cotton Research, Nagpur-440010*

CPF-1 is a Cotton (*Gossypium hirsutum*) mutant with pink filament. Pink filament is relatively uncommon in *G. hirsutum* although it is diagnostic in few other *Gossypium* species (Fryxell 1984 and Wilson 1987). Inheritance of pink filament (Wilson, 1987) is conditioned by two complementary dominant gene pairs, which were designated Pf_1 and Pf_2. CPF-1 is a spontaneous mutant with pink anther filament. The mutant identified bred true to type and lacks petal spots in initial stage of flowering and very light petal spot is visible only at full blooming on the inner sides of the petals, unlike that of the mutant identified by Wilson (1987) with prominent petal spots at the initial stage. It was identified from the population of AKH-0308 (a strain derived from the combination of *Gossypium* species (*G. hirsutum* x *G. barbadense*) x *G. hirsutum*) x Derivative (*G. hirsutum* x *G. anomalum* x *G. sturtianum*), All the species involved in the parent culture were obtained from PKV Akola had yellow anther filament colour. The mutant trait is governed by a dominant gene action (as indicated in crosses of RS-2013 x CPF-1 and CPF-1x RS-2013). Possess good fibre properties and agronomic attributes and therefore, can serve as morphological genetic marker in mapping, for varietal identification and in production of superior hybrids (Table 1).

Table 1. Distinctive Morpho-agronomic characters of Pink filament mutant CPF-1

Character	Mutant CPF-1	AKH-0308 (parent)
Plant height(cm)	140.00	111.00
Number of monopodial branches/plant	7.0	4.00
Number of sympodial branches/plant	12.33	11.5
Days to maturity	165	170-180
Stem Colour	Purple	Green
Internode length(cm)	5-10	8-10
Leaf lobing	Small (5 lobed)	3 lobed
Leaf colour	Dark green	Dark green
Leaf surface	Lower surface hairy	Hairy
Nectary/leaf	1-3	1-2
Bolls/plant	**32.0**	**64.0**
Boll weight (gm)	**3.5**	**3.4**
Seed cotton yield/plant(g)	90.0	130.0
Ginning Out Turn (%)	34.5	36.5
Petal colour	Yellow	Light yellow
Petal spot	Very light at full blooming	Absent
Anther filament	Pink	Cream
Fruit Shape	Oval pointed	Oval
Seeds/locule	7-8	5-7
Seed index (g)	7.50	7.1
Fibre 2.5% span length (mm)	27.6	25.8
Fibre uniformity ratio (%)	49.0	50.0
Fibre micronaire value 10^{-6}g/in	4.7	4.3
Fibre maturity coefficient (%)	75	75
Fibre tenacity (g/tex) (3.2mm)	22.2	21.6

bred true to type. The mutant colour identified is governed by a dominant gene (as indicated in crosses of RS-2013 x CSPF-1 and CSPF-1x RS-2013), possess good fiber properties and agronomic attributes and therefore, can serve as morphological genetic marker in genetic mapping, varietal identification and in production of superior hybrids (Table 1).

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Character	Normal F_3 Plant	Pink flower mutant
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Bolls/plant	35-40	50-60
Boll weight (g)	2.97	3.0
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Ginning Out Turn(%)	33.3	35.3
Petal colour	Cream	Pink
Seed index (g)	7.50	8.1
2.5% span length (mm)	26.2	28.6
Uniformity ratio (%)	52.0	45.0
Micronaire value 10^{-6} g/in	4.6	3.9
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Tenacity (g/tex) (3.2mm)	21.3	24.0

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CPF-1 is a Cotton (*Gossypium hirsutum*) mutant with pink filament. Pink filament is relatively uncommon in *G. hirsutum* although it is diagnostic in few other *Gossypium* species (Fryxell 1984 and Wilson 1987). Inheritance of pink filament (Wilson, 1987) is conditioned by two complementary dominant gene pairs, which were designated Pf_1 and Pf_2. CPF-1 is a spontaneous mutant with pink anther filament. The mutant identified bred true to type and lacks petal spots in initial stage of flowering and very light petal spot is visible only at full blooming on the inner sides of the petals, unlike that of the mutant identified by Wilson (1987) with prominent petal spots at the initial stage. It was identified from the population of AKH-0308 (a strain derived from the combination of *Gossypium* species (*G. hirsutum* x *G. barbadense*) x *G. hirsutum*) x Derivative (*G. hirsutum* x *G. anomalum* x *G. sturtianum*), All the species involved in the parent culture were obtained from PKV Akola had yellow anther filament colour. The mutant trait is governed by a dominant gene action (as indicated in crosses of RS-2013 x CPF-1 and CPF-1x RS-2013). Possess good fibre properties and agronomic attributes and therefore, can serve as morphological genetic marker in mapping, for varietal identification and in production of superior hybrids (Table 1).

Table 1. Distinctive Morpho-agronomic characters of Pink filament mutant CPF-1

Character	Mutant CPF-1	AKH-0308 (parent)
Plant height(cm)	140.00	111.00
Number of monopodial branches/plant	7.0	4.00
Number of sympodial branches/plant	12.33	11.5
Days to maturity	165	170-180
Stem Colour	Purple	Green
Internode length(cm)	5-10	8-10
Leaf lobing	Small (5 lobed)	3 lobed
Leaf colour	Dark green	Dark green
Leaf surface	Lower surface hairy	Hairy
Nectary/leaf	1-3	1-2
Bolls/plant	**32.0**	**64.0**
Boll weight (gm)	**3.5**	**3.4**
Seed cotton yield/plant(g)	90.0	130.0
Ginning Out Turn (%)	34.5	36.5
Petal colour	Yellow	Light yellow
Petal spot	Very light at full blooming	Absent
Anther filament	Pink	Cream
Fruit Shape	Oval pointed	Oval
Seeds/locule	7-8	5-7
Seed index (g)	7.50	7.1
Fibre 2.5% span length (mm)	27.6	25.8
Fibre uniformity ratio (%)	49.0	50.0
Fibre micronaire value 10^{-6}g/in	4.7	4.3
Fibre maturity coefficient (%)	75	75
Fibre tenacity (g/tex) (3.2mm)	22.2	21.6

References

Fryxell PA (1984) Taxonomy and germplasm resources. In Kohel RJ and CF Lewis (eds.): *Cotton. Agronomy Series No. 24 Am. Soc. Agron.*, Madison pp. 27-57.

Kohel RJ, TR Richmond and CF Lewis (1970) Texas marker-1. Description of a genetic standard for *Gossypium hirsutum* L. *Crop Sci.* **10:** 670-71.

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37. CS 53 (IC553273; INGR07037) Jute (*Corchorus olitorious*) Germplasm with Premature Flowering Resistance, Chocolate Seed and Finer Quality Fiber

S Chattopadhyay, SK Chaudhury and PG Karmakar

Central Research Institute for Jute and Allied Fibres, Barrackpore, Kolkata-700120

CS 53, a tossa jute mutant with chocolate seed coat colour was developed at Central Research Institute for Jute and Allied Fibres, Barrackpore, West Bengal through hybridization between the jute varieties JRO 632 and the irradiated pollen (12kR X-Ray) of JRO 878 (Chattopadhyay and Mitra,1994). The mutant was isolated from the segregating population and stabilized at F_8 generation through selfing. It was tested for its yield and fibre quality in multilocation trials under All India Co-ordinated Project (Chattopadhyay *et al.*, 2006). Plant height of CS 53 is 3.5-4.0 m, stem is green, 1.4-2.4 cm in diameter, unbranched with rudimentary axillary buds in leaf axils, leaf is green, lanceolate, semi erect (50^0), length, width and leaf area are 14.46 cm, 5.0 cm and 47.65 sq cm respectively. Flower yellow, elongated (8-10 cm) producing non-dehiscent fruit. Thousand seeds weight is 1.940 g. The seed coat colour is chocolate and is governed by monogenic recessive gene. Mean days to 50 per cent flowering is 190-195 days when sown in mid-March and seed to seed maturity is 180-185 days for June sown crop.

It is resistant to premature flowering, thereby suitable for early sowing and it produces finer quality (2.4 tex) and moderately strong fibre (24.5 g/tex), which will be more acceptable to the industry for the production of value added products. The potential dry fiber yield range from 26.23 to 36.94 with an average of 29.43 q/ha and is suitable for whole tossa jute growing belt of the country where jute is followed by transplanted paddy. CS 53 has expressed field resistance to major pests (yellow mite, stem weevil, semilooper and hairy caterpillar) and diseases (stem rot, root rot and anthracnose) in All India Coordinated Trials.

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38. CoSnk 0344 (IC526807; INGR0738) a Sugarcane (*Saccharum spp.*) Germplasm with Resistance to Sugarcane Wooly Aphid

S Patil, PS Tippannavar, BM Khadi, N Balasundram, SA Patil, S Lingappa, PM Salimath and NS Kambar

Agricultural Research Station, Sankeshwar, UAS, Dharvad

Sugarcane is favorably adapted to a wide range of agricultural situations but its productivity is generally limited by abiotic and biotic stresses. Efforts were made to identify environment specific and widely adapted Sugarcane Wooly Aphid (SWA) caused by *Ceratovacuna lanigera* Zenther, resistant clones. Screening of a large number accessions against SWA at Agricultural Research Station, Sankeshwar, University of Agricultural Sciences, Dharwad, Karnatka resulted in identification of CoSnk 0344 as a wooly aphid resistant clone, which is widely adapted. It is highly tolerant to moisture and salinity water logged complex stresses. It has thick, green, solid, cylindrical zigzag internodes without splits, bud groove is present and the canopy is open and droopy. This clone has been found to be superior to the recommended check both under natural and artificial inoculation conditions and is a stable source.

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39. BS35 (IC553284; INGR07039) a Chilli (*Capsicum frutescens*) Germplasm Resistant to Leaf Curl Virus Disease

Sanjeet Kumar, B Singh, M Singh, SK Rai, S Kumar and M Rai
Indian Institute of Vegetable Research, Varanasi

BS-5 is a pepper leaf curl resistant genotype of (*Capsicum annuum*) identified at Indian Institute of Vegetable Research, Varanasi. The initial screening of 304 genotypes of four cultivated and one wild species of *Capsicum* resulted in identification of BS 35. It was then subjected to viruliferous white fly under glass house conditions. Using scion and root stalk of susceptible genotype, Pusa Jawala, it was further challenged through grafting and alternate grafting. When subjected to PCR amplification with degenerated primers, designed to detect Pep marker associated with LCV, the genotype didn't show any amplification suggesting that this genotype is free from LCV viruses and thereby resistant.

40. JN-189 (IC553285; INGR07040) a Potato (*Solanum tuberosum)* Germplasm with Resistance to Leaf Hopper Burn and Potato Stem Necrosis Tospi Virus

RB Singh, SK Pandey, SM Paul Khurana and P Manivel
Agricultural Research Station, Central Potato Research Institute, Ummedganj, Kota

JN-189 hybrid was identified following the recurrent breeding selection method from the F_1 progeny of a cross Kufri Jawahar x *S. andigena* (Cross was made in 1974) by CPRI, Shimla at Agricultural Research Station Ummedganj, Kota (Rajasthan). The morphological description of JN-189 is presented in Table 1. JN-189 yields between 27-30 t/ha in crop duration of 90-100 days with 5-7 per cent disease incidence of PSND and 2-3 per cent incidence of leaf hopper burn under 'hot spot' conditions.

Potato stem necrosis disease (PSND) caused by a Tospo virus is a serious problem in early potato crop in the Central & Western parts (including plateau) of India. The disease causes economic losses, which vary from place to place and year to year and have been estimated to range from 15 to 30 per cent. Leafhoppers (*Amrasca* sp.) are another problem mostly in early potato crop exposed to higher temperatures. The important symptom of leafhopper feeding is the typical hopper burn and severe feeding can cause up to 30 per cent reduction in crop yields depending on the variety, location and crop growth phase. Screening of potato germplasm at Kota (Rajasthan), identified as the hot spot for both the diseases, genetic stock JN-189 consistently showed high resistance against both the diseases. It is a medium maturing culture and produces attractive light purple, oval tubers with medium deep eyes and pale yellow flesh. It can be used as a donor parent in developing potato varieties with combined resistance to PSND and leafhoppers.

Table 1. Morphological description of indigenous potato hybrid JN-189

Character	Description
Plant	Medium height, plant canopy semi-compact, stem thick, predominantly purple, secondary colour green, and wings feebly developed and straight.
Foliage	Leaves structure intermediate, leaflet width broad, leaflet coalescence frequency nil, rachis and midrib pigmentation absent.
Flowers	Flowering shy, floral stalk light purple, floral stalk-pedicel articulation clearly visible and located above the middle, calyx completely pigmented, bud purple, corolla light purple, corolla shape stellate, anther yellow and cone normally developed, stylar length longer than stamen column and stigma bi-lobed.
Tubers	Tuber round, skin colour predominantly creamy white, secondary colour light purple splashed through out, eyes deep, eyebrows normal, and flesh white.
Sprouts	Sprout red-purple predominantly and white to green at the apex, shape conical, pubescence of base slight and sprout tip closed.

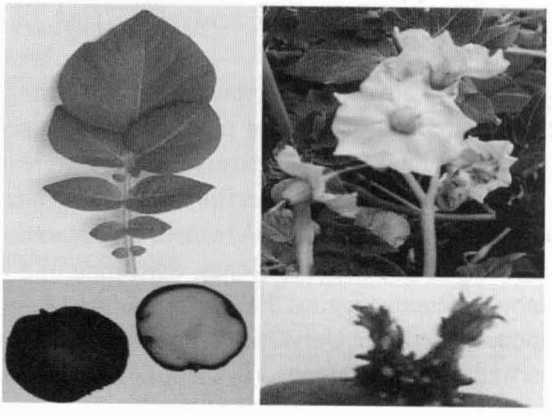

Figure1

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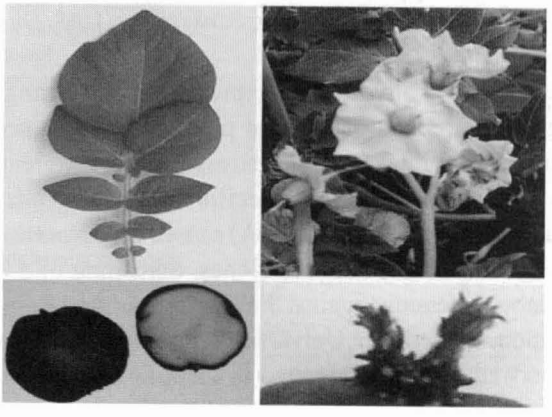

Figure1

41. NRC AP-2 (IC548348; INGR07041), a Kalmegh (*Andrographis paniculata*) Germplasm with Compact Plant Type with Higher Andrographoloide Contents

KA Geetha, Satyabrata Maiti and Narendra Gajbhiye
National Research Centre for Medicinal and Aromatic Plants, Boriavi, Anand

In medicinal and aromatic plants there has been effort for search of plant types that produces higher quantities of main ingredient of economic importance. The screening of Kalmegh *Andrographis paniculata* germplasm at National Research Centre for Medicinal & Aromatic Plants, Boriavi, Anand resulted in identification NRC AP-2, which is a compact plant morpho-type and produces comparatively higher andrographoloide content (0.83 gram/plant). The fresh herbage yield is 209g/plant and dry herbage yield is 76.6g/plant .The plant reaches a height of 57.2 and with a spread of 107 cm.

42. NIC 023413 (IC522963; INGR07042) a Rose Geranium (*Pelargonium graveolens*) Germplasm with Quality Aroma

KS Negi[1], KC Muneem[1], VK Pant[1], Poonam Suneja[2], KC Pant[1] and ML Maheshwari[3]
[1] *National Bureau of Plant Genetic Resources, Regional Station Bhowali-263132, Niglat, Dist. Nainital (Uttarakhand)*
[2] *National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012*
[3] *E8, Street, E, Mayapuri, New Delhi-110064*

Scented Rose Geranium (*Pelargonium graveolens* L' Herit) was introduced to dooryard/ backyard/ kitchen garden of Almora, Uttarakhand in 1988. Stem cuttings of rose geranium were obtained from Mr. V Joshi, Gardener, Mohalla- Bakshikhola, P.O. and Distt. Almora, Uttarakhand. These are being maintained at herbal garden of National Bureau of Plant Genetic Resources (NBPGR), Regional Station Bhowali. NIC 23413 is a genetic stock with high quality aroma identified at NBPGR, Bhowali. The essential oils obtained from NIC 23413 under Uttarakhand conditions are acceptable in the industry. It has good major chemical constituents, such as, Cis-rose oxide 0.918 per cent, Trans-rose-oxide 0.295 per cent, Iso-menthone 17.10 per cent, Linalool 11.565 per cent, Citronellol 62.03 per cent and Geraniol 4.07 per cent. NIC 23413 is accepted for its high contents of citronellol compounds and lemon or odomas like odour. NIC 23413 is a perennial hairy or scabrous plant (up to seven years) with creeping rhizomatous root stocks, 120-180 cm tall; leaves light green, sub-orbicular, palmately (5-7) lobed, 25 cm across, segments irregularly lobed, pubescent on both surfaces, lower leaves petiolate, upper ones sessile, dark green; flowers pale pink-purple with dark purple centre/veins, one cm across, solitary or 8-10 together; sepals 5, free, 4-5 mm long, lanceolate, acute; petals 5 free 8-10 mm long, obovate; capsule 1-2 cm long, forming beak, single seeded, enclosed by persistent erect calyx.

This genotype is evergreen resistant to frost, diseases and pests. Terminal shoot- apex with 4-6 nodes of the stem froms healthy plants with profuse branching that are good to multiply and regenerate round the year except rainy season. Plantation of geranium is done with 30 cm plant-to-plant and row-to-row distance, yielding about 1200-1500 quintals herbage (leave and tender stem) after four cuttings (at three months interval) with and a yield of 84-105 kg of essential oil per ha/year. Large scale extraction of geranium herbage through steam and hydro distillation units yielded 0.07 and 0.14 percent essential oil respectively.

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43. UPG-16 (IC522969; INGR07043) a Jasmine (*Jasminum ritchiei*) Germplasm with Variegated Leaves

PA Jose, AG Pandurangan and M Abdul Jabbar
Tropical Botanic Garden and Research Institute, Palode, Thiruvananthapuram-695562

Jasminum ritchiei Clarke, a wild jasmine belonging to the family Oleaceae, is distributed in India and Sri Lanka. The plant is a branched climbing shrub having green leaves with obtuse base and acuminate apex. Flowers are 3-7, arranged in cyme and are milky white with mild fragrance. It usually flowers in August-October. UPG-16 is a variegated leaved natural genetic stock collected and established in the campus of Tropical Botanic Garden and Research Institute, located at Palode, Thiruvananthapuram, Kerala. The clonal multiplication in 5 successive generations retained the parent variegation confirming stability of character (Jose and Jacob Thomas, 1994; 1999; Jose *et al.* 2006).

It is a branched climbing shrub with variegated leaves, where the upper surface has characteristic mosaic of white patches. Leaf shape ranges from ovate-obovate to oblanceolate with acute base. Leaves are simple with size varying from 2.3-3.2 x 1.5-1.9 cm. The flowers are 1-4, loosely arranged in a cyme. The plant naturally reproduces by the root sprouts produced from the mature plants. Clonal propagation through stem cuttings is an ideal and easy method for the multiplication. Tolerance of the plants towards insect-pest incidence extends its agronomic success in cultivation. By virtue of being habituated at mean sea level, it is an excellent flower cum foliage jasmine for the plains.

References

Jose PA and Jacob Thomas (1994) A spontaneous mutant of *Allamanda neriifolia*. *Indian Horticulture* **39:** 36-37.

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44. B-159 (IC396388; INGR07044) a Snap Melon (*Cucumis melo mormordica*) Germplasm with Downy Mildew Resistance

S Pandy, B Singh, M Rai and KK Pandey
Indian Institute Vegetable Research, Varanasi

Downy mildew has been one of the major biotic stresses causing severe yield losses in case of melons, particularly musk melon. There have been efforts to identify lines with resistance to downy mildew and therefore a large number of accessions have been screened against this disease. Screening of germplasm at Indian Institute Vegetable Research, Varanasi resulted in identification B-159, a snap melon genetic stock with resistance to downy mildew. The identified line is easily crossable with muskmelon and therefore can be utilized in breeding for resistant hybrid and varieties. The fruits B-159 are long and light green in colour. The mature fruit weighs 0.82 kg with average length of 37 cm and average diameter of 7.22 cm. The average number of fruits per plant is 2.75.

43. UPG-16 (IC522969; INGR07043) a Jasmine (*Jasminum ritchiei*) Germplasm with Variegated Leaves

PA Jose, AG Pandurangan and M Abdul Jabbar
Tropical Botanic Garden and Research Institute, Palode, Thiruvananthapuram-695562

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45. HI 8591 (IC537351; INGR07045) a Durum Wheat (*Triticum durum*) Germplasm with High Yield, Resistance to Stem, Leaf and Stripe Rusts

HN Pandey, RS Thakur, SV Sai Prasad, RC Bhawsar, AN Mishra and PK Varma
Indian Agricultural Research Institute, Regional Station, Indore-452001 (MP)

Durum wheat went out of cultivation in Central India due to poor yield and susceptibility to stem and leaf rusts. Hence, an urgent need was felt to identify few good durum wheat genetic stocks having high yield along with resistance to rusts and other diseases. **HI 8591** is a semi-dwarf, high yielding multiple disease resistant genotype of durum wheat (*Triticum turgidum var. durum*), evolved at Indian Agricultural Research Institute – Regional Station, Indore through pedigree method from the cross "HI 8144 / NI 8625". In its 3 years (1998-1999 to 2000-01) of evaluation in All India Co-ordinated Wheat trials, it performed on par with popular durum variety, HI 8498. It showed high levels of field resistance to black rust (*Puccinia graminis tritici*), leaf rust (*Puccinia triticina*) and stripe rust (*Puccinia stritiformis*) over years including virulent pathotypes 77-2, 77-5, 104-2 and 12-2 of leaf rust and 40A, 40-1, 122 and 117-6 of stem rust. It also showed good resistance to Karnal bunt and foot rot.

HI 8591 has 80 – 85 cm height and erect growth habit. It is medium early in maturity, non-lodging and non-shattering. Spikes are dorsally pressed, fusiform with pubescent glumes and black awns at maturity. Grains are amber, bold and lustrous with > 50 g thousand grain weight.

46. KRL 99 (IC546936; INGR07046) a Wheat (*Triticum durum*) Germplasm for Salinity, Sodicity and Waterlogging Stresses

KN Singh[1], Neeraj Kulshreshtha[1] and Ravish Chatrath[2]
1. *Central Soil Salinity research Institute, Karnal-132001*
2. *Directorate of Wheat research, Karnal-132001*

KRL 99, a salt and waterlogging tolerant genotype has been developed at Central Soil Salinity Research Institute, Karnal through recombination breeding involving the parentage KRL 3-4/CIMK 2//KRL 1-4. The genotype is unique with respect to amber oblong and medium size grain and very high level of tolerance to different stresses mentioned above. It has dark green foliage with medium waxiness and semi erect growth habit. The plant has medium height and long light brown ears.

All India Coordinated salinity / alkalinity tolerance varietal trial data for 2002-03, 2003-04 and 2004-05 indicated that KRL 99 was significantly superior to the best check over the years. Its performance was the best both under high sodic microplots (pH: 9.3) and under waterlogged (pH: 9.3) conditions in comparison to PBW 343, HD 2009, HD 4530, KRL 19 and Kharchia 65. The percent reduction in grain yield in KRL 99 was much less under stress (11%) in comparison to other tolerant varieties KRL 19 (34%) and Kharchia 65 (22%) (Table 1). The high yielding variety PBW 343 incurred much reduction (81%) and the other genotypes HD 2009 and HD 4530 could not even survive.

Table 1. Grain yield per plant of wheat genotypes under waterlogged sodic conditions in comparison to normal soil

Genotype	Grain yield per plant (gm)		% reduction from Normal
	Normal (pH: 8.1)	*Waterlogged sodic (pH: 9.3)*	
KRL 99	8.39	7.45	11
KH 65	8.67	6.75	22
KRL 19	8.83	5.86	34
PBW 343	8.90	1.71	81
HD 2009	5.23	0.67	87
HD 4530	4.71	0.10	98
C.D.	0.62	1.24	

Figure 1

45. HI 8591 (IC537351; INGR07045) a Durum Wheat (*Triticum durum*) Germplasm with High Yield, Resistance to Stem, Leaf and Stripe Rusts

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KRL 99 is much improved from Kharchia 65 (red grains), on account grain colour (amber), improved plant type, along with high level of sodicity and water logging tolerance. It gives its best expression under low sodic/ reclaimed sodic and normal sown conditions. However under high sodic conditions (pH more than 9.3), the genotype can provide much better yield than the prevalent variety PBW 343.

47. HD2819 (IC546938; INGR0704) a Wheat (*Triticum durum*) Germplasm with Resistance to Leaf and Stripe Rust, Karnal Bunt, Loose Smut, Root Aphids and High Protein Content

B Singh, SMS Tomar, Vinod, Rajendra Singh and Anil Kumar
Division of Genetics, Indian Agricultural Research Institute, New Delhi-110012

Wheat rust caused by *Puccinia* spp. inflicts heavy damage to wheat production world over. In India leaf rust is prevalent throughout the country. Stem rust *Puccinia graminis tritici* occurs in comparatively warmer areas of Central and Peninsular India, while stripe rust caused by *P. striiformis* is confined to cooler areas of northern hill zone, tarai regions of Himachal Pradesh, Uttarachal and Uttar Pradesh and occasionally in entire North Western Plains Zone when congenial environment prevails during the crop season. Karnal Bunt (*Neovossia indica*) is also an important disease of wheat which makes the grain unfit for human consumption, if incidence crosses the prescribed limit of 0.5 per cent. Similarly, Loose smut (*Ustilago nuda*) occurs in all wheat zones and reduces grain quality and yield by approximately 2 per cent in susceptible genotypes.

Development of resistant genetic stocks is an important pre-requisite for breeding disease resistant varieties with high protein content. HD2819 derived from CPAN 3004/WR447 (RL6043*[5]/NAC76) //HW2007 exhibited adult plant resistance to all the three rusts, Karnal bunt and Loose smut. Seedling test against leaf rust races indicated that HD2819 presumably carry *Lr*24, which is linked with *Sr*24. HD2819 also showed <10 per cent average coefficient of infection against all the three rusts at adult plant at multi-locations over the years. This novel stock also expressed resistance to root aphids. The multiple resistances to diseases and pests seem to be derived from exotic genotypes involved in its pedigree.

In general, protein content in commercially grown wheat varieties in India ranges from 9 to 11 per cent. HD2819 has 12.74 per cent grain protein content on average and its mixography characters indicate better mixing time along with suitably high loaf volume. This genetic stock also possesses high *Glu*-1 score that matches with a popular wheat variety C306 which possess very high chapati making characteristics. The observations with respect to disease resistance, pest resistance and quality characters recorded at multi locations over the years (2001-2004) indicated that HD2819 is a novel genetic stock. Since HD2819 having less than 100 cm plant height and performed favorably under rain fed and timely sown conditions, its novelty is enhanced. The use of such genotypes in breeding programmes will encourage the development of high quality wheat.

48. FRL282 (IC279125; INGR07048) a Pea (*Pisum sativum*) Germplasm with Bold Seed Size with 100 Seed Weight (50.14 gm)

JC Rana[1], OP Chaurasia[2], K Pradheep[1] and VD Verma[1]
National Bureau of Plant Genetic Resources, Regional Station, Shimla-171004
Field Research Laboratory, DRDO, Leh

IC279125, is an important dual purpose crop grown for vegetable as green pod and for grain. Majority of the varieties are small seeded. Accession IC279125 recorded highest 100-seed weight (50.14g) among all the pea germplasmm aintained at NBPGR. Generally, the bold seeded lines have less seeds/pod and short pod length, while this accession has good pod length (5.3 cm/pod) and seeds/pod (6.0), which is better than general average. It also showed moderate resistance to powdery mildew and *Ascochyta* blight. Owing to its good pod length and

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Table 1. Characteristic feature of the germplasm accessions IC279125

Characters	Mean value	Characters	Mean value
Plant height (cm)	86.5	Score for powdery mildew (0-5 scale)	2
Days to flowering	74.0	Score for *Ascochyta* blight (0-5 scale)	2
First flowering node height (cm)	32.00	Early plant vigor	V. good
No. of clusters/plant	17.0	Plant growth habit	Indeterminate
No. of pods/plant	36.0	Flower colour	White
Pod length (cm)	5.3	Flowering habit	Intermediate
No. of primary branches	4.0	Leaf size	Large
Day to maturity	126.0	Pod thickness	Medium
Seeds/pod	6.0	Pod shape	Straight
Seed yield/plant (g)	32.46	Leaf colour	Green
100-seed weight (g)	50.14	Seed shape	Round
		Seed surface	Smooth

seed size, it is good for vegetable purpose and can be used in breeding both vegetable and pulse type varieties. Interestingly, it has also given high yield compared to check varieties, hence being multiplied for testing in All India Coordinated Trials.

49. BN-RED (IC538546; INGR07049) a Cotton (*Gossypium hirsutum*) Germplasm with Resistance to Spotted, Pink and *Heliothis* Bollworms

SL Ahuja[1], SK Banerjee[2], Jagmail Singh[3], BM Khadi[2], SKVerma[1], VV Singh[2], D Monga[1], OP Tuteja[1] and LS Dhayal[1]

1. Central Institute for Cotton Research, Regional Station, Sirsa-125055, Haryana

2. Central Institute for Cotton Research, Nagpur-440010

3. Division of Genetics, Indian Agricultural Research Institute, New Delhi-110012

BN- Red is a semi naked seeded morphological diverse genetic stock line with red pigmented plant body. The genetic stock has been developed through back cross method (BC_8 generation) using germplasm line Mec Namara Wine Sap as non-recurrent parent and BN (Bikaneri Narma), a well adapted *G. hirsutum* cultivar as recurrent parent. Red pigmentation has effect on resistance to pests as reported by various workers (Lukefar *et al.* 1969, 1975; Ahuja *et al.* 1998). This has been reported that BN-Red has high amount of gossypol content in stem and squares, flavanol in leaves and squares and total phenol contents in squares and low amount of total sugars in squares (Ahuja *et al.*, 2001). Studies of other workers (Lulefer *et al.*, 1969; Deterline, 1975; Leigh, 1975; Agarwal *et al.* 1976) have indicated that high amount of gossypol, flavanol and phenols contents in plant parts account for lower bollworm infestation. The bollworms incidence (bollworm complex; spotted, pink and *Heliothis* bollworms) in BN-Red was considerably low as compared to Bikaneri Narma and its improved cultivar H-777 (Table 1).

Table 1. Distinctive morpho-agronomic characters of BN-Red

Character	BN-Red	Bikaneri Narma
Plant type	Spreding/Bushy	Lanky
Plant height(cm)	110	143.00
Number of monopodial branches/plant	5-6	2.67
Number of sympodial branches/plant	11.33	12.0
Stem hairiness	Dense hairy	Hairy
Colour	Red	Light pink
Leaf lobing	Small (3 lobed)	Narrow
Leaf colour	Upper red and lower green	Medium green
Nectary/leaf	1-3	1-2
Bolls/plant	50.67	45.0
Boll weight (gm)	2.40	2.58
Seed cotton yield/plant(g)	100.00	91.00
Ginning Out Turn (%)	31.0	33.00
Lint index (g)	3.60	3.49
Petal colour	Cream with red side margins	Cream
Shape and colour	Oval pointed small red boll	Oval and green
Seeds/locule	5-6	8

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Character	BN-Red	Bikaneri Narma
Plant type	Spreding/Bushy	Lanky
Plant height(cm)	110	143.00
Number of monopodial branches/plant	5-6	2.67
Number of sympodial branches/plant	11.33	12.0
Stem hairiness	Dense hairy	Hairy
Colour	Red	Light pink
Leaf lobing	Small (3 lobed)	Narrow
Leaf colour	Upper red and lower green	Medium green
Nectary/leaf	1-3	1-2
Bolls/plant	50.67	45.0
Boll weight (gm)	2.40	2.58
Seed cotton yield/plant(g)	100.00	91.00
Ginning Out Turn (%)	31.0	33.00
Lint index (g)	3.60	3.49
Petal colour	Cream with red side margins	Cream
Shape and colour	Oval pointed small red boll	Oval and green
Seeds/locule	5-6	8

Seed index (g)	8.40	7.1
Fibre 2.5% span length (mm)	25.5	26.7
Fibre uniformity ratio (%)	49.0	45.0
Fibre micronaire value 10^{-6} g/in	4.4	4.3
Fibre maturity coefficient (%)	75	75
Fibre tenacity (g/tex) (3.2mm)	21.2	22.1
Biochemical attributes	*L ST SQ*	*L ST SQ*
Gossypol (mg/g)	2.29 6.92 4.01	2.91 4.03 2.72
Reducing sugar (mg/g)	3.62 2.26 1.40	2.56 1.91 4.81
Flavanol (mg/g)	1.98 2.18 1.40	1.58 2.33 0.92
Total phenol (%)	3.65 4.62 3.37	3.80 4.62 2.97
Total sugar (mg/g)	5.65 5.24 3.14	7.18 5.49 8.80
Bollworm incidence (%)	40.92*	71.02*

Where L=leaves, ST= stem and SQ= square; * Five years avareage

References

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50. BN OKRA (IC538547 INGR07050) a Cotton (*Gossypium hirsutum*) Germplasm with Resistance to Spotted, Pink and *Heliothis* Bollworms

SL Ahuja[1], SK Banerjee[2], Jagmail Singh[3], BM Khadi[2], SK Verma[1], VV Singh[2], D Monga[1], OP Tuteja[1] and LS Dhayal[1]

[1] *Central Institute for Cotton Research, Regional Station, Sirsa-125055, Haryana*

[2] *Central Institute for Cotton Research, Nagpur-440010, Maharashtra*

[3] *Division of Genetics, Indian Agricultural Research Institute, New Delhi-110012*

American cotton (*G. hirsutum* L) cultivars have palmate (normal) leaf shape. BN-Okra is a morphological diverse genetic stock with lanceolate (super okra) leaf shape. It has been developed through backcross method (BC_8 generation) using germplasm line, Reba Okra Isogenic Line-3 (ROIL-3) and BN (Bikaneri Narma), a well adapted *G. hirsutum* cultivar as recurrent parent. Super okra leaf shape has effect on resistance to pests as reported by various workers (Lukefar *et al.,* 1969; 1975 and Ahuja *et al.,* 1998). This has been reported that BN-Okra has high amount of gossypol in leaves and stem, flavanol in leaves, stem and squares and total phenol in leaves and squares and low amount of total sugars in stems (Ahuja *et al.,* 2001). Studies of other workers (Lulefer *et al.,* 1969; Leigh, 1975 and Agarwal *et al.,* 1976) indicate that high amount of gossypol, flavanol and phenols contents in plant parts account for lower bollworm infestation. The bollworms incidence (bollworm complex; spotted, pink and *Heliothis* bollworms) in BN-Okra was considerably low as compared to Bikaneri Narma and its improved cultivar H-777 (Table 1).

Table 1. Distinctive Morpho-agronomic characters of BN-Okra

Character	BN-Okra	Bikaneri Narma
Plant type	Spreading/Bushy	Lanky
Plant height(cm)	130-150	143.00
No. of sympodial branches/plant	8.67	12.0
Stem colour	Brown	Light pink
Leaf size	Large	Medium
Leaf shape	Lanceolate	Palmate
Lobing	Very deep	Narrow
Colour	Green	Medium green
Surface	Hairy	Margin hairy
Nectary/leaf	2-3	1-2
Bolls/plant	40.67	45.0
Boll weight (g)	2.50	2.58
Seed cotton yield/plant(g)	53.57	91.00
Ginning Out Turn (%)	33.0	33.00
Lint index (g)	3.50	3.49
Pollen colour	Yellow	Cream
Petal spot	Dirty yellow spot on petals	Absent
Fruit shape	Oval round with pointed tip	Oval
Seeds/locule	6-7	8
Fibre 2.5% span length (mm)	23.8	26.7
Fibre uniformity ratio (%)	4.9	45.0
Fibre micronaire value 10^{-6} g/in	52.0	4.3
Fibre maturity coefficient (%)		75
Fibre tenacity (g/tex) (3.2mm)	21.3	22.1

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Reducing sugar (mg/g)	3.62 2.26 1.40	2.56 1.91 4.81
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Flavanol (mg/g)	2.29 3.10 1.87	1.58 2.33 0.92
Total phenol (%)	6.00 4.25 3.02	3.80 4.62 2.97
Total sugar (mg/g)	7.81 5.00 7.25	7.18 5.49 8.80
Bollworm incidence (%)	39.36*	71.02*
Jassid resistance	1.31	1.30

Where L=leaves, ST= stem and SQ= square; * Five years average

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