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ISOZYME DIVERSITY IN RELATION TO DOMESTICATION OF GAUR (*Cyamopsis tetragonoloba* (L.) TAUB.)

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A survey of isozyme systems in a relatively little known legume, the guar (clusterbean), *Cyamopsis tetragonoloba* L.) Taub., has been reported for the first time. The plant material included seven landrace accessions from India, six released cultivars from the United States, and two wild species populations of *C. senegalensis* and *C. serrata*. Starch gel electrophoresis protocols for seven isozyme systems, viz., MDH, IDH, PGD, ADH, PGI, GOT and ME were largely developed. The combination of cotyledons as the plant tissue, and Tris-HCl with ascorbic acid, PVP, PVPP and 2-mercaptoethanol as the extraction buffer provided the best resolution of isozymes. Out of the four gel-electrode buffer systems attempted, the Histidine system was selected to study the patterns of diversity. All the cultivated species accessions were uniformly monomorphic. Two isozyme phenotypes were recorded for ADH in *C. senegalensis*, and for GOT in *C. serrata*. A preliminary interpretation of the banding patterns in relation to domestication of guar has been made.

Key words : Guar, isozymes, diversity, genetic distance

Guar (*Cyamopsis tetragonoloba* (L.) Taub.) has been cultivated in India, Pakistan, Indonesia and other parts of southern and south-eastern Asia as a vegetable and forage crop for a long time (Whyte *et al.*, 1953; ICAR, 1970). Guar gum is used extensively by the paper, mining, explosive, food, pharmaceutical, cosmetic, textile and oil industries around the world (Hymowitz and Maltock, 1963). Guar seed protein also has great industrial potential, both for human diet and cattle feed.

The genus *Cyamopsis* is (tribe Indigofereae, Family : Leguminosae, Sub-family; Papilionoideae) consists of three species viz., *C. tetragonoloba, C. senegalensis* and *C. serrata* (Gillett, 1958; 1971). The forms intermediate between the latter two wild species and found in south-western Africa alongwith *C. serrata* were named as *C. dentata* by Torre (1960). Whistler and Hymowitz (1979) followed Gillett's taxonomic treatment of *Cyamopsis*. In cytological studies, Senn (1938) had suggested close relationship between the Genus *Cyamopsis* and *Indigofera*, but Gillett (1958) preferred to retain *Cyamopsis* as a distinct genus. *Cyamopsis* is a uniformly diploid genus with 2n = 14.

The relationship between the guar cultigen, *C. tetragonoloba*, grown in the Indian sub-continent and its allied wild species has not been studied in depth experimentally. Linguistic evidence to ascribe antiquity is also very poor (Hymowitz, 1972). On morphological grounds, however, the cultigen appears to be closest to the wild species, *C. senegalensis*, found from north-east and north-west Africa and as far north as Arabia. The other related species, *C. serrata* and *C. dentata*,

have been found in south-western Africa, a region distant from the distribution of *C. senegalensis*. No conspecific wild forms of *C. tetragonoloba* have been found, nor any remains in any Neolithic site in the Indo-Pakistan sub-continent. Gillett (1958) was also not sure of the cultigen's presence of Asia east of Arabia and did not record its presence in Arabia. Linnaeus (1767) indicated that the distribution of *C. tetragonoloba* was Arabia. Hymowitz (1972) has reviewed the history of domestication of guar, and suggested that the focus of its domestication should be concentrated towards the drier regions in north-western India and adjacent lands of Pakistan, where hot dry climates allow it to flourish as a field crop. The possibility of its domestication in other parts of the sub-continent has been ruled out, other regions having high soil moisture conditions or drizzling weather with high humidity in which the pathogens cause appreciable damage to the cultigen. The paradox of an apparent domestication of guar in the Indian sub-continent far removed from the African continent can be explained by the trans-domestication concept of Hymowitz (1972). His thesis takes support from the history of Arab-Indian trade in early times. Horses were a major item of import to Indian ports and the Arabs must have taken on board their ships huge quantities of fodder to feed horses while on the seas, and perhaps sold any remaining fodder to the Indians. Seed of *C. senegalensis* probably came with the fodder, and since the climatic conditions in the dry regions of Indo-Pakistan sub-continent are similar and quite favourable, any seed brought along by the Arabs, and which subsequently germinated, could have easily formed the basis for development through selection of the present day *C. tetragonoloba*. The arrival of *C. senegalensis* in the sub-continent is thought to have occurred between the 9th and 13th centuries A.D. when extensive trade took place between the Arabs and Indians. Thus, the African wild species, *C. senegalensis*, appears to be the ancestor of the west Asian domesticate, *C. tetragonoloba*. The domestication process took place in not very distant times in dry areas of the north-western region of the Indo-Pakistan sub-continent.

Despite the morpho-agronomic diversity in guar germplasm collections (Dabas *et al.*, 1989), variation in isozymes in germplasm accession populations have not been studied to provide additional set of data to interpret genetic diversity in a still greater depth. Research work reported here is one small attempt to understand isozyme diversity in this relatively little known legume, the guar (clusterbean); *Cyamopsis tetragonoloba*. Isozyme survey work has not been reported in this crop, and was considered appropriate in view of the economic importance of crop. The objectives of the research work were to (1) develop starch gel electrophoresis protocols for analysis of seven enzyme systems; and (2) compare isozyme diversity in the primitive landrace accessions from India alongside the released cultivars from the United States, and the two wild relatives.

MATERIALS AND METHODS

(i) Plant materials

Seven landrace accessions, IC Nos. 40034(1), 40052(2), 40057(3), 40284(4), 40348(5), 40378(6) and 41110(7) from guar growing Rajasthan state of India, obtained from NBPGR, New Delhi, India; six US cultivars viz., Brooks (8), Esser (9), Hall (10), Kinman (11), Lewis (12) and Santacruz (13) and samples of the two wild relatives viz., *C. senegalensis* (14) and *C. serrata* (15) and US cultivars were obtained from USDA, Beltsville, Maryland, USA.

(ii) Seed germination

Seeds were scarified with dilute sulphuric acid (1:8) for 10 minutes for the cultivated types and for 30 minutes for the wild species. Seeds were then thoroughly washed with distilled water, and sown in 'Professional All-Purpose Compost' from the Sinclair Horticulture and Leisure Co.

(SHL), UK in 6-inch size pots in a controlled environment chamber maintained at a temperature of 28-30°C. Germination was rapid (2 days), and seedlings suitable for isozyme analysis could be obtained in 7 days.

(iii) Selection of plant tissue and extraction buffer

Four plant tissues representing different organs of seedlings viz., cotyledons, hypocotyls, roots and primary leaves were evaluated for the extraction of enzymes using five different extraction buffers from Catty and Jackson (1989) viz., i) Tris- HC1, ii) Tris-HC1 with 2-mercaptoethanol, iii) Tris-HC1 with ascorbic acid, PVP, PVPP and 2-mercaptoethanol; iv) Tris-HC1 with $NaNO_3$ and NaCl, and v) distilled water. The performance of separation of isozymes was evaluated using three criteria viz., level of enzyme activity expressed on the starch gel, clarity in the separation of bands, and the intensity of arcing. Thus, coyledons were selected for study of the patterns of isozyme variation using 0.1M Tris-HC1 extraction buffer (pH 7.2) containing ascorbic acid (0.03%), polyvinylpyrrolidone-40(4%), polyvinyl polypyrrolidone (2%) and 2-mercaptoethanol (1 μ/ml) per 1 cm^2 cotyledonous tissue in 2ml of extraction buffer to extract the enzymes. Since deep freezing (–40°C) of extracted homogenate did not yield better results, fresh plant material was used every time a gel was run.

(iv) Selection of buffer systems with differential gel and electrode buffers

Four gel and electrode buffer systems, first three from Catty and Jackson (1989) and fourth from Chen (1985), viz., i) Histidine system: Electrode buffer (E.b.) = 0.2M trisodium citrate $2H_2O$, pH 7.0; Gel buffer (G.b.) = 0.005 L-histidine monohydrochloride, pH 7.0 ii) Buffer System 1 : E.b. = 0.135 M tris, 0.043 M citric acid, pH 7.0; G.b. = diluting 20 ml of E.b. to 300 ml; iii) Buffer system F : E.b. = 0.3M sodium borate (boric acid), pH 8.3; G.b. = 0.0036M citric acid, 0.152 M tris, pH 7.6; and iv) Tris/Citrate and Lithium Borate System; Buffer (A) E.b.) = 0.2 M Lithium borate, Buffer (B) = 0.05 M tris citrate; G.b. = 9B:1A; were evaluated.

The concentration of starch (Sigma, USA) in the gel was maintained at 38g in 300 ml of gel buffer. On the basis of three criteria viz., separation of bands, quality of staining and duration of the run, Histidine system was selected for seven selected enzyme systems viz., alcohol dehydrogenase (ADH), phospho glucoisomerase (PGI), glutamate-oxaloacetate transminase (GOT), isocitrate dehydrogenase (IDH), malate dehydrogenase (MDH), malic enzyme (ME) and 6-phosphogluconate dehydrogenase (PGD) using the staining recipes described in Catty and Jackson (1989). The electric current was maintained at 30 mA at the start of electrophoresis, and 25 mA after the removal of wicks. The electrophoresis was run for 5-5.5 hrs at 4°C in a refrigerator. To keep the electrophoretic conditions as cool as possible, the gel was covered with a polythene cling film sheet after the removal of the wicks, and some ice was placed is a small tray on the top of the cling film. Buffer system 'F' gave additional resolution for ME for the two wild species.

(v) Data analysis

The isozyme profiles obtained for the seven polymorphic enzyme systems were scored for "allelic" differences within and among the three species. Although this scoring was based on the analysis of individual seedlings from each germplasm accession, a genetic confirmation of the interpretation is required for more accurate analyses. The species X allele datamatrix for 26 allelic variants from seven enzyme systems was used to calculate genetic distances among the three species (Nei, 1972). The genetic distances were used to construct a UPGMA-based dendrogram to depict inter-relationships among

the species. All the statistical calculations were performed using NTSYS-pc, version 1.80 software package (Rohlf, 1992).

RESULTS AND DISCUSSION

All the accessions of the cultivated species, *C. tetragonoloba*, whether landrace accessions from Rajasthan (India) or US cultivars, were uniformly monomorphic for all the severn enzyme systems. The population of *C. senegalensis* indicated two isozyme phenotypes for ADH. The population of *C. serrata* expressed two phenotypes for GOT. The diagrammatic representation in the forms of zymograms and representative photographs are given in Fig. 1 and 2 respectively.

Malate drhydrogenase (MDH)

There were indications of two zones of activity. The fast migrating zone consistently displayed well-resolved equally- spaced three bands at Rf = 0.311, 0.338 and 0.365. However, in just a few cases of individual plants, there was an indication of a fourth faint band at Rf = 0.233 (e.g. in IC 40034, IC 40052, IC40057) or at Rf = 0.455 (e.g. IC 40284, IC 40438). It was difficult to determine whether these were extra bands or just artefacts. Likewise, the slow migrating zone, from Rf = 0 to 0.085, was very faint and was not observed in all the gels screened.

Isocitrate dehydrogenase (IDH)

The cultivated accessions consistently displayed a single band at Rf = 0.263. However, in the populations of *C. senegalensis* and *C. serrata*, the single band was fast migrating compared to the cultivated accessions, at Rf = 0.337.

6-Phosphogluconate dehydrogenase (PGD)

Two isozyme bands at Rf = 0.549 and 0.396 were common in both the cultivated and wild accessions. There was a third slow migrating band at Rf = 0.212 in the cultivated accessions, and at Rf = 0.321 in the two wild accessions.

Alcohol dehydrogenase (ADH)

Two isozyme bands at Rf = 0.309 and 0.480 were uniformly expressed in all the cultivated accessions. The slow migrating band was generally faint in expression. In *C. senegalensis*, two isozyme phenotypes were noticed. One phenotype (freq. = 0.03) was observed to be the same as in the cultivated accessions. However, the other phenotype was throughout consistent (freq. 0.97). This phenotype consisted of two bands at Rf = 0.412 and 0.516 i.e. the isozyme forms were fast migrating compared to the forms in the cultivated

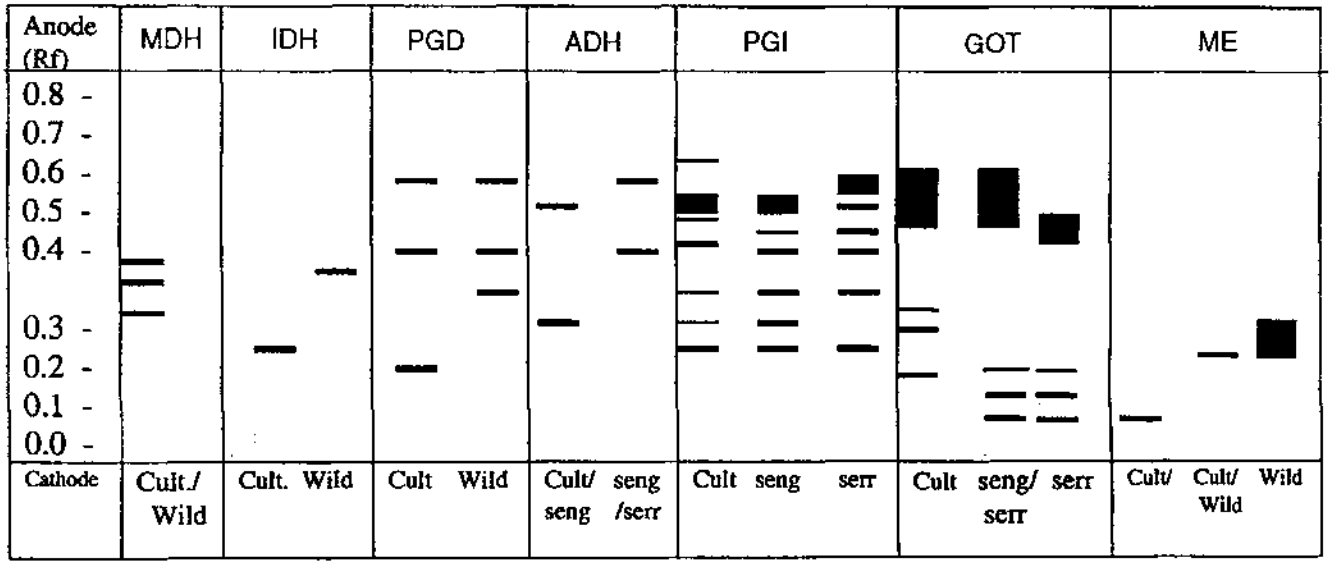

Fig. 1. Representative zymograms of the seven enzyme profiles analysed in *C. tetragonoloba, C. serrata* and *C. senegalensis*

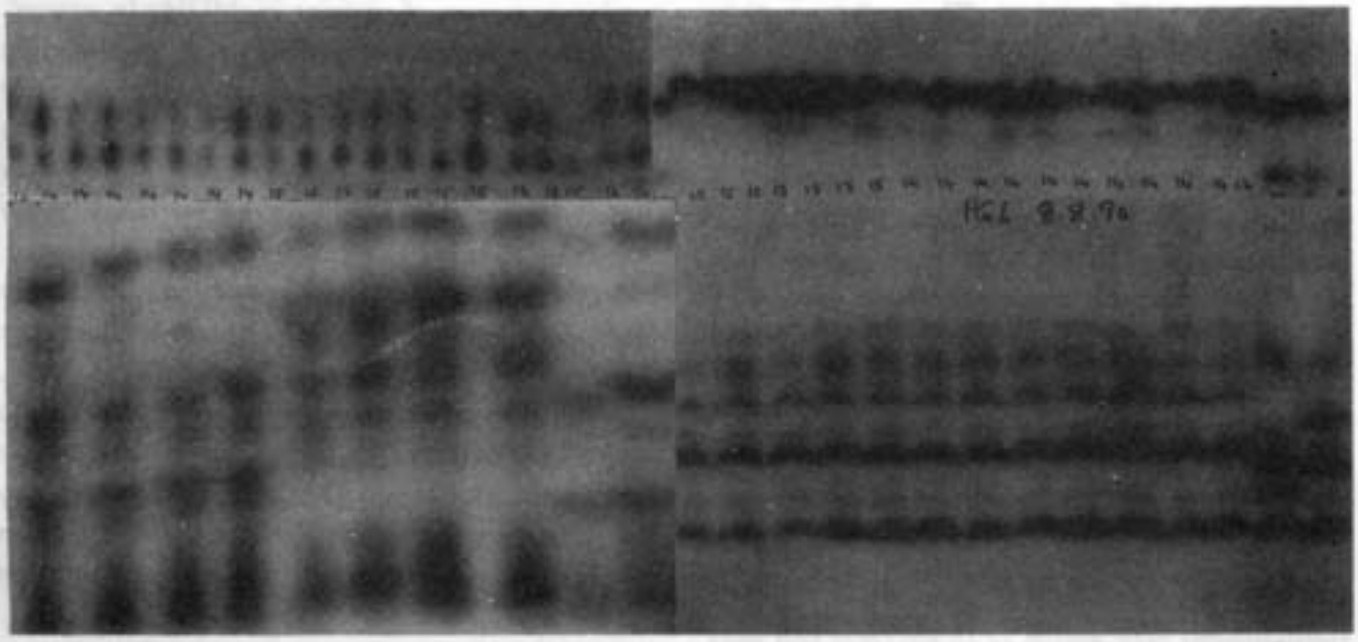

Fig. 2. Representative isozyme profiles for phosphoglucoisomerase (top panel), 6-phosphogluconate dehydrogenase (left half of lower panel) and alcohol dehydrogenase (right half of lower panel) in *C. tetragonoloba*, *C. serrata* and *C. senegalensis*

accessions. The population of *C. serrata* also uniformly expressed the common phenotype of *C. senegalensis* population.

Phosphoglucoisomerase (PGI)

Apparently, there were two zones of activity in the cultivated accessions. The slow migrating Zone I expressed two strongly staining bands at Rf = 0.225 and 0.371, and three faint bands at Rf = 0.281, 0.303 and 0.404. The fast migrating Zone II displayed two strongly staining bands at Rf = 0.467 and 0.528, and a faint band at Rf = 0.607. The two strongly staining bands of Zone II expressed diffused activity between these bands in all the individuals of cultivated accessions and did not indicate the presence of any faintly staining bands as in Zone I. The two zones together were same in all the individuals of the cultivated accessions.

The isozyme phenotype was uniformly different in the two wild species. In *C. senegalensis*, the isozyme phenotype corresponding to Zone 1 of the cultivated accessions, expressed strong enzyme activity at Rf = 0,225, 0.281, 0.303 and 0.371, and faint acticity at Rf = 0.404. Corresponding to Zone V, it expressed a strong but diffused zone of activity between Rf = 0.482 and 0.528. In *C. serrata*, the isozyme phenotype, corresponding to Zone I of the cultivated accessions, expressed strong activity at Rf = 0.225, 0.303 and 0.371. Corresponding to Zone II, it expressed two additional strongly staining bands at Rf = 0.428 and 0.459 and a strong but diffused zone of activity between Rf = 0.482 and 0.528, as observed in the population of *C. senegalensis*.

Glutamate-oxalo-acetate transaminase (GOT)

Two zones of activity could be visualised. The slow migrating Zone I expressed two strongly staining bands at Rf = 0.195 and 0.253, and a faint band at Rf = 0.310. The fast migrating Zone II did not separate a strong but diffused zone of activity between Rf = 0.460 and 0.575. In *C. senegalensis*, the enzyme activity corresponding to Zone I of the cultivated accessions, was comparatively slow migrating. In this case, the Zone I expressed two strongly staining bands at Rf = 0.136 and 0.146, and a

faint band at Rf = 0.195. The enzyme activity corresponding to Zone II of the cultivated accessions was similar to cultivated accessions. In *C. serrata*, the enzyme activity in Zone I was similar to that in *C. senegalensis*. Corresponding to Zone II, two phenotypes were observed. One phenotype (freq. 0.86) was the same as in *C. senegalensis*. The other rare phenotype (freq. 0.14) expressed a comparatively slow migrating Zone II between Rf = 0.432 and 0.465. In one gel, where two individuals each of the seven Indian accessions and three US cultivars were screened, the pH of the gel buffer was modified to 7.9. This modification could resolve the Zone II into three clear strongly staining bands of Rf = 0.453, 0.558 and 0.604. In this case, the bands of Zone I were weak in expression, and were observed at Rf = 0.244, 0.291 and 0.337.

Malic enzyme (ME)

This enzyme system was screened in both the Histidine ad F gel-electrode buffer systems. In the Histidine system, the cultivated accessions and also *C. senegalensis* consistently expressed a single band at Rf = 0.122. In *C. serrata*, the expression was very faint, and some enzyme activity was expressed near the origin with streaking upto R. = 0.122. In the F buffer system, the isozyme phenotype of the cultivated accessions was different compared to the two wild populations. The cultivated accessions expressed a single strongly staining band at Rf = 0.270. The two wild species expressed faint bands at Rf = 0.191 and 0.270 with diffused activity between these bands.

Development of starch gel electrophoresis protocols

Some limitations observed in the developed protocols are as follows. The problem of arcing in isozyme bands in MDH, IDH, ADH, PGI and ME is still present to a certain extent. The isozymes of PGD could only be expressed as 'blobs', and not as discrete and tight bands. It was not possible to resolve adequately the slow migrating zone of activity in MDH. In general, the two wild species have expressed weak enzyme activity, and the arcing of bands was relatively acute in some of the gels run. These observations suggest the need for attempting further modification particularly in the extraction buffer used for releasing enzymes from the plant material. Several workers have also noted that the choice of extraction buffer was one of the most important factors affecting enzyme resolution (Kephart, 1990). The selected extraction buffer was chosen based on its generally better performance on the cultivated accessions. Thus, the wild species may require some further modification in the extraction buffer to provide better resolution of isozyme bands.

The cotyledons were selected as the organ for extraction of enzymes based on greater enzyme activity. However, it becomes a destructive approach and poses limitations on the seedling to mature into a full-grown plant. Rhoades and Cates (1976) have indicated that the concentration of phenolics and other secondary compounds can vary inversely with age. It may be possible that if more research is conducted in the modifications of the extraction buffer, the primary leaf, which gives slightly less enzyme activity with the identified extraction buffer, may become the ideal plant part of better resolution of isozymes. In a survey through a questionnaire to scientists using starch gel electrophoresis, Kephart (1990) found that the respondents rated pH, chemical composition and molarity as the most important factors in selecting the gel-electrode buffer systems. It is quite possible that some further modification in any of these factors may help in better resolution of isozymes from the primary leaf.

The isozyme phenotypes have been determined using one set of electrophoretic conditions (except in ME) used. Coyne *et al.* (1978) have found that the additional variation is proportional to the variation detected by one

condition. Thus, the general picture of variation for an enzyme is not changed after additional analysis, and the preponderance of evidence in the literature also suggests the same (Gottlieb, 1981). The study of Coyne *et al.* (1979) is particularly significant because a number of different electrophoretic techniques were utilised to investigate 6-glycerophosphate dehydrogenase heterogeneity within and between species of *Drosophila.* No additional variation was detected within species but additional variation among species was documented. Gottleib (1979) also did not find any additional variation in *Stephanomeria matheurensis* with additional electrophoretic analyses, using several different conditions of pH and pore size, in acrylamide gels as compared to that detected with starch gels. The evidence to date also suggests that in most instances the increased variation detected with different electrophoretic conditions will cause little if any change in systematic and phylogenetic inferences made from original surveys using only one condition (Ayala, 1982; Gottleib, 1981).

Interpretation of zymogram patterns

The zymograms for MDH, IDH, PGD, ADH and ME expressed simple banding patterns. As such, a preliminary interpretation is made of the number of gene loci involved, and their nature, whether homozygous or heterozygous.

MDH - This is a dimeric enzyme. The presence of three equally- spaced bands throughout the cultivated and wild accessions is perhaps indicative of 'fixed heterozygosity' for this locus.

IDH - The single band detected for this enzyme indicated that this IDH locus is uniformly homozygous. However, the nature of this gene locus is different in the two wild species populations as it yields a comparatively fast migrating form of the isozyme.

PGD - The three bands at different Rf positions could perhaps be interpreted as products of three different homozygus gene loci. The two fast migrating isozymes occupy the same position in both the cultivated and wild accessions, and this may represent two homologous gene loci. The third slow migrating isozyme occupies different positions in the cultivated accessions vis-a-vis the two wild species populations. Thus, the nature of this gene locus is apparently different in the two cases.

ADH - The two bands consistently observed in all the cultivated accessions and the wild species could also be interpreted as two homozygous loci. Two gene loci for ADH have also been reported in many other diploid plant species (Gottleib, 1981). The isozyme forms of the two homozygous gene loci observed in *C. serrata* were comparatively fast migrating. In *C. senegalensis,* the two homozygous gene loci were either similar to the cultivated accessions or to the population of *C. serrata.*

ME - The single band observed in the Histidine system throughout the cultivated accessions and *C. senegalensis* also apparently represents a homozygous gene lcus. However, the gene locus expressed in the F system was observed as heterozygous in the two wild species populations, but homozygous in the cultivated accessions.

It was difficult to interpret the zymogram patterns for PGI and GOT in terms of the number of gene loci involved. For PGI, there appears at least three gene loci (two for Zone I, andone for Zone II) for the cultivated accessions. In the two wild species, the number of loci appears more than the cultivated accessions. The banding pattern perhaps further suggests that the number of gene loci involved is more in *C. serrata* than in *C. senegalensis.* In GOT, there appears at least two gene loci for Zone I and one locus for Zone II, for both the cultivated accessions and the two wild species populations.

Isozyme phenotypes in cultivated accessions vs. wild species

The multiple forms of enzymes recorded in the seven enzyme systems studied arise due to the phenomenon of gene duplication. This is more intensity depicted in the case of PGI and GOT resulting in complex banding patterns. The excessive number of strongly staining bands for PGI, particularly in *C. serrata*, is indicative of more gene duplication in this primitive species. The greater number of bands makes the interpretation more difficult. In the presence of faint as well as strongly staining bands, it is difficult to know whether each product represents a different locus or is a result of intergenic interactions, or is just a 'ghost' band. The interpretation of such complex patterns is perhaps possible only after formal genetic analysis or progeny tests. Only an appropriate genetic analysis could allow the distinction to be made between different forms of enzymes that are allozymes or isozymes. This is particularly difficult in this case where these phenotypes are monomorphic.

Essentially, the cultivated accessions have been found uniformly monomorphic for all the gene loci involved in the seven isozyme systems studied. The gene loci for MDH and ME, and two fo the lci in PGD are apparently same in the cultivated species and its supposed progenitor *C. senegalensis*. The two gene loci of ADH in the cultivated species have also been found the same in *C. senegalensis* in the rare phenotype. In GOT, the cultivated species and *C. senegalensis* appear the same for the activity Zone II. In PGI, all the bands in activity Zone I occupy the same position in both the cultivated species and *C. senegalensis* although there are differences in the intensity of enzyme activity. The enzyme activity corresponding to Zone II in PGI is also partly similar in the cultivated species and *C. senegalensis*. On the other hand, the two wild species together express the same phenotype for the gene loci involved in MDH, IDH, PGD, ADH and ME. There is some similarity in the banding patterns between the two wild species for PGI and GOT also.

Thus, the overall picture indicates that while there have been some changes in the isozyme phenotypes during the process of domestication from the progenitor species, *C. senegalensis*, to its derivative domesticate, *C. tetragonoloba*, the indicated similarities in the two wild species suggest that the geographical separation of *C. serrata* in south-western Africa from the *C. senegalensis* of northern Africa has perhaps not brought about many differences at the level of isozymes.

The electrophoretic results in other diploid annual plant species related as progenitor and derivative have suggested that the genome of each derivative species was extracted from the repertoire of genetic polymorphisms already present in its progenitor (Gottlieb, 1981). Thus, the evolution of the cultivated *C. tetragonoloba* from *C. senegalensis* as a result of domestivation, and the differentiation between *C. senegalensis* and *C. serrata* as a result of geographical separation, is supported from the evidence of similarities in isozyme banding patterns. Minimal genetic divergence between two tomato species (Rick *et al.*, 1976) and between various animal species (Sene and Carson, 1977; Nevo and Cleve, 1978) in the electrophoretic data has also been reported. Gottlieb (1981) has indicated that it may be that differences between species do not involve electrophoretically detectable differences at large number of single genes, and Wilson *et al.* (1974) have postulated that the differences between species are rather the changes in regulatory sequences. Also the genus *Cyamopsis* is a self-compatible annual, and autogamy has often been associated with accelerated species formation in many annual groups (Grant, 1963). In at least one instance (*Tetramolopium*), speciation apparently has been rapid, with morphological divergence

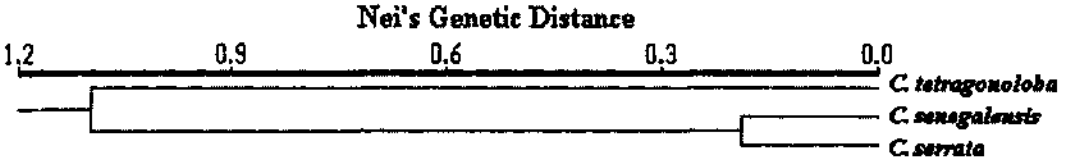

Fig. 3. UPGMA dendrogram based on allozyme variations depicting the relationships among *C. tetragonoloba, C. serrata* and *C. senegalensis*

accompanying radiation into different habitats yet with little divergence at isozyme loci (Crawford, 1983). The case of *Cymaposis* appears the same.

Relationships among *Cyamopsis* species

The allozyme variation observed within and among the three *Cyamopsis* species as well as the UPGMA-dendrogram (Fig. 3) supports the earlier view that *C. tetragonoloba* is closer to *C. senegalensis* than to *C. serrata*. The genetic distance between *C. tetragonoloba* and *C. senegalensis* was 0.63 as against a distance of 1.56 between *C. tetragonoloba* and *C. serrata*. The zymogram presented in Fig 1 also substantiates this evidence. These findings are comparable to the earlier views (Hymowitz, 1972) based on the patterns of variations observed for morphological traits in *C. tetragonoloba, C. senegalensis* and *C. serrata*. However, in the present study, at these ten isozyme loci the cultivated species appear to have diverged from its putative ancestor species.

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REFERENCES

Ayala, F. J. 1982. The genetic structure of species. *In*: R. Milkman (ed.), Perspectives on Evolution. Sinauer Associates Inc., Sunderland, Mass, USA, p. 60-82.

Catty, J. P. and M. T. Jackson. 1989. Starch Gel Electrophoresis of Isozymes: A Laboratory Manual. School of Biological Sciences. The University of Birmingham, Birmingham, UK. (Unpublished).

Chen, Weiping 1985. Isozyme studies of *Solanum aethiopicum* L. and related species. M.Sc. Thesis, The University of Birmingham, Birmingham, U.K.

Coyne, J. A., A. A. Felton and R. C. Lewontin. 1978. Extent of genetic variation at a highly polymorphic esterase locus in *Drosophila pseudoobscura*. *Proc. Nat. Acad. Sci. (USA)* 75: 5090-5093.

Coyne, J. A., W. F. Eanes, J. A. M. Ramshaw and R. K. Koehn. 1979. Electrophoretic heterogeneity of glycerophosphate dehydrogenase among many species of *Drosophila*. *Syst. Zool.* 28: 164-175.

Crawford, Daniel J. 1983. Phylogenetic and systematic inferences from electrophoretic studies. *In*: S. D. Tanksley and T. J. Orton (eds), Isozymes in Plant Genetics and Breeding, Part A. Elsevier Science Publishers, B. V. Amsterdam, Netherlands, p. 257-287.

Dabas, B. S., T. A. Thomas, Ranjna Nagpal and D. P. Chopra. 1989. Catalogue on Guar (*Cyamopsis tetragonoloba* (L.) Taub.) Germplasm. National Bureau of Plant Genetic Resources, New Delhi, India.

Gillett, J. B. 1958. *Indigofera (Microcharis)* in trodpical Africa with the related genera *Cyamopsis* and *Rhynchotropis*. *Kew Bull. (Addl. Ser.)* 1: 1-166.

Gillett, J. B. 1971. 'Indigofereae'. *In*: Flora of tropical east Africa, 'Leguminosae', part 3 and 4. p. 212-330, 1013-1041.

Gottleib, L. D. 1979. The origin of phenotype in a recently evolved species. *In*: O. T. Solbrig, S. Jain, G. B. Johnson and P. Raven (eds), Topics in Plant Population Biology, Columbia Univ. Press, New York, USA, p. 264-286.

Gottlieb, L. D. 1981. Electrophoretic evidence and plant populations. *In*: L. Reinhold, J. B. Harborne and T. Swain (eds), Progress in Phytochemistry, Pergamon Press, Oxford, U.K, 7: 1-46.

Grant, V., 1963. The Origin of Adaptations, Columbia Univ. Press. New York, USA.

Hymowitz, T. 1972. The trans-domestication concept as applied to guar. *Econ. Bot.* **26**: 49-60.

Hymowitz, T. and R. S. Maltock. 1963. Guar in the United States. *Okla Agr. Exp. Sta. Bull.* B 611 : 1-34.

ICAR 1970. Pulse Crops in India. Indian Council of Agricultural Research, New Delhi, India.

Kephart, Susan R. 1990. Starch gel electrophoresis of plant isozymes : a comparative analysis of techniques, *Amer. J. Bot.* 77(5): 693-712.

Linnaeus, C. 1767. Mantissa Plantarum 1767 and 1771. Tomus VII Historiae naturalis Classca. J. Cramer, Weinheim, Hafner Publication Company, New York, USA.

Nei, M. 1972. Genetic distance between populations. *Am. Natur.*, **106**: 283-292.

Nevo E. and H. Cleve 1978. Genetic differentiation during speciation. *Nature* 275: 125

Rhoades, D. and R. Cates, 1976. Toward a general theory of plant-herbivore chemistry. *Recent Adv. Phytochem.* **10**: 168-213.

Rick, C. M., E. Kesicki, J. F. Fobes and M. Holle. 1976. Genetic and biosystematic studies on two new sibling species of *Lycopersicon* from interandean Peru. *Theor. Appl. Genet.* 47 : 55-68.

Rohlf, F. J. 1992. NTSYS-pc Numerical taxonomy and multivariate analysis system-version 1 80. Exeter Software, New York, USA, p. 13-10.

Sene, F.M. and H. L. Carson, 1977. Genetic variation in Hawaiian *Drosophila*. IV. Allozymic similarity between *D. silvestris* and *D. heteroneura* from the island of Hawaii. *Genetics* 86: 187-198.

Senn, H. A. 1938. Chromosome number relationships in Leguminosae. *Bibliographia Genetica* 12: 175-336.

Torre, da A. R. 1960. Taxa Anglonesia nova vel minus congnita-1. *Mem. Junta invest. Ultramar (2a ser.)* **19**: 23-66.

Whistler, R. K. and T. Hymowitz. 1979. Guar : Agronomy, Production, Industrial Use and Nutrition. Purdue University Press, West Lafayette, Indiana, USA.

Whyte, R. O., G. Nilsson-Leissner and H. C. Trumble. 1953. Legumes in Agriculture. FAO Agricultural Studies No. 42. Food and Agricultural Organisation of the United Nations, Rome, Italy.

Wilson, A. C., L. R. Maxson and V. M. Sarich 1974. Two types of molecular evolution-evidence from studies of interspecific hybridisation. *Proc. Nat. Acad. Sci. (USA)* 71 (7): 2843-2847.

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ANALYSIS OF GENETIC DIVERGENCE OF SUNFLOWER INBRED LINES (*Helianthus annuus* L.)

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Genetic divergence of 77 inbred lines of sunflower for 11 characters were assessed by using Mahalanobis's D^2 statistic. The genotypes were grouped into 10 clusters. No relationship between geographic origin and genetic diversity was observed. Based on inter cluster distance, maximum genetic diversity was observed between genotypes belonging to cluster II and VII. Hence, the genotypes belonging to above clusters will be very useful in the crossing programme and may result high amount of heterosis. Characters viz., plant height, number of filled seeds per head and head diameter contributed more towards genetic divergence.

Key words : Sunflower, genetic divergence

Sunflower is one of the important oilseed crop. Hybrid development is of much value for increasing the production and selection of parents based on the genetic divergence is a pre-requisite in a hybrid programme. Asthana and Pandey (1980) reported that the geographic diversity may not necessarily be related with genetic divergence. Therefore, the selection of lines for breeding should be based on genetic divergence rather than geographical diversity. For the choice of diverse parents, multivariate analysis using Mahalanobis's D^2 statistic has been extensively used as a quantitative measure of genetic divergence. It is a powerful tool in quantifying the degree of genetic divergence among parents. Though sunflower has number of desirable features, the yield is low and unstable in India which necessiates the improvement by adopting suitable breeding strategies. In this direction, the present study deals with genetic divergence in inbred lines for selection of appropriate germplasm material in sunflower breeding programmes.

MATERIALS AND METHODS

The present investigation consisted of 77 inbred lines developed from Directorate of Oilseed Research, Hyderabad were grown in 2 rows of 5 m length with a spacing of 60 × 30 cm in a randomised block design (R.B.D.) with 2 replications at College of Agriculture, Rajendranagar, Hyderabad during *rabi*, 1997. Observations were recorded on 5 random plants on 11 characters viz., plant height, days to 50 per cent flowering, stem girth, no. of leaves per plant, head diameter, days to maturity, no. of filled seeds per head, no. of unfilled seeds per head, test weight, oil per cent and seed yield. To study genetic diversity the data were analysed by using Mahalanobis's D^2 statistic as described by Rao (1952). The genotypes were grouped into different clusters according to Toucher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant

differences exists between genotypes for yield, yield component characters. All the 77 genotypes were grouped into 10 clusters (Table 1). The cluster I comprising of 19 genotypes was the longest followed by cluster VII and VIII. Remaining clusters had 3-8 genotypes. These genotypes were

Table 1. Distribution of 77 germplasm stocks of sunflower in different clusters

Cluster	No. of genotypes	Genotypes						
I	19	DRM82	DRM69	DRM59	DRM63	DRM5	DRM6	DRM12
		DRM60	DRM71	DRM86	DRM78	DRM3	VND NB10	DRM77
II	3	DRM7	DRM1	DRM68				
III	7	DRM85	DRM93	DRM11	DRM83	DRM81	DRM91	DRM15
IV	6	GP11949	R-17	R-856	IV55NB-13	VNDNB7	VNDNB2	
V	4	ARM241	ARM249	88-2	GP11937			
VI	3	X-15NB-5	X-15NB-2	P-356-R				
VII	12	R-272-II	234-B	LIB02M-14	GP11669	R-298	RHA271	R- 265
		LIB02M-1	LIB02M-3	LIB02M-6	6D-1	RHA859		
VIII	10	GP1529 88-4	GP11288 88-9	GP11519 88-8	GP1545	GPI3001	GPII499	R-272-1
IX	8	GPI255 ARM238	ARM250	ARM247	ARM244	ARM240	ARM242	ARM245
X	5	GP12324	ARM239	GPI594	ARM248	ARM246		

Table 2. Average intra and inter cluster distance (D values)

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	23.382 M	30.313 H	28.568 M	36.792 H	46.024 H	41.790 H	45.674 H	40.107 H	40.816 H	48.739 H
II		33.494 H	39.762 H	48.296 H	59.131 H	58.039 H	60.621 H	47.283 H	53.244 H	57.714 H
III			25.027 M	41.548 H	46.162 H	41.556 H	45.334 H	44.495 H	43.302 H,H	50.441
IV				H	31.321 H	40.977 H	35.822 H	38.823 H	44.865 H	39.631 H
V					31.109 H	40.752 H	35.142 H	43.617 H	36.112 H	41.751 H
VI						26.977 M	35.303 H	53.455 H	45.932 H	58.786 H
VII							30.410 H	49.100 H	39.807 H	51.382 H
VIII								40.260 H	36.803 H	39.915 H
IX									26.556 M	35.546 H
X										30.456 H

H : Highly divergent (above 30); Moderately divergent (23-30); M

generally extraordinary for one or more characters which made them divergent from the other clusters. Maximum distance (60:621) was observed between cluster II and VII (Table 2) followed by II and V (59.131), while the clusters I and II were the lowest (28.568).

The cluster means (Table 3) indicated appreciable variation among various clusters. An examination of cluster means revealed that the clusters VI (6.95) and VII (6.74) were low seed yielders and cluster V recorded maximum seed yield per plant. For plant height (159.62 cm), stem girth (2.00 cm), no. of leaves per plant (26.33) and unfilled seeds per head (151.92) cluster X recorded maximum and cluster V recorded maximum for days to 50% flowering and days to maturity. The genotypes grouped into cluster III recorded maximum test weight (4.98 gm) and cluster VI recorded highest oil per cent (39.60).

Table 3. Mean of cluster from 77 germplasm lines of sunflower for 11 characters

Cluster	Plant height	Days to 50% flowering	Stem girth	No. of leaves per plant	Head diameter	Days to maturity	No. of filled seeds/head	No. of unfilled seeds/head	Test weight	Oil per cent	Seed yield/plant
I	94.984	54.816	1.745	19.592	12.006	77.237	387.984	85.918	4.022	34.656	15.654
II	84.433	55.167	1.793	19.300	14.533	77.167	493.958	98.375	4.053	32.593	20.030
III	92.950	55.429	1.793	18.314	11.429	77.643	279.018	77321	4.988	33409	13.957
IV	99.508	59.500	1.339	19.158	9.105	81.417	358.250	63.000	3.311	36.539	11.577
V	132.150	67.625	1.793	22.988	10.565	89.625	351.063	134.313	3.537	31.300	12.345
VI	93.317	57.333	1.315	19.367	8.297	79.000	195.583	79.292	3.533	39.660	6.952
VII	115.042	60.333	1.645	18.508	8.743	83.917	235.552	66.978	2.882	32.501	6.742
VIII	130.000	62.800	1.775	23.075	12.300	84.950	465.187	107.379	4.228	32.156	19.901
IX	142.400	64.688	1.778	25.163	10.892	86.250	402.234	71.313	3.956	35.122	15.798
X	159.620	64.600	2.005	26.330	13.251	87.000	475.475	151.925	4.461	32.860	21.298

In the present study, maximum inter cluster distance was existed between cluster II and VII. Hence crossing between genotypes belonging to these clusters may result in high heterosis. The characters which contributed maximum genetic divergence (Table 4) are the plant height (23.92%), filled seeds per head (20.78%), head diameter (18.22%). These results are in agreement with the findings of Yadav *et al.* (1980). Among the studies on evolution on understanding the effect of change in breeding system on genetic divergence between populations would be of considerable interest (Murthy and Arunachalam 1996; Singh *et al.*, 1980)

In the present study, it appears that the clusters II, VIII and X had high mean performance of the desirable characters (no. of filled seeds, head diameter and test weight). These clusters were very useful in the crossing programmes of sunflower to develop a good hybrid. Several reports on sunflower path analysis revealed that the characters number of filled seeds per head, head diameter and test weight were directly correlated with seed yield per plant. Hence, breeder should select the parents from these clusters which are having high mean performance of above characters and those parents will be very useful in breeding programmes to develop with yielding hybrids in sunflower.

Selection of genotypes from divergent clusters, might prove to be more useful, if these are also selected with due consideration of *per se*

performance. However looking at subjective and arbitrary nature of grouping with D^2 statistic (Singh and Ramanujan, 1981) and depending on breeders interest more than one genotype from a cluster could be selected for hybridization programme.

REFERENCES

Asthana, A. N. and V. R. Pandey. 1980. Genetic divergence in linseed. *Indian J. Genet.* **40**: 247-250.

Murthy, B. R. and V. Arunachalam. 1996. The nature of divergence in relation to breeding system in some crop plants. *Indian J. Genet.* **26A**: 188-198.

Rao, L.R. 1952. Advanced statistical methods in biometrical research. John Willey and Sons, New York.

Singh, S. P. and S. Ramanujam. 1981. Genetic divergence and hybrid performance in *Cicer arietinum* L. *Indian J. Genet.* **41**: 268-276.

Yadav, R. K., B. K. Behl and T. P. Yadav. 1988. Assessment of diversity among sunflower collections. *Crop Improvement* **15**: 160-162.

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HIERARCHICAL CLUSTER ANALYSIS IN EXOTIC INTRODUCTIONS OF MULBERRY

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The natural variability of germplasm samples is often very high and their crossing offers a simple way to recover large number of new combinations. Fifty-six exotic entries of different geographic origin varying in their yield potential were subjected to hierarchical cluster analysis to classify the variability. Twenty one agronomic traits viz., leaf yield, stomatal frequency, stomatal size, cuticle thickness, total leaf thickness, palisade to spongy parenchyma ratio, length of the root, dry weight of the root, root to shoot ratio by length and by weight, moisture retention capacity, moisture percentage, number of primary branches, length of the shoot, inter-nodal distance, number of leaves per meter length of the shoot, leaf area, weight of 100 leaves, percentage of sprouting and rooting and total chlorophyll content were measured. Studies revealed that 56 mulberry entries fell in five clusters. Considerable genetic diversity was observed among the entries studied. On the basis of inter and intra-cluster distances, parents could be selected for breeding purpose.

Key words : Mulberry, agronomic traits, hierarchical clustering, genetic divergence

Hanson (1972) stressed the importance of diverse germplasm pools in increasing the genetic diversity for selection and in improving the frequency of genes for potentially valuable plant characteristics. The efficient utilisation of genetic resources required that, they be adequately classified and evaluated. Germplasm collections that have been established for many crop species generally contain a large number of entries. Studies on several crops have pointed out that an incredible amount of variation occurs in these collections (Ashri 1973; Narayan and Macfield 1976; Hussaini *et. al.*, 1977; Camussi, 1979 and Tolbert *et al.*, 1979). All the desirable materials cannot easily be evaluated or located from large collections (Holden, 1984). Only a relatively small number of the collection has been fully described for morphological and physiological characters in mulberry (Susheelamma and Jolly, 1986). This is an important prerequisite for effective and efficient utilization of germplasm collections in breeding programmes (Duvick, 1884).

Since, univariate approaches to exploit data on the germplasm lack precision principally because of G × E interactions, hierarchical cluster analysis could become a useful tool for the management of the variation and also to estimate the segregation potential of germplasm in crosses (Peters and Martinelli, 1989). Multivariate statistical techniques have been suggested to measure genetic and phenotypic divergence among entries to aid in planning crosses among genotypes belonging to different clusters (Bhatt, 1970; Camussi *et al.*, 1983).

The multivariate approach increases the precision and at the same time decreases the complexity introduced otherwise by increasing replications of estimates for a given variable or by increasing the number of variable and decreasing the characteristics of the sample. The established computer algorithms developed in the field of multivariate statistics allow the mixing of both qualitative and quantitative data thereby, facilitating the usage of all available data on an entry. A difficulty in using this statistics is the choice of the algorithm. Sokal (1986) and Rohlf Wooten (1988) have reported that UPGMA clustering analysis (group average or average linkage) generally yield most accurate results, although there are other reports stating that the results obtained from six of the most commonly used methods were nearly identical (Lebeda and Jendrulik, 1987).

Mulberry is a tropical East Asian genus distributed in temperate, sub-tropical and tropical regions of the world. It is distributed to north and west Asia, European, South and Central American continents of the world (Sastry, 1984). Fifty-six germplasm entries representing 12 countries spread over Europe, Asia, Australia, South America and the Far East, being maintained at the germplasm bank, CSRTI, Mysore, India were studied with respect to twenty-one agronomic traits. The entries were clustered on the basis of their degree of relatedness with regard to twenty-one agronomic traits measured from the Germplasm samples, enabling to use them with more accuracy in directed breeding programme.

MATERIALS AND METHODS

In the present study, fifty-six entries collected from diverse geographic countries viz., Japan, Bangala Desh, Indonesia, Myanmar, China, erstwhile U.S.S.R., France, Italy, Australia, Paraguay and Brazil were critically analysed for twenty-one agronomic traits. All the germplasm entries, which were utilised for evaluation, were maintained in the field under identical conditions at Central Sericultural Research and Training Institute, Mysore, India. The spacing maintained between rows and plant to plant was 150 cm and 120 cm respectively. The field was maintained following package of practices as recommended by Krishnaswami (1978). All the plants were pruned during the month of June and were allowed to grow. After 70 days of pruning (i.e., during August-rainy season), five plants were selected at random and growth observations contributing to yield were recorded. During the subsequent two seasons of the year (December-Winter season, April-Summer season) yield attributes viz., length of the shoot, inter-nodal distance, number of primary branches per plant, 100 leaves weight, number of leaves per meter length of the shoot, and leaf yield were further recorded. For stomatal studies, 5^{th}, 6^{th} and 7^{th} leaves from the top of three months old shoots of randomly selected plants from each entry were collected. Stomatal impressions were peeled out and frequency was determined. Twenty microscopic fields were observed for each entry. The average length and breadth of stomatal aperture was determined on 20 measurements from all the three leaves for final consideration. For total leaf and cuticle thickness, free hand sections of tender, medium and mature leaves were used. Thickness of leaf, cuticle and ratio of palisade parenchyma to spongy parenchyma were measured (in μm). In all the cases, a minimum of 20 observations were taken during three seasons and the mean of calculated. To determine the moisture content (MC) and moisture retention capacity (MRC), 100 leaves from all the age groups were collected at 9 A.M. in polythene bags and fresh weight (FW) noted. Thereafter, the leaves were kept in the open at laboratory temperature for 12h and the weight (IW) was recorded. Then the leaves were dried in oven for 72 hr. at 80°C for complete dryness and dry weight (DW) was recorded. Moisture content

Table 1. Mean and range estimates of the twentyone agronomic traits in fiftysix exotic introductions used for clustering analysis

Variable	Mean	Std. Dev.	Minimum	Maximum	C.V (%)
AYPY	2.60	1.33	0.20	5.31	51.15
STOFRE	636.60	189.69	306.46	1244.00	29.00
STOSI	206.20	43.66	118.57	313.00	21.17
CUTTHI	4.85	2.20	1.67	10.47	45.34
TOTHI	152.81	25.24	114.97	247.90	16.51
PALI	1.38	0.34	0.88	2.50	25.34
ROOL	23.57	14.44	5.09	62.00	61.37
DWROOT	1.78	1.74	0.10	8.64	97.37
RSRL	0.91	0.59	0.20	3.33	64.96
RSRW	0.45	0.14	0.08	0.80	31.80
MRC	60.21	4.64	47.73	68.28	7.71
NPBP	12.27	6.93	2.00	37.00	56.49
SHOOTL	153.96	53.68	57.60	303.68	34.87
IND	4.14	0.80	2.25	5.86	19.29
NLPML	24.35	4.46	17.00	36.00	18.31
LAREA	154.66	22.72	105.38	220.25	14.69
W100L	455.12	191.53	137.46	940.00	42.08
MP	69.85	3.04	62.28	76.86	4.35
SPRP	34.56	27.46	2.00	96.60	79.44
ROOTP	37.00	27.71	2.00	95.40	74.89
TCC	2.25	0.43	1.49	3.62	18.97

AYPY: Avg. leaf yield; STOFRE : Stomatal frequency; STOSI : Stomatal size; CUTTHI : Cuticle thickness; TOTHI : Total thickness of leaf; PALI : Palisade parenchyma ratio; ROOL : Length of the root; DWROOT : Dry Wt. of the root; RSRL : Root to shoot ratio by length; RSRW : Root to shoot ratio by Wt.; MRC : Moisture retention capacity; NPBP: No. of primary branches; SHOOTL : Shoot length; IND : Internodal distance; NLPML : No. of leaves/Mtr. of length; LAREA : Leaf area; W100L : Wt. of 100 leaves; MP : Moisture percentage; SPRP : Sprouting percentage; ROOTP : Rooting percentage; TCC : Total chlorophyll content.

(MC) and moisture retention capacity (MRC) was calculated using the formula :

$$MC = \frac{FW - DW}{FW} \times 100$$

$$MRC = \frac{IW - DW}{IW} \times 100$$

Table 2. Analysis of variance for 21 agronomic variables as realised from the operation of SPSS/PC+" Quick cluster programme". (The programme was executed after Z-transformation of the estimates of variables)

Variable	Cluster MS	Error MS	DF	F	Prob
ZAYPY	0.8206	1.0141	51.0	0.8092	0.525
ZSTOFRE	3.7392	0.7852	51.0	4.7623	0.002
ZSTOSI	1.4261	0.9666	51.0	1.4754	0.223
ZCUTTHI	7.1077	0.5210	51.0	13.6434	0.000
ZTITHI	3.6487	0.7923	51.0	4.6055	0.003
ZPALI	1.4727	0.9629	51.0	1.5294	0.208
ZROOL	4.6083	0.7170	51.0	6.4271	0.000
ZDWROOT	8.3118	0.4265	51.0	19.4873	0.000
ZRSRL	2.9771	0.8449	51.0	3.5235	0.013
ZRSRW	3.2891	0.8205	51.0	4.0088	0.007
ZMRC	5.8297	0.6212	51.0	9.3845	0.000
ZNPBP	4.5719	0.7199	51.0	6.3512	0.000
ZSHOOTL	7.6653	0.4772	51.0	16.0620	0.000
ZIND	4.6828	0.7112	51.0	6.5848	0.000
ZNLPML	4.0830	0.7582	51.0	5.3851	0.001
ZLAREA	2.6809	0.8682	51.0	0.0880	0.024
ZW100L	7.1488	0.5177	51.0	13.8076	0.000
ZMP	1.7428	0.9417	51.0	1.8507	0.134
ZSPRP	7.8581	0.4621	51.0	17.0049	0.000
ZROOTP	8.1702	0.4376	51.0	18.6690	0.000
ZTCC	1.1903	0.9851	51.0	1.2083	0.319

For root proliferation studies, equal sized cuttings from mature shoots of all the accessions were planted in earthen pots of 80 × 40 × 40 cm (height × breadth × width) dimension and were allowed to grow for three months. These were watered once in four days. The three months saplings were uprooted without damaging the root system. Roots were washed thoroughly and the length of the root and shoot, and the fresh weight of the root and shoot were recorded which later

were dried for 72 hr. at 80°C in oven for complete dryness and weight of dried roots and shoots were recorded separately. Root to shoot ratio by length and weight were calculated. To determine the percentage of sprouting and rooting, one hundred cuttings prepared out of ten months old shoots were taken from each entry and planted separately in nursery beds. After 20 days of planting, sprouting percentage was recorded and the percentage of rooting was recorded after three months of planting on the basis of survival rate. The data on leaf yield were collected for two years from five plants, which were selected at random. Total chlorophyll content was estimated following the colorimetric method of Arnon (1949). Leaf area was recorded by using LICOR-3100 leaf area meter. All the observations were recorded on twenty-one agronomic traits were further analysed.

Clustering methodology

The data on the twenty-one characters computed and agglomerative hierarchical clustering was done using SPSS/PC + software (Microsoft ware Dept. SPSS Inc., Chicago III), employing the method of average linkage between groups (Romesburg, 1984) under UPGMA (unweighted pair-group method using arithmetic averages). The clustering is based on the squared Euclidean distances with distance $(x, y) = \Sigma_i (x_i - y_i)^2$. The average linkage between groups is taken as the average of the distance between all pairs of cases with one member of each group.

RESULTS AND DISCUSSION

Five groups were obtained through clustering, based on twenty-one variables. The degree of variability is evident from the data presented in Table-1. Among the variables studied, maximum variability was observed in case of dry weight of root (CV % 97.37) followed by percentage of sprouting (CV% 79.44) and percentage of rooting (CV% 74.89). Minimum variability was recorded for moisture percentage (CV% 4.35). A persual of Table-1 indicates, that leaf yield per plant per year ranged between 0.20-5.31 kg in different entries studied. Stomatal frequency, stomatal size, cuticle thickness, total leaf thickness and palisade parenchyma to spongy parenchyma ratio ranged from 306.46-1244 per mm^2, 118.57-313 μm^2, 1.67-10.47 µm, 114.97-247.90 µ, and 0.88-2.50 respectively. Length of the root, dry weight of the root, moisture retaining capacity and moisture content ranged between 5.09-62.00 cm, 0.10-8.64 g, 47.73-68.28 per cent and 62.28-76.86 per cent respectively, where as number of primary branches per plant, inter-nodal distance, 100 leaves weight and total chlorophyll content ranged between 2.00-37.00, 2.25-5.86 cm, 137.46-940.00 g and 1.49-3.62 mg/g fresh weight respectively.

Application of quick clustering

The quick cluster provision of SPSS/PC + was used with a five cluster command. The analysis of variance for the twenty-one agronomic variables and the final cluster centers for these variables are presented in Table 2. Except in the case of average leaf yield (AYBY), stomatal size (STOST), ratio of palisade parenchyma to spongy parenchyma (PALI), moisture percentage in leaf (MP) and total chlorophyll content of the leaf (TCC), in all the other variables the cluster variance was found to be substantially higher than the error variance. A persual of Table- 4 indicates that cluster 4 has the highest indices for leaf yield (AYPY), length of the root (ROOL), dry weight of the root (DWROOT), inter-nodal distance (IND), whereas, cluster 3 has the highest indices for 100 leaves weight (W100L), palisade parenchyma to spongy parenchyma ratio (PALI) and total chlorophyll content (TCC). On the other hand, cluster-2 has the highest indices for moisture percentage (MP), moisture retention capacity (MRC), number of primary branches per plant (NPBP) and root to shoot ratio by length (RSRL). Cluster-1 has the highest indices for total

Table 3. Result of quick cluster with five cluster command showing final cluster centers for twentyone variables (With z-transformation) as realised for five clusters

Cluster	ZAYPY	ZSTOFRE	ZSTOSI	ZCUTTHI
1	–0.0188	0.4058	–0.2503	1.2383
2	–0.3973	1.2135	–0.6447	0.0095
3	0.1957	0.0813	–0.1313	–0.1679
4	0.6974	0.0777	0.0948	–0.8123
5	–0.1695	–0.5832	0.3824	–0.5507
Cluster	ZTOTHI	ZPALI	ZROOL	ZDWROOT
1	0.7814	–0.1223	–0.4664	–0.7144
2	0.6040	–0.2495	0.8340	–0.0987
3	–0.1207	0.4991	–0.4638	–0.1383
4	–0.3553	–0.4730	1.6334	2.9319
5	–0.4789	–0.1989	0.2624	0.1549
Cluster	ZRSRL	ZRSRW	ZMRC	ZNPBP
1	0.0499	–0.3385	–1.0560	0.1583
2	1.4466	–0.8341	1.0031	1.2572
3	–0.4625	–0.3220	0.4441	–0.7605
4	–0.0697	0.5432	0.7377	0.8260
5	0.0587	0.5630	0.0198	0.1301
Cluster	ZSHOOTL	ZIND	ZNLPML	ZLAREA
1	1.2107	0.7086	–0.6426	0.3895
2	0.3757	0.3512	–0.4804	–0.2715
3	–0.7724	–0.7370	0.7201	0.2764
4	–0.5767	0.9774	–0.7511	0.7338
5	–0.1577	–0.0879	0.0504	–0.5300
Cluster	ZW100L	ZMP	ZSPRP	ZROOTP
1	–0.9578	0.0008	0.6140	0.6847
2	–0.8575	1.1221	0.5623	0.6189
3	0.9207	0.0971	–0.9298	–0.9555
4	0.2274	–0.0272	1.9463	1.8537
5	0.0234	–0.2985	–0.0597	–0.0825
Cluster	ZTCC			
1	0.1374			
2	–0.0904			
3	0.3645			
4	–0.4551			
5	–0.294			

thickness of leaf (TOTHI), cuticle thickness (CUTTHI) and length of the shoot (SHOOTL). The cluster membership is presented in Table 4. Five clusters have clearly been identified. The cluster-1 comprises thirteen genotypes viz, three entries from Japan, three from Indonesia, five from Pakistan and remaining two entries, one each from Myanmar and Bangala Desh. Cluster-2 comprises four entries, one each from Japan, Indonesia, Paraguay and Australia. Cluster-3 has sixteen entries. Out of them, fourteen are from Japan and remaining two from Brazil and France. Cluster-4 has the minimum membership of three entries, one each from Japan, China and France. Cluster-5 has the maximum entries consisting of twenty genotypes viz., eleven belonging to Japan, two from erstwhile U.S.S.R., two from Bangala Desh, two from Paraguay and of the remaining three, one each from China, Italy and Myanmar. It is also clear from the data in Table-5, that all the high yielding genotypes have fallen in Cluster-3 and low yielding genotypes in clusters-1 and 2. However, Japanese genotypes were found in all five clusters and genotypes from Indonesia, France, Myanmar and Paraguay in more than one cluster. The inter-cluster distances are presented in Table 5. It is evident that the diversity is the highest between the clusters 3 and 4 as reflected by the inter-cluster distance of 6.46 followed by the distance between clusters 1 and 4 (6.0675).

The present study pointed out to the existence of enormous variability in the germplasm and establishes that, in order to manage collections more effectively, the clustering method can be employed. The presence of entries from Japan, Myanmar, erstwhile USSR, China, Italy, Bangala Desh and Paraguay in a single cluster suggests that genetic diversity in not directly related to geographic distribution although; it is generally associated with geographic diversity. Similar findings have been reported by Singh and Singh (1979), Singh and Gupta (1968) and Murthy

Table 4. Number of entries by country of origin in an exotic collection of Mulberry. The five cluster groups are based on quick cluster with five cluster command

Acc. No.	Origin	Cluster	Distance	Acc No.	Origin	Cluster	Distance
246	Pakistan	1	0.996	168	Japan	3	4.985
245	Japan	1	2.880	128	Japan	3	6.021
247	Pakistan	1	3.254	126	Japan	3	6.138
248	Pakistan	1	3.479	101	Japan	3	6.436
239	Myanmar	1	4.321	160	Japan	3	6.536
250	Pakistan	1	4.364	122	Japan	4	1.119
233	Indonesia	1	4.418	104	China	4	5.512
236	Indonesia	1	4.565	132	France	4	5.884
257	Japan	1	5.268	134	USSR	5	1.285
178	Bangala Desh	1	5.848	131	Myanmar	5	4.299
235	Indonesia	1	6.091	167	Japan	5	4.360
249	Pakistan	1	6.330	176	Itali	5	4.383
231	Japan	1	6.778	164	Japan	5	4.471
136	Japan	2	0.918	174	Japan	5	4.570
125	Paraguay	2	5.247	184	Japan	5	4.575
220	Australia	2	5.558	129	Japan	5	4.657
234	Indonesia	2	6.772	149	Japan	4	4.658
169	Japan	3	1.079	190	Japan	5	4.664
186	Brazil	3	2.702	189	Paraguay	5	4.695
173	Japan	3	4.325	133	USSR	5	5.178
171	Japan	3	4.325	238	Japan	5	5.330
192	France	3	4.508	124	Japan	5	5.386
127	Japan	3	4.522	180	Bangala-Desh	5	5.387
182	Japan	3	4.552	137	Japan	5	5.388
181	Japan	3	4.696	147	China	5	4.451
177	Japan	3	4.959	179	Bangala-Desh	5	5.466
183	Japan	3	4.962	191	Paraguay	5	5.521
102	Japan	3	4.963	205	Japan	5	6.954

and Arunachalam (1966). The study also confirms the superiority of multivariate approaches in studying the relationships between genotypes by bringing together genotypes, which show wide diversity in more than one character. The usefulness of the method is further realised by the fact that the agronomical, physiological and quality related traits could be taken into consideration at a time, for grouping the collections.

The groupings of collections from Bangladesh, Pakistan in 5th and 1st cluster respectively suggest the closeness among the genotypes. At the same time, the presence of entries from geographically distant and diverse countries in the same cluster indicates the fact that the correspondence between genetic divergence and geographic diversity is obscured when the species have been the object of intense breeding effort (Jain and Wu, 1977; Tolbert *et al.*, 1979). This material probably has been exchanged among breeders of different countries so that, the difference between germplasm from countries with sharply contrasting agro-ecological conditions have been consistently reduced. This might be the cause for finding genotypes from the erstwhile USSR and Bangala Desh; two geoecologically diverse countries in the same cluster. This is in confirmation with the findings of Zohary (1970) and Spagnoletti Zeuli and Qualset (1987) who reported that the geographical position does not correspond with the phenotypic grouping. The present findings

Table 5. Matrix of cluster distances as realised from quick clustering with a five cluster command

Cluster	1	2	3	4
1	0.0			
2	3.8519	0.0		
3	4.8567	5.1341	0.0	
4	6.0675	5.2356	5.4600	0.0
5	3.9456	4.1074	3.0093	4.8478

have clearly illustrated that, sampling from different clusters would be more effective in achieving great allelic diversity for hybridization, rather than confining to selection based on geographic diversity or based on limited number of many agronomical characters. Frankel and Brown (1984) have opined that computer facilitated data reduction can simplify sampling of large collections for breeding or research purpose or in establishing 'core collections' to study genetic variation.

A systematic search based on combining ability among the exotic germplasm and improved varieties is likely to uncover yet unknown yield promoting genetic resources (Frankel and Brown, 1984). Choosing parents from distant clusters showing highest cluster indices for the particular desired quantitative agronomic character would be highly beneficial in the directed breeding programme.

REFERENCES

Arnon, D. L. 1949. Copper enzymes in isolated Chloroplasts. Polyphenol oxidase in Beta vulgaris. *Plant Physiol.* 24: 1-15.

Ashri, A. 1973. Divergence and evolution in the safflower genus carithamus L. Final report, USDA. P.L 480 project. Jerusalem.

Bhatt, G. M. 1970. Multivariate analysis approach to selection of parents for hybridisation aiming at yield improvement. *Aust. J. Agric. Res.* 21: 1-7.

Cammussi, A. 1979. Numerical taxonomy of Italian population of maize based on quantitative traits. *Maydica* 24: 161-174.

Cammussi, A., Spagnoletti zeuli, P. L. and Melchiorre, P. 1983. Numerical taxonomy of Italian maize populations, Genetic distances on the basis of heterotic effects. *Maydica* 28: 411-424.

Duvick, D. N. 1984. Genetic diversity in major farm crops on the farm and in reserve. *Econ. Bot.* 38: 161-178.

Frankel, O. H. and A. H. D. Brown. 1984. Plant genetic resources today. A critical appraisal. *In*: J.H.W. Holden and J. T. Williams (ed). Crop Genetic Resources Conservation and Evaluation. Allen and Unwin Inc. Winchester, M.A.

Hanson, A. S. 1972. The biology and Utilisation of grasses, (ed) V.B. Younger and C. M. Mekell. Academic Press NT, Sanfrancisco, London, p 36.

Holden, J. H. W. 1984. The second ten years in *In*: J. H. W, Holden and J. T. Williams (ed). Crop Genetic Resources, Conservation and Evaluation. Allen and Unwin Inc. Winchester, M.A. p 276-285.

Hussaini, S. H., M. M. Goodman and D. H. Timothy. 1977. Multivariate analysis and the geographical distribution of the world collection of finger millet. *Crop Sci.* 17: 257-263.

Jain, S. K. and K. K. Wu. 1977. A note on germplasm diversity in the world collection of safflower. *Econ. Bot.* 31: 72-75.

Krishnaswami, S. 1978. Mulberry cultivation in south India. CSR & TI, Bulletin No. 1. Central Silk Board, India.

Lebeda, A and T. Jendrulek. 1987. Cluster analysis as a method for evaluation of genetic similarly in specific host parasite interaction (*Lactuca sativa - Bremia lactucae*). *Theor. Appl. Genet.* 75: 194-199.

Murthy, B. R and V. Arunachalam. 1966. The nature of divergence in relation to breeding system in crop plants. *Indian J. Genet.* 26A: 188-198.

Narayan, R. K. J. and A. J. Macfield. 1976. Adoptive responses and genetic divergence in a world collection of chick pea (*Cicer arietinum* L.). *Theor. Appl. Genet.* 47: 179-187.

Peters, J. P. and J. A. Martinalli. 1989. Hierarchical cluster analysis as a tool to manage variation in germplasm collection. *Theor. Appl. Genet.* 78: 42-48.

Rohlf, F. and M. C. Wooten. 1988. Evaluating of restricted maximum likelihood method for estimating phylogenetic trees using simulated allele frequency data. *Evolution* 2: 581-595.

Romesburg, H. C. 1984. Cluster analysis for researchers. Lifetime learning publications Belmont California.

Sastry. 1984. Mulberry varieties, exploration and pathology. *Sericologia* 24: 333-359.

Singh, R. B. and M. P. Gupta. 1968. Multivariate analysis and divergence in upland cotton. *Indian J. Genet.* 28: 151-167.

Singh, H. N. and S. B. Singh. 1979. Genetic divergence in sugarcane ISSCT 17: 1198-1202.

Sokal, R. R. 1986. Phenetic Taxonomy, Theory and methods. *Annual Rev. Ecol. Sys.* 17: 423-442.

Spagnoletti, P.L. Zeuli and C. O. Qualset. 1987. Geographical diversity for quantitative spike characters in a world collection of burum wheat. *Crop Sci.* 27: 235-241.

Susheelamma, B. N. and M. S. Jolly. 1986. Evaluation of morphological parameters associated with drought resistance in mulberry. *Indian J. Seric.* 25: 6-14.

Tolbert, D. M., C. O. Qualset, S. K. Jain and J. C. Craddock. 1979. A diversity analysis of a world collection of barley. *Crop Sci.* 19: 789-794.

Zohary. 1970. Centres of diversity and centres of origin. In Frankel, O.H. and Bennett, E. (ed) Genetic resources in plants. Their exploration and conservation. Blackwell, Oxford, England p 33-42.

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GENETIC VARIABILITY, CHARACTER ASSOCIATION AND PATH ANALYSIS OF YIELD AND ITS COMPONENT CHARACTERS IN LENTIL

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Genetic variability, character association and path analysis between yield and its contributing traits were studied in 41 genotypes of cultivated lentil. Highly significant differences between genotypes were recorded for most of the characters studied except internode length, number of seeds/pod and seed weight. High phenotypic and genotypic coefficients of variation coupled with high heritability and high genetic advance in 100 seed weight, harvest index, biological and grain yields per plant and also seeds and pods per plant indicate the predominance of additive gene effects in controlling these traits. Correlation and path coefficient analysis revealed that biological yield/plant, 100 seed weight, number of pods and seeds per plant were the most important characters for realizing improvement in grain yield in lentil.

Key words : Lentil, genetic variability, path analysis, gcv, pcv

Development of high yielding cultivars requires a thorough knowledge of the existing genetic variation and also the extent of associations among yield contributing characters. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, the estimate of heritability alone does not provide an idea about the expected gain in the next generation but it has to be considered in conjunction with genetic advance. Correlation and path analysis will establish the extent of association between yield and its components and also bring out relative importance of their direct and indirect effects and thus give a clear understanding of their association with yield. The present paper deals with the above genetic constants and character associations in 41 genotypes of lentil.

MATERIALS AND METHODS

Forty one genotypes of cultivated lentil (mostly cultivars) belonging to microsperma group of *Lens culinaris* Med. procured from different research institutes/universities of Uttar Pradesh were grown in a randomized block design with three replications at the Department of Agricultural Botany Research Farm, Ch. Charan Singh University, Meerut during rabi 1997-1998. Each genotype was evaluated in a plot of two rows of 5-m length. Observations were recorded on five random plants per genotype in each replication for 11 quantitative characters including plant height, number of leaves, pods and seeds per plant, seeds per pod, biological and grain yields per plant, seed weight and harvest index. Standard statistical procedures were followed for estimating genetic constants - phenotypic and genotypic coefficients of variation (Burton, 1952), heritability (Hanson *et al.*, 1956) and genetic advance (Johnson *et al.*, 1955). Genotypic and phenotypic correlation coefficients were calculated following Searle (1961) and path analysis following the method of Dewey and Lu (1955).

RESULTS AND DISCUSSION

A wide range of phenotypic variability was observed for almost all the characters studied. The analysis of variance recorded highly significant differences between genotypes for most of the characters studied with the exception of internode length, number of seeds/pod and 100 seed weight. This suggests that there is considerable amount of intervarietal variability in lentil.

The data on yield and its contributing traits, phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (H^2) and genetic advance (GA) are presented in Table 1. The variability estimates, in general, reveal that the phenotypic variance (PCV) was higher than the corresponding genotypic variance (GCV) for different characters though the extent of difference between the two was relatively low. The estimates of PCV and GCV indicated the existence of fairly high degree of variability for grain and biological yields, seed weight, number of pods and seeds per plant and harvest index. Moderate variability was observed for plant height and internode length. Relatively low PCV and GCV were recorded for days to maturity and seeds per pod. The genotypic coefficient of variation ranged from a minimum of 2.2 per cent for days to maturity to a maximum of 41.1 per cent for plant grain yield. The number of leaves per plant showed the highest PCV value of 49.81 in comparison to GCV of 14.69 suggesting more environmental influence on this character, which was confirmed by its low heritability. The difference between PCV and GCV was minimum for days to maturity; harvest index and 100 seed weight suggesting that these traits are least affected by environment. This observation draws support from the very high values of heritability (> 92.5) recorded for these traits (Table 1).

Since broad sense heritability includes both additive and epistatic effects, it will be reliable only when accompanied by high genetic advance. Heritability estimates along with genetic advance are more useful than heritability alone in predicting the effectiveness of selection. High estimates of heritability (> 85%) and genetic advance (> 47%) were obtained for traits like grain yield and biological yield per plant, seed weight and harvest index. Selection for these traits is likely to

Table 1. Data on mean, range and genetic parameters in 41 genotypes of lentil

S. No.	Character	Mean	Range	PCV (%)	GCV (%)	H (%)	GA	GA as % of mean
1.	Plant height (cm)	36.51	30.55-43.70	18.29	16.84	20.5	12.32	33.75
2.	Internode length (cm)	2.24	2.04-2.55	8.20	5.68	48.0	0.18	8.03
3.	Leaves/plant	114.68	72.87-149.0	49.81	14.69	8.7	10.24	8.92
4.	Days to maturity	147.93	141.0-154.0	2.28	2.20	92.5	6.44	4.35
5.	No. of pods/plant	75.21	38.0-111.2	24.75	19.32	61.0	23.37	31.07
6.	No. of seeds/plant	109.49	56.93-154.8	24.54	19.57	63.0	35.21	32.15
7.	No. of seeds/pod	1.48	1.33-1.60	5.98	3.58	35.9	0.06	4.05
8.	Grain yield/plant (g)	1.99	0.65-3.75	43.81	41.18	88.4	1.59	79.89
9.	Biological yield/plant	6.85	2.89-11.42	33.59	31.12	85.9	4.07	59.41
10.	100 seed weight (g)	1.81	0.93-3.34	31.42	30.63	95.0	1.12	61.87
11.	Harvest index (%)	28.94	19.66-46.01	23.66	23.37	97.5	13.76	47.54

H: heritability, G.A : genetic advance

accumulate more additive genes leading to further improvement of their performance and hence, these traits may be used as selection criteria. Simple selection procedures like mass selection, family selection would be effective for improvement of these traits. Moderate heritability with moderately high genetic advance was observed for number of pods and seeds per plant, which indicate that additive gene effects also govern these traits.

Moderate heritability with low genetic advance was found in respect of internode length, and number of seeds per pod indicating non-additive gene action. The heritability is being exhibited due to favourable influence of environment rather than genotype and selection for such traits may not be rewarding. Low heritability with moderate genetic advance was observed for plant height. It reveals that additive gene effects govern plant height. The low heritability is being exhibited due to high environmental effects and selection may be effective in such cases. Low heritability with low genetic advance was found in respect of number of leaves per plant indicating that this character is highly

Table 2. Phenotypic (P) and genotypic (G) correlation coefficients among eleven characters in lentil

S. No.	Character		1	2	3	4	5	6	7	8	9	10	11
1	Plant height	P	-	0.306	0.073	0.232	0.289	0.308	0.039	0.157	0.17	0.289	0.264
		G	-	0.344	0.322	0.262	0.337*	0.364*	0.03	0.163	0.172	0.314	0.298
2	Internode length	P		-	−0.002	−0.213	0.262	0.28	0.009	0.209	0.163	0.231	0.29
		G		-	0.400**	−0.31	0.284	0.328*	0.229	0.238	0.223	0.315*	0.392*
3	Leaves/plant	P			-	0.142	−0.05	−0.031	0.096	−0.004	0.035	−0.008	0.013
		G			-	0.417**	−0.238	−0.189	0.277	−0.037	0.246	−0.09	0.028
4	Days to maturity	P				-	0.007	0.028	0.125	0.093	0.197	−0.029	0.101
		G				-	0.032	0.055	0.199	0.11	0.21	−0.034	0.116
5	Pods/plant	P					-	0.971**	−0.148	0.666**	0.33*	0.466**	0.732**
		G					-	0.982**	−0.052	0.661**	0.442**	0.555**	0.756**
6	Seeds/plant	P						-	0.077	0.715**	0.395**	0.494**	0.791**
		G						-	0.137	0.713**	0.517**	0.588**	0.822**
7	Seeds/pod	P							-	0.204	0.265	0.026	0.217
		G							-	0.384*	0.460**	0.094	0.412**
8	Biological yield/plant	P								-	0.828**	0.558**	0.868**
		G								-	0.910**	0.588**	0.869**
9	100 seed weight	P									-	0.122	0.722**
		G									-	0.129	0.795**
10	Harvest index	P										-	0.433**
		G										-	0.454**
11	Plant grain yield	P											-
		G											-

**Significant at 1% level; *Significant at 5% level.

influenced by environmental effects and selection would be ineffective. Thus, expression of this trait can be modified through hybridization followed by selection. Singh and Singh (1969), Singh and Dixit (1970), Nandan and Pandya (1980), Singh (1981) and Luthra (1986) reported similar observations.

Grain yield of a crop is the result of interactions of a number of interrelated characters. Therefore selection should be based on these component characters after assessing their correlation with grain yield. Character associations reveal the mutual relationship between two characters, and it is an important parameter for taking a decision regarding the nature of selection to be followed for improvement in the crop under study. In the present investigation, plant grain yield was found to be significantly and positively correlated with number of pods and seeds per plant, biological yield per plant, seed weight and harvest index (Table 2). Therefore, these characters should be kept in mind while making selection for yield improvement in lentil. Harvest index showed positive and highly significant correlations with 100 seed weight, number of seeds and pods per plant at both genotypic and phenotypic levels and with plant height and internode length at genotypic level only. On the other hand, 100 seed weight showed positive and significant correlation with biological yield, number of seeds and pods per plant at both levels while with number of seeds per pod at genotypic level. Significant positive correlations of biological yield per plant with pods and seeds per plant; number of seeds/plant with number of pods per plant,

Table 3. Path coefficient analysis of phenotypic and genotypic correlation coefficients to determine the direct and indirect effects of different traits on grain yield in yield

S. No.	Character		1	2	3	4	5	6	7	8	9	10	CCwith GY@
1	Plant height	P	**–0.001**	0.009	0.001	0.004	0.084	–0.058	–0.004	0.095	0.031	0.102	0.264
		G	**–0.14**	0.035	0.028	0.036	–0.047	0.062	–0.019	0.177	–0.02	0.186	0.298
2	Internode length	P	0	**0.031**	0	–0.003	0.076	–0.052	0.001	0.127	0.03	0.082	0.29
		G	–0.048	**0.102**	0.035	–0.043	–0.883	0.957	–0.147	0.259	–0.026	0.187	0.392*
3	No. of leaves/plant	P	0	0	**0.01**	0.002	–0.015	0.006	0.009	–0.002	0.006	–0.003	0.013
		G	–0.045	0.041	**0.087**	0.058	0.738	–0.552	–0.178	–0.04	–0.028	–0.053	0.028
4	Days to maturity	P	0	–0.007	0.001	**0.016**	0.02	–0.005	0.011	0.056	0.036	–0.01	0.101
		G	–0.037	–0.032	0.036	**0.139**	–0.099	0.159	–0.127	0.12	–0.024	–0.02	0.116
5	No. of pods/plant	P	0	0.008	0	0	**0.291**	–0.182	–0.013	0.404	0.06	0.164	0.732**
		G	–0.047	0.029	–0.021	0.004	**–0.103**	0.863	0.033	0.719	–0.051	0.329	0.756**
6	No. of seeds/plant	P	0	0.009	0	0	0.282	**0.587**	0.007	0.434	0.072	0.174	0.791**
		G	–0.051	0.033	–0.016	0.008	–0.046	**0.917**	–0.088	0.776	–0.059	0.348	0.822**
7	No. of seeds/pod	P	0	0	0.001	0	–0.043	–0.014	**–0.49**	0.124	0.049	0.009	0.217
		G	–0.034	0.023	0.024	0.028	0.161	0.399	**–0.64**	0.418	–0.053	0.056	0.412**
8	Biological yield/plant	P	0	0.006	0	0.002	0.194	–0.134	0.018	**0.606**	0.132	0.043	0.868**
		G	–0.023	0.024	–0.003	0.015	–0.052	0.08	–0.246	**0.588**	–0.091	0.077	0.869**
9	100 seed weight	P	0	0.005	0	0.003	0.096	–0.074	0.024	0.438	**0.183**	0.153	0.828**
		G	–0.024	0.023	0.021	0.029	–0.371	0.508	–0.295	0.864	**–0.115**	0.269	0.910**
10	Harvest index	P	0	0.007	0	0	0.135	–0.092	0.002	0.074	0.079	**0.353**	0.558**
		G	–0.044	0.032	–0.008	–0.005	–0.724	0.715	–0.06	0.141	–0.052	**0.592**	0.588**

@Correlation coefficient with grain yield. **Significant at 1% level; *Significant at 5% level.

plant height and internode length; number of pods per plant and internode length with plant height; days to maturity with number of leaves per plant; and number of leaves per plant with internode length were recorded (Table 2).

Yield is the sum total of several component characters which directly or indirectly contribute to it. The information derived from the correlation studies indicates only mutual association among the characters. Whereas, path-coefficient analysis helps in understanding the magnitude of direct and indirect contribution of each character on the dependent character like grain yield. Partitioning of correlation coefficient into direct and indirect effects provides the information about the nature and magnitude of effects of other characters on grain yield. The results of the present investigation on path coefficient analysis (Table 3) reveal that characters like number of pods and seeds per plant, biological yield per plant and harvest index had maximum positive direct effect on grain yield, while number of seeds per pod and plant height had direct but negative effects. On the other hand, positive indirect effects on grain yield were realized from characters including biological yield per plant via seed weight, number of pods per plant and number of seeds per plant.

In the light of the above findings it may be concluded that improvement in characters like number of pods and seeds per plant, biological yield, harvest index and seed weight will help in improving the grain yield in lentil both directly and indirectly. Therefore, these characters should be considered for yield improvement in lentil breeding programmes.

REFERENCES

Burton, G. W. 1952. Quantitative inheritance in grasses. Proc. 6th Int. Grassland Congr. Vol. 1: 227-283.

Dewey, D. R. and K. H. Lu. 1959. A correlation and path-coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 51: 515-518.

Hanson, C. H., H. F. Robinson and R. E. Comstock. 1956. Biometrical studies of yield in segregating population of Korean lespedza. *Agron J.* 48: 268-272.

Johnson, H. W., H. F. Robinson and R. E. Comstock. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.* 47: 314-318.

Luthra, S. K. 1986. Variability, character association and genetic divergence in lentil. M.Sc. Ag. Thesis, Meerut Univ., Meerut.

Nandan, R. and B. P. Pandya. 1980. Correlation, path-coefficient and selection indices in lentil. *Indian J. Genet.* 40: 399- 404.

Searle, S. R. 1961. Phenotypic, genotypic and environmental correlations. *Biometrics* 57: 474-480.

Singh, B. and R. K. Dixit. 1970. Genetic variability and interrelationship studies on yield and other quantitative characters in lentil. *Indian J. Agric. Sci.* 39: 737-741.

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GENETIC DIVERSITY OF WEST BENGAL INDICA RICE LANDRACES USING ISOZYME AND SITE SPECIFIC PUTATIVE TRANSPOSON SEQUENCE AMPLIFICATIONS

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A study on genetic variability in indica rice landraces at both the protein and DNA levels was made using isozyme and Site Specific Putative Transposon Sequence Amplification (SSPTSA) analyses. The results showed that the level of polymorphism between the two methods varied widely, ranging from only 12.38% (isozymes) to 46.66% (SSPTSA). Genetic dissimilarity matrix between the two methods, tested by the Spearman Rank Correlation analysis, indicated a moderate correlation between isozymes and SSPTSA (rs = 0.36). It was concluded that the DNA based markers (SSPTSA) will be more useful than isozyme markers in detecting genetic diversity among the indica landraces of West Bengal.

Key words : Rice landraces, isozymes, plant transposon, genotyping, genetic diversity

Landraces are generally considered to be a rich source of genetic variation for cultivar development. Because of the ancient origin and wide spread distribution of rice, enormous numbers of landraces have been accumulated (Chang, 1976), and portions of these landraces have been collected and maintained in the form of gene banks in several national and International germplasm programs. However, there are very few reported studies designed to assess the relative richness of genetic variability in these landraces in comparison to modern cultivars.

Isozyme analysis is a valuable tool for studying genetic variation in natural population, identification of species and hybrids and to delineate clones (reviewed in Nevo, 1988a, Rajora, 1990, Linhart and Grant, 1996), providing many advantages over morphological methods. However, allozyme studies are limited by the number of enzymes and loci that can be resolved, and reveal only genetic changes in coding regions of the genome that have resulted in changed amino-acid sequences. On the other hand, transposable elements are integral components of most, if not all, genome. The majority of middle or interspersed repetitive DNA may be composed of transposons (Flavell, 1986). Few dispersed mobile DNA families were identified and found to be associated with genes in several plant species including rice (Bureau *et al.*, 1996). If the conserved domains of mobile genetic elements are amplified, they would reveal polymorphism and may be used for genotyping.

Studies comparing marker techniques in detecting genetic diversity are recently appearing (Russel *et al.*, 1997; Sun *et al.*, 1999). However, no studies on applying Site Specific Putative Transposon Sequence Amplification (SSPTSA) and

isozyme markers to the same set of individuals have been reported. Such a study would provide experimental data to verify the relative merits of the different methods and would indicate whether genetic diversity obtained by one method is similar to that obtained by other method. The objectives of our study were (i) to evaluate levels of genetic variability in indica rice landraces at both the protein and DNA levels with isozyme and SSPTSA markers; (ii) to compare the results obtained from these two methods with each other; and (iii) to determine a suitable strategy to characterize indica rice germplasm.

MATERIALS AND METHODS

Plant material

Seeds of 11 landraces and one cultivar (IR8) (listed in Table 1), procured from the Rice Research Station (CRRS), Chinsurah, West Bengal.

Table 1. Details of the rice cultivar/landraces

Code	Cultivar	Accessions
1	CB1	Chinsurah Boro-1
2	CB2	Chinsurah Boro-2
3	Bhasamanik	Chinsurah-3
4	Patnai23	Chinsurah-7
5	Rupsail	Chinsurah-13
6	Kumargore	Chinsurah-19
7	Latisail	Chinsurah-25
8	Tilakachari	Chinsurah-31
9	SR26B	Chinsurah-45
10	Matla	Chinsura
11	Jaldhi I	Chinsurah
12	IR8	Chinsurah

Extraction of protein and DNA

Crude enzymes from approximately 200 mg of 4 to 6 days old, etiolated seedlings were extracted in 400 µml of 100 mM Tris-HCl buffer, pH 6.8 and centrifuged at 15,000 rpm for 20 minutes at 4°C. The supernatant containing crude enzymes was taken for isozyme analysis. DNA was extracted from 5 to 10 days old etiolated seedlings raised in a growth chamber using a modified protocol of Walbot (1988).

Polyacrylamide gel electrophoresis and staining for isozymes

To obtain a good separation of proteins, slab gel electrophoresis was performed with 7.5 per cent polyacrylamide (Davis, 1964) in Tris-glycine buffer, pH 8.3. Gels were run at 30 mA constant current for 4 hours at 4°C. After electrophoresis, the gels were stained as per standard procedures for Esterase, Peroxidase, Superoxide Dismutase (SOD) and Alcohol Dehydrogenase (ADH) (Kephart, 1990). When the bands were visible, the gels were fixed in a solution of methanol/water/ glacial acetic acid in a ratio of 4:5:1 and photographed by placing the gels on frosted glass and providing fluorescent lights from below. Line drawings of the visible bands were made manually and the gels scanned in a Pharmacia LKB densitometric scanner (model 2210) at 632.8 nm wave length provided from a Helium Neon Laser.

Sequencing of RG104 clone

The RFLP marker RG104 (a gift from Prof. S.D. Tanksley of Cornell University, USA) was cloned from the supplied pUC8 into an expression vector (pBluescript II), at the *Pstl* site and was sequenced using the (-29) universal primer by dideoxynucleotide chain termination method (Sanger *et al.*, 1977). The sequence was reported in the EMBL data bank as OSY07612.

PCR primers

From the repeat motifs of the RG104, a total of twelve primers, each 12 nucleotides long were designed. The primers along with their positions on the RG104 sequence are described elsewhere (Prasad *et al.*, 2000).

Polymerase chain reaction

DNA amplification was carried out in 50-µl reaction mixtures, each containing 100 ng template DNA, 200 ng primer, 200 µM each of the dNTPS, 2.5 mM $MgCl_2$, 1X PCR buffer and 1U *Taq* DNA polymerase using the following PCR profile in a Perkin Elmer DNA thermal cycler 2400. Initial denaturation at 95°C for 5 min; followed by 35 cycles of 95°C for 1 min, 37°C for 1 min, 72° C for 2 min, and final extension at 72°C for 5 min. The amplification products were resolved on 1.5 per cent agarose gels.

Data analysis

For the purpose of assessing genetic diversity leading to the preparation of a dendrogram, gels (Allozyme profiles and Amplification profiles) were scored in binary format, with the presence of a band scored as unity and its absence scored as zero. Nei's dissimilarity indices [1- (2 × No. of shared bands/Total no. of bands)] were calculated (Nei and Li, 1979) and clustering was done using unweighted pair group with arithmetic mean (UPGMA) method (Sneath and Sokal, 1973). Correlation between assays were calculated using Spearman Rank Correlation (SRC).

RESULTS AND DISCUSSION

Fingerprinting

Four enzyme systems (Esterase, Peroxidase, Alcohol dehydrogenase and Superoxide dismutase) were used in this study due to their activity, high resolution and polymorphism. A schematic representation of allozyme profiles of one enzyme (Esterase) is given in Fig. 1. A total of 226 isozyme bands was recorded over the four enzyme systems (Table 2). Twenty-nine (12.83%) bands showed polymorphism across the tested samples. Clear polymorphism in banding pattern was observed in each zymograms, though estarase and peroxidase activities are more polymorphic than that of other two enzymes. Data on the number

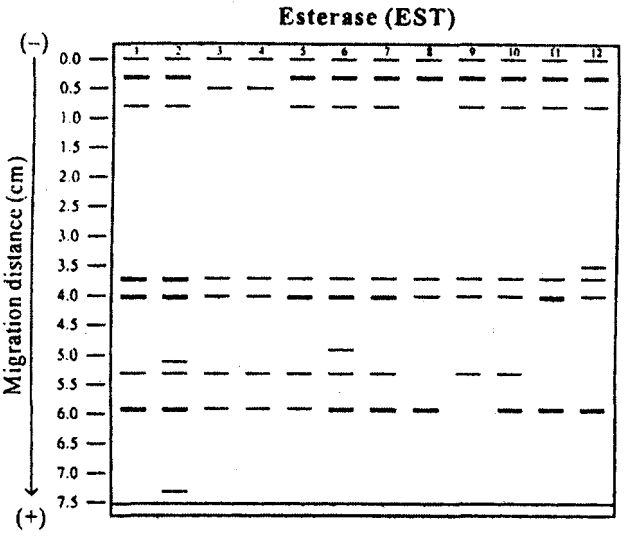

Fig. 1. Diagrammatic representation of the Esterase isozyme profiles in the twelve rice landraces/cultivars. Lane 1, Tilakachari; lane 2, IR8; lane 3, Bhasamanik; lane 4, CB1; lane 5, Kumargore; lane 6, Latisail; lane 7, Rupsail; lane 8, CB2; lane 9, Jaladhi1; lane 10, Patnai23; lane, 11, Matla; lane 12, SR26B

of allozymes and number of polymorphic allozymes for four enzymes is given Table 2. From the zymograms, it is apparent that in several cases though the banding patterns are similar but the band intensity are different, thereby indicating polymorphism.

Table 2. Name of enzyme, number and number of polymorphic allozymes in indigenous rice germplasm

Enzyme	Total bands	Dissimilar bands	% polymorphism
Esterase	69	9	13.04
Peroxidase	56	10	17.85
SOD	50	7	14.00
ADH	51	3	05.88

The unusual high frequency of short repeats and the presence of a transposon-like element in the RG104 sequence led to the thought that this region in the rice genome may be hypervariable amongst different cultivars (Chaudhuri *et al.*, 1996). Based on this rationale, from the repeat motif of the RG104, a total of twelve primers,

each 12 nucleotides long were designed (named as RCP5-RCP16). The primers along with their positions on the RG104 sequence are described elsewhere (Prasad *et al.*, 2000). Reproducible DNA amplification profiles of the rice cultivars were obtained using the "hot start" method in which the *Taq* DNA polymerase was added to the reaction tubes at 72°C 9the third step in the second cycle). A total of 105 bands was scored, resulting in an average of 4.08 fragments per primer with a range of one to seven fragments per primer. Primer RCP8 generated the highest number of polymorphic fragments among the 12 primers used (Fig. 2). The level of polymorphism

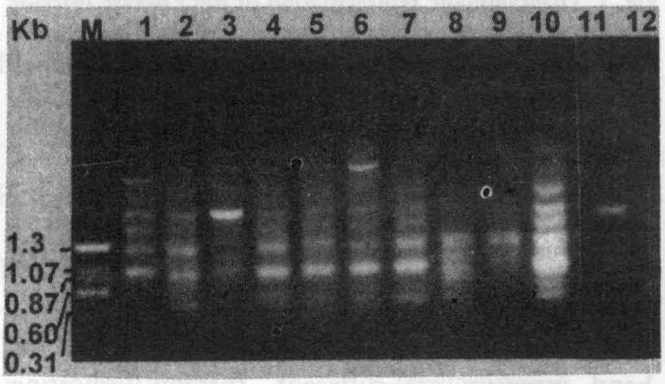

Fig. 2. Amplification profiles of eleven landraces and one cultivar (IR8) obtained using primer RCP8. Lane M, φX174/HaeIII molecular weight (Kb) marker; lane 1, SR26B; lane 2, Matla; lane 3, Rupsail; lane 4, Latisail; lane 5, Bhasamanik; lane 6, Patnai23; lane 7, Tilakachari; lane 8, Kumargore; lane 9, CB1; lane 10, CB2; lane 11, IR8; lane 12, Jaladhi I.

between the two methods varied widely, ranging from only 12.83% (isozymes) to 46.66%) (SSPTSA). The intrinsic differences between the two entire genome of both coding and non-coding regions, in case of SSPTSA, whereas, isozymes reflect polymorphism only in the coding regions that codes for certain enzymes. Moreover, considerations of the genetic code and of electrical properties of amino acids suggest that only one third of all amino acid replacements are detectable by gel electrophoresis which consequently underestimates the variation actually present. Higher degree of variability for RAPD over isozymes has also been reported on other species e.g. *Tylophora indica* (Parani and Parida, 1997) and *Elymus caninus* (Sun *et al.*, 1999).

Assessment of genetic diversity

The diversity in rice germplasm based on PCR analysis has also been initiated (Parsons *et al.*, 1997; Nadarajan *et al.*, 1999) for exploitation of this technology in rice improvement. Pairwise dissimilar values for the different combinations of cultivars were calculated from the compiled zymogram of four enzymes and also from the compiled amplification profile of twelve primers. The coefficient values ranged from 17.54 (CB1 and CB2) to 45.61 (Rupsail and IR8) for the isozymes and from 6.25 (Bhasamanik and Patnai23) to 61.65 (SR26B and IR8) for SSPTSA. Dendrograms based on dissimilarity values from

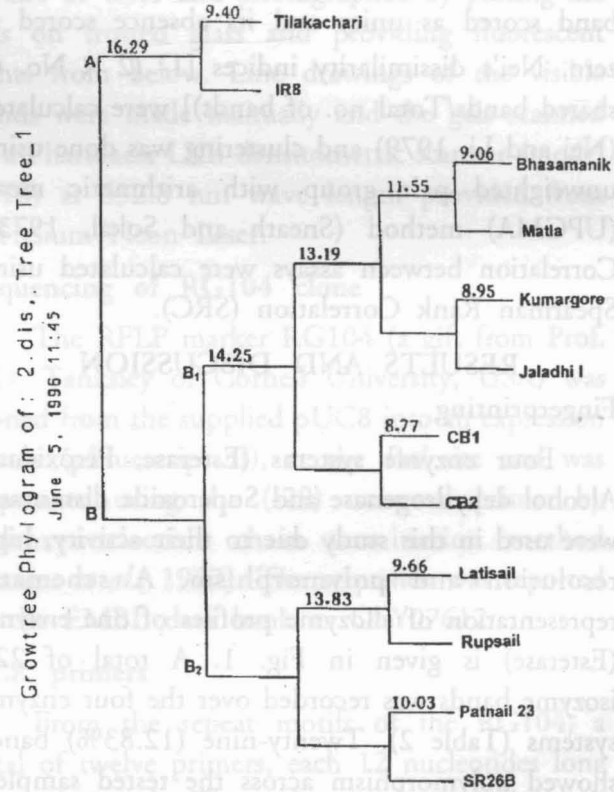

Fig. 3. Dendrogram based on culster analysis fo isozyme data showing the genetic relatedness between cultivars. Accessions are indicated at the end of each branch and numbers on the branches indicate the unit distance.

isozyme and SSPTSA data were constructed to reveal similarities between accessions. Two independent dendrograms for the two types of markers were generated (Figs. 3, 4) and several clusters were recognised from the two dendrograms. The grouping of accessions based on isozyme and SSPTSA data differed from each other. However, some of them occupied in the same relative position in both the dendrograms. Similar discrepancies was also reported by Parani and Parida (1997) in *Tylophora indica* and Sun *et al.*, (1999) in *Elymus caninus*. A possible explanation for the differences found among the two dendrograms might be based on the kind of information provided by each type of marker. Isozyme variation reflects only differences in protein-coding genes and is environment sensitive. Coding sequences are under a greater selection pressure to maintain functional sequences. On the other hand, SSPTSA can detect variation in both coding and non-coding regions and environment independent.

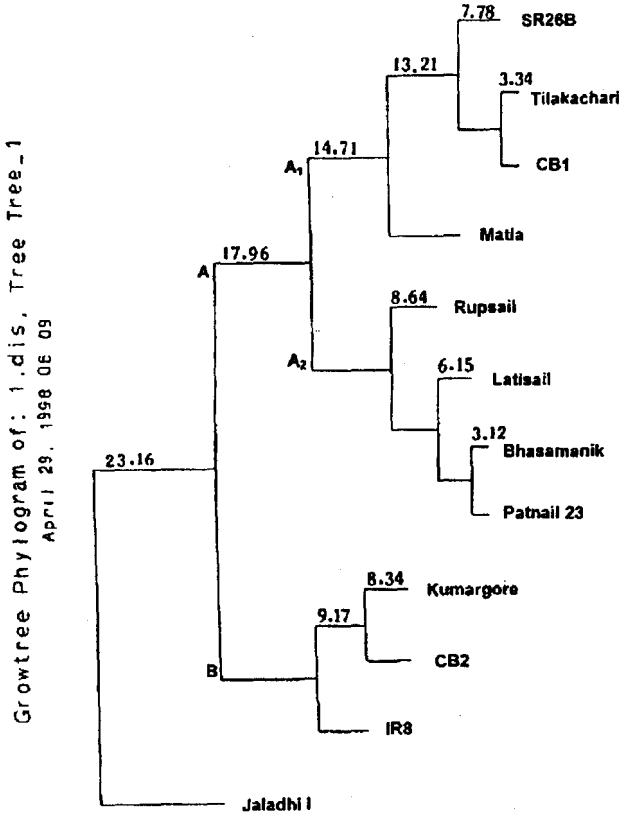

Fig. 4. Dendrogrambased on cluster analysis of DNA amplification profile data showing the genetic relatedness between cultivars. Accessions are indicated at the end of each branch and numbers on the branches indicate the unit distance

The correlation between the two genetic dissimilarity matrices was tested using the Spearman Rank Correlation (SRC). The results for SRC (which compares how each system ranks pairwise similarities) gave moderate correlation between isozymes and SSPTSA (rs = 0.36) and over 40 per cent of the genotypes ranking in the same order. In several recent studies, fingerprints based on different markers were compared using genotypes from different species. Lanner-Herrera *et al.*, (1996) also recorded a moderate Spearman's Rank Correlation (r = 0.38) between RAPD and isozyme distances in *Brassica oleracea*. Similar results were also reported by Beer *et al.*, (1993) and Heun *et al.*, (1994) in *Avena sterlis* L., and by Sun *et al.*, (1999) in *Elymus caninus*.

The results of the present study on isozyme and SSPTSA patterns, in general, provided an insight into the interrelationships among the studied varieties and have thereby helped to formulate phylogenetic hierarchies. Further, to the best of our knowledge, this has been the first report of analysis of evolutionary relationship s among the landraces of West Bengal, some of which have been extensively used in variety development programmes nationally and internationally, using biochemial (isozyme) and DNA markers. Overall, it could be concluded that the DNA based markers (SSPTSA) will be more useful than isozyme markers in detecting the genetic diversity among the landraces of West Bengal.

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REFERENCES

Beer, S. C., J. Goffreda, T. D. Philips, J. P. Murphy and M. E. Sorrells. 1993. Assessment of genetic variation in *Avena sterilis* using morphological traits, isozyme, and RFLPs. *Crop Sci.* 33: 1386-1393.

Bureau, T. E., P. C. Ronald and S. R. Wessler. 1996. A computer- based systematic survey reveals the predominance of small inverted-repeat elements in wild-type rice genes. *Proc. Natl. Acad. Sci.* 93: 8524-8529.

Chang, T. T. 1976. The origin, evolution, cultivation, dissemination, and diversification of Asian and African rices. vol.*Euphytica* 25: 425-441.

Chaudhuri, R. K., A. Mitra, M. Prasad and I. Chaudhuri. 1996. Possible existence of transposon footprints in a rice genomic DNA. *The Nucleus* 39: 24-28.

Davis, B. J. 1964. Disc electrophoresis II. Method and application to human serum proteins. *Ann. N. Y. Acad. Sci.* 121: 404-427.

Flavell, R. B. 1986. Repetitive DNA and chromosome evolution in plants. Philos. *Trans. R. Soc., Lond. Ser. B* 312: 227-242.

Heun, M., J. P. Murphy and T. D. Philips. 1994. A comparison of RAPD and isozyme analyses for determining the genetic relationships among *Avena sterlis* L. accessions. *Theor. Appl. Genet.* 87: 689-696.

Kephart, S. R. 1990. Starch gel electrophoresis of plant isozymes: a comparative analysis of techniques. *Am. J. Bot.* 77: 693-712.

Lanner-Herrera, C., M. Gustafsson, A.S. Falt and T. Bryngelsson. 1996. Diversity in natural populations of wild *Brassica oleracea* As estimated by isozyme and RAPD analysis. *Genet. Res. Crop. Evol.* 43: 13-23.

Linhart, Y. B and M. C. Grant. 1996. Evolutionary significans of local genetic differentiation in plants. *Annu. Rev. Ecol. Syst.* 27: 237-277.

Nadarajan, N., P. Vivekanandan and R. J. Henry. 1999. Use of molecular markers for diversity analysis in rice. *Indian J. Genet.* 59: 247-259.

Nei, M and W. Li. 1979. Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proc. Natl. Acad. Sci.*, USA 76: 5269-5273.

Nevo, E. 1988a. Genetic diversity in nature: Patterns and theory. *Evol. Biol.* 23: 217-247.

Parani, M and A. Parida. 1997. Allozyme and RAPD polymorphism in *Tylophora indica* (Burm. f.) Merr. *J. Plant Biochemistry and Biotech.* 6: 29-33.

Parsons, B. J., H. J. Newbury, M. T. Jackson and B. V. Fordlloyd. 1997. Constrasting genetic diversity relationships are revealed in rice (*Oryza sativa* L.) using different marker types. *Mol. Breeding* 3: 115-125.

Prasad, M., A. Mitra, I. Chaudhuri and R. K. Chaudhuri. 2000. Genotyping indica rice landraces and cultivars with site specific putative transposon sequence amplification. *Cereal Res. Commun.* (communicated)

Rajora, O. P. 1990. Marker allozyme genes and alleles for differentiation of *Populus deltoides, P. nigra, P. maximowiczii* and their interspecific hybrids. *Can. J. Bot.* 68: 990-998.

Russell, J. R., J. D. Fuller, M. Macaulay, B. G. B. Hatz, A. Jahoor, W. Powell and R. Waugh. 1997. Direct comparison of levels of genetic variation among barley accessions detected by RFLPs, AFLPs, SSRs and RAPDs. *Theor. Appl. Genet.* 95: 714-722.

Sanger, F. S., S. Nicklen and A. R. Coulson. 1977. DNA sequencing with chain termination inhibitors. *Proc. Natl. Acad. Sci.*, USA 74: 5463-5467.

Sneath, D. H. A. and R. Sokal. 1973. Numerical taxonomy. W. H. Freeman and company, San Fransisco, USA.

Sun, G. L., O. Diaz, B. Salomon and R. von Bothmer. 1999. Genetic diversity in *Elymus caninus* as revealed by isozyme, RAPD, and microsatellite markers. *Genome* 42: 420-431.

Walbot, V. 1988. Preparation of DNA from single rice seedling. *Rice Genetics Newsletter* 5: 149-151.

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GENETIC DIVERSITY IN RELATION TO GRAIN YIELD AND NEUROTOXIN IN GRASSPEA (*Lathyrus* sp.) GENETIC RESOURCES

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Genetic divergence as measured by D^2 technique was studied for grain yield, its components and neurotoxin content in 65 genotypes of grasspea. The genotypes were grouped into six clusters and the maximum intra-cluster distance was observed in cluster III comprising 16 genotypes. Clusters I and II followed by I and IV were identified as genetically divergent. Considering the cluster means and cluster distances, RLS 6, Pusa 24, BioL- 212, LS 157-14 and BioR-202 of cluster IV (for 100-seed weight); RLS 3, BioR-231, RLS 12, Bio I-222, P94-3 of cluster V (for low ODAP and earliness); RLS 9630, RLS 617, RLS 9625, RLS 9622, RLS 9603, RLS 7 of cluster III (for number of pods plant^{-1}) are expected to give promising and desirable recombinants of high yield with low neurotoxin content.

Key words : *Lathyrus*, grasspea, cluster analysis, genetic diversity, neurotoxin, grain yield

The long neglected grasspea crop has been an important food, feed and fodder legume crop of dryland agriculture. The drought tolerance and the low cost of production make an insurance and dependable crop of poor families, especially during famine conditions when the production of other crops is impossible due to excessive drought. Thus, its ability to provide an economic yield under most adverse conditions has made it a popular crop in subsistence farming. The objectives in grasspea improvement programme are to improve its yield potential, adaptability to different biotic and abiotic stresses and nutritional quality through reduction in its neurotoxin content causing neurolathyrism in human beings (Adiga *et al.*, 1963; Murthy *et al.*, 1964).

Therefore, future efforts in the improvement of grasspea should be geared to : (i) Hybridization for low or toxin free varieties (ii) Development of early, high yielding varieties. In the present study 65 genotypes including low ODAP somaclonal variants, breeding lines and germplasm accessions were evaluated. (i) to determine the magnitude of variability among the genotypes for yield, its components and ODAP content. (ii) to determine the grouping pattern of genotypes into different clusters and (iii) to identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme aimed at improving grain yield potential of grasspea and reducing the toxin content present in its seeds.

MATERIALS AND METHODS

The material for the study comprised 52 germplasm accessions, 6 breeding lines, 4 somaclonal variants and 3 checks viz., Pusa 24, BioL-212 and Local cultivar of grasspea genotypes. These were evaluated in randomized complete block design with three replications at Research Farm, Indira Gandhi Agricultural University, Raipur. Each entry represented single row of 2m length with a spacing of 30 cm between rows

and 10 cm between plants in a row. A recommended package of practices was adopted to grow a normal crop. Observations on metric traits were recorded on five randomly selected plants of each accession per replication (Table 1). ODAP content in dry seeds was estimated using colorimetric method as suggested by Rao *et al.* (1978). The data were subjected to the Mahalanobis D^2 statistic (1936) to measure the genetic divergence. The varieties were grouped into a number of clusters by Tocher's method as described by Rao (1952).

Table 1. Parameters of genetic variability

Character	Mean	Range		GCV %	PCV %	h^2 BS %	GA
		Min	Mix				
Days to 50% flowering	56.42	50.33	62.67	4.30	4.96	75.30	4.34
Days to maturity	107.89	98.67	119.67	5.36	5.65	90.20	11.32
Plant height (cm)	43.34	33.00	54.87	9.88	11.69	71.30	7.45
No. of pods plant^{-1}	19.74	10.53	33.20	23.52	27.77	71.70	8.10
No of seeds pod^{-1}	2.81	2.30	3.47	7.82	10.89	51.50	0.32
100-seed weight (g)	8.11	6.17	11.87	11.54	14.01	67.90	1.59
Grain yield plant^{-1}	0.86	0.35	1.54	25.97	33.77	59.10	0.36
ODAP%	0.37	0.07	0.66	44.19	45.44	94.60	0.33

RESULTS AND DISCUSSION

The results of the present study exhibited low to high variability for all the eight characters under study. Considerable genetic divergence was also present among the genotypes indicating adequate scope for selection of superior and diverse genotypes.

The data presented in Table 1 showed the estimates of PCV and GCV were high for ODAP content, grain yield plant^{-1}, number of pods plant^{-1}, and 100-seed weight. Wide range of variation was observed for ODAP content ranging from 0.07 to 0.66 per cent grain yield plant^{-1} (0.35 to 1.54 g), number of pods plant^{-1} (1053 to 33.20) and seed size (6.17 to 11.87 g/100 seeds). This reveals that there is ample scope of selection of superior genotypes for grain yield and low neurotoxin. Large variation in seed ODAP ranging from 0.1 to 1.0 per cent has also been reported in landraces by Jain *et al.* (1972) and Pandey *et al.* (1997). High heritability with high genetic advance for days to maturity, number of pods plant^{-1}, plant height and days to 50 per cent flowering indicated that selection may be effective for these traits. High heritability coupled with low genetic advance for ODAP content and grain yield clearly indicated that more attention should be paid while exercising selection for these traits.

Based on the relative magnitude of D^2 values, 65 genotypes were grouped into six clusters (Table 2). Maximum number of 22 cultivars were accommodated in cluster VI followed by 16 in cluster III, 8 in cluster V, 7 in cluster II and 6 each in cluster I and IV. The average intra-cluster distance between the members of cluster III was maximum followed in descending order by cluster IV, V, VI, II and I (Table 3), suggesting that genotypes in cluster III were relatively more diverse than the genotypes in the above clusters. The minimum intra-cluster distance exhibited by cluster I indicated limited genetic diversity among the constituent genotypes.

The relative divergence of each clusters from other clusters (inter-cluster distances) indicated greater divergence between cluster I & II (D = 5.180) followed by clusters I & IV (D = 4.700), II & V (D = 4.507) and IV & V (D = 2.506). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for yield and ODAP content which may enable further selection and improvement of these traits. The hybrids developed from the selected genotypes within the limits of

Table 2. Clustering of 65 grasspea genotypes based on D^2 statistics

Cluster	No. of genotypes included	Genotypes
I	6	RLS 9641, Pusa 24, BioL-212, RLS-6, LS 157-14, BioR-202
II	7	RLS 9604, RLS 9605, RLS 9606, RLS 9607, RLS 9610, RLS 9614, RLS 9615
III	16	RLS 9617, RLS 9619, RLS 9620, RLS 9622, RLS 9625, RLS 9628, RLS 9630, RLS 617, LS 9311-8, RLS 7, RLS 9602, RLS 9603, RLS 9611, RLS 9612, RPL 26, LS 157-12
IV	6	LS 155-6, LS 193-10, RLS 9601, RLS 9613, BioL-208, RLS 11
V	8	RLS 3, BioR-231, RLS 9, RLS 10, RLS 12, Biol-222, P 94-3, Local
VI	22	RLS 9616, RLS 9618, RLS 9621, RLS 9623, RLS 9624, RLS 9626, RLS 9627, RLS 9629, RLS 9631, RLS 9632, RLS 9633, RLS 9634, RLS 9635, RLS 9636, RLS 9637, RLS 9638, RLS 9639, RLS 9640, RLS 9642, RLS 9608, RLS 9609, RLK 273-1

compatibility of these clusters may produce high magnitude of heterosis or desirable transgressive segregants which would be rewarding in grasspea breeding programme. Quader (1985) and Vedna Kumari *et al.* (1996) also reported sufficient diversity even in a limited number of genotypes of grasspea.

The inter-cluster distance analysis revealed the maximum divergence between cluster I & II followed by cluster I & IV, II & V and IV & V (Table 3). Due emphasis in breeding programme should be given to RLS 9641, Pusa 24, BioL-212, RLS 6, LS 157-14, BioR-202 of cluster 1; RLS 9604, 9605, 9606, 9607, 9610, 9614, 9615 of cluster II; LS 155-6, LS 193-10, RLS 9601, RLS 9613, BioL-208, RLS 11 of cluster IV; RLS 3, BioR-231, RLS 9, RLS 10, RLS 12, BioL-222, P94-3 and local cultivar of cluster V.

Table 3. Mean intra-cluster (diagonal and bold) and inter-cluster distances among six characters

Cluster	I	II	III	IV	V	VI
I	**1.692**	5.180	3.068	4.700	2.130	3.793
II		**1.774**	3.480	2.925	4.507	3.043
III			**2.083**	3.561	2.965	2.289
IV				**1.901**	4.506	3.049
V					**1.859**	3.098
VI						**1.852**

Note : D values given above in the diagonal and non-diagonal

Crosses among parents having genetic divergence are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. Two important factors to be considered are :

(i) Choice of particular cluster from which genotypes are to be used as parents in crossing scheme, and

(ii) Selection of particular genotypes from selected groups

The cluster mean values for all the traits are furnished in Table 4. There was a wide range of variation in the cluster mean values for most of the characters except for number of seeds pod^{-1}. The maximum and minimum mean values for characters viz., days to 50% flowering, 60.33 (ii) and 53.87 (V); days to maturity; 117.00 (II) and 100.71 (V); plant height, 50.29 (I) and 39.24 (II); number of pods plant^{-1}, 25.14 (III) and 16.66 (IV); number of seeds pod^{-1}, 3.11 (I) and 2.60 (II); 100-seed weight, 10.23 (IV) and 7.68 (V); grain yield, 1.30 (I) and 0.57 (IV); ODAP per cent, 0.54 (VI) and 0.19 (V), respectively were observed. This indicates that while planning hybridization programme cultures like RLS-3, BioR-231, RLS 12, Biol-222 and P 94-3 from cluster v hold like RLS-3, BioR-231, RLS 12, Biol-222 and P 94-3 from cluster V hold be considered for low ODAP and earliness. Similarly,

Table 4. Cluster means for different characters

C*	Genotypes included	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of pods plant^{-1}	No. of seeds pod^{-1}	100-seed weight (g)	Grain yield plant^{-1}	ODAP (%)
I	6	55.61	101.72	50.29	17.67	3.11	8.23	1.30	0.26
II	7	60.33	117.00	39.24	18.05	2.60	7.89	0.66	0.23
III	16	55.65	109.50	45.72	25.14	2.95	7.72	0.84	0.36
IV	6	57.56	113.33	43.78	16.66	2.67	10.23	0.57	0.33
V	8	53.87	100.71	42.93	16.90	2.88	7.68	1.17	0.19
VI	22	56.56	106.64	41.04	18.80	2.70	8.00	0.80	0.54

C*-Cluster

RLS 9630, RLS 617, RLS 9625, RLS 9622, RLS 9603 and RLS 7 (cluster III) for number of nods plant^{-1}; RLS 6, Pua 24, BioL-212, LS 157-14 and BioR-202 (cluster I) for grain yield plant^{-1}; BioL-208, LS 193-10, RLS 9613 (cluster IV) for 100- seed weight. Thus, these genotypes hold great promise as parents to obtain promising hybrids and create further genetic variability for these characters.

REFERENCES

Adiga, P. R., S. L. N. Rao and P. S. Sharma. 1963. Some structural features and neurotoxic action of compound from *Lathyrus sativus* seeds. *Curr. Sci.* 32: 153-155.

Jain, H. K., P. L. N. Somayajulu and G. K. Barat. 1972. Investigations in *Lathyrus sativus* L. In: Annual Report of PL. 480 Research Project : 3-4.

Mahalanobis, P. S. 1936. On the generalised distances in statistics. Proc. Natl. Acad. Sci., India, 2 : 49-59.

Murthy, V. V. S., T. R. Seshadri and T. A. Venkatsubramanian. 1964. Neurotoxic compound of the seed of *Lathyrus sativus*. *Phytochemistry* 3: 73-78.

Pandey R. L., M. W. Chitale, R. N. Sharma and A. K. Geda. 1997. Evaluation and characterisation of grasspea germplasm (*Lathyrus sativus* L.) *Journal of Medicinal and Aromatic Plant Sciences* 19(1): 14-16.

Quader, M. 1985. Genetic analysis of neurotoxin content and some aspects of reproductive biology in *Lathyrus sativus* L. Ph. D. thesis, I.A.R.I., New Delhi.

Rao, C. R. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York.

Rao, S. L. N. 1978. A sensitive and specific colorimetric method for the determination of a α, β - diaminopropionic acid and the *Lathyrus sativus* L. neurotoxin. *Analytical Biochemistry* 86 : 386-395.

Vedna Kumari, R. B. Mehra, G. K. Barat, D. B. Raju and K. Himabindu. 1996. Genetic diversity in relation to ODAP content in Grasspea. *Indian J. Genet.* 56: 8-11.

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EMS INDUCED VARIABILITY IN *Artemisia pallens* Wall.*

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Davana (*Artemisia pallens*) is native to India and has gained considerable importance in industry for its fragrance. Because the crop is harvested at pre-flowering stage, there is threat to its extinction, and thus variability is also reduced. This paper revealed that a wide range of variability could be generated through the induced chemical mutagenesis in *A. pallens*.

Key words: Davana, Artimisia pallens, induced mutagenesis, variability

The genus *Artemisia* comprises a large number of economically important species, some of which yield essential oil while others have medicinal properties (Anonymous, 1985). Among theses, *Artemisia pallens* Wall. popularly known as davana is a native of India and has gained considerable industrial importance. The davana oil, prized for its fruity fragrance, is mainly used in perfurmery, flavouring and cosmetic industries. There is a huge demand of the oil in the foreign market. But the oil produced in India is not keeping pace with the increasing demand of the oil. As such necessity has been felt for the development of the crop. In view of the fact that cultivation of the crop is confined to a limited area and crop is harvested at pre-flowering stage, there is hardly any variability in the crop (Farooqi *et al.*, 1990), which is a pre-requisite for any improvement programme. Thus one of the best options available is to generate variability through induced mutations. The present study on induced mutagenesis in *Artemisia pallens* was carried out with a view to assess the amount of variability, which can be induced by Ethyl methane sulphonate (EMS).

MATERIAL AND METHODS

A set of selfed, dry and viable seeds with 8-10 per cent moisture were treated with aqueous solution of EMS prepared in distilled water. Concentrations of EMS used ranged from 0.01-0.1 per cent. Another set of same concentrations was prepared by dissolving the mutagen in 2 per cent Dimethyl Sulphoxide (DMSO). Three replicates, each of 200 seeds, were used for each treatment along with the controls. All the treatments lasted for 8 hrs at a temperature of 25 ± 1°C with intermittent shaking. At the end of treatments, seeds were thoroughly washed. Following each treatment, 50 treated seeds along with respective controls were separately placed in petridishes for germination and cytological studies. The remaining seeds were sown in pots to raise the nursery. The seedlings about 5-8 cm tall were transplanted to experimental beds to raise M_1 generation. The biological effects of different treatments were evaluated with respect to the germination, seedling growth, survival percentage and other agronomic characteristics of the plants and compared to the control. All the observations in the control were

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taken as 100%. M_1 abnormalities scored from seedling stage to maturity were determined from the percentage of the M_1 plants survived. Pollen fertility was estimated by Aceto-carmine staining test over 2,000 pollen grains per treatment. Impact of EMS treatments has been assessed on mitotic and meiotic systems. The cytological studies were carried out as described by Sharma and Sharma (1980). Data on plant height, capitulum number/plant, herbage and flower yield per plant were recorded on 25 plants per replicate from each treatment. Oil percentage of the herb was determined by hydro-distillation in Clevenger apparatus.

Selfed seeds from M_1 plants were harvested individually and grown to raise M_2 generation as progeny rows the following year. These progenies were studied for various parameters like M_1 plants. The data collected for quantitative traits were put to statistical analysis. The statistical significance of the difference in mean values between the control and treated plants was calculated by applying student's t-test. The variance of the control and treated plants was compared by applying variance ratio (F) test.

RESULTS AND DISCUSSION

Germination and survivality were adversely affected under all the treatments of EMS. These physiological processes revealed a parallel relationship and showed a decreasing trend with the increasing doses. Application of EMS dissolved in DMSO induced more reduction than the corresponding concentration in water. The concentration of EMS used and seedling height bear inverse relation. Maximum reduction to 48.87% was observed at 0.1% EMS dissolved in DMSO (Table 1). The observed decrease in survival and germination is attributed to disturbed metabolic activity in the treated seeds and also to the damage caused to the meristimatic cells (Konzak *et al.*, 1965).

Table 1. Seed germination, seedling growth and seedling survival following various EMS doses in *Artemisia pallens* seeds in M_1 generation

Treatment (EMS)	Germination (%)		Seedling height (cm)		Survival % of control
	Mean	% of control	Mean	% of control	
Control	92.00	100.00	2.73 ± 0.09	100.00	100.00
0.01%/H_2O	85.00	92.39	2.37 ± 0.11**	86.18	90.64
0.05%/H_2O	71.50	77.50	2.24 ± 0.15**	81.45	74.65
0.10%/H_2O	56.34	51.74	1.86 ± 0.14**	67.63	52.58
DMSO (2%)	88.36	100.00	2.66 ± 0.08	100.00	100.00
0.01%/DMSO	74.74	84.59	1.66 ± 0.13**	81.20	81.50
0.05%/DMSO	63.28	71.62	1.84 ± 0.12**	69.17	64.04
0.10%/DMSO	48.35	42.73	1.30 ± 0.11**	48.87	54.63

EMS induced a number of morphological aberrations which were mostly confined to leaves. Leaf curling was the most predominant effect. The frequency of these abnormalities were dose related (Table 2). These abnormalities fail to re-appear in the M_2 generation. This class of variation represent the outcome of physiological imbalance or biochemical disturbances caused by mutagen (Gunckel and Sparrow, 1961).

All the EMS treatments induced significant reduction in plant height in M_1 generation. Mean values for this character skewed towards positive direction following 0.01 and 0.05% EMS treatments in water during M_2 generation and all the treatments exhibited a significant increase in variance. A dose related increase in pollen fertility was observed in the treated plants and was found enhanced in case of treatments applied in presence of DMSO. All the concentrations

Table 2. Morphological abnormalities induced by various doses of EMS in M_1 generation of *Artemisia pallens*

Treatment (EMS)	Abnormal plants (%)	Types of morphological abnormalities (%)				
		Curled leaves	Fused leaflets	Albino seedlings	Colour changes	Other types
Control	-	-	-	-	-	-
0.01%/H_2O	9.39	3.21	2.22	-	2.00	1.96
0.05%/H_2O	16.45	5.05	4.13	0.55	3.08	3.64
0.10%/H_2O	18.52	12.22	2.86	-	1.44	2.00
DMSO (2%)	-	-	-	-	-	-
0.01%/DMSO	19.94	8.36	5.94	-	3.33	2.28
0.05%/DMSO	26.74	14.84	4.31	0.84	2.12	4.63
0.10%/DMSO	29.54	13.09	9.99	-	3.46	3.00

widened the range of pollen fertility in M_2 and more variability has been induced by EMS treatments dissolved in DMSO (Tables 3 and 4).

Reduced fertility has been ascribed to the physiological damage produced by the hydrolic products of the alkylating chemicals (Gaul *et al.*, 1966). Stimulatory effect on capitulum count per plant was observed as a result of EMS (0.01 and 0.05%) treatments in M_1 generation. All other treatments showed reduction. Herbage and flower yield per plant also suffered reduction except at the treatment 0.05 per cent EMS/H_2O An appreciable increase in oil percent was noticed at all the treatments. This increase was not linear to the concentration of EMS applied (Table 5). Variance was increased significantly for most of the treatments for all the parameters under study during M_2 generation. Range got further widened than within the control (Table 6 & 7). Increased variability in these traits is much desired aspect of mutagenic treatments.

The stimulatory effect of low EMS doses observed on some yield attributing characters has been attributed to the rapid turn over of auxin

Table 3. Plant height and pollen fertility following EMS treatment in *Artemisia pallens* in M_1 generation

Treatment (EMS)	Plant height (cm)		Pollen fertility (%)	
	Average	% of control	Range	Average
Control	59.32 ± 0.69	100.00	54.22 - 93.81	77.63
0.01%/H_2O	56.72 ± 0.97*	95.62	56.64 - 77.03	68.91
0.05%/H_2O	52.00 ± 0.70*	87.66	48.19 - 85.93	69.74
0.10%/H_2O	47.80 ± 0.91**	50.58	52.00 - 70.81	61.75
DMSO (2%)	57.64 ± 0.52	100.00	69.74 - 89.99	78.32
0.01%/DMSO	52.61 ± 0.62**	91.27	50.96 - 90.02	70.98
0.05%/DMSO	47.52 ± 1.03**	82.44	33.63 - 90.02	53.32
0.10%/DMSO	37.69 ± 0.82**	65.39	37.93 - 60.64	48.20

Table 4. Variation in plant height and pollen fertility in M_2 generation raised after treatment with EMS in *Artemisia pallens*

Treatment (EMS)	Plant height (cm)			Pollen fertility (%)	
	Range	Average	% of control	Range	Average
Control	47.20 - 70.50	85.84 ± 1.41	100.00	76.82 - 90.50	82.23
0.01%/H_2O	46.30 - 72.40	61.76 ± 1.59	104.96	68.88 - 87.21	79.07
0.05%/H_2O	50.50 - 77.00	66.56 ± 1.44**	113.12	64.52 - 83.68	75.91
0.10%/H_2O	39.40 - 68.20	54.40 ± 1.85*	92.45	55.85 - 81.87	69.23
DMSO (2%)	53.10 - 70.40	60.36 ± 0.94	100.00	69.14 - 86.99	78.44
0.01%/DMSO	39.40 - 70.00	55.92 ± 1.82**	92.64	46.86 - 89.91	69.36
0.05%/DMSO	36.70 - 66.50	51.44 ± 1.75**	85.22	49.99 - 73.63	62.51
0.10%/DMSO	32.60 - 60.00	47.28 ± 1.57**	37.33	38.85 - 74.22	57.39

Table 5. Effect of various doses of EMS on different yield attributing characters in *Artemisia pallens* in M_1 generation

Treatment (EMS)	Capitula count/plant		Herbage yield/plant (g)		Flower yield/plant (g)		Oil (%)
	Mean	% of control	Mean	% of control	Mean	% of control	
Control	370.70 ± 9.52	100.00	31.08 ± 0.89	100.00	13.63 ± 0.45	100.00	0.20
0.01% / H_2O	424.40 ± 3.24**	114.49	28.04 ± 1.36*	90.22	14.12 ± 0.79	103.22	0.36
0.05% / H_2O	397.95 ± 15.91	107.35	33.28 ± 1.40	107.07	15.12 ± 0.72*	110.52	0.32
0.10% / H_2O	313.95 ± 15.99**	84.60	26.48 ± 123**	85.20	12.36 ± 0.65	90.35	0.30
DMSO (2%)	374.00 ± 11.59	100.00	32.56 ± 0.78	100.00	13.55 ± 0.47	100.00	0.24
0.01% / DMSO	355.43 ± 13.64	94.50	29.04 ± 1.07**	89.18	12.53 ± 1.32	93.57	0.37
0.05% / DMSO	321.94 ± 14.08**	86.06	26.07 ± 1.35**	81.69	11.60 ± 0.98	84.61	0.37
0.10% / DMSO	301.37 ± 16.31	80.58	24.00 ± 1.15**	73.71	10.08 ± 0.67*	74.39	0.39

Table 6. Variation in capitulum count and herbage yield/M_2 plants raised following treatments with EMS

Treatment (EMS)	Capitula count/plant			Herbage yield/plant (g)		
	Range	Mean	% of Control	Range	Mean	% of control
Control	280-450	373.04 ± 10.00	100.00	25-38	30.92 ± 0.86	100.00
0.01% / H_2O	290-510	401.24 ± 11.47*	107.56	22-48	33.92 ± 1.43*	109.13
0.05% / H_2O	190-525	359.20 ± 15.15	96.29	28-48	38.08 ± 1.22**	122.52
0.10% / H_2O	260-445	334.92 ± 10.53**	89.78	21-38	29.44 ±1.26	94.72
DMSO (2%)	291-420	355.04 ± 7.72	100.00	28-37	32.66 ± 0.79	100.00
0.01% / DMSO	280-512	373-28 ± 11.00	105.14	22-40	34.10 ± 1.00	104.40
0.05% / DMSO	245-425	340.76 ± 9.63	95.97	18-36	30.14 ± 1.24*	92.28
0.10% / DMSO	240-410	329.20 ± 9.22*	92.72	15-36	28.54 ± 1.23**	87.38

Table 7. Variation in flower yield and oil yield/M_2 plant raised following treatments with EMS

Treatment (EMS)	Flower yield/plant (g)			Oil yield (%)	
	Range	Average	% of control	Range	Average
Control	9.5-17.4	12.64 ± 0.57	100.00	0.16-0.32	0.23
0.01%/H_2O	7.7-22.3	14.18 ± 0.64*	112.21	0.26-0.38	0.32
0.05%/H_2O	4.5-20.0	12.17 ± 0.96	96.32	0.26-0.35	0.30
0.10%/H_2O	4.6-19.4	11.71 ± 0.99	92.66	0.22-0.33	0.28
DMSO (2%)	8.9-17.1	12.00 ± 0.48	100.00	0.18-0.28	0.22
0.01%/DMSO	7.5-15.6	11.38 ± 0.93	94.84	0.21-0.34	0.28
0.05%/DMSO	5.8-16.3	10.80 ± 0.52*	90.04	0.26-0.36	0.32
0.10%/DMSO	4.5-162	10.28 ± 0.80*	85.72	0.23-0.36	0.29

± Standard error; *Significant at 5% probability level; **Significant at 5% probability level

in metabolically active tissue and increase in cell division or size of cells (Sax, 1962). Similar results have been recorded in *Sorghum* (Wanjari and Kutarekar, 1977). Treatment with EMS induced no change in the cytological behaviour of treated plants. Therefore no alteration was observed in the chromosome complement during mitosis as well as meiosis. Chromosome synapsis was perfect and 8 bivalents were observed at prophase I and metaphase I. They disjuct and 8 chromosomes segregate to each pole at anaphase I.

The use of DMSO as solvent modified the mutagenic effectiveness of EMS. All the biological parameters were reduced as compared to corresponding EMS treatments in water. However, the mean value for oil content was increased. The role of DMSO in increasing mutagenecity of EMS has been reported in many other plants also and it has been attributed to its property of enhancing penetration and absorption of the mutagen (EMS) by the treated tissues (Bhatia, 1967; Singh and Chaturvedi, 1982).

The mutagenic effects of EMS in *A. pallens* are in conformity with the results obtained in a large number of plants under similar treatments (Ram and Kaul, 1991; Padmavathi *et al.*, 1992; Mary and Jayabalan, 1995; Kumar and Mani, 1997; Singh *et al.*, 2000). Moreover, variability observed in M_1 generation was manifested through M_2 generation suggesting the genetic origin of these variations. This variability seems to be of great practical utility as its exploitation through selection could provide ample scope for selection of desired genotypes. The present investigation shows that a wide range of variability could be generated through the induced chemical mutagenesis in *A. pallens*.

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REFERENCES

Bhatia, C. R. 1967. Increased mutagenic effect of EMS when dissolved in dimethyl sulphoxide. *Mut. Res.* 4: 375-376.

Farooqi, A. A., N. D. Dasharatha Rao, K. A. Devaiah and R. L. Ravi Kumar. 1990. Genetic variability in Davana (*Artemisia pallens*). *Ind. Perfum.* 34: 42-43.

Gaul, H., K. Bender, E. Ulonska and M. Sato. 1966. "EMS-induced genetic variability in barley; the problem of EMS - induced sterility; and a method to increase the efficiency of EMS treatment". *In*: Mutations in plant Breeding, Symp. FAO/IAEA, Vienna. p 63-84.

Konzak, C. F., R. A. Nilan, J. Wagner and R. J. Foster. 1965. Efficient chemical mutagenesis. *Rad. Bot. (Suppl.)* 5: 49.

Gunckel, J. E., A. H. Sparrow. 1961. Ionization radiations - biological, physiological and morphological aspects of their effects on plants. *In*: Encyclopaedia of Plant Physiol, 16: 555-611.

Kumar, R. and S. C. Mani. 1997. Chemical mutagenesis in Manhar variety of rice (*Oryza sativa* L.). *Indian J. Agric. Sci.* 63: 27-33.

Mary, R. J. and N. Jayabalan. 1995. EMS induced variability in sesame. *Crop Improv.* 22: 170-174.

Padmavathi, T., Pratibha Devi and V. Kiranmai. 1992. Induced variability for different biological parameters in soybean. *J. Cytol. Genet.* 27: 175-177.

Ram, G. and B. L. Kaul. 1991. Biological effect of X-rays, Ethyl methane sulphonate and sodium azide in *Solvanum khasianum* Clerke. *Ind. Jour. Forest.* 14: 275-281.

Sax, K. 1963. The stimulation of plant growth by ionizing radiation. *Rad. Bot.* 3: 179-186.

Sharma, A. K. and A. Sharma. 1980. Chromosome techniques-Theory and Practices (3rd ed.) Butterworths, London.

Singh, V. P. and S. N. Chaturvedi. 1982. Comparative mutagenic effects of EMS and NMU in *Vigna radiata* (L.) Wilzek with DMSO. *Ind. Jour. Bot.* 5: 54-57.

Singh, V. P., Man Singh and J. P. Lal. 2000. Gamma rays and EMS induced genetic variability for quantitative traits in urdbean (*Vigna mungo* L. Hepper). *Indian J. Genet.* 60 (1): 89-96.

Wanjari, K. B. and D. R. Kutarekar. 1977. A study of some M_1 parameters in different combination treatments of gamma rays and chemical mutagens in *Sorghum*. *Jour. Cytol. Genet.* 12: 55-61.

Wlth India. 1985. The Wealth of India. Vol. 1 (Revised Edition) CSIR, New Delhi. p. 434-442.

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VARIABILITY AND INTERRELATIONSHIP STUDIES FOR YIELD COMPONENTS IN *G. arboreum* COLLECTED FROM NORTH-EASTERN HILL REGION AND GUJARAT

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Twenty three single plant selections (twenty of *G. arboreum* race *cernuum* and three of *G. arboreum)* made from the collections done in North-East region of the country and Gujarat were evaluated for analysis of seed cotton yield, boll number per plant, boll weight, ginning outturn percentage and 2.5% span length. Seed cotton yield showed positive correlation with all the component traits. The analysis confirmed that plant type with high boll weight, high number of bolls per plant and long fibres have high seed cotton yield.

Key words : *G. arboreum*, variability, interrelationship, yield components

The National Bureau of Plant Genetic Resources, New Delhi in collaboration with Central Institute for Cotton Research, Nagpur has a joint mandate to collect genetic diversity in cotton from India by exploration and exotic collections through exchange programme. During 1990-1994, CICR, Regional Station, Sirsa, Haryana participated in four explorations conducted in various regions of India. One hundred eight collections of *G. arboreum* race *cernuum* characterized by big long bolls, high boll weight, high ginning out turn, high seed number and high locule retentivity were made from N. E. region of the country. In *G. arboreum*, variability in *mathio* types with open, relatively small bolls, red and green plants, long fibre, greater strength and high ginning percent was collected from Saurashtra and Kachchh regions of Gujarat. The population sample consisted of single boll per plant from 20-25 random plants (as per availability) was picked up to represent diversity and to study variability within and between populations. To exploit variability present in a population sample collected, single plant selections were made and their progeny were raised. With the help of certain parameters like coefficient of variability, heritability and genetic advance and the interrelationship among different yield component traits from single plant selection and other land races collections efficient breeding programme for yield improvement would be possible.

MATERIALS AND METHODS

Twenty single plant selections for yield and yield contributing traits were made from the collections of *G. arboreum* race *cernuum* types (CSA types) done from North East regions during 1992. Similarly, three single plant selections were made (CSG types from the *mathio* type *G. arboreum* collection made from Gujarat). These 23 single plant selections were selfed and multiplied and evaluated in a Randomized Block Design with three replications during Kharif 1995 alongwith 2 local cultivars i.e., RG 8 and LD 327. Each strain was allotted a three rows plot

Table 1. Mean performance of *G. arboreum* collections

Sr. No.	Variety	Yield kg/ha	Yield/plant	Boll no.	Boll wt.	G.O.T.	2.5% span length
1	CSA 5-92	1938.72	64.07	36.43	3.03	38.00	24.3
2	CSA 5-92-1	2121.62	66.50	34.77	2.67	39.00	15.3
3	CSA 5-92-2	2322.81	83.47	33.33	3.00	39.00	19.3
4	CSA 5-92-3	2487.42	86.30	35.00	3.13	40.00	15.0
5	CSA 4-93-1	3072.69	88.57	34.53	3.50	39.50	18.0
6	CSA 8-93-1	2633.74	82.57	26.20	3.83	41.00	15.3
7	CSA 12-93-1	3145.85	92.03	33.23	3.37	39.50	18.3
8	CSA12-93-2	1200.29	50.80	27.10	3.90	42.50	17.7
9	CSA 13-93-1	2999.50	103.97	30.57	3.93	40.50	16.7
10	CSA 17A-93-1	2597.16	77.10	32.13	2.70	36.50	15.3
11	CSA 23-93-1	1774.11	81.10	36.67	4.23	40.00	16.3
12	CSA 5-93-4	2472.79	84.97	35.20	3.33	36.50	24.3
13	CSA-17A	1682.67	121.80	33.13	4.27	41.50	17.7
14	CSA-8	1646.09	113.37	35.80	3.73	40.00	20.7
15	CSA-11	987.65	135.00	30.57	4.40	42.00	17.7
16	CSA-13	2286.52	126.83	33.43	3.87	42.00	18.2
17	CSA-11-1	2085.04	95.53	33.47	3.40	42.00	17.8
18	CSA-13-1	2176.49	93.83	36.80	3.37	36.33	15.0
19	CSA 22-327	1810.69	105.60	33.00	3.37	39.50	19.0
20	CSA9A-13	1470.50	71.93	29.10	2.27	36.00	20.7
21	CSG-24	1975.30	65.73	32.67	2.27	31.00	17.0
22	CSG-18	2030.17	64.30	29.10	3.07	34.00	15.3
23	CSG-27	2121.62	84.67	35.87	1.83	38.00	16.3
24	RG-8	2090.98	90.07	33.63	2.47	36.00	16.2
25	LD327	1969.08	71.00	32.67	2.27	37.00	15.7
	$\bar{X}$	2167.18	88.04	32.98	3.25	38.69	17.72
	CV (%)	27.64	24.08	13.60	4.93	2.70	1.48
	S.E (d)	489.09	17.31	3.66	0.13	0.85	0.21

Table 2. Analysis of variance for yield and its component traits in *G. arboreum*

Source of variation	d.f.	Yield (kg/ha) (1)	Yield/plant (2)	Boll no. (3)	Boll wt. (4)	G.O.T. (5)	2.5% span length (6)
Replication	2	316792.0	6362.00	93.62	0.69	0.39	0.15
Genotypes	24	9462449.0*	1305.30*	24.38	1.45**	0.42**	19.93**
Error	48	358809.5	449.42	20.14	0.26	0.06	0.07
h^2 (%)		35.31	38.83	6.56	94.89	87.08	98.98
G.A.		541.64	21.68	0.63	1.38	5.22	5.27
G.C.V. (%)		20.42	19.18	3.61	21.23	7.02	14.52
P.C.V. (%)		34.36	30.79	14.08	21.80	7.52	14.59

of 5.4 m length with a spacing of 67.5 × 30 cm. The data was recorded on 10 random competitive plants in each treatment for seed cotton yield per plant and number of bolls per plant. Seed cotton yield kg per hectare was obtained by weighing the plot yield. G.O.T. (%) was recorded by weighing per cent of amount of lint obtained from 100 gm seed cotton. 2.5% span length in mm was measured by CIRCOT unit at CICR RS Sirsa. The genotypic coefficient of variation (Burton and Devane, 1953), heritability in broad sense (Lush, 1940), correlations (Robinson *et al.*, 1951), direct and indirect effects (Dewey and Lu, 1959) were calculated as per standard statistical methods.

RESULTS AND DISCUSSION

Significant genotypic differences were obtained for the traits, seed cotton yield kg/ha, seed cotton yield per plant, boll weight, G.O.T. (%) and 2.5% span length (Table 2). This indicated that adequate variability was present among the genotypes for these traits. Heritability value (6.56%) and genetic advance value (0.63) were low for number of bolls per plant. This indicated that the collections made have undergone considerable change during selection pressure and are maintained as small populations. Therefore, improvement through correlated characters could be more effective. Selection for seed cotton yield both on plot basis (35-31, 541.64) and per plant (38.83, 21.68) basis, boll weight (94.84, 1.38) G.O.T.% (87.08, 5.22) and mean fibre length (98.98, 5.27) would be effective and satisfactory for practical purposes as their genetic components (heritability, genetic advance) are of high value. Duhoon (1989), Sambamurthy and Reddy (1995) also observed high heritability and genetic advance for these traits.

The genotypic correlation coefficient (Table 3) of seed cotton yield/ha based on plot basis

Table 3. Correlation coefficients among yield components in *G. arboreum*

Character	Yield (kg/ha) (1)	Yield/ plant (2)	Boll no. (3)	Boll wt. (4)	G.O.T. (5)	2.5% span length (6)
G	1.00	–0.32	0.90**	–0.21	–0.14	–0.23
(1) P	1.00	0.16	–0.16	–0.13	–0.14	–0.14
E	1.00	0.45*	–0.45*	–0.09	–0.20	–0.20
G		1.00	0.60**	0.72**	0.63**	0.08
(2) P		1.00	0.04	0.38	0.37	0.05
E		1.00	–0.07	–0.30	–0.00	–0.01
G			1.00	–0.33	–0.34	0.48*
(3) P			1.00	–0.09	–0.03	0.13
E			1.00	–0.06	0.16	0.16
G				1.00	0.73**	0.08
(4) P				1.00	0.66**	0.08
E				1.00	–0.02	0.18
G					1.00	0.03
(5) P					1.00	0.03
E					1.00	0.14
G						1.00
(6) P						1.00
E						1.00

G = Genotypic correlation, P = Phenotypic correlation,
E = Environmental correlation

Table 4. Direct and indirect effects keeping yield/plant as dependent variable and others characters as independent

Character		Boll no./ plant (1)	Boll wt. (2)	G.O.T. (3)	2.5% span length (4)	Correlation with yield/ plant
Boll no.	G	(1.35)	–0.28	–0.16	0.31	0.60
(1)	P	(0.07)	–0.02	0.00	0.00	0.40
Boll wt.	G	–0.44	(0.87)	–0.34	–0.05	0.72
(2)	P	–0.01	(0.26)	–0.13	–0.00	0.38
G.O.T.	G	–0.45	0.64	(–0.47)	0.02	0.63
(3)	P	–0.01	0.17	(–0.20)	0.00	0.37
2.5% span length	G	0.65	–0.07	–0.01	(0.65)	0.08
(4)	P	–0.01	–0.02	0.00	(0.01)	0.05

In parentheses given values for, direct effects.
Residual effect G = –0.68; P = 0.83

were negative with seed cotton yield per plant,

Table 5. Direct and indirect effects keeping yield kg/ha as dependent variable and others characters as independent

Character		Yield/plant	Boll no./plant	Boll wt.	G.O.T.	2.5% span length	Correlation with yield kg/ha
Yield/plant	G	(–2.69)	–0.999	–1.50	0.56	0.04	–0.32
	P	(–0.29)	–76.38	–0.07	–0.05	–0.01	0.16
Boll no.	G	–1.61	(–1.67)	0.680	0.300	0.27	1.20
	P	–0.01	(–0.18)	0.02	–0.300	0.02	–0.16
Boll wt	G	1.93	–0.55	(–2.09)	0.65	0.044	–0.21
	P	0.11	–0.02	(–0.17)	–0.08	–0.01	–0.14
G.O.T.	G	1.70	–0.56	–1.52	(0.89)	0.02	–0.14
	P	0.11	–0.01	–0.11	(–0.13)	0.00	–0.14
2.5% span length	G	–0.21	–0.81	–0.17	–0.02	(0.56)	–0.23
	P	–0.02	–0.02	–0.01	–0.00	(0.11)	–0.14

In parentheses are given direct effects; Residual effect G = 3.43, P = 0.87

boll weight, ginning outturn and 2.5 per cent span length. Boll number per plant was the only trait which showed significant positive indirect contributor to seed cotton yield. None of the traits studied, showed positive indirect effect with G.O.T. At genotypic and phenotypic level number of bolls per plant showed negative association with boll weight and G.O.T. percentage, but its association was positive with fibre length. Boll weight showed significant positive associations at genotypic (0.73) and phenotypic level (0.66) with ginning outturn. Mean fibre length gave very weak association with traits *viz*; yield per plant, boll weight and G.O.T. percentage. Therefore selection of a plant type possessing high number of bolls per plant, high boll weight and long fibres should be made for increasing the seed cotton yield.

REFERENCES

Burton, G. W. and E. H. De Vane. 1953. Estimating heritability in tall fescue from replicated clonal material. *Agron. J.* 45: 478-487.

Dewey, D. R. and K. H. Lu. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 51: 515-518.

Duhoon, S. S. 1989. Variability, correlations and path analysis of nine characters in *Gossypium arboreum* L. *J. Indian Soc. Cotton Improv.* 14(1): 39-44.

Kumar, Chakresh, P. Joshi and R. P. Bhardwaj. 1992. Path analysis in Gossypium arboreum L. *J. ISCI.* 17(1): 23-26.

Lush, J. L. 1940. Intra-sire correlations or regression of offspring on dam as a method of estimating heritability of characteristics. *Ann. Proc. Amer. Soc. Anim. Produ.* 33: 293-301.

Robinson, H. F., R. E. Comstock and P. H. Harvey. 1951. Genotypic and phenotypic correlations in corn and their implications in selection. *Agron. J.* 43: 262-67.

Samamurthy, J. S. V. and B. M. Reddy. 1995. Genetic variability, correlation and path analysis in cotton. *ISCI J.* 20(2) : 133-139.

Singh, V., H. Singh, S. S. Verma, S. S. Tonk and S. S. Faroda. 1990. Correlation and path coefficient analysis of seed cotton yield and its components in cotton. *J. Indian Soc. Cotton Improv.* 15(2): 104-106.

Tomar, S. K. and S. P. Singh. 1992. Correlation and path-coefficient studies over environments in desi cotton (*G. arboreum* L.) *Indian J. Genet.* 52 (2): 187-191.

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GERMPLASM CHARACTERIZATION IN INDIGENOUS BLACKGRAM (*Vigna mungo* (L.) HEPPER)

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Three hundred twenty indigenous accessions, collected from diversity zones of Uttar Pradesh, were evaluated for 10 quantitative and 25 visual characters in incomplete block design, augmented with 4 checks. The characters, seed yield per m^2, pods per cluster and pods per plant exhibited high variability while the remaining seven traits, plant height, pod length, 100-seed weight, seeds per pod, days to flowering, relative chlorophyll index and days to maturity showed moderate to low variability. Full range of variability was observed for all the visual characters. About 60 and 10% accessions exhibited resistance reaction to yellow mosaic and leaf crinkle virus diseases, respectively.

Key words : Blackgerm, germplasm, characterization

Blackgram or urdbean (*Vigna mungo* (L.) Hepper) is a major pulse crop in asiatic region. The diversity of this crop is found maximum in India being a primary center of origin of this crop. The productivity of this crop has been far from satisfactory thus genetic improvement through exploitation of germplasm can be a priority area for vertical and horizontal expansion of this crop. A thrust for germplasm collection and evaluation is of utmost significance to have a dynamic breeding programme. The superior donor parents are urgently required for incorporating desirable characters in the plant type (Paroda, 1990). The explorations were carried out in diversity zones that is Hardoi, Bareilly, Barabanki, Sitapur and Kumaun and Garhwal divisions (Uttaranchal). The collections were also obtained from NPBGR, New Delhi for field evaluation purpose. The whole set of germplasm was evaluated under field conditions to characterize specific traits. The characterization has been done for 10 quantitative and 25 visual characters including diseases like yellow mosaic and leaf crinkle viruses.

MATERIALS AND METHODS

Three hundred twenty accessions along with 4 checks Narendra Urd-1, Type-9, Pant Urd-19 and Pant Urd-35 were sown at Crop Research centre, Pantnagar in an augmented block design with 16 blocks having 20 plots each in *Kharif* 1998. The check variaties were randomly replicated alongwith the test genotypes within the block and replicated as many times as the number of blocks. each accessions had two row plot of 4 m length, with row to row and plant to plant distance of 30 cm and 10 cm, respectively. The trial was unprotected for diseases. The data on 10 quantitative and 25 visual characters were recorded as per descriptor list published by IBPGR (1985).

The data obtained was subjected to statistical analysis for augmented design using method given by Federer and Raghav Rao (1975) and Peterson (1985) for 10 quantitative characters. The values of accession means were adjusted for the block effects as measured by check plots. The mean

values for all characters were utilized for estimation of mean, variance and range. The visual characters have been reported as such and their frequencies were only calculated.

RESULTS AND DISCUSSION

Mean and least significant differences of accessions and checks and range of accessions are presented in Table 1. On the basis of block errors the mean values for characters were 55 days for 50% flowering and 93 days for maturity. The mean value for plant height was 97.47 cm. The mean pods per plant came out to be 27.05, pods per cluster, 3.34, pod length 4.71, seeds per pod 6.51, 100-seed weight 3.03, seed yield per m^2 84.24 g and relative chlorophyll index as 36.29. The maximum values fo check means for seed yield per m^2 (149.72 g) was recorded for Type-9. The highest mean values of checks were observed for days to 50% flowering (51) and days to maturity (87) in case of Pant Urd-35 whereas Pant urd-19 had maximum plant height (123.76 cm). Check variety, narendra urd-1 had highest number of pods per plant (38.36), pods per cluster (3.68), pod length (5.00 cm), seeds per pod (6.66) and 100-seed weight (3.43 g).

The high variability among accessions was observed for seed yield per m^2 (cv = 36.87%; range 0.33 to 395.57 g), pods per cluster (cv = 21.54%; range 1.77 to 6.97) and pods per plant (cv = 19.10%; range 2.18 to 76.95). Minimum variability was observed for days to maturity (cv = 3.63%; range 67 to 130), followed by relative

Table 1. Mean, range and least significant differences in urdbean accessions and checks

Characters	Accessions	Checks				Coeffi-cient of variation (%)	Least significant difference			
		Check 1	Check-2	Check-3	Check-4		CM	AVSB	AVDB	AVAC
		Naren-dra urd-1	Type-9	Pant Urd-19	Pant urd-35					
Days to 50% flowering	55.00 (41-73)	46	47	48	51	4.47	1.49	5.94	6.64	4.84
Days to maturity	93.00 (67-130)	85	84	86	87	3.63	2.15	8.61	9.62	7.01
Plant height (cm)	97.47 (34.90-197.62)	107.04	118.99	123.76	109.81	9.08	7.23	28.92	32.33	23.57
Pods per plant	27.05 (2.18-76.95)	38.36	31.30	27.79	33.26	19.70	4.46	17.84	19.94	14.54
Pods per cluster	3.34 (1.77-6.97)	3.68	3.62	3.68	3.29	21.55	0.53	2.13	2.38	1.74
Pod length (cm)	4.71 (3.34-6.22)	5.00	4.73	4.83	4.80	7.83	0.26	1.05	1.18	0.86
Seeds per pod	6.51 (4.29-12.44)	6.66	6.58	6.48	6.62	5.98	0.27	1.09	1.22	0.89
100-seed weight (g)	3.03 (1.87-4.90)	3.43	3.28	3.14	2.94	6.07	0.13	0.54	0.60	0.44
Seed yield per m^2 (g)	84.24 (0.33-395.57)	121.34	149.72	115.74	120.68	36.87	32.41	129.65	144.94	105.65
Relative chlorophyll index	36.29 (13.50-54.60)	42.30	40.71	39.54	39.45	4.16	1.17	4.66	5.22	3.80

Note : Range given in parentheses ( ), CM = Between check means, AVSB = Between adjusted mean of two test genotypes in the same block, AVDB = Between adjusted mean of two test genotypes in different blocks, AVAC = Between an adjusted mean of a test genotypes against check mean

Table 2. Classification of visual characters in urdbean germplasm on the basis of frequency of character

Sl. No.	Character	Scale	No. of entry	Percentage of entry
1.	Hypocotyl colour			
	- Green	1	88	27.16
	- Green-purple	2	207	63.89
	- Purple	3	29	8.95
	- Dark purple	4	-	0.00
	- Mixed	5	-	0.00
2.	Seedling vigour			
	- Poor	3	11	3.40
	- Intermediate	5	247	76.23
	- Vigorous	7	66	20.37
3.	Growth habit			
	- Erect	1	16	4.94
	- Semi-erect	2	266	82.10
	- Spreading	3	42	12.96
4.	Growth pattern			
	- Determinate	1	145	44.75
	- Intermediate	2	179	55.25
5.	Branching pattern			
	- Basal	1	56	17.28
	- Central	2	228	70.37
	- Top	3	35	10.80
	- All over	4	5	1.54
6.	Primary leaf shop			
	- Ovate-lanceolate	1	323	99.69
	- Lanceolate	2	-	0.00
	- Apple shape	3	1	0.31
7.	Terminal leaf let shape			
	- Deltate	1	20	6.17
	- Ovate	2	299	92.28
	- Ovate-lanceolate	3	2	0.62
	- Lanceolate	4	2	0.62
	- Rhombic	5	-	0.00
	- Obovate	6	-	0.00
	- Apple shape	7	1	0.31
8.	Leaf pubescence			
	- Glabrous	0	1	0.31
	- Very sparsely pubescent	1	266	82.10
	- Puberulent	3	43	13.27
	- Moderately pubescent	5	13	4.01
	- Densely pubescent	7	1	0.31
9.	Leaf colour			
	- Light green	3	47	14.51
	- Intermediate green	5	249	76.85
	- Dark green	7	28	8.64
10.	Leafness			
	- Sparse	3	9	2.78
	- Intermediate green	5	86	26.54
	- Abundant	7	229	70.68
11.	Terminal leaflet length			
	- Short	3	5	1.54
	- Intermediate	5	239	73.77
	- Long	7	30	24.69
12.	Terminal leaflet width			
	- Narrow	3	4	1.24
	- Intermediate	5	232	71.60
	- Broad	7	88	27.16
13.	Leaf senescence			
	- No visible senescence	0	4	1.23
	- Slight visible senescence	3	218	67.28
	- Moderate senescence	5	85	26.23
	- Conspicuous concurrent senescence	7	17	5.25
14.	Petiole colour			
	- Green	1	37	11.42
	- Green with purple spots	2	144	44.44
	- Greenish purple	3	140	43.21
	- Purple	4	3	0.93
	- Dark purple	5	-	0.00
15.	Stem colour			
	- Light green	1	8	2.47
	- Dark green	2	42	12.96
	- Light purple	3	193	59.57
	- Dark purple	4	81	25.00
16.	Pod attachment to peduncle			
	- Penchant	3	9	2.78
	- Sub-erect	5	293	90.43
	- Erect	7	22	6.79
17.	Immature pod colour			
	- Light green	1	292	90.12
	- Dark green	2	32	9.88
18.	Mature pod colour			
	- Straw	1	8	2.47
	- Tan	2	1	0.31
	- Brown	3	47	14.51
	- Brown and black	4	229	70.68
	- Black	5	39	12.04
19.	Pod pubescence			
	- Glabrous	0	1	0.31
	- Puberulent	3	97	29.94
	- Moderately pubescent	5	222	68.52
	- Densely pubescent	7	4	1.23
20.	Pod shattering in field			
	- Absent	0	319	98.46

	- Present	1	5	1.54
21.	Seed shape			
	- Globose	1	37	11.42
	- Ovoid	2	149	45.99
	- Drum-shaped	3	138	42.59
22.	Seed colour			
	- Light green	1	11	3.40
	- Greenish brown	2	51	15.74
	- Brown	3	109	33.33
	- Chocolate	4	28	8.64
	- Black	5	63	19.44
	- Mottled	6	63	19.44
23.	Hiluym			
	- Concave	1	-	0.00
	- Non-concave	2	324	100.00
24.	Disease reaction			
	Yellow mosaic virus			
	- Resistance	1	195	60.19
	- Low susceptibility	3	55	16.98
	- Medium susceptibility	5	25	7.77
	- High susceptibility	7	17	5.25
	- Susceptible	9	32	9.88
	Leaf crinkle virus			
	- Resistance	1	33	10.18
	- Low susceptibility	3	79	24.38
	- Medium susceptibility	5	113	34.88
	- High susceptibility	7	81	25.00
	- Susceptible	9	18	5.55

chlorophyll index (cv = 4.15%; range 13.50 to 54.60), days to 50 per cent flowering (cv = 4.45; range 41 to 73). Moderate variability was observed for seeds per pod (cv = 5.98%; range 4.29 to 12.44), 100-seed weight (cv = 6.07%; range 1.87 to 4.90 g), pod length (cv = 7.83%; range 3.34 to 6.22 cm) and for plant height (cv = 9.08%; range 34.90 to 197.62 cm).

Accessions ShU9626 and ShU9630 showed flowering in 41 days and were earlier than all the checks. Similar was the pattern for days to maturity where the minimum days (67) were observed in ShU 9608 which was significantly earlier than the earliest check Type-9 (84 days). This was a collection from village Tursapathi in Bareilly district of Uttar Pradesh.

The range for various characters in the present collection indicates the presence of extreme types of all characters indicating high variability. The late maturing types (130 days) were distinct in their growth habit also. Similarly the seeds per pod upto 12.44 suggests an ample scope of variability utilization.

The shortest plants were found in accession SDI-43 and ShU9621 with mean value 34 and 35 cm. The tallest genotype recorded was IC 201886 with height of 197.62 cm. The accession ShU9534 which is a collection from Baniganj in Hardoi district of Uttar Pradesh had the highest number of pods per plant (76.95) which is significantly higher than all other genotypes followed by ShU9508 (68.82). The minimum number of pods per plant (2.18) was obtained in PLU-270 which had high foliage with less pods. The accession GV-400 had 6.97 pod per cluster followed by PLU-11300 (6.47) and PLU-1149 (6.14).

The largest pods were recorded in ShU9640 with average pod size of 6.22 cm, followed by NIC14632 (6.02 cm). The highest number of seeds per pod recorded was 12.44 in IC 201893 which had an entirely different plant type and very small seed size. It had trifoliate, apple shaped leaves. The plant remained green with shattering habit of pods. Among the typical urdbean genotypes, the highest seed per pod were found in NIC 14632 (8.99) followed by PLU-360 (8.59) and ShU9736 (8.09). The boldest grain were recorded in ShU9606 whih is a collection from Shergarh area in Bareilly district. The seed size recorded was 4.90 g per 100 seeds. The highest chlorophyll index was recorded for SD-1-61.

The high yielding genotypes like PLU-289 and ShU9682 with yields 395.57 g and 376.83 g, respectively were indicative of the facts that higher yielding germplasm are still available. Further testing of such accessions in wide areas will be needed. The evaluation data for quantitative

Table 3. Genetic donor for different characters

(1) **Days to 50 per cent flowering**

(a) Early type :

ShU9523, ShU9524, ShU9607, ShU9608, ShU9612, ShU9614, ShU9615, ShU9617, ShU9618, ShU9626, ShU9630, PLU-289 and PLU-317

(b) Late type :

ShU9508, ShU96126, PLU-305, PLU-346, PLU-1292, IC-37176, IC-38676, IC-38987, NIC-15271-1, NIC-15274, NIC-16446-A, NIC-16446-B, SD-3765, DPU-256, DPU-1018, NC-61003, H-6838, NKG-43

(2) **Days to maturity**

(a) Early type :

ShU9503, ShU9504, ShU9506, ShU9507, ShU9508, ShU9509, ShU9511, ShU9517, ShU9518, ShU9520, ShU9521, ShU9522, ShU9524, ShU9527, ShU9528, ShU9529, ShU9537, ShU9538, ShU9539, ShU9540, ShU9604, ShU9606, ShU9607, ShU9608, ShU9611, ShU9612, ShU9613, ShU9615, ShU9618, ShU9622, ShU9626, ShU9629, ShU9630, ShU9636, ShU9639, ShU9641, ShU9642, ShU9643, ShU9644, ShU9645, ShU9667, ShU96114, PLU-289, PLU-1278, IC-15270, IC-201889, INC-14632, NIC-16447-A, JBI-1133, JBT-2154, N-55, Type-9, VL-310

(b) Late type :

ShU9501, PLU-36, PLU-73, PLU-94, PLU-168, PLU-169, PLU-185, PLU- 187, PLU-118, PLU-189, PLU-190, PLU-199, PLU-205, PLU-226, PLU-227, PLU- 257, PLU-271, PLU-285, PLU-286, PLU-300, PLU-305,PLU-309, PLU-317, PLU-329, PLU-336, PLU-341, PLU-342, PLU-346, PLU-360, PLU-366, PLU-369, IC- 37176, IC-38676, NIC-15271-1, NIC-15274, DPU-5, DPU-87-14, DPU-88-5, DPU-256, DPU-1018, SDI-29, 2183-32, SV-2445, JV-566 and NE-15266.

(3) **Plant height**

(a) Tall type :

ShU9633, ShU96127, ShU9724, ShU9727, PLU-169,PLU-257, PLU-297, PLU- 360, PLU-1040, IC-73264, NIC-23231, K-6113

(b) Dwarf type :

ShU9618,ShU9621,SDI-43

(4) **Pods per plant**

ShU9502, ShU9505, ShU9508, ShU9534, ShU9543, ShU9606, ShU96100, ShU9724, PLU-384.

(5) **Pods per cluster**

PLU-297, PLU-1149, PLU-11300, NIC-16446-A, GV-400

(6) **Pod length**

ShU9508, ShU9509, ShU9518, ShU9598, ShU9603, ShU9604, ShU9606, ShU9607, ShU9617, ShU9627, ShU9628, ShU9633, ShU9634, ShU9639, ShU9640, ShU9641, ShU9642, ShU9645, ShU9667, ShU9682, ShU96129, PLU-433, 2183-32, NIC-14632.

(7) **Seeds per pod**

ShU9503, ShU9677, ShU9685, ShU96100, ShU96109, ShU96110, ShU96113, ShU96114, ShU9724, ShU9727, ShU9736, PLU-227, PLU-228, PLU-279, PLU-285, PLU-286, PLU-309, PLU-347, PLU-360, PLU-433, IC-16048, IC-23231, IC-38987, IC-201893 (With 12.436 seeds per pod), NIC-14361, NIC-14632, NIC-15274, 2183-32, 7PU-3

(8) **100-seed weight**

ShU9509, ShU9505, ShU9518, ShU9606, ShU9612, ShU9632, ShU9640, ShU9680, PLU-277, PLU-433, IC-292, IC-110649, K-61113, K-73302, JBT-9193, JBT-17152A, SDI-428-1, BDJ-85, VKP-574, 7PU-3, Pusa-105.

(9) **Seed yield per m^2**

ShU9609, ShU9627, ShU9630, ShU9637, ShU9677, ShU9681, ShU9682, ShU9684, ShU96100, ShU96109, ShU96133, ShU9723, ShU9724, PLU-26, PLU-224, PLU-228, PLU-237, PLU-251, PLU-277, PLU-279, PLU-289, PLU-317, PLU-363, PLU-433, PLU-1278, IC-292, IC-110649, IC-38987, IC-73301, IC-201887, IC-201893, NIC-14361, SD-1-61, K-61113, H-61, H-68, H-68, JBT-9194, SDI-428-1

(10) **Relative chlorophyll index**

ShU9502, ShU950, ShU9513, ShU9709, ShU9716, PLU-188, PLU-199, PLU- 228, PLU-260, PLU-261, PLU-264, PLU-270, PLU-271, PLU-285, PLU-360, PLU- 603, PLU-731, IC-16048, IC-223231, IC-201893, SD-1-61, K-1724, K-2543, K- 10-51, K-19-45, H-62, SDI-43, BDJ-116, N-832, Pusa-105.

(11) **Resistant genotype to yellow mosaic and leaf crinkle virus diseases**

ShU9511, ShU9513, ShU9603, ShU9606, ShU9612, ShU9614, ShU9621, ShU9716, ShU9727, ShU9736, PLU-289

characters clearly suggests the richness of variability in existing collection and scope of improvement over existing checks. Hawkes (1981) and Sharma *et al.* (1981) also emphasized the need of evaluation and use of diverse germplasm in crop plant.

The range and frequency of visual characters obtained in urdbean germplasm are presented in Table 2, it showed enough range of variation for visual characters also. Intermediate seedling vigour was obtained for 76.23% accessions while vigorous seedlings were observed in 20.37% accessions. Poor seedling vigour was recorded for 3.40% accessions.

Pod pubescence and leaf pubescence are thought to play a major role in insect resistance. Full range of variation for it was present in the germplasm studied. Majority of accessions (82.10%) showed very sparse pubescent leaves while glabrous leaves was observed for one accession i.e., IC 201893 (0.31%) Accession 2183-37 showed dense pubescent leaves.

Moderate pod pubescence was recorded for 68.52 per cent accessions while glabrous type pod pubescence was lowest in frequency (0.31 per cent). Being monogenic and dominant nature of pubescent character (Pathak and Singh, 1961 and Dwivedi and Singh, 1986) can be transferred easily into cultivated variety from the characterize germplasm lines. In majority of accessions (98.46%) pod shattering in field was absent, only 1.54 per cent accessions showed pod shattering in the field which is an undesirable character.

More than half of accessions (67.28%) showed slight visible senescence including ShU9514, ShU9515 and 5.25 per cent accessions including ShU9501, ShU9505, IC-201893 were found non-senescence which can be utilized in breeding programme to breed photoinsensitive lines. Ovoid seed shape was observed for 45.99 per cent accessions whereas globose and drum-shaped seed was obtained for 11.42 per cent and 45.99 per cent accessions, respectively. Full range of variation for seed colour was present but majority of accessions (33.33%) showed brown colour of seeds. The light green colour was obtained in 3.04 per cent of accessions. All accessions (100%) had protruded hilum on the seed.

Majority of accessions (60.19%) showed resistance against yellow mosaic virus while high susceptibility was observed only in 15.13 per cent accessions. About 25 per cent accessions showed low to medium susceptibility to yellow mosaic viruses (Table 2). About 10 per cent accessions were found resistant to leaf crinkle virus while major of accessions (59.26%) showed low to medium susceptibility against leaf crinkle virus disease. About 31 per cent accessions were found highlysusceptible to leaf crinkle virus disease (4.3). Accessions ShU9511, ShU9513, ShU9603, ShU9606, ShU9612, ShU9621, ShU9716, ShU9727, ShU9736 and PLU-289 were found resistant to yellow mosaic and leaf crinkle virus diseases both and can be utilized in the disease resistance breeding programme.

Based on the screening of different quantitative and visual characters of 320 accessions, some of the accessions were identified as donor for desirable character (presented in Table 3), can be utilized in breeding programme for improvement of a particular character. The seed of all these accessions will be deposited at National Gene Bank at NBPGR for long term conservation and utilization.

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REFERENCES

Dwivedi, S. and Singh, D. P. 1986. Inheritance of pod pubescence and seed coat colour in urdbean. *Crop Improv.* 13: 54-57.

Federer, W. T and Raghava Rao, D. 1975. On augmented designs. *Biometrics.* **31**: 29-35.

Hawkes, J. G. 1981. Germplasm collection, presentation and use. Frey, J. J. ed. Plant Breeding. Vol. 11. Iowa State University. 57-84.

IBPGR 1985. Descriptor for *Vigna mungo* (Revised). IBPGR (now IPGRI), Rome, 23 p.

Paroda, R. S. 1990. Production and improvement of pulse. Crops. *In* : Genetic improvement of pulse crops ed : Jafar Nizam and Irfan A. Khan and S. A. Farook.

Pathak, G. N. and Singh, K. P. 1961. Inheritance of hairy characters on pods in blackgram. *Curr. Sci.* **30**: 434-435.

Peterson, R. G. 1985. Augmented design for preliminary yield trials (Revised). RACHIS. *Barley and Triticale News Letter.* ICARDA 4(1): 27-32.

Sharma, H. C.; J. G. Waines and Foster, K. W. 1981. Variability in primitive and wild wheat for useful genetic Characters. *Crop Sci* **21** (4) : 555-559.

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A NOTE ON AUGMENTED DESIGNS

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The optimum number of replications of the control treatment(s) in each of the blocks of an augmented randomized complete block design or comparing test treatments with control treatment(s) has been worked out. This replication number maximises the efficiency per observation of the best linear unbiased estimates (BLUE) of the test treatment vs control treatment contrasts. An augmented randomized complete block design with a single control appearing exactly once in each of the blocks has been shown as A- and MV-optimal for making test treatments-control comparisons in a general block design set up. Such a block design is a connected block design with minimum number of observations. The combinations of number of test treatments and number of blocks for which such A- and MV-optimal designs maximise the efficiency per observation have also been obtained.

Key words : Augmented designs, efficiency per observation, designs with minimum number of observations, A-optimality, MV-optimality

In many agricultural situations, experiments are often conducted where the existing practices called control treatments or check varieties are to be compared with new varieties or germplasm collected through exotic or indegenous collections, called test treatments. The experiment material for test treatments is scarce and it is not possible to replicate them in the design. However, enough material is available for replicating control treatments in the design. These kind of experimental situations encountered by Federer (1955) in screening new strains of sugarcane and soil fumigants used in pineapples. Augmented (Hoonuiaku) designs were introduced by Federer (1956) to fill a need arising in screening new strains of sugarcane at Experimental Station of Hawaiian Sugarcane Planters Association on the basis of agronomic characters other than yield. An augmented experimental design is any standard experimental design in standard (control) treatments to which additional (new or test) treatments have been added. The additional treatments require enlargement of either the complete block or the incomplete block in the block design setting and the complete or incomplete rows and (or) columns in the row-column design settings, etc. The augmented design for 1-way elimination of heterogeneity settings is known as augmented block design. The block sizes in these designs may be unequal. Augmented designs eliminating heterogeneity in two directions are called augmented row-column designs. Federer (1956, 1961) gave the analysis, randomization procedure and construction of these designs by adding the new treatments to the blocks of a randomized complete block (RCB) design and balanced lattice designs. Federer (1963) gave procedures and designs useful for screening material inspection and allocation with a bibliography. Federer and Raghavarao (1975) have given a general theory of augmented designs. They obtained the augmented block designs using RCB

designs and linked block designs for 1-way elimination of heterogeneity and augmented row-column designs using a Youden square design. Federer, Nair and Raghavarao (1975) gave general methods of construction of augmented row column designs. They also provided formulae for standard errors of estimable treatment contrasts.

A survey of the literature reveals that generally such experiments are conducted using an augmented randomized complete block design. However, the experimenters would often like to know how many times the control treatments be replicated in each of the blocks so as to maximize the efficiency per observation for making test treatments vs control treatment(s) comparisons? To make the idea clearer, consider the following examples:

METHODOLOGY

Example 1 : Consider an experimental situation where 16 tests are to be compared with a single control treatment. The experiment can be laid out in a block design with four blocks, but there is no scarcity of experimental units and the blocks may contain almost 16 experimental units. The four blocks may have unequal number of experimental units. There is enough material available on control treatment that can be replicated but the test treatments can be replicated only once. We studied three possible designs (D1, D2 and D3) in which the replication of the control in each block was one, two and three, respectively. Thus, in the three designs, the control is replicated four, eight and twelve times. The average variance of the BLUE of the tests vs control contrasts and efficiency per observation for the three designs is as given below :

Design	Variance	Efficiency/ observation
D1: w = 16, u = 1, = 4, r = 1, n = 20	$2\sigma^2$	$(1/40)\ \sigma^{-2}$
D2:w = 16, u = 1, b = 4, r = 2, n = 24	$(3/2)\ \sigma^2$	$(1/36)\ \sigma^{-2}$
D3:w = 16, u = 1, b = 4, r = 3, n = 28	$(4/3)\ \sigma^2$	$(3/112)\ \sigma^{-2}$

In the table w denotes the number of test treatments, r the number of times the control is replicated in each of the blocks, b the total number of blocks, n the total number of experimental units and σ^2 the error variance. One can see that in the above example D2 is better than D1 and D3 according to efficiency per observation criterion. It can also be observed that efficiency per observation doesn't increase with the increase in the number of replication of the control in each block (r).

Example 2 : Consider another experimental situation where 36 test treatments are to be compared with two control treatments. The experiment can be laid out in a block design with three blocks. The blocks may have unequal number of experimental units. There is enough material to have replications on controls but the test treatments can be replicated only once. We studied three possible designs (D1, D2 and D3) in which the replication of the control in each block was one, two and three, respectively. Thus in the three designs each of the control treatments is replicated three, six and nine times. The average variance of the BLUE of the test vs control contrasts and efficiency per observation for D1, D2 and D3 is given in the following table.

Design	Variance	Efficiency per observation
D1 : w = 36, u = 2, b = 3, r = 1, n = 42	$(15/9)\ \sigma^2$	$(1/70)\ \sigma^{-2}$
D2 : w = 36, u = 2, b = 3, r = 2, n = 48	$(12/9)\ \sigma^2$	$(1.64)\ \sigma^{-2}$
D3 : w = 36, u = 2, b = 3, r = 3, n = 54	$(11/9)\ \sigma^2$	$(1.66)\ \sigma^{-2}$

One can see that in the above example D2 is better than D1 and D3 according to efficiency per observation criterion. It can also be observed that efficiency per observation doesn't increase with the increase in the number of replication of the control in each block (r). Therefore, it is important to answer the above question and in

section 2, we have made an attempt to answer this question.

RESULTS AND DISCUSSION

Consider an experimental situation in which $w = \sum_{j=1}^{b} k_j$ test treatments are to be compared with u control treatments each replicated r times in each of the b blocks such that j^{th} block size is $k_j + ur$, $j = 1, \ldots, b$. The total number of experimental units are $w + ubr$ and the total number of treatments is $w + u$. If we denote $1, \ldots, w$ as test treatments and $w + 1, \ldots, w + u$ as control treatments, then the coefficient matrix of reduced normal equations for estimating treatment effects is given by :

$$C = \begin{bmatrix} A_1 & 0 & \cdots & 0 & -\frac{r}{k_1+ur} 1_{k_1} 1_u' \\ 0 & A_2 & \cdots & 0 & -\frac{r}{k_1+ur} 1_{k_1} 1_u' \\ \vdots & \vdots & \cdots & \vdots & \vdots \\ 0 & 0 & \cdots & A_b & -\frac{r}{k_b+ur} 1_{k_b} 1_u' \\ -\frac{r}{k_1+ur} 1_u 1_{k_1}' & -\frac{r}{k_2+ur} 1_u 1_{k_2}' & \cdots & -\frac{1}{k_b+ur} 1_u 1_{k_2}' & br\, 1_u - \left(r^2 \sum_{j+1}^{b} \frac{1}{k_j+ur} \right) 1_u 1_u' \end{bmatrix}$$

$$C = \begin{bmatrix} 1_{k_1} + \frac{1}{ur} 1_{k_1} 1_{k_1}' & 0 & \cdots & 0 & 0 \\ 0 & 1_{k_2} + \frac{1}{ur} 1_{k_2} 1_{k_2}' & \cdots & 0 & 0 \\ \vdots & \vdots & \cdots & \vdots & \vdots \\ 0 & 0 & \cdots & 1_{k_b} + \frac{1}{ur} 1_{k_b} 1_{k_b}' & 0 \\ 0 & 0 & \cdots & 0 & \frac{1}{br}\left[1_u - \frac{1}{u} 1_u 1_u' \right] \end{bmatrix}$$

The contrasts of main interest are those between test treatments and control treatments and it is easy to see that the design in variance balanced with respect to these contrasts and variance of BLUE of each of these contrasts is given by

$$\text{Var}\ (\hat{\tau}_t - \hat{\tau}_c) = \left(\frac{ubr + b + u - 1}{ubr} \right) \sigma^2;$$

$$\forall t = 1, \ldots, w,\ c = w + 1, \ldots, w + u \quad (2.1)$$

where σ^2 is the error variance.

Therefore, Average variance, $\overline{V} = \sigma^2 \left(\frac{ubr + b + u - 1}{ubr} \right)$

$$\text{Efficiency} = \frac{\sigma^{-2}\, ubr}{ubr + b + u - 1}$$

$$\text{Efficiency/Observation} = \frac{\sigma^{-2}\, ubr}{(ubr + b + u - 1)\,(w + ubr)}$$

$$= \sigma^{-2}\, \varphi\,(b, w, u, r) \qquad \ldots (2.2)$$

For fixed b, u and w, φ behave as a function of r and is independent of $k_1, \ldots, k_b$ separately. It depends on the k_j's only through $w = \sum_{j=1}^{b} k_j$

$$\varphi(b,w,u,r) = \frac{-b-u+1}{(w-b-u+1)\,(ubr+b+u-1)} + \frac{-w}{(-w+b+u-1)\,(w+ubr)}$$

$$= \frac{1}{w-b-u+1}\left[\frac{-b-u+1}{ubr+b+u-1} + \frac{w}{w+ubr}\right]$$

$$\varphi'(r) = 0$$

$$\Rightarrow \frac{-w}{(w+ubr)^2} + \frac{u+b-1}{(ubr+b+u-1)^2} = 0$$

$$\Rightarrow \frac{\sqrt{w}}{w+ubr} = \frac{\sqrt{u+b-1}}{ubr+b+u-1}$$

$$\Rightarrow \sqrt{w}\, ubr + \sqrt{w}\,(b+u-1) = w\sqrt{u+b-1} + ubr\sqrt{u+b-1}$$

$$\Rightarrow ubr\,(\sqrt{w} - \sqrt{u+b-1}) = \sqrt{u+b-1}\,\sqrt{w}\,(\sqrt{w} - \sqrt{u+b-1})$$

$$\Rightarrow ubr = \sqrt{u+b-1}\,\sqrt{w}$$

$$\Rightarrow r = \frac{\sqrt{u+b-1}\,\sqrt{w}}{ub}$$

$$\Rightarrow r = \frac{1}{u}\sqrt{\frac{u+b-1}{b}}\,\sqrt{\frac{w}{b}} \qquad \ldots (2.3)$$

$$\varphi''(r)\Big|_{r=\frac{1}{u}\frac{\sqrt{u+b-1}}{b}\sqrt{\frac{w}{b}}} < 0$$

requires that $b+u-1 \le w$. Therefore, the efficienty per observation is maximized when r is as given in (2.3) provided b + u − 1 ≤ w. For example, consider the problem of obtaining the optimum number of replications of the controls in an experiment with w = 24, u = 3, b = 4. We have

$$r+\frac{1}{3}\sqrt{\frac{6\times 24}{4\times 4}} = 1.$$

Similarly, for w = 98, u = 2, b = 7, we have

$$r+\frac{1}{3}\sqrt{\frac{8\times 98}{7\times 7}} = 2$$

Remark 2.1 : For a single control situation, i.e. u = 1, the expression (2.3) reduces to $r=\sqrt{\frac{w}{b}}$ and it can easily be seen that for $u=1, b$, which is always true.

There may, however, arise many combinations of w, u and b for which expression (2.3) does not yield a positive integer value of r. In such situations, a question arises as to what integer value of r should be taken. For this efficiency per observation has been calculated of $w \le 100, b \le 25$ and $u \le 10$ such that $b+u-1 \le w$ and r has been taken as $r^* = int(r)$ and $int(r)+1$ in the expression (2.3) besides taking r = 1. A close scrutiny reveals that if value of r > #. 42 then take $r^* = int(r)+1$ and for values of r smaller than or equal to #. 42 take $r^* = int(r)$ for $u \ge 2$. For u = 1, the same rule applies but the value of r is taken as #. 45 instead of #. 42.

The augmented design with u = 1 and r = 1 are the designs with minimum number of observations i.e., number of observations (n) = number of treatments (w + 1) + number of blocks (b) − 1. These designs can be obtained by allocating control treatment to each of the blocks once and allocating the treatments 1, ..., w to the remaining units of the blocks such that a treatment appears in only one block. For example, a design with w + 1 = 9, b = 4, k = 3 is

9	9	9	9
1	3	5	6
2	4	6	8

These designs have been shown to be A- and MV- optimal for making test treatments-control comparisons in a proper block design set up by Dey, Shah and Das (1995). Through simple algebra on the lines of Lemma 4.1 and Theorem 5.2 of Dey, Shah and Das (1995), it can be shown that the above procedure gives A- and MV-optimal designs for making test treatments control comparisons under a non-proper block design set up as well. At this stage, one may pose a question whether A- and MV-optimal designs for making test treatments-control comparisons also maximizes the efficiency per observation or not. To answer this question, the combinations of w and b which maximizes the efficiency per observation have been obtained through empirical investigations as described earlier for obtaining the value of r, and are given in the following table.

b	w
2	3 to 4
3	4 to 6
4	5 to 8
5	6 to 10
6	7 to 12
7	8 to 14
8	9 to 16
9	10 to 18
10	11 to 20

11	12 to 22
12	13 to 24
13	14 to 26
14	15 to 28
15	16 to 30
16	17 to 32
17	18 to 34
18	19 to 36
19	20 to 38
20	21 to 40
21	22 to 42
22	23 to 44
23	24 to 46
24	25 to 48
25	26 to 50

It is to be noted that analysis of the designs so generated does not pose any problem as a g-inverse of C, C^- is given and adjusted treatment total vector can be obtained as per procedure of general block designs and other sum of squares can be obtained as per established procedures and various types of contrasts can be estimated using contrast analysis.

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REFERENCES

Dey. A, K. R. Shah and A. Das. 1995. Optimal block designs with minimal and nearly minimal number of units. *Statistica Sinica* 5(2): 547-558.

Federer, W. T. 1955. Experimental Design : Theory and Applications. McMillan, New York.

Federer, W. T. 1956. Augmented designs. *Hawaiin Planters' Record* 55: 191-208.

Federer W. T. 1961. Augmented designs with one way elimination of heterogeity. *Biometrics* 17: 447-473.

Federer, W. T. 1963. Procedures and designs useful for screening material in selection and allocation with a bibliography. *Biometrics* 19: 553-587.

Federer, W. T. and D. Raghavarao. 1975. On augmented designs. *Biometrics* 31: 39-45.

Federer, W. T., R. C. Nair and D. Raghavarao. 1975. Some augmented row column designs. *Biometrics* 31: 361-374.

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PEST RISK ASSESSMENT ON NEMATODE DISEASES OF ROSES OF INDIA

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An analysis of the risk to rose plants in India from possible introduction of plant parasitic nematodes is done by assembling relevant biological, climatic and commercial information. The risk presented by different exchange propagules is assessed and phytosanitary measures to reduce the risks are proposed. The conclusions of the PRA, based on EPPO guideline No.1, is that nematodes of species not yet reported from India, present a serious risk to the industry. All sorts of exchange of live material should be rooted through quarantine inspection.

Key words : Rose, pest risk analysis, PRA, nematodes, floriculture

Floriculture has become a potential money-spinner for the developing countries. It is a multi million rupee industry in India. The liberalisation of industrial and trade policies in July 1991, paved way for development of export oriented production of cut flowers. The seed policy of 1988 had already made it possible to import planting material of international varieties. Floriculture was included in the export and import policy as one of the areas eligible for setting up exports oriented units (EOU's). Various measures are being taken up at the Government level to support this sector.

More than 140 countries are now involved in floriculture trade. Netherlands is the largest producer and exporter of cut flowers with as much as 63 per cent share of the total world exports. Germany is the largest importer, its share in World Trade being around 37 per cent. The largest consumer of flowers and plants is Norway followed by Switzerland, Denmark, Sweden and Germany. India's share in the export of floriculture products in World market is less than 1 per cent.

The important floriculture crops in the international cut flower trade are rose, camation, chrysanthemum, orchids, tulip, anthurium, lilies, iris and liasanthus. According to a report of Agricultural and Processed Food Products Export Development Authority (APEDA) and National Horticulture Board (NHB), for India the estimated area and production under ornamentals in 1994-95 were 53000 hectares and 4 lakh tonnes respectively. Government of India allows subsidy on airfreight, import duty and customs duty. Units engaged in floriculture are permitted duty free imports. Soft loans at 4-5 percent are available from the NHB.

Pest Risk Assessment

Information was collected in the format of EPPO PRA Guideline No. 1 "Checklist of information required for PRA (OEPP/EPPO, 1993)". Analysis could not be made due to non-availability of basic data.

Part A : Information for PRA

Section 1 : The Organisms (Potential disease causing organism)

List of plant parasitic nematodes reported on roots in rhizosphere of the plants along with

country of occurrence are in Table 1. There are no reports of plant parasitic nematodes on cut flowers or other above ground parts of rose plants.

Table 1. Some important nematode species reported on roses

Pratylenchus crenatus	Nurseries in Poland	Wojtowicz & Sobilo, 1994
P. penetrans	Poland	- do -
P. projectus	Poland	- do -
P. vulnu	Poland	Schneider et al. 1995
P. coffeae	Bulgaria	Katalan & Budurova 1979
P. brachyurus	Pakistan	Saeed *et al.* 1988
P. zeae	Pakistan	Saeed *et al.* 1988
P. penetrans	Belgium	Ann. 1975
P. penetrans	Denmark	Jakobsen 1976
P. vulnus	Denmark	Santo 1974
P. vulnus	Europe	EPPO 1977
P. vulnus	Japan	Hayashi 1976
P. vulnus	Florida, USA	Lehman 1982
P. penetrans "	Florida, USA	
P. vulnus	Italy	Lamberti *et al.* 1987
Meloidogyne hapla	Nurseries in Poland	Wojowicz & Sobilo 1994
M. javanica	Pakistan	Zaina & Maqbool 1995
M. incognita	Pakistan	- do -
M. hapla	Netherland	Ann. 1978
M. incognita	U.P.,India	Hasseb *et al.* 1978
M. hapla	Belgium	Ann. 1975
M. hapla	Denmark	Santo 1974
M. hapla	Japan	Hayashi 1976
M. hapla	Florida, USA	Lehman 1982
Longidorus elongatus	Nurseries in Poland	Wojtowics & Sobilo 1994.
L. alaskaensis	Alaska	Robbins and Brown 1996
L. paralaskaensis	Alaska	- do -
L. bernardi	Alaska	- do -
L. ala	Alaska	- do -
L. macrosoma	Florida, USA	Lehman, 1982
Xiphinema cobbi	U.P. India	Sharma & Saxena 1981
X. indica	U.P. India	- do -
X. basiri	Rajasthan, India	Roy 1980
X. diversicaudatum	Florida, USA	Lehman 1982
X. brevicolle	Florida, USA	Lehman 1982
X. americanum	Pakistan	Saeed *et al.* 1988
Tylenchorhynchus rosei	Pakistan	Zarina & Maqbool 1991
T. microdoratus Bulgaria	Katalan & Budurova 1979	
T. brassicae	U.P., India	hasseb *et al.* 1978
T. annulatus	Pakistan	Saeed *et al.* 1988
T. martini	Pakistan	Saeed *et al.* 1988
T. mashhoodi	Pakistan	Saeed *et al.* 1988
Helicotylenchus sp.	T.N., India	Sundara & Vadivelu 1988
H. verecundus	Pakistan	Zarina & Maqbool 1991
H. shakili	H.P., India	Sultan,1981
H. dihystera	H.P., India	Sultan,1981
H. valecus	H.P., India	Sultan,1981
H. indicus	U.P.,India	Haseeb et al 1978
Rotylenchus gracilidens	Bulgaria	Katalan & Budurova 1979
R. calvus	Bulgaria	- do -
R. reniformis	U.P.,India	Hasseb *et al*, 1978
R. reniformis	Pakistan	Saeed *et al*, 1988
Ditylenchus pumilus	Bulgaria	Katalan & Budurova 1979

1.1. Relationship with known quarantine pests

Some important nematode pests associated with rose plants are *Pratylenchus vulnus, P. penetrans, meloidogyne indica, M. hapla, Longidorus* sp., *Xiphinema americanus.* Most of the countries would not import material grown in nursery/field infested with these nematodes. Plants, rootstock, soil adhered to roots or plant debris in the packing material could be carried for the nematode species.

1.2 Methods of identification for inspection purposes

Nematodes are identified and classified, based on morphology and morphometrics measurements. Observations are taken with the help of high power microscopes, using guidance from taxonomic literature. DNA fingerprinting and PCR techniques are now being used to distinguish certain closely related species. Microsatellite dot blot technique is also useful for differentiating species. The modern techniques are available only to few laboratories and have not yet been developed sufficiently to be reliable tool for routine diagnosis.

1.3 Methods for detection

Nematodes are associated with roots and occur in rhizosphere. Some of them are endoparasites; semi endoparasites while others are ectoparasites. For detection of ectoparasites, processing of soil from the rhizosphere could give a fair idea about not only presence or absence but also its population per unit of soil. For detection of endo and emiendo parasitic nematodes roots are either stained or soaked in water for at least 24 hours at 15-20 C. Active nematodes move into the water suspension and could be examined after concentration through sieves. Aerial parts of rose are generally free from nematodes, but thorough washing of stem/budwood cuttings or flowers with water would further ensure and prevent, if any, nematode adhering within aerial parts and flowers. Expertise is required to distinguish plant parasitic nematodes and correct identification.

Section 2 : Biological characteristics of pest and its vectors

2.1 Life Cycle

Immediately after the larva comes out of egg, it tries to locate host plant. All the laral and adult stages feed on cells of the host roots. Endoparasitic nematodes penetrate epithelial and cortical cells; some cells of the stele grow into giant cells/nurse cells to support nematodes. Two genera of plant parasitic nematodes on roses - *Longidorus* sp. and *Xiphinema* sp. are vectors of viral diseases. After continuous feeding, nematodes moult to adult, mate inside or outside - in soil and begin to lay eggs. During this propagative stage of multiplication, the nematode population is composed of males, females and four juvenile stages.

2.2 Dissemination and dispersal

Rose parasitic nematodes are restricted to aquatic environment - i.e. roots and soil. Movements of soil and plants/rooted cuttings from nurseries/fields to new areas assist in dispersal of nematodes. Human activities are known to be the principal route for dispersal over greater distances. *Pratylenchus* sp., *Meloidogyne* sp. and *Tylenchorhynchus* sp. have been intercepted on a number of occasions during international exchange of rooted plants, rootstock or with soil - as contaminant along with plants/packing material.

2.3 Survival under adverse conditions

The nematodes have temperature dependent life cycles and are adapted to survive periods of low moisture (eggs, cysts and other anhydrobiotic stages), low and high temperatures stages. Nematodes inside the plant root are safe and survive for a very long period. Finding differential temperatures to kill nematodes, without injuring its hosts, for salvaging is generally a tedious job.

2.4. Adaptability

Nematodes have remarkable flexibility in its biology. They are able to enter the ecosystem in an area for outside its normal geographic range; adapting to different host species and different climatic conditions. They are known to have different biotypes and races. DNA profiles indicate considerable plasticity in the nematode genome. Populations from different parts of world show small differences in morphology and pathogenicity (biodiversity)

Section 3 : Geographical distribution of pests

Sufficient data is not available for the distribution of nematode species in or outside India. Information is scattered and most of the research papers are on taxonomic identification. Many of the survey reports are indicative of the distribution of Nematologists rather than nematodes themselves.

The overall distribution of nematodes is again host, moisture, temperature, soil type and soil pH dependent. Some species are prevalent in one area while others are dominant in another.

3.1 Area of origin and history of spread

Data is not available and predictions have not been made about origin or spread of nematode pests of roses, though nurseries play an important role in sporadic spread. Inter national/continental movements are through exchange of amterial/human activities.

3.2. Overlap of world distribution of the pests with that of major hosts

Consolidated literature about worldwide distribution of nematode pests of roses is not available. Most of the reported nematodes on roses have very wide host range.

Section 4 : Host plants of the pests

4.1 Host plants reported in areas where the pest now occurs

Most of the nematode pests of roses have very wide host range. Data on full host range/plants reported in the PRA (India) area or where the pest now occurs is not available.

4.2 Host plants growing in PRA area (i.e. India)

Data is not availale on weeds, crop rotation, alternate crops, and mixed crops, grown along with roses and their pests. The area under rose cultivation is wide spread and native crops grown in the area are not studied. The reported nematode pests are known to have very wide host range.

Section 5 : Potential of the pest for establishment in the PRA area

5.1 Climatic conditions for pest development

The optimal conditions for the pest development are the same as required for the host/rose development and survival. There are optimum temperature and moisture conditions for the host and pest multiplication, therefore extent of damage on roses depends upon climatic conditions of the area..

5.2. Data on climatic conditions in PRA area

India being a big country has got all types of climates, starting from temperate in the north, to tropical, subtropical and xerophytic in the west. Rose pests, coming along with host or otherwise from other countries could easily accommodate themselves in rose growing areas.

Section 6 : Control of the pests

6.1. Control measures

Growing of rootstock in pest free area is important and desirable wherever the material is for movement. Fumigation, hot water treatments and pesticidial dip/spray treatments are being used as a precautionary measure for plants, rooted cuttings, cut flowers under exchange.

6.2. Records of eradication of the pest

There is no record of any successful eradication programme from a field/region. Populations have been managed below threshold level for *Pratylenchus* sp. under glass house/nurseries by steaming soil and using nematode free rootstocks. Plants/rooted cuttings could be salvaged for exchange through hot water and nematicidal treatments.

Section 7 : Transport of the pest

7.1. Methods of natural spread elsewhere in the world

Natural but slow spread of nematodes occurs

through movement of soil, rooted plants from fields/nurseries, wind storms, irrigation canals and through farm machinery. Nematodes on their own can move, a few inches in a year. Long distance movements are through the man.

7.2. Pattern of international trade in the major host plants of the pest

Most of the international trade and exchange of germplasm for improving quality, takes place through cut flowers, but wood/stem cuttings which in general does not impose threat of nematode spread along with it. Additional precautions could be taken to wash stem cuttings with running water at the place of origin and packing them in pest/soil free material.

To some extent material exchanged for commercial use are either grafted plants or rootstocks. These could carry nematodes. In no case soil should be allowed to come along with the exchanged material. Plants exchanged as far as possible, should have been grown on a disease/pests free nursery. Suitable treatments are advised for salvaging at the point of export and verification of the same at the country of import. Still there are chances of escape of few pests especially from a bulk consignment.

7.3 Records of interception of the pest

Important nematode pests - *Pratylenchus* sp., *Tylenchorhynchus* sp. and *Meloidogyne* sp. have been intercepted along with international shipments of roses. The nematodes are known to survive in roots for at least a year in dominant stage and could therefore survive shipment to any destination from any source.

7.4 Records of movement of the pest not associated with host plants

Apart from movement of nematode pests along with plants and rooted cuttings, there are reports of movement of live nematodes along with non-hosts, in soil clods and damp packing material.

7.5 Specific pathways for movement of the pests to the PRA area

Nematode pests reported on roses are of very wide host range, so it is not necessary that they should enter in the PRA area through rose germplasm/commercial material. All the exchanged planting material should be thoroughly examined to confirm pest free movement of plants/seeds.

Section 8 : Economic impact of the pest

8.1 Recorded economic impact

Rose is an important ornamental crop of India. Cut flowers are in great demand in national and international market. Nematodes are known to not only reduce yield but also have drastic effect on their quality. Quality/size of the cut flowers makes a big difference on economy of the crop. Therefore all precautions and measures should be taken to reduce the chances of entry of a new nematode (pest) species through imported consignment or through infested nurseries.

8.2 Estimated effect of the presence of the pest on exported commodities

Cost fetched in the international market would be drastically reduced for the cut flowers as their size and quality goes down. Export of plants because of quarantine reasons and plant products (cut flowers) because of quality will not be possible once the pests (nematodes) get introduced in the nurseries/fields. Although treatments are available but no country would prefer to risk their own flower production/industry by importing plants from diseased regions/nurseries, as 100% control (eradication)is seldom achieved.

8.3 Costs and side effects of control measures

There are no side effects of salvaging treatments if proper time and temperature combinations is used for curing plants/planting material of roses through hot water treatment. Cost involved is negligible.

CONCLUSIONS

From the assessment of the information available, potential nematodes -

Pratylenchus vulnus, P. projectus and Meloidogyne hapla, pose a threat to roses in Indian subcontinent. There are two pathways for the nematodes to enter, firstly through introduction of infested plants/root stock of roses or any other host plant and secondly by contamination of soil clods mixed with seeds/packing material. Conditions are favourable for establishment of the nematodes as appropriate host plants roses, ornamental and fruit crops are widely grown with favourable climatic factors.

Inter population mating and development of hybrids of other rose parasitic nematodes already present in our country are possible (Riga *et al.* 1992). Such hybrids may alter pathogenicity traits and survival strategies.

Exchange of rose plants and rootstock involves a great risk from nematode pest. Cut flowers and stem cuttings are comparatively risk free. Therefore as far as possible exchange of germplasm should be through stem cuttings while international trade should be restricted to cut flowers only.

REFERENCES

Riga, E., K. Beckenbach and J. M. Webster. 1992. Taxonomic relationships of *Bursaphelenchus xylophilus* and *B. mucronatus* based on interspecific and intraspecific cross hybridisation and DNA analysis. Fundamentals and *Applied Nematology* **15**: 391-395.

OEPP/EPPO. 1993. Guideline on pest risk analysis. No.1. Check list of information required for pest risk analysis (PRA). *Bulletin OEPP* **23**: 191-198.

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COLLECTION AND EVALUATION OF HILL RICE GENOTYPES OF ASSAM

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In an exploration undertaken in the hills zone of Assam, comprising Karbi Anglong and North Cachar Hills districts, a total of 76 hill rice genotypes were collected from 42 sampling sites. High variation was observed among the genotypes for all the traits studied. GCV and PCV were recorded high (> 50%) for yield per plant. Heritability estimates were recorded high for all the traits. A high estimates of genetic advance were recorded for grain yield per plant, grains per panicle, tillers per plant and spikelets per panicle. High heritability coupled with high genetic advance was observed in yield per plant, grains per panicle, tillers per plant and spikelets per panicle, which revealed predominance of additive gene action in inheritance of these traits. Three cultivars *viz.* Maibee Socket and Banglai were identified promising for grain yield per plant.

Key words : Rice, collection, evaluation, genotype, variability, heritability, genetic advance

Hills zone of Assam comprised Karbi Anglong and North Cachar Hills districts. Here rice is grown mostly in the hilly slopes as *jhum* (shifting cultivation through burn and slush method) and also in terraces. A number of hill rice cultivars are grown by the farmers of these two districts. These cultivars are mainly poor in yielding ability but highly adaptable to the existing agro-ecological condition. Most of these cultivars are tolerant/ resistant to water stress, major diseases and insects-pests. Moreover, they possess lot of other agronomically important traits. These local cultivars are facing imminent danger of extinction due to recent trends in agricultural development. Hence, collection and evaluation of these genotypes for various morpho-physiological traits is an important breeding aspects for identification of outstanding genotypes to use as such and also for development of suitable rice varieties for the region. Keeping this view in mind, the present work was planned to collect and evaluate the hill rice germplasm of Assam.

MATERIALS AND METHODS

Agro-ecology

The hills zone of Assam has diverse agro-ecological situations resulting from variation in slope (0-80%), altitude (95m to 1000m above mean sea level), temperature (3.7°C to 40.1°C) and average annual rainfall (1000mm to 2500mm). Hill rice cultivars are mainly grown in hilly slopes as *jhum* (shifting cultivation through burn and slash) and also in terraces either as mixed or mono-crop under direct seeded rainfed condition. Micro- environments such as day to day and day and night temperature and also soil characteristics differ markedly from place to place and within a short distance. All these factors lead to accumulation of enormous variability among the rice cultivars grown in this zone.

Collection strategy

An itinerary for collection of germplasm was prepared in consultation with the State Department

Table 1. Range, mean and mean squares of different quantitative traits in hill rice genotypes of Assam

Characters	Range	Mean ± SE	Mean Square	
			Variety	Replication
Days to 50% flowering	81.00-145.00	101.36 ± 1.46	485.532**	98.450**
Days to maturity	113.50-162.50	126.86 ± 1.35	414.812**	0.161
Plant height (cm)	88.85-161.80	127.62 ± 1.69	652.019**	142.453**
Tillers/plant	3.35-12.50	8.45 ± 0.26	15.945**	0.011
Leaf length (cm)	40.65-73.70	57.54 ± 0.96	200.218**	3.561
Flag leaf length (cm)	21.80-49.15	34.30 ± 0.64	93.114**	20.271*
Leaf breadth (cm)	1.22-2.20	1.66 ± 0.03	0.171**	0.110**
Flag leaf breadth (cm)	0.973-1.88	1.42 ± 0.03	0.138**	0.018
Panicle length (cm)	19.70-31.85	25.64 ± 0.30	19.808**	1.303
Spikelets/panicle	81.75-293.00	181.77 ± 5.24	6252.752**	312.053
Grains/panicle	51.50-243.25	131.47 ± 4.96	5619.908**	2007.484**
100 grain weight (g)	1.17-3.00	1.84 ± 0.04	0.432**	0.003
Yield/plant (g)	5.05-35.35	15.26 ± 0.92	194.364**	2.524

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

of Agriculture, Assam, and the areas covered are given in Fig. 1. Farmer's field was taken as a unit area and random samples from the populations and biased samples of the elite materials were collected (Chang, *et al.*, 1972, Chang, 1976, Pandravada and Reddy, 1990). Germplasm samples were also collected from threshing yards and farm stores (Pandravada *et al.*, 1996). Each germplasm sample was given an accession number and name of the farmer, place and date of collection were also recorded.

Materials and Design

All the 76 rice genotypes were grown in randomized block design with three replications during summer 1998 at Regional Research Station, Diphu (25° 50' N longitude, 90° 30' E latitude and altitude of 180m above m.s.l). Observations were recorded for 13 yield and yield attributes *viz.* days to 50% flowering, days to maturity, plant height, tillers per plant, leaf length, flag leaf length, leaf breadth, flag leaf breadth, panicle length, spikelets per panicle, grains per panicle, 100 grain weight and grain yield per plant. The data were subjected to analyze variances. Genotypic and phenotypic co-efficient of variances (GCV and PCV) were worked out according to the formulae suggested by Burton (1952) while heritability (broad sense) and genetic advance (GA) as percentage of mean were obtained using the formulae of Hanson *et al.* (1956).

RESULTS AND DISCUSSION

Seventy-six hill rice germplasm were collected from 42 sampling sites of Karbi Anglong and North Cachar Hills districts of Assam (Fig. 1). Significant variations were observed among the genotypes for all the traits studied (Table 1). Wider ranges of mean performances were observed for all the traits indicating greater magnitude of variability among the genotypes. Grain yield per plant ranged from 5.05 to 35.35g. High GCV

Table 2. Genetic variability and its related parameters in hill rice genotypes of Assam

Characters	6^2g	6^2pm GCV(%)	PCV(%)	Heritabilit (b.s)%		GA% of mean
Days to 50% flowering	159.49	166.55	12.46	12.73	95.76	25.12
Days to maturity	137.49	139.83	9.24	9.32	98.33	18.88
Plant height (cm)	208.93	234.16	11.33	11.99	89.22	22.04
Tillers/plant	5.07	5.81	26.65	28.53	87.20	51.24
Leaf length (cm)	63.62	72.98	13.86	14.85	87.17	26.66
Flag leaf length (cm)	29.58	33.95	15.86	16.99	87.13	30.49
Leaf breadth (cm)	0.05	0.07	13.47	15.94	71.43	23.45
Flag leaf breadth (cm)	0.04	0.05	14.47	16.41	77.78	26.29
Panicle length (cm)	6.21	7.39	9.72	10.60	84.12	18.37
Spikelets/panicle	1951.45	2349.84	24.30	26.67	83.05	61.51
100 grain weight (g)	0.14	0.15	20.58	20.75	98.42	42.03
Yield/plant (g)	64.23	65.91	52.52	53.20	97.45	106.80

and PCV were recorded for grain yield per plant (52.52% and 53.20% respectively) indicating maximum variability among the genotypes for this trait. While, moderate GCV and PCV values 20% to 50% were recorded for grains per panicle, tillers per plant and 100-grain weight. The remaining traits showed relatively low GCV and PCV estimates. Heritability estimates were recorded high for all the traits studied. It ranged from 71.43 per cent in leaf breadth to 98.42 per cent in 100-grain weight. Higher estimates of heritability revealed lower environmental influence in expression of these traits depicting reliability for phenotypic selection. Genetic advance as percentage of mean were observed high for yield per plant (106.80%), grains per panicle (61.51%), tillers per plant (51.24%) and spikelets per panicle (45.63%). The remaining traits exhibited relatively low genetic advances. High heritability coupled with high genetic advance as observed in yield per plant, grains per panicle, tillers per plant and spikelets per panicle indicated predominance of additive gene effects in inheritance of these traits and thus revealed relatively higher feasibility for phenotypic selection. Similar observations were also reported by Kihupi and Dote (1989), Marimuthu *et al.* (1990), Deb Choudhury and Das (1998).

On the basis of mean performances of genotypes, few promising lines were identified for various agronomic traits (Table 3). One cultivar, Izong was found suitable for semidwarf plant type (88.85 cm) while four cultivars *viz.*, Maigogang, Baodm, Maidaola, and Banglai were selected for tall plant type (153.00 to 161.80 cm). Ten genotypes *viz.* Maibee, Miren, Maiju Guphu, Baodum, Izong, Petchiam, Maitotai, Bairing, Mailong Chang and N.D.C were found promising for more numbers of tillers per plant (11.00 to 12.50). Petchiam and Maiguangang were two genotypes selected for longer panicle (30.30 to 3.185 cm), while, Bairing and Maichu were identified promising for more grains per panicle (243.25) and more test weight (30.00g) respectively. Three genotypes *viz.*, Maibee, Socket and Banglai were identified promising for grain yield per plant (33.80 to 35.35 g). These three genotypes may be recommended as such for cultivation by the farmers of the region after elaborate yield traits. All these genotypes identified

Table 3. Promising cultivars identified for various agronomic traits on the basis of their mean performances

Characters		Promising cultivars
1.	Semi dwarf plant type (88.85 cm)	Izong
2.	Tall plant type (153.00 to 161.80 cm)	Maigogang, Baodum, Maidaola, Banglai
3.	More tillering ability (11.00 to 12.50 tillers/ plant)	Maibee, Miren, Maiju Guphu, Baodum, Izong, Petchiam, Maitotai, Bairing, Mailong Chang, NDC
4.	Longer panicle (30.30 to 31.85 cm)	Petchiam, Maiguangang
5.	More grains/panicle (243.25 grains/panicle)	Bairing
6.	More grain weight (test weight (30g/1000 grains)	Maichu
7.	More grain yield/plant (33.80 to 35.35 g/plant)	Maibee, Socket, Banglai

for various traits may be used as suitable breeding material for future breeding purposes.

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REFERENCES

Burton, G.W. 1952. Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Cong.*, 1: 277-283.

Chang, T.T. 1976. Manual on the genetic conservation of Rice Germplasm for evaluation and utilization. IRRI, Los Banos, Philippines.

Chang, T.T., S.D. Sharma, C.R. Adair and A.T. Perez. 1972. Manual for field collectors of rice. p. 32. IRRI, Los Banos, Philippines.

Deb Choudhury, P.K. and P.K. Das. 1998. Genetic variability, correlation and path co-efficient analysis in deep water rice. *Ann. Agric. Res.* **19**(2): 120-124.

Hanson, G.H., H.F. Robinson, and R.E. Comstock. 1956. Biometrical studies of yield in segregating populations of *Korean lespedeza. Agron. J.* 48: 268-272.

Kihuphi, A.N. and A.L. Dote. 1989. Genotypic and environmental variability in selected rice characters. *Oryza* **26**(2): 129-134.

Marimuthu, R., S. Rajasekaran, and G. Soudrapondian. 1990. Association of yield and its components in rice (*Oryza sativa* L.), *Madras agric. J.* 77 (9-12): 443-446.

Pandravada, S.R. and B.R. Reddy. 1990. Paddy Germplasm collection in Nellore district and adjoining areas, Andhra Pradesh. *In*: M.N. Koppar, S.S. Duhoon, Umesh Srivastava and Anjula Pandey (eds). *Germplasm Collection Reporter*, Vol. **1**(1), p. 2-7, NBPGR, New Delhi.

Pandravada, S.R., N. Sivraj, and K.R.K. Murthy. 1996. Collection of rice germplasm from Adilabad district, Andhra Pradesh, India. *Indian J. Pl. Genet. Resources* **9**(2): 255-259.

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Short Communication

APPLICATION OF INDEX SCORING METHOD FOR SELECTION OF MULBERRY GENOTYPES

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In mulberry (*Morus* spp.) which is sole food plant of silkworm, breeding objectives are mainly concentrated on qualitative and quantitative improvement of foliage in contrast to fruit trees. With a view to select potential parents, 60 accessions of mulberry from diverse origin were evaluated for propagation, foliage yield and quality parameters. In the present study, for selection of promising genotypes, index scoring method was used where the index values are determined by Euclidian distance. Based on index values, 10 genotypes were selected as potential parents over checks.

Key words: Mulberry, evaluation, index scoring method

The objectives of breeding mulberry (*Morus* spp.) are mainly concentrated on the quantitative and qualitative improvement of foliage in contrast to fruit trees and cereals. Since mulberry is a perennial crop grown under varied agro- climatic conditions, cultivation of high yielding strains with good quality leaf and adaptability to specific regions is the cheapest and long standing method to realize higher income. To meet the above breeding objectives, large scale and long term breeding programmes are necessary for which adequately conserved broad spectrum genetic variability is a pre-requisite. The conserved germplasm genotypes need to be evaluated for identifying potential parents for successful hybridization. In the present study, the exotic genotypes were evaluated for different unrelated characters and potential parents have been identified using Index scoring method.

Germplasm genotypes of various geographical origin maintained at CSR&TI, Mysore were used for the study. Among the 60 exotic genotypes evaluated, maximum of 26 were from Japan, five accessions were from Pakistan, four from Indonesia, four from Paraguay, three from China, three from Bangla Desh, two from Italy, two from France, one from USSR, one from Burma and 10 exotic accessions (origin not known). 60 accessions maintained as high bushes at 45 cm height under 1.5 × 1.5 m spacing were used for the study and recommended package of practices for irrigated mulberry (Krishnaswamy, 1978) were followed. Observations on propagation, growth yield and quality parameters like sprouting, rooting, plant height, number of branches, internodal distance, weight of 100 fresh leaves, area of 100 leaves and moisture percentage were recorded following the methods suggested by Jolly and Dandin (1986).

For analysis of the data on various unrelated parameters, Index scoring method was followed as suggested by Barreto and Raun (1991) of International wheat and Maize improvement Centre (CIMMYT), Mexico. The programme computes a variable called 'INDEX' which

Table 1. Genotypes of different geographic origin included in the study

Origin	Names of genotypes/Acc. No.
Japan	Kosen, KNG, Kairyoroso, Mizusawa, Tsukasagawa, Goshoerami, Kokuso-27, Roso, Kenmochi, Kokuso-21, Ichihei, Katania, Roko-kuyaso, Ensatakasuke, Shimanochi, Kokuso-20, Atsubamidori, Okinawa, Kasuga, Togowase, Acc. 167, Ichinose, Limoncina; Shin-ichinose, Senmatsu, Tomeisc.
China	China white, China peking, MR-1
Pakistan	PKS-1-12, PKS-1-11, PKS-1-9, PKS 1-4, PKS-1-2
Indonesia	*M. australis, M. multicaulis, M. nigra,M. cathayana*
Paraguay	Ferno-dias, Calabresa, Paraguay, Miuraso
Bangladesh	Shrim-2, Shrim-5, Shrim-8
Italy	Cattaneo, Italian sarnal
France	English black, France
USSR	Sannish-5
Burma	Burma-8
Exotic	Acc. 107, Acc. 116, Acc. 123, Acc. 134, Acc. 135, Acc. 148, Acc. 151, Acc. 152, Acc. 165

mathematically incorporates all the characters indicated by the user's objective. The best genotype is the one that has the smallest index value and closely relates with the desired objectives.

The genotypes included in the study and their place of collection is presented in Table 1. The data on maximum, minimum, average values and CV% of different parameters is presented in Table 2. The i ndex values along with the different parameters of the top 10 genotypes selected by index scoring method are presented in Table 3.

The sprouting percentage ranged from 0.00 to 97.00 per cent average being 41.744 per cent the rooting percentage ranged from 0.00 to 96.67 per cent average value being 33.705 per cent. Plant height varied from 32.40 cm to 207.40 cm with an average value of 115.103 cm. Number of branches ranged from 2.00 to 36.00 with an average value of 13.852. The minimum internodal distance recorded was 2.25 cm and the maximum was 7.69 cm, the average value being 4.411 cm. Weight of 100 fresh leaves ranged from 101.69 g to 896.00 g with an average value of 355.189g. Area of 100 leaves ranged from 4781.00 cm^2 to 34200.00 cm^2 with an average value of 13035.180 cm^2. Moisture percentage ranged from 60.81 to 78.09 with an average value of 73.62%. The variability was maximum for rooting character (104.80%) followed by sprouting (86.81%) and number of branches (58.75). The variability in weight of fresh leaves and leaf area was almost same (38.09% & 38.07% respectively). The variability for plant height and internodal distance were 34.48% and 22.01% respectively. The variability was lowest (4.27%) for moisture percentage.

Table 2. Maximum, minimum, average values and CV% for different parameters

Parameter	Maximum	Minimum	Average	St. dev.	CV %
Sprouting (%)	97.00	0.00	41.744	36.239	86.81
Rooting (%)	96.67	0.00	33.705	35.324	104.80
Plant height (cm)	207.40	32.40	115.103	39.692	34.48
No. of branches	36.00	2.00	13.853	8.138	58.75
Int. distance (cm)	7.69	2.25	4.411	0.971	22.01
Weight of 100 fresh leaves (g)	896.00	101.69	355.189	135.308	38.09
Area of 100 leaves (g)	34200.00	4781.00	13035.180	4963.674	38.07
Moisture (%)	78.09	60.81	73.621	3.142	4.27

Table 3. Listing of top genotypes selected by index scoring

Name of the genotype	Origin	Index value	Sprouting (%)	Rooting (%)	Pl. ht. (cm)	No. Branches	Int. distance (cm)	Fr.wt. of 100 leaves (g)	Area of 100 leaves (cm^2)	Moisture (%)
Mizusawa	Japan	17.2	90.00	80.00	149.80	28.0	5.50	580.80	20889.0	72.86
English Black	France	17.7	57.54	95.40	105.80	36.0	4.19	455.00	13987.0	74.05
Kairyo roso	Japan	18.2	84.60	79.50	136.40	15.0	4.01	406.98	16185.0	74.50
Miuraso	Paraguay	18.6	83.00	85.00	207.40	23.0	5.43	355.57	14061.0	75.33
M. multicaulis	Indonesia	19.1	23.30	76.67	143.80	10.0	5.16	896.00	34200.0	74.80
China peking	China	19.3	42.90	40.90	129.80	28.0	5.00	393.55	16036.0	74.90
Shrim-5	Bangladesh	19.4	97.00	83.00	193.60	32.0	5.68	281.47	12100.0	75.98
MR-1	China	19.7	66.00	66.00	109.50	19.0	6.23	693.00	28230.0	73.66
Kosen	Japan	19.7	10.00	10.00	119.70	28.0	4.53	490.17	16690.0	74.29
China White	China	19.9	96.60	89.70	131.80	20.0	4.33	322.17	13956.0	71.99

In mulberry the main aim is to increase the leaf yield, improve leaf quality and bolster the resistance against disease or climatic hazards (Hazama, 1967). This can be achieved through various ways and the most successful one being hybridization among desirable parents and selection of superior hybrids. The tropical mulberry genotype have been endowed with good rooting, growth and yield characters but are medium or poor in quality parameters. On the other hand, the temperate genotypes show medium yield and good quality but are poor in rooting and growth characters. For combining these desirable traits in the progeny through hybridization, identification of potential parents is the first step. As mulberry is vegetatively propagated, once a desirable genotype is obtained it can be multiplied without any segregation.

While selecting a mulberry genotype many unrelated characters have to be considered to arrive at a conclusion as to the superiority of a genotype. Different parameters like propagation, growth, yield and quality are involved in the present study. Values of some of the attributes need to be high and some low, for judging the superiority of the genotype. When selection is made separately for different attributes no single common genotype would appear to be listed hence rendering it difficult for the breeder in selection procedure. Under such a condition, a comparative assessment irrespective of quantitative or qualitative character has to be made and index scoring method was found to be more suitable method. Based on the index scoring values, top 10 genotypes viz., Musizawa, English Black, Kairyo roso, Miuraso, M. multicaulis, China peking, Shrim - 5, MR-1, Kosen and China white were selected. Of the 10 genotypes selected, three were from Japan, three from China, one from France, one from paraguay and one from Bangladesh. These 10 genotypes have been identified as potential exotic parents for future hybridization programmes in mulberry.

REFERENCES

Barreto and Raun. 1991. MST data assistant. Intnatl Wheat & Maize Improvement Centre (CIMMYT), Mexico.

Hazama K. 1967. Breeding of mulberry tree. JARQ 3: 15-19.

Jolly M. S. and S. B. Dandin. 1986. Collection, conservation and evaluation of mulberry (*Morus* spp.) germplasm. CSR & TI, Mysore, 44 p.

Krishnaswamy, S. 1978. Mulberry cultivation in South India. CSR&TI Bull. No. 1 CSRTI, Mysore, 18 p.

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Short Communication

FIELD SCREENING OF MUSKMELON GERMPLASM AGAINST CUCUMBER GREEN MOTTLED MOSAIC VIRUS

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Forty germplasm lines of muskmelon were screened for cucumber green mottled mosaic virus (CGMMV) under field conditions and on the basis of two-year observations, average per cent disease index (PDI) was calculated. The maximum disease incidence was observed in Bagpat Local while phoot (*Cucumis melo* var. momordica) showed minimum disease incidence of CGMMV. Out of 40 germplasm, 16 were observed to be resistant while 17 and 7 germplasm, showed moderately resistant and susceptible reaction respectively. The resistant germplasm can be utilized for evolving disease resistant varieties with desirable quality traits.

Key words : Muskmelon, CGMMV, screening, resistance

Cucumber Green Mottled Mosaic Virus (CGMMV) is one of the most limiting factor for muskmelon production in the garden land as well as in the river beds of north India (Roychaudhuri and Varma, 1975). Research on screening and resistance breeding aspects for this disease was hardly undertaken in India barring the reports of More *et al.* (1993) and Pan and More (1996). Keeping in view the above facts, the present investigation was conducted at IARI, New Delhi during spring summer season of 1996-97 and 1997- 98 to screen muskmelon germplasm against CGMMV under field condition. Forty (40) germplasm consisting of released varieties, local collections, exotic collections, breeding lines [cross derivatives of phoot (R) × M4 (S) and FM1 (R) × Pusa Madhuras (S)] and wild species were undertaken for the study. The crop was sown in rows, 2.5 cm apart with a spacing of 45 cm between the plants. All the recommended agronomical packages were followed to grow a successful crop in spring summer season. However, no insecticide was applied during the entire period of crop. Out of 12 plants, 10 were marked for taking observations of the disease reaction. The screening was done on the basis of weekly observation on occurrence of the above disease in each genotype throughout the growing period. For scoring the resistance, the scale from resistance to susceptibility ranging from 0 to 5 was assigned. The scale used on the basis of symptom expression is given below :

0	No symptoms	Immune (I)
1	Slight vein clearing,very light mottling of light and dark green colour in younger leaves	Resistant (R)
2	Mottling of leaves with light and dark green colour	Moderately Resistant (MR)
3	Blisters and raised surface on leaves	Moderately Susceptible (MS)
4	Distortion of leaves	Susceptible (S)
5	Stunted growth with negligible or no flowering and fruiting	Highly Susceptible (HS)

Table 1. Percent disease index and reaction of muskmelon germplasm against CGMMV

Sl. No.	Germplasm	P.D.I. (%)		Average (%)	Reaction
		1996-97	1997-98		
1	Pusa Madhuras	34.8	24.6	29.7	MR
2	Pusa Sarbati	52.8	62.7	57.7	S
3	Punjab Sunheri	34.9	28.9	31.9	MR
4	Lucknow Safeda	28.6	37.2	32.9	MR
5	Chittidar	66.5	57.8	61.6	S
6	Harela	19.8	16.3	18.0	R
7	Ravi	58.5	62.8	60.5	S
8	T-96	39.3	54.9	47.1	MR
9	Punjab Rasila	12.3	16.9	14.6	R
10	Batti-1	30.8	26.8	28.8	MR
11	Batti-2	22.6	29.7	26.1	MR
12	Batti-3	24.8	39.8	32.3	MR
13	Batti-4	37.0	19.8	28.4	MR
14	Batti-5	25.4	27.9	26.6	MR
15	Batti-6	24.9	29.4	27.1	MR
16	Bagpat Local	67.0	76.8	71.9	S
17	NDM-5	42.6	49.8	45.6	MR
18	NDM-9	39.8	44.7	42.3	MR
19	Honey Dew	29.8	33.4	31.6	MR
20	Joublen	72.8	62.7	67.8	S
21	51-2	7.5	5.9	6.7	R
22	53-5	4.9	6.2	5.5	R
23	31-1-2	4.3	5.9	5.1	R
24	29-1	6.9	7.6	7.2	R
25	7-12	9.8	16.3	13.1	R
26	43-6	4.8	4.1	3.9	R
27	42-4	3.9	5.8	4.8	R
28	5-10A	5.1	4.6	3.4	R
29	5-10B	3.9	6.8	5.3	R
30	Gurbeli	29.9	37.5	33.7	MR
31	M3	36.8	41.6	39.2	MR
32	Durgapura Madhu	62.6	53.8	58.2	S
33	Hara Madhu	32.6	23.3	27.9	MR
34	Charantris	19.8	13.6	16.7	R
35	Topmark bush	29.3	38.4	33.8	MR
36	PI 414723	11.6	8.2	9.9	R
37	PI 124122	7.8	4.3	6.0	R
38	Mau	59.8	67.4	63.6	S
39	Phoot (*C. melo* var. momordica)	2.7	3.6	3.1	R
40	Kochri (*C. callosus*)	11.8	19.4	15.6	R

The scoring was done in the morning to avoid the confusion between the resistant and moderately resistant plant. On the basis of symptoms expressed by the individual plant, per cent disease index (PDI) values for each germplasm were calculated as suggested by Silbernayel and Jafri (1974) and Bos (1982). On the basis of two-year data, average PDI was calculated and five reaction categories were made as suggested by Pan (1993).

Average PDI values of 40 germplasm and their reaction on the basis of five reaction categories are presented in Tables 1 and 2. The average PDI values varied from 3.1 per cent to 71.9 per cent. The maximum value was observed in Bagpat Local (71.9%), while phoot (*Cucumis melo* var. *momordica*) showed minimum incidence (3.1%). The breeding lines 51-2, 53-5, 31-1-2, 29-1, 7-12, 43-6, 5-10A and 5-10B derived from crosses, Phoot (resistant) × M4 (susceptible) and FM1 (resistant) × Pusa Maduras (susceptible) at Division of Vegetable Crops, were observed to be quite promising (Table 1). Out of 40 germplasm screened, 16 were observed to be resistant, while 17 and 7 germplasm, showed moderately resistant and susceptible reaction towards CGMVV. None of the germplasm was found to be either immune or highly susceptible.

The germplasm observed to be resistant, will be utilized in breeding programme to develop CGMMV resistant/tolerant varieties with desirable horticultural characters.

Table 2. Reaction of muskmelon germplasm against cucumber green mottled mosaic virus based on five categories

P.D.I(%)	Reaction category	Number of genotypes
0	Immune (I)	0
1-25	Resistant (R)	16
26-50	Moderately Resistant (MR)	17
26-50	Susceptible (S)	7
76-100	Highly Susceptible (HS)	0

REFERENCES

Bos, L. 1982. Crop losses caused by viruses. *Advances in Virus Research* 2: 31-57.

More, T. A., A. Verma, V. S. Seshadri, R. G. Somkumar and L. Rajamany. 1993. Breeding and development of cucumber green mottled mosaic virus (CGMMV) resistant lines in melon (*Cucumis melo* L.). *Cucurbit Genetics Cooperative* 16: 44-46.

Pan, R. S. 1993. Breeding for multiple disease resistance in muskmelon (*Cucumis melo* L.) Ph.D. Thesis, Division of Vegetable Crops, IARI, New Delhi.

Pan, R. S. and T. A. More. 1996. Screening of melon (*Cucumis melo* L.) germplasm for multiple disease resistance. *Euphytica* **88**(2): 125-128.

Roychaudhuri, M. and A. Varma. 1975. Virus diseases of cucurbits in Delhi. *Proc. 62nd Ind. Sci. Congr.* **Part III**, 74 pp.

Silbernagel, M. J. and A. M. Jafri. 1974. Temperature effects on curly top resistance in *Phaseolus vulgaris*. *Phytopath.* **64**: 825-827.

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Short Communication

CONTRIBUTION OF EXOTIC GERMPLASM IN WHEAT BREEDING IN INDIA

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Indian wheat programme has released/identified about 212 wheat varieties till date since 1965. Of these, 162 varieties have exotic germplasm in their pedigree either as a direct release or as a parent in a cross. An increasing reliance on exotic germplasm threatens our local material. A judicious use of local germplasm from different sources is suggested to make further gains in productivity.

Key words : Wheat, exotic germplasm, pedigree, direct selection

Introduction has always been an important breeding method in any crop. Early varietal improvement work has witnessed movements of plant material across the continents at massive scale. Indian agriculture has benefitted a great deal from this important tool of crop improvement. Some notable examples are Sonora 64, Lerma Rojo, Sonalika, Kalyansona (wheat), TN1, IR8, IR21, IR28 (Rice), Bonneville, Arkel (garden pea), Delchrest, Virginia Gold Tobaco (*N. tabacum*), Bragg, Lee (soybean), and Sioux (tomato) etc. The list is endless and very impressive as these have been the landmark varieties in their respective crops.

Establishment of International research institutes gave a further impetus to the movement of plant genetic material across the international boundaries. Wheat (*Triticum aestivum* L.) improvement work across the globe benefits from the movement of wheat germplasm affected through international nurseries and trials coordinated by International Center for Maize and Wheat Improvement (CIMMYT), Mexico. Indian wheat improvement work has also been benefitted by these activities ever since its inception (Sharma and Mishra, 1999).

Indian wheat programme has so far released over 200 varieties till date during post green revolution phase (Table 1). Of these, about 76 per cent have exotic germplasm or foreign introductions in their pedigree either as direct release (Table 2) or as a parent (Table 3). About 28 per cent of all the released varieties are the direct release of foreign introduction or a selection in the introduction and an overwhelming 48 per cent of all the varieties involve exotic germplasm as a parent. A study conducted by Jag Shoran *et al.*, (1998) revealed that 40 per cent of advance test entries in All India Coordinated Wheat Improvement Trials during 1991-92 to 1995-96 were exotic germplasm, however it was interesting to note that among the final year test entries, the proportion of better yielding indigenous genotypes was quite high (32%) as compared to exotic material which stood at 23 per cent. However, an interesting observation has been that though the relative importance of exotic germplasm is coming down but its acceptability as a direct

Table 1. Number of wheat varieties released/identified in India after 1965

Period	Varieties involving exotic germplasm as			Others	Total
	Direct release	Parent in pedigree	Total		
1965-1970	7 (29.2)	13 (54.2)	20 (83.4)	4 (16.6)	24
1971-1980	15 (27.3)	30 (54.5)	45 (81.8)	10 (18.2)	55
1981-1990	15 (19.7)	44 (57.9)	59 (77.6)	17 (22.4)	76
1991-1999	23(40.4)	15 (26.3)	38 (66.7)	19 (33.3)	57
Total	60(28.3)	102(48.1)	162(76.4)	50(23.6)	212

Table 2. Wheat varieties released/identified in India from 1965 till date which are either direct introductions or selections from introductions

Sl. No.	Variety	Year	Pedigree
1	Sonora 64	1965	YT54/N10B//2*Y54
2	PV 18	1966	KALYANSONA SIB
3	Chhoti lerma	1967	LR64 SIB/HUAR
4	Sonalika	1967	MIDA-U/K-117A//2*TH3/FN/4*TH/4/AN/5/YT54/N10B//LR/6/B494
5	Kalyansona	1967	PJ SIB/GB55
6	Safed Lerma	1968	Y50/N10B//L52/3/3* LR
7	UP301	1970	LR64/SN64
8	UP310	1973	KLRE/RAF//LR64/2* SN64
9	UP319	1973	CNOSIB//SN64/KLRE/3/8156
10	VL404	1973	KT/BAGE//FN/GU/3/ST464(DR)/P174106(DR)
11	VL Gehun 401	1973	FKN/N10B
12	K852	1973	SEL.S308=SKA SIB
13	K816	1973	CNOSIB//SN64/KLRE/3/8146
14	Arjun (HD2009)	1974	LR64A/NAI60
15	Shera	1974	LR64A/SON64
16	UP215	1974	TZPP/SN64
17	UP368	1974	LR64/SN64
18	CC 464	1979	BB/CNO/SN64
19	GW40	1979	INIA66*2/7C
20	HP1102	1979	8156(B)/NAD63
21	VL GEHUN421	1979	SN64//Y50E/GTO
22	UP 2003	1980	BB/2*7C
23	HW 517	1981	BB/CC/3/CNO/NO//PI
24	RAJ 1482	1982	NAPO/TOB SIB//8156/3/KAL/BB
25	ROHINI	1983	BON//CNO/SN64/3/KAL/BB
26	MANGLA	1989	GLL/AUSTII61/157//CNO.NO/3/KAL/BB
27	PURBALI	1984	KVZ/TI//TITO
28	MALVIYA 206	1985	KVZ/BUHO//KAL/BB
29	HW 741	1985	HW 517 SIB
30	CPAN 1796	1985	NAPO/TOB SIB//8156/3/KAL/BB
31	GW 120	1985	INIA66/CNO/INIA66/BB/3/Y50E/3*KAL
32	GW 405	1985	CNO/INIA66//BB/3/CNO//PI/GLL
33	WL 2265	1985	NAPO/TOB SIB//8156/3/KAL/BB
34	HI 977	1988	GLL/AUSTII61.157//CNO/NO/3/Y50E/3*KAL
35	HS 207	1989	KVZ/BUHO//KAL/BB
36	HS 240	1989	AU//KAL/BB/3/WOP/4/PVN
37	HS277	1991	KVZ/CGN

Sl. No.	Variety	Year	Pedigree
38	HS295	1991	CQT/AZ//IAS55/ALDML SIB/3/ALDML SIB/NAFN/4/PJN/SIB.PEL 1276.69
39	MACS 2496	1991	VEE#5
40	WH 542	1992	HPW 42
41	HPW 42	1992	VEE/3/PVN SIB/CNO SIB//JAR/ORZ SIB
42	SANGAM	1992	GLL/AUSTII61-157//CNO/ NO/3/VEE
43	WH533	1993	VEE#5
44	DWR 162	1993	KVZ/BUHO//KAL/BB
45	AKW 1071	1994	VEE/3/FLN/ACC//ANA
46	HP 1731	1995	URES//PRL "S"/TONI
47	DWR195	1995	SH1#4414/CROW"S"
48	PBW 343	1996	ND/VG7944//KAL//BB/3/ YACO"S"/4/VEE#5"S"
49	PBN 51	1996	BUC SIB/FLK SIB
50	PBW 373	1997	ND/VG7944//KAL//BB/3/ YACO"S"/4/VEE"S"
51	HD 2643	1997	VEE"S"/CPAN 2407/HD2329
52	HW 2004	1997	REGENT1974/3*CHZ//*ZC 591/3P-19/C-281
53	NIAW 34	1997	CNO79/PRL"S"
54	VL 738	1997	NS12.07/LIRA"S"/VEE"S"
55	HP 1744	1997	CNO/PRL//CHILERE/ GARUDA
56	NW 1012	1998	PARANA//JUP/BJY"S"/3/ VEE//5"S"/JUN"S"
57	NW 1014	1998	HAHN"S"
58	DWR 1006	1998	SULA/CREX//AAZ
59	PBW 396	1999	CNO67/MFD//MOM "S"/VEE "S"

release has increased tremendously during nineties. Out of a total of 57 varieties released during 1991-1999, about 23 were direct release (Table 2). Plant breeding aims at accumulating all possible desirable alleles in one background. Exotic germplasm represents a very important source of desirable and diverse alleles for different traits. efforts need to be made to bring together these desirable alleles in one background by including a judicious selection of germplasm sources in breeders' crossing plots.

Table 3. Wheat varieties released/identified in India from 1965 till date which have foreign introductions in their pedigrees

Sl. No.	Variety	Year	Pedigree
1	C 306	1965	RGN/CSK31/2*C591/3/C217/NI4//C281
2	DURGAPURA 65	1965	RS31*5//TH/NP 165
3	HYB 663	1965	LOCAL//KC6042/GUL
4	NI 747-19	1965	RFP196/MOY3
5	NI 917	1965	C591//KC6042/GUL
6	NP 818	1965	DO/C518//SPP/NP114/3/WIS245 SIB
7	NP 846	1965	RN/NP760
8	NP 852	1965	KF/2*NP761
9	GANGA SONAHERI	1966	EG953/RS31
10	KHARCHIA 65	1966	KHLC*5/EG593
11	SHARBATI SONARA	1968	AMBER MUTANT OF SONARA 64
12	NP 884	1969	KC6042//GUL//PLT/3/K58/N/4/NP755
13	HIRA	1970	YT54/N10B//SN64
14	NARBADA 4	1971	GB-AUS/NI4/3/PW5//TH/NP165
15	PUSA LERMA	1971	AMBER MUTANT OF LERMA ROJO 64
16	MOTI	1971	YT54/N10B//NP852
17	GAUW 10	1973	S308/WS217
18	GIRIJA	1973	CJ60/3/SPO/MTA//MQ/2*RNW
19	NI 5643	1973	N/NI345 SIB
20	WG 357	1973	PV 18/C273
21	WG 377	1973	WG143/USA265//PV18
22	DESHRATNA	1974	S503/NP835
23	JANAK	1974	YT54/N10B//HD845
24	HD 2135	1975	BB SIB/5/SL BIB/NP853/4/PJ SIB/P14//KT54B/3/K65
25	SHAILAJA	1975	PJ SIB/P14//KT54B/3/SKA
26	RAK 821	1977	NP875//LR64/2*SN64

Sl. No.	Variety	Year	Pedigree
27	RAJ1114	1977	SKA/INIA66
28	UP 262	1977	S308/BJ66
29	WH 147	1977	PJ SIB/P14//KT54B/3/C286/ C273/4/S339/PV18
30	WH 157	1977	NP876/S308//CNO/8156
31	BITHOOR	1978	MULTILINE (KALYANSONA) OF NINE COMPONENTS
32	HD 2177	1979	SL SIB/NP852/4/PJ SIB/P14//KT54B/3/K65/5/ KAL
33	HD 2189	1979	36896/CJ54//P4160E/3/SN6 3/5/MY54/N10B//LR64/3/T ACSIB/4/LR64//TLPP/Y54
34	HD 2204	1979	BJ66 SIB//NAD63/LR64A/5/SL SIB/NP852/4/PJ SIB/P14//KT54B/3/K65
35	HP 1209	1979	N10B/Y53//Y50/3/KT54B/4/ PJ KLRE/NP830
36	HW 657	1979	TG/K65
37	K-POORVI	1979	K816 SIB/KAL
38	MALVIYA 12	1979	NP876/CNO]
39	TAWA 267	1979	BB/7C
40	UP115	1979	RIDLEY/NP710/3/PJ SIB/P14//KT54B/4/PJ SIB/GB856//TZPP/NAI60
41	WL 410	1979	SN63/4/36896//CJ54/P4160 E/3/HUAR/5/KAL
42	WL 711	1979	S308/CHR//KAL
43	WL 1562	1979	KAL/JN//UP301
44	AJANTA	1981	PW5/Y53
45	IIS 86	1981	TII/MIDA-U//MCM/EX/3/ S227/4/S308
46	KEERTHI	1981	SKA.TOB
47	KSHIPRA	1981	CNO SIB/NO/3/C273//NP875/PI SIB/4/HD 1981
48	KSML-3	1984	MULTILINE (KALYANSONA) OF SIX COMPONENTS
49	LOK-1	1981	S308/S331
50	MLKS-11	1981	MULTILINE (KALYANSONA) OF EIGHT COMPONENTS
51	MALVIYA 37	1982	KAL/S331//HD1982
52	PBW 12	1982	CNO SIB/GLL//WL 711
53	SKML 1	1982	MULTILINE (SONALIKA) OF SIX COMPONENTS
54	HD 2281	1983	HD2160//7/36896//CJ54/ P4160E/E/HUAR/6/KAL SIB/5/SL SIB/NP852/4/PJ SIB/P14//KT54B/3/K65
55	K 72	1983	PV18/K68
56	MALVIYA 55	1983	PJ SIB/P14//KT54B/3/HD1982 /4/INIA66/5//HD2189
57	PARVATI	1983	CNO SIB NO/3/C273//NP875/PI SIB/6/36896//CJ54/P4160E/ 3/HUAR/4/KAL/5/SL SIB/NP852/4/F SIB/P14/KT54B/3/K65
58	SAGARIKA	1983	NP798/KAL
59	UTKALIKA	1983	DG65/C306// FAO1061-68R
60	GW 89	1984	KAL SIB/LR64A//SKA
61	HUW 234	1984	HUW12/SPRW//HUW12
62	RAJ 1972	1984	C306/NP852/3/GB-AUS/ N10B//2*LR/5/SL SIB/NP852/4/PJ SIB/P 14//KT54B/3/K65/5/ HD 2160
63	UP 2121	1984	NAI60//KAL//UP301/3/ SAM68
64	HD 2285	1985	3689//CJ54/P4160E/3/ HUAR/4/KAL SIB/5/SL SIB/NP852/4/PJ SIB/P14//KT54B/3/K65/6/ HD2160/7/SL SIB/NP852/4/PJSIB/P14// KT54/3/K65/5/2*SKA
65	HD 2337	1985	SL SIB/NP852/4/PJ SIB/P14//KT54/3/K65/5/ SKA/6/HD2160

Sl. No.	Variety	Year	Pedigree
66	HD 2329	1985	SL SIB/NP852/4/PJ SIB/P14//KT54B/3/K65/5/ SKA/6/UP262
67	HP 1493	1985	KLRE/NP830
68	MALVIYA 213	1985	NO/MOTI//HD2160
69	PRAGATI	1985	LR64/2*SN64//S308
70	RAJ 2184	1985	SN64/Y50E//GTO/3/8156/ 4/HD2135 SIB
71	UP 2113	1985	UP 301//KAL/HY65/3/WG377
72	WH392	1985	SHERA/3/N10B/K68//BB
74	TRIVENI	1986	KAL/HD 1982
75	VL 616	1986	SKA/P46
76	PBW 65	1987	USA255/K816/3/S738/ C306//KAL
77	AKW381	1988	SKA/NI5439
78	HD 2270	1988	SL SIB/NP852/4/PJ SIB/P14//KT54B/3/K65/5/ CNO SIB/NO/3/C273//NP875/ PI SIB/6/TOB/CNO SIB//BB/4/NAI60 SIB*2//TT/SN64/3/LR/ SN64
79	HD 2402	1988	HD 2177//CNO67/BB/3/HD216 0/4/HD2236
80	MAGHAR	1988	NP875/4/N10B/Y53//Y50/3/ KT54B/5/2*K852
81	HD 2380	1989	HD2135 SIB/SKA/3/TOB/CNO SIB//BB/4/NAI60*2//TT/SN 64/3/LR64/SN64/5/HD2160 /HD2170
82	PBW 175	1989	HD2160/4/JN/GAGE//JN/ KAL/3/PV18/C273
83	PBW 226	1989	C591/RN//JN/3/CIIR/HIRA
84	GW 496	1990	HD2285/4/CNO/NO//CC/ INIA66/KAL/BB
85	GW 503	1990	TOB SIB/NAPO//CC/INIA66 SIB/3/CNO/NO/4/CTFN/ CNO SIB/3/JAR SIB//MENG/856
86	HDR 77	1990	PTZ/2*HD2204
87	RAJ 3077	1990	HD2177/3/CNO67/BB//HD 2160/4/RAJ1482/5/BB//INIA 66 SIB/NAPO
88	HUW 318	1991	HUW206//KAL/MUS
89	K 88	1991	VEE/WL711
90	PBW 299	1992	BB/KAL//WL711/PBW65
91	SONALI	1992	TH*6/TF//6*SKA
92	GW 190	1993	VEE/3/BB SIB/SKA//ARJUN
93	K 8962	1993	K816 SIB/PV18//HD2160
94	VAISHALI	1993	KAL*4//TR380/27*4/3AG3/ 3/HD2281
95	HD 2610	1993	VEE'S'/HD2402
96	HD 2643	1997	VEE'S'/CPAN2407/ HD2329
97	HP 1761	1997	RL6010/6*INIA66// 3*KAUZ
98	DL788-2	1997	K7537/HD2160/HD2278// L24K-4-14
99	HS 365	1997	HS207/SONALIKA
100	HPW 89	1997	INTERMEDIO RODI/HD2248
101	PBW 435	1998	HD2160/CALIDAD
102	HW2044	1999	SUNSTAR/6/C80-1/6/ PBW226

REFERENCES

Anonymous. 1998. Distinguishing Characters of Indian wheat varieties. Research Bulletin No. 4. Directorate of Wheat Research. Karnal.

Anonymous, 1991. Directorate of Wheat Research, 1999. Results of the All India coordinated Wheat and Triticale Trials (Jag Shoran *et al.*) DWR, Karnal.

Jag Shoran, D Mohan, B. S. Tyagi and J. Kumar. 1998. Yield trials/nurseries: Information and benefits at what cost? *In*: S. Nagarajan, G. Singh, and B. S. Tyagi, eds. Wheat Research Needs Beyond 2000 A.D. Narosa Publishing House, New Delhi, p 89-99.

Jain, K.B.L. 1994. Wheat cultivars in India. ICAR/CIMMYT.

Sharma, Rajiv K. and S. K. Mishra 1999. Wheat breeding in India: Past achievements, current status and future prospects. *Ann. Agric. Res.* **20** 2: 137-143.

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Short Communication

WILD FOOD PLANTS USED BY SOME TRIBES OF SINGRAULI REGION (MADHYA PRADESH)

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This paper presents the results of a survey of the wild plants used as food by various tribes namely Gond, Baiga, Kol, Kahirwar, Panika and Agaria of the Singrauli region of Madhya Pradesh. Sixty species of flowering plants used as food were recorded.

Key words : Wild food plants, Singrauli, Madhya Pradesh

Forests form an integral part of tribal life. Since they practice very little agriculture, they obtain most of their food from wild plants. The food plants used by various tribes in India have received considerable attention the recent past (Jain, 1964; Oommachan, 1977, 1992; Maheshwari, 1986; Vartak, 1990 and Basu, 1996). However, Singrauli region is yet to be explored. It is one of the foremost coal and power producing region of the country. It is located in district Sidhi in Madhya Pradesh. It lies between 23°49' N to 24°42' N latitude and 81°18' to 82°50' E longitude with a total area of 1904 sq. km. More than 42 per cent of the area is covered by forests, having great plant diversity. The forest region is inhabited by various tribes namely Gond, Baiga, Kol, Khairwar, Panika and Agaria. They mainly depend upon forests for food.

Table 1. Wild plant exploited for food in Singrauli region

Botanical Name	Local name	Family	Habit	Place of Collection	Frequency of Occurance	Edible Part
Aegle marmelos (L) Corr.	bel	Rutaceae	Tree	Harrai (3)	Common	Fruit
Amaranthus spinosus L	Katili cholai	Amaranthaceae	Herb	Goniari (2)	Common	Leaves & Seeds
A. vrdis L	Cholai	Amaranthaceae	Herb	Harrai (3)	Common	Leaves & seeds
Amorphophallus paenoniifolis (Dennst) Nicol	Sooran	Araceae	herb	He Sidhi Kalan (6)	Occasional	Cornm.
Angoeissus latifolia Bedd	Dhaura	Comber taceae	tree	Padari (13)	Frequent	Gum
Artocarpus heterophyllus Lamk	Kathal	Moraceae	Tree	Tiara (5)	Ocassional	Fruit
Asparagus recemosus Wild	Satawar	liliacaeae	Climber	Utani(25)	Ocassional	Roots
Bauhinia verigata L	Kath Mohila	Cassalpiniaceae	Tree	Godoria (14)	Common	Flower bud
Begonia picta Sm	Khatti bhaji	Bigoniaceae	Herb	Utani (25)	Rare	Whole plant
Bombax ceiba L	Semul	Bombacaeaceae	Tree	Modholi (12)	Occasional	Flower buds
Buchnania lanzan Spreng	Char	Anacardiaceae	Tree	Mada (30)	Common	Fruits & seeds
Butea monosperma (Lamn) Taub.	Chiula	Fabaceae	Tree	Makrohar (07)	Frequent	FLower buds
Canavalia gladiata (Jock) D.C.	Bansemi	Fabaceae	Climber	Sasan (04)	Frequent	Fruit
Carissa opaca stapfex Hains	Karonda	Apocynaceae	Shrub	Gadaria(14) Frequent	Fruit	

Table 1. (Contd.)

Botanical Name	Local name	Family	Habit	Place of Collection	Frequency of Occurance	Edible Part
Cassia fistuala L	Dhanbad	Caesalpiniaceae	Tree	Rondi (31)	Frequent	Flower buds
Cassia tara L	Chakoda	Caesalpiniaceae	Herb	Waidhan(01)	common	young leaves & seeds
Cayratia trifolia (L) Domin	Amlola	Vitaceae	Climber	Mada (30)	Occasional	Fruits
Chenopodium album L	Bathua	Chenopodiaceae	Herb	Ganiari(02)	Common	Whole plant
Coccinia grandis (L) Voigt	Berai,Kundru	Cucurbitaceae	Climber	Naugarh(11)	Common	Fruit
Commelina bengalensis L	Kukaua	Commelinaceae	Herb	Waidhan(1)	Common	Leaves
Cordia dichotoma Foosts f.	Beohar	Cordiaceae	Tree	Mdhauli(12)	Occasional	Fruits
Coastus speciosus (Koen) Sm.	Gona	Costaceae	Herb	Utani(25) Rare	Tubers	
Cucumis melo var *agrastis* Noud	Pehta	Cucurbitaceae	Climber	Sasan(4)	Occasional	Fruits
Cyperus esculantus L	Gozila	Cyperceae	Grass	Sasan94)	Frequent	Bulbs
Dendrocalamus strictus Nees	Bans	Poaceae	Culm	Gadaria (14)	Common	Young shoot
Digera Muricata (L) Mart.	Lesua	Amaranthaceae	Herb	Khutar (22)	Frequent	Leaves
Dioscorea bulbifera L	Gaenthi	Discoreaceae	Twinner	Sasan(4)	Occasional	Tubers
D. daemons Roxb.	Baichandi	Discoreaceae	Twinner	harrai(3)	Occasional	Tubers
D. deltoides L.	Khanima	Discoreaceae	Twinner	Gadaria(14)	Occasional	Tubers
D. opposiifolia L.	Kathar	Discoreaceae	Twinner	Harrai(3)	Common	Tubers & Bulbil
D. pentaphylla	Kanda	Discoreaceae	Twinner	medhouli(12)	Occasional	Tubers
Diospyros melanoxylon Roxb.	Tendu	Ebanaceaea	Tree	Mada(30)	Common	Fruits
Emblica officinalis Gaertn.	Amla	Euphorbiaceae	Tree	Sasan(4)	Frequent	Fruit
Eugenia heyneana Wall.	Kath Jamthi	Myrtaceae	Tree	Gobha(9)	Frequent	Fruits
Feronia limona (L) Swingle	Kaitha	Rutaceae	Tree	Mada(30)	Occasional	Fruits
Flacourtia indica (Burm f.) Merr.	Katai	Flacourticeae	Shrub	Mada(30)	Occasional	Fruits
garuga pinnata Roxb.	Kekad	Burseraceae	Tree	Gobha(9)	Occasional	Fruit
grewia hirusta Vahl.	Gursankar	Tiliaceae	Shrub	Sasan(4)	Occasional	Fruit
Holarrhena antidysentrica (Roth) A.D.C.	Khirna	Apocynaceae	Tree	Medhauli(12)	Common	Flower buds
Ipomoea pestigrids L	Bilaripath	Convolvulaceae	Herb/Clim Ber	Waidhan(1)	Rare	Seeds
Madhuca latifolia (Roxb.) Chev.	Mohua	Sapotaceae	Tree	Medholi(12)	Common	Flowers,Fruits
Manilkara hexandra Roxb. Dub.	Khirni	Sapotaceae	Tree	Gobha(9)	Occasional	Fruits
Momordica diocia Roxb. ex. Wild	Kheksa	Cucurbutaceae	Climber	Rondi(31)	Occasional	Fruit & Root
Phoenix acaulis Buch Hamex *Roxb.*	Cheer	Aracaceae	Shrub	Godaria(14)	Common	Fruit
Physalis minima L	Patko	Solanaceae	Herb	Ganiari(2)	Occasional	Leaves & Fruits
Pithecellobium dulce (Roxb) *Benth.*	Jangal Jalebi	Papilionaceae	tree	Mada(30)	Occasional	Aril of seed
Portulaca oleraceae L.	Lonia	Portulacaceae	Herb	Waidhan(01)	Occasional	Whole plant
Puereria tuberosa DC	Patal Kumrha	Fabaceae	Twinner	Chargoda(01)	Rare	Young tubers
Rumex deutatus L.	Jangali Palak	Polygonaceae	Herb	Waidhan (01)	Common	Leaves
Schleichera oleosa (Lour) Okem	Kosam	Sapindaceae	Tree	Tiara(05)	Rare	Aril of seed
Semecarpus anacardium l.f.	Bhela	Anacardiaceae	tree	Medhauli(12)	Common	Thalamus
Solanum nigrum L.	Makoi	Solanaceae	Herb	Waidhan(01)	Common	Fruits
spondias pinnata L.f. Kurz	Amra	Anacardiaceae	tree	Mada(30)	Rare	Fruit
Sterculia urens Roxb.	Kullu	Sterculiaceae	tree	Godaria(14)	Rare	Gum & seeds
Syzygium cumini (L) Skeels.	Jamthi	Myrtaceae	tree	Godaria(14)	Common	Fruit
tamarindus indica L.	Imli	Caesalpiniaceae	Tree	Padari(13)	Rare	Fruit,Leaves

Table 1. (Contd.)

Botanical Name	Local name	Family	Habit	Place of collection	Frequency of occurance	Edible Part
tamarindus indica L.	Imli	Caesalpiniaceae	Tree	Padari(13)	Rare	Fruit,Leaves
Terminalia bellirica (Gaertn.) Roxb.	Bhera	Combretaceae	Tree	Sasan(4)	Common	Seed Kernel
Woodfordia fruiticosa Kurz	Dhawai	Lythraceae	Shrub	Sasan(4)	Common	Young buds
Ziziphus nummularia (Burm f.) W & A	Ber	Rhamnaceae	Shrub	Dongari(26)	Common	Fruit
Z. oenoplia (L) Mill	Makoi	Rhamnaceae	Climber	Dongari(26)	Common	Fruit

MATERIALS AND METHODS

Ethnobotanical exploration were undertaken during past three years (1997, 1998 and 1999) in twenty tribal villages of this region. The information regarding the plants was collected by interviewing a large section of various tribes. The distribution and frequency of food yielding plants was made in the forest. Plants were collected, identified and preserved as herbarium specimens. These are listed in alphabatical order followed by local name, family, habit, place of collection, frequency of occurrence, edible parts in Table 1.

OBSERVATIONS AND DISCUSSION

It is evident from Table 1, 23 trees, 6 shrubs, 14 herbs 14 climbers and 2 grasses belonging to 60 species of angiosperms are used by various tribes of Singrauli region. It is evident from the data that some of these species are rare and are at the verge of extinction. Therefore, the conservation of germplasm of these species requires immediate attention.

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REFERENCES

Jain, S.K. 1964. Wild plant foods of tribals of Bastar (M.P.) *Proc. Nact. Inst. Sci. India.* 30(B): 56-80.

Maheshwari, J. K. and K. K. Singh. 1986. Ethnobotany of tribals of Mirzapur District. (U.P.) NBRI Lucknow.

Vartak, V. D. Observations on wild edible plants from Hilly region of Maharashtra and Goa. Contribution to Ethnobotany of India. 1990 p 230-241.

Basu, R. and P. K. Mukherjee. 1996. Food plants of the tribe 'Paharia of Purulia' *Ad. Plant Sci.*, 9(2): 209-210.

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Short Communication

GRAIN SORGHUM AND SMALL MILLET GERMPLASM COLLECTION FROM NANDURBAR DISTRICT OF MAHARASHTRA STATE

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Sorghum is the staple food of the majority of people of the predominantly tribal areas in newly constituted tribal district Nandurbar (Maharashtra). These tribals in the hills of Satpura ranges grow traditional varieties of sorghum and certain small millets. They attributed the preference to local cultivars to their good processing characteristics, acceptable quality and storability as prepared food. The local sorghum varieties like dadar are costlier than hybrids even in the neighbouring districts of adjoining Gujarat State. The present paper reports certain landraces of sorghum and small millets collected form these areas.

Key words : Sorghum, small millets, germplasm collection

The collection was undertaken in Shahada and Dhadgaon talukas of Nandurbar district (earlier Dhule). The soil of area is mainly clay. The annual rainfall ranges from 450 mm in Shahada (180 MSL) to 1000 mm in Toranmal (110 MSL) which is the highest peak in Satpuda Hills.

Morphological description and utility

Sorghum samples were classified into different races according to Harlan and Dewet (1972) and small millets were identified with help of established flora (Blatter and McCann, 1935; Cooke, 1908; and Shah, 1978). The plants were observed in the field and morphological characters were recorded. Grain samples of the cultivars were collected from farmer's store. The samples were preserved at Department of Botany, P.S.G.V.P. Mandal's College, Shahada. The morphology of the plants and grains of the collected sorghum cultivars were briefly described in table 2. Badi Jowar (VB-1) and Dadar (VB-3) were collected by ICRISAT but from other localities of Dhule district. Preliminary investigation in this laboratory showed that these two cultivars are resistant to NaCl salinity (unpublished data). Chikni (VB-5) was not available among the 37,000 and odd accessions of ICRISAT. The present collection is red grained and used only in papad making. Andheri Dadar (VB-4) however is not found with any of sorghum germplasm collection centers (Personal communication). It is close to Dadar in morphology but differs with it in making quality. It is grown for its popping qualities. It is not generally attacked by birds because the kernels are not seen from outside. They are hidden between the large red glumes. Hence the name 'Andheri Dadar'. Murthy *et al.* (1982) recorded that of the 9682 accessions screened for popping qualities, only 36 were found to be better. VB-4 must also be screened for its usefulness in breeding programmes which will help improving this quality.

Table 1. Vernacular names, sources of collection of sorghum and small millet germplasm from Nandurbar district, Maharashtra, India

Collection No	Vernacular Name	Rabi/ Kharif	Race	Village
VB-1	Badi Jowar	Kharif	Durra	Rampur
VB-2	Mani Jowar	Kharif	Candatum	Shahada
VB-3	Dadar	Rabi	Durra	Shahada
VB-4	Andheri Dadar	Rabi		Shahada
VB-5	Chikni	Kharif	Durra	Rampur
VB-6	Ramkel	Rabi	Durra	Rampur
VB-7	Varai	Kharif	*Panicum Sumatrance*	Ranipur
VB-8	Safed Sangri	Kharif	*Echinocola colonum* Var. *frumentacea*	Kotbandh-ani
VB-9	Kali Sangri	Kharif	*Echinocola*	Kotbandhani
VB-10	Banti	Kharif	*colonum* Var. *frumentacea*	Kotbandhani
VB-11	Mordhan (Mor)	Kharif	*Panicum psilopodium* Trin	Kotbandhani
VB-12	Bhagar	Kharif	*Panucun miliacium* Linn	Kotbandhani

VB-1 is a six months crop and is known to be mold resistant. Mani Jowar (VB-2) is popular among farmers as its stalk and leaves form good fodder. Cattle not only like it most but also give thick fatty milk when fed with mani jowar fodder. Looking to the sweet taste of its bread, VB-2 may be evaluated for sweet sorghum status. It may find usefulness in jaggery production as envisaged by Ghanekar (1987) and also for malt production. This is an indication of high lipid content of this cultivar. In Nandurbar district, the cultivar of Ramkel (VB-6) is restricted to Rampur Village only. It is not as popular as the other cultivars.

Table 2. Morphology of plants and the making quality of the grains of sorghum cultivars

Collection No.	Name	Morphology	Making Quality
VB-1	adi Jowar	2.5 to 3.5m height,flag leaf close to drooping panicle,Grain white & bold	White bread easy to digest
VB-2	Mani Jowar	1.5 to 2m height,flag leaf 30-50cm below inflorence straight panicle,grain blue and bold but with black glume	Black bread sweet in taste
VB-3	Dadar	2-3m height,flag leaf 20-30 cm from inflorence straight panicle,small pale yellow grain	Bread hard to digest
VB-4	Andheri Dadar	2-3m height,flag leaf close to infloresence straight panicle,small and yellow grain with red glume	flake making
VB-5	Chikni	2-3m height,flag leaf close to infloresence drooping panicle,red grain	Papad Making

All the samples of small millets were collected from Satpuda hills. Kotbandhani is near Toranmal while Dhadgaon is an important trading center for tribals of these hills. Safed Sangri (VB-8) and Kali Sangri (VB-9) were identified as same species (*E. colonum*). It closely resembles with the description of *Echinocloa colona* var. *frumentacea* of Blatter and McCann (1935). Patil (D. A. Patil-personal communication) opines it to be *Echinocloa stagnina.* In an earlier publication (Bhasker, 1999); it was reported as *E. stagnina.* Further confirmation is needed. The only morphological difference between these two is the seed colour. Safed Sangri is white seeded while the latter is black seeded. Cytological and chemical analyses are, however, needed to establish their taxonomic relationship. These two small millets are not seemed to be cultivated elsewhere; either

in Maharashtra or in the adjoining tribal areas of Gujarat and Madhya Pradesh. Mordhan (VB-11) is cultivated in Kotbandhani and Dhadgaon. According to natives it is also cultivated in the adjoining areas of M.P. All these small millets are used to make roti or pudding, the latter is more common. Bhagar (VB-12) is eaten as pudding on fasting days by Maharashtrians in towns and cities as well. Thus it is a widely grown small millet in many parts of the state.

Flours of hybrids and local sorghums differ in their fermentation characteristics as determined by swelling volume of the batter (Subhramanian and Jambunathan, 1992). Andheri Dadar, the popping type, described in the present study seems to be a promising source for beverage industry owing to its small size, white creamy colour and medium thick pericarp. However, all these local cultivars must be screened for malt and fermentation characteristics. Studies on comparative evaluation of Dadar and Andheri Dadar and their improvement are already underway. Similar studies on other samples and small millets are required. A collaborative evaluation programme between collection centers like ICRISAT and NBPGR and analytical centers like universities and other institutions located close to the origin of the genotype would yield more fruitful results.

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REFERENCES

Blatter, S. J. and C. McCann. 1935. The Bombay grasses. p. 149 Bishan Singh Mahendrapal Singh, Dehradun, India 1984.

Bhaskar, V. V. 1999. Tribal ecology of Toranmal forest region in Satpuda Hills. *J. Eco. Env. & Cons.* 5(4): 307-311.

Cooke. T. 1965. The Flora of Presidency or Bombay No./II P. Bishan Singh Mahendrapal Singh, Dehradun.

Ghanekar, A. R. 1987. Sweet sorghum for jaggery production: problems and prospects. p 197-202. *In*: Proceedings on the National Seminar on Technology and Applications for alternative uses of sorghum (Ingle, U.M., Kulkarni, D. N. and Throat, S. S. eds.), Marathwada Agricultural University, Parbhani, Maharashtra, India.

Gopal Reddy, V. and V. D. Verma. 1996. Rabi sorghum germplasm collection in Maharashtra and adjoining areas of Karnataka. Genetic Resources Progress Report 85. International Crops Research Institute for the Semi-Arid Tropics, Andhra Pradesh, India.

Harlan, J.R. and J. M. J. de Wt. 1972. A simplified classification of cultivated sorghum. *Crop. Sci.* 12: 172-176.

Murthy, D. S., H. D. Patil, K. E. Prasada Rao and L. R. House. 1982. A note on screening the Indian sorghum collection. *J. Food Sci. and Tech.* 19: 79-80.

Prasada Rao, K. E., M. H. Mengesha and V. G. Reddy. 1989. International use of sorghum germplasm collection. *In*: "The Use of Plant Genetic Resources: p 49-47 (ADH Brown O. H. Frankel, O. R. Marshell and J. T. Williams eds.) Cambridge University Press, Cambridge.

Shaha. G. L. 1978. Flora of Gujarat State Part II p. 818 Sardar Patel University, Vallabh Vidyanagar.

Subhramanian, V. and R. Jambunathan. 1992. Laboratory procedures for evaluating rain and good quality of sorghum and pearl millet: problems and prospects. p 143-150. *In*: Utilization of sorghum and millets. (Gomez, M. L. Rooney, L. W. and Dendy, D.A.V. eds.), ICRISAT, Patanchery, A.P. 502 324, India

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Short Communication

'SELECTION 212' — A NEW RUST RESISTANCE SOURCE FROM RYE (*Secale cereale*)

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The search for new genes from secondary and tertiary genepool and incorporating them into cultivar helps in genetic diversification. Rye (*Secale cereale*, RR, 2n = 14) is known for several valuable traits namely, resistance to diseases and pests, hardiness, high photosynthetic activity. With permutation and combination, in BC1F7 generation, cytologically stable plants were identified. Studies revealed identification of a line "Selection 212" which was found resistant to both leaf and stem rust diseases.

Key words: Wheat, *Triticum aestivum, Secale cereale*, resistance, stem rust, leaf rust

Building multiple disease resistance into high yielding varieties is one of the main strategies for improving productivity and yield stability as well as restrict the use of chemicals in controlling diseases. The search for new genes, so called gene hunting, in wild-species and incorporating them into present day cultivars helps in genetic diversification. For enhancing the genetic potential of cultivated wheats, the secondary and tertiary gene pool of wheat was considered important (Mujeeb- kazi, 1995). Rye (*Secale cereale*, RR, 2n = 14), a species of tertiary gene pool is known for several valuable traits like resistance to diseases and pests, hardiness, high protein, high photosynthetic activity, high spikelet number and plant vigour (Rajaram *et al.*, 1983).

In an endeavour to tap the genetic potential of rye, attempts were made by exploiting recombination between homoeologous chromosomes. In this approach, a monosomic line (2n = 41) of cultivar Chinese Spring deficient for chromosomes 5B was crossed with rust resistant, self compatible, amber seeded strain of diploid (2n = 14) rye obtained through gamma - radiation from a red seeded self-incompatible rye, accession number PI366498, procured from USDA. A wheat-rye F_1 hybrid with 27 chromosomes which lacked chromosome 5B of *Triticum aestivum* exhibited extensive chromosome pairing of homoeologous chromosomes (Table 1). This F_1 hybrid was backcrossed to a hexaploid wheat cultivar Sonalika, BC_1F_2 families of (CS mono 5B × rye) F_1 × Sonalika produced a spectrum of aneuploids. Segregating populations were grown at Wellington (South India), a hot spot for rust diseases and only rust resistant derivatives were selected. In BC_1F_7 generation cytologically stable ($2n = 42 = 21^{II}$) plants were identified. A line found resistant to leaf rust (*Puccinia recondita* f.sp. *tritici*) and stem rust (*Puccinia graminis* f.sp. *tritici*) was designated 'Selection 212' (Singh, 1991).

'Sel. 212' has features like aestivum wheat. It is 110 cm tall having amber, long, bold, lustrous seeds. The 1000 kernel weight ranges from 40-44 gms. The days to flowering and

Table 1. Meiotic chromosome pairing in the F_1 hybrids involving monosomic 5B of Chinese Spring and amber rye strains

No. of Chromosome	No. of cells analysed	Univalents	bivalents	trivalents	tetravalents	Chaismata
28	1032	24.27 ± 0.07	1.86 ± 0.04	0.02 ± 0.004	-	1.9 ± 0.04
27	231	10.18 ± 0.17	6.51 ± 0.12	1.14 ± 0.07	0.09 ± 0.02	12.34 +–.0.17

maturity are slightly more than Sonalika i.e. 84 days and 126 days respectively. Sel. 212 is semi-erect in early growth stages having good straw strength but shy tillering. leaves are slightly waxy. Spikes are medium long and medium dense with pseudo black chaff. Auricles have purple pigmentation. Sharma (1997) generated the information regarding effectiveness of this stock to leaf and stem rust pathotypes and inheritance and chromosome location of rust resistance genes in this wheat-rye recombinant.

Seedling tests against 25 pathotypes of leaf rust and 20 pathotypes of stem rust suggested that Sel. 212 is resistant to all the pathotypes. Adult plant tests with most virulent pathotype 77-5 and 40A of leaf and stem rust pathogen respectively also showed high level of field resistance.

Inheritance studies in seedlings against highly virulent pathotypes (77-1, 77-3, 77-4 and 77-5 revealed that a recessive undesignated gene is providing resistance to leaf rust. Inheritance studies at adult plant stage in field with most virulent pathotype 77-5 suggested the presence of an additional adult plant resistance gene, which is likely to be *Lr34* probably derived from Chinese Spring, a parental line of Sel. 212. When inheritance was studies against two selected stem rust pathotypes 122 and 40, it showed that an unknown resistance gene is providing resistance to stem rust. Adult plant inheritance studies for stem rust resistance against pathotype 40A suggested the presence of an adult plant resistance gene *Sr2* in the stock which may have derived from Sonalika, the parent of Sel. 212. Test of allelism detected the presence of stem rust resistance gene *Sr11*, may also be derived from Sonalika.

Linkage analysis established the close linkage between undescribed leaf and stem rust resistance genes. Chromosome location studies using monosomic analysis located these linked leaf and stem rust resistance genes in chromosome 2B of Sel. 212. Cytological analysis of F_1 hybrids of Sel. 212 and parental rye indicated the presence of rye chromatin in Sel. 212.

These undescribed linked leaf and stem rust resistance genes are tentatively named Lr Sel. 2121 and Sr Sel. 2121 respectively. These leaf and stem rust resistance genes effective to all existing leaf and stem rust pathotypes respectively are expected to be of immense value in diversifying the genetic base of rust resistance in the country. The transfer of these linked leaf and stem rust resistance genes would facilitate the breeders in incorporating these novel resistances to both the pathogens.

REFERENCES

Mujeeb-Kazi, A. 1995. Conclusions and a look to the future. *In*: A. Mujeeb-Kazi and G. P. Hettel (eds.), Utilizing wild grass biodiversity in wheat improvement: 15 years of wide cross research at CIMMYT. CIMMYT Research Report No. 2: 102-106.

Rajaram, S, C. E. Mann, G. Ortiz-Ferrara and A. Mujeeb-Kazi. 1983. Adaptation, stability and high yield potential for certain 1B/1R CIMMYT wheats. *In*: S. Sakamoto (ed.), Proc. 6th Int. Wheat Genet. Symp., Kyoto, Japan, p 613-621.

Singh, D. 1991. Wheat rye recombinant resistant to all three rusts of wheat. *Ann. Wheat Newsl.* 37: 68.

Sharma, J. B. 1997. Inheritance and location of rust resistance genes in a wheat-rye recombinant 'Selection 212'. Ph.D. Thesis, Indian Agricultural Research Institute, New Delhi.

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Short Communication

FORAGE GENETIC RESOURCES IN ORISSA AND THEIR CONSERVATION

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This paper deals with distribution of forages viz., 224 species of legumes and 268 species of grasses in Orissa. The distribution of tropical/subtropical/temperate species has been discussed. The causes of genetic erosion, notes on rare/threatened/endemic species have also been dealt with in detail. Conservation aspect of rare species and important forage species for improvement of grasslands/rangelands has been highlighted. *In-situ* conservation of *Cajanus cajanifolia, Rhynchosia hainesiana, Rhynchosia suaveolens, Dimeria orissae, Themeda mooneyi, Mucuna minima* has been suggested. Conservation and domestication of *Stylosanthes fruticosa* which is the only species available in India for pasture development have been highlighted.

Key words : Forage legumes, grasses, rare/threatened/endemic species, distribution, conservation

Orissa, one of the coastal state lies between 81° 27' and 87° 29' east longitudes, and 17° 49'-22°34' N latitude. It is situated in the eastern peninsula with a coast line of 482 kms and is bounded by West Bengal on the north-east, Bihar in the north, Madhya Pradesh in the West, Andhra Pradesh in the South and Bay of Bengal in the east. It covers an areas of 155,707, Sq kms. having forest cover of 68,150 sq. kms. approximately.

Geologically, it is a part of Gondwanaland landmass and gifted with big rivers like Mahanadi, Brahmani, Rushikulya, Budhabalanga and Baitarani etc. Besides these, hills and mountains like Similipal-Meghasam (1162 m), Malayagiri (1188 m), Mankadanacha (1110 m), Mahendragiri (1525 m), Devagiri (1363 m) etc are also met with in this state. So due to peculiar climatic condition coupled with various edaphic factors, Orissa is very rich and diverse in genetic resources in general and forage resources in particular.

Once upon a time, the forest cover was *ca* 40 per cent of the state cover but due to operation of biotic factors and human interference, it is reduced to 13 per cent only. As a result of which, many species have been vanished andsome are on the verge of extinction. Due to these activities, there is serious degradation of grassland/range lands, which are the main sources of forages. Now this is high time to conserve our genetic resources in general and forage resources viz., legumes and grasses in particular for future generation to use. Because livestock population is really the backbone of the rural population which not only increase the socio-economic condition of the country in general but also the people in particular. Again India is about 2 per cent of the total geographical area of the world sustains as much as 15 per cent of the world's livestock population. So the fodder and feed resources is

very less than demand. This widening gap is increasing day by day as there is severe pressure on grassland/range lands due to habitat destruction. So proper management of grassland/rangelands through improved technique is the need of hours. This can only be achieved through introduction and domestication of indigenous legumes/grasses in the grasslands and augmentation of native diversity through exploration, collection, conservation and domestication of indigenous legumes and grasses. Realising the importance of fodder resources this paper highlighted the diversity of legumes and grasses in Orissa their distribution pattern, sociability etc. and notes on rare/endemic/ threatened species, have been discussed in detail. Conservation strategies and future research have also been given.

EXTENT OF DIVERSITY

(a) **Legumes** : In India, the family Leguminosae is represented by about 400 species-60 genera only, 21 genera are useful as forages. (Mehra and Magoon, 1974). But Hussain and Kapoor (1990) reported 1150 species of legumes from India, Kaines (1921-25), the pioneer plant explorer, reported 200 species of which 62 species are reported from Orissa. Subsequently Mooney (1950) added 47 species to the previous list while Saxena and Brahaman (1996) reported 224 number of species under 64 genera from Orissa. Besides many sporadic reports have also been made by various workers (Saxena *et al.*, 1980; Choudhury and Patnaik, 1985). Bairiganjan *et al* (1985) reported 147 species and 7 varieties from Orissa during his cytotaxonomic studies of Fabaceae, of these 12 species are new records for Orissa. From the previous reports, it is evident that Orissa is very rich in legume genetic resources. Most of the legumes are used as fodder, green manure and pasutre development. The ecology and diversity of legumes having forage value have been discussed here. In Orissa, 29 genera are represented by single species. These species are *Abrus precatorius, Dolichos biflorus, Dumasia villosa, Eriosema himalaicum, Gliricidia sepium, Medicago sativa, Ormocarpum cochinchinense, Pachyrrhizus erosus, Paracalyx scariosa, Pongamia pinnata, Pseudarthria viscida, Psophocarpus tetragonoloba, Pueraria tuberosa, Rothia indica, Shuteria densiflora, Stylosanthes fruticosa, Taveniania cuneifolia* etc. The number of species in other genera are given in Table 1. The dominant genera are *Crotalaria* (31), *Desmodium* (19), *Indigofera* (17), *Vigna* (16) etc. The species of Leguminosae are found in different diverse ecological habitats. The species of

Table 1. Distribution of legumes/grasses species in Orissa and India

Name of Genus	Orissa	India	Name of Genus	Orissa	India
Aeschynomene	3	3	*Aristida*	4	15
Alysicarpus	8	12	*Arthraxon*	5	20
Atylosia	4	20	*Arundinella*	4	16
Butea	3	3	*Bothriochloa*	2	16
Canavalia	3	4	*Chrysopogon*	6	15
Clitorea	2	2	*Coix*	3	4
Crotalaria	31	82	*Dicanthium*	2	8
Desmodium	19	44	*Digitaria*	6	22
Flemingia	12	15	*Dimeria*	10	18
Glycine	2	3	*Echinochloa*	4	46
Indigofera	17	44	*Eleusine*	2	5
Lathyrus	2	9	*Eragrostris*	23	28
Macrotyloma	2	6	*Eulalia*	3	13
Melilotus	2	3	*Heteropogon*	2	7
Milletia	2	12	Isachne	3	20
Mucuna	6	15	*Iseilema*	4	4
Rhynchosia	8	23	*Oplismenus*	2	4
Sesbania	7	8	*Oryza*	5	6
Smithia	2	13	*Panicum*	16	24
Teramnus	2	3	*Paspalum*	4	14
Vigna	16	15	*Pennisetum*	6	16
Zornia	2	2	*Setaria*	6	11
			Sporobolus	8	14
			Themeda	9	17

Aeschynomene, Sesbania, Smithia, Neptunia are usually found in aquatic, semiquatic and marshy habitats of eastern Orissa. Similarly *Rothia indica, Indigofera glabra, I. asphalthoides Canavalia maritima, Dicerma biarticulatum, Tephrosia purpurea* var. *maritima, Macrotyloma ciliatum, Mucuna gigantea* are found in sandy sea shore and tidal forests of Orissa. The species viz., *Canavalia gladiata, Phaseolus lunatus, Psophocarpus tetragonolobus, Vigna aconitifolia* are cultivated in various tribal pockets of western Orissa. The species such as *Lablab purpureus, Vigna radiata, Vigna mungo, Vigna unguiculata, Phaseolus vulgaris, Macrotyloma uniflorum, Glycine max, Arachis hypogaa, Cajanus cajan* etc. are cultivated in western and eastern Orissa with striking variabilities. Hence these species require special attention for exploration and germplasm conservation. The temperate species viz., *Centrosema pubescens, Desmodium tortuosum, Macroptilium lathyroides* var., *semierecta* and *Tephrosia noctiflora* are exotic in nature and now naturalised in Orissa.

Cajanus cajanifolia (syn. *Atylosia cajanifolia*) is the wild relative of pigeonpea. Till now it exists in its type locality which was reported by Haines (1921-25). This species needs immediate conservation *in-situ* and *ex-situ. Stylosanthes* is one of the important genus used in fodder researches and pasture improvement. All the species of Stylo are temperature in nature. Only *Stylosanthes fruticosa* is indigenous to India and found in wild state in Orissa and adjoining Andhra Pradesh.

Exploration, conservation and utilisation of this species is the need of hour, which will help in development of improved variety of Stylo. There are many species which occur abundantly and few species are of rare occurrence in specific habitats. The species viz., *Abrus precatorius, Alysicarpus vaginalis, Alysicarpus monilifer, Aeschynomene aspera, Atylosia scarabioeides, Desmodium gangeticum, Desmodium heterocarpon, D. pulchellum, Indigofera cordifolia, Sesbania bispinosa, Albizia lebbek* etc. are very common throughout Orissa. In addition, *Zornia gibbosa, Desmodium triflorum* are also very common in sandy and swampy localities which help in pasture development. Orissa is the meeting ground of South and North Indian flora. So the vegetation is mostly tropical, subtropical and rarely temperate in nature. The tropical species viz., *Alysicarpus racemosus, A. scarious, Canavalia maritima, Desmodium alysicarpoides, D. biarticulatum, Flemingia wightiana, Flemingia nilgherensis, Indigofera trifoliata, Macrotyloma ciliatum, Pseudarthria viscida, Rhynchosia rufescens, Rothia indica, Sesbania speciosa, Stylosanthes fruticosa, Vigna dalzelliana, Albizia amara* are similar to the flora of South India. Very few species are similar to North India. These are *Albizia procera, Dichostachya cineraria, Mimosa himalayana, Desmanthus virgatus, Pithecelobium dulce, Vicia hirsuta, Rhynchosia bracteata, Mucuna nigricans, Melilotus alba, Lathyrus aphaca, Indigofera prostrata* etc.

Grasses : Poaceae, one of the dominant family comprised 10,000 species under 1620 genera, distributed in different agro-ecological zones of world. (Hubard, 1954). This family is represented by about 245 genera and 1250 species of which 21 genera and 139 species are endemic (Mehra and Magoon, 1971). Agrostological analysis reveals that species belonging to the tribe *Andropogoneae, Paniceae, Eragrosteae, Festuceae, and Agrostideae*, being 30, 15, 9, 7 & 5 per cent respectively of the total number of grasses. Bor (1960) reported that 1/3 of grasses of India are considered of forage value. The centre of concentration of tropical grass species is the humid belt of South west India.

In Orrisa, Haines (1921-25) reported 214 number of species from different regions. Thereafter Mooney (1950) explored the hilly western Orissa and most of the species are endemic. Recently Saxena and Brahman (1996) reported

268 number of species. Which are mostly tropical and subtropical in nature. Rich diversity occur in western Orissa, Eastern Ghats and Similipal regions. The species have got similarity with Western ghats and Himalayan regions. The dominant genera are *Eragrostis* (23), *Panicum* (16), *Dimeria* (10), *Themeda* (9), *Brachiaria* (9) etc. forty seven genera are represented by single species which includes *Zoysia matrella, Vetiveria zizanoides, Thysanolaena maxima, Phragamites karka, Myriostachya, wightiana, Hackeolochloa granularis, Leersia hexandra, Apluda mutica, Dendrocalamus strictus, Dactyloctenium aegyptium* etc. The common species occurring throughout Orissa are *Brachiaria kurzii, B. ramosa, Coix lacryma jobi, Allopteropsis, cimicina, Apluda mutica, A. uaginata, Bothriochloa pertusa, Leersia hexandra, Cynodon dactylon, Dactyloctenium aegyptium*, etc. Most of the species are tropical and similar to the flora of the South India. These species are *Brachiaria mutica, B. reptans, Chloris virgata, Coix gigantea, Chrysopogon aciculatus, Arundinella benghalensis, Iseilema laxum, Myriostachya wightiana, Panicum antidotale, Paspalum cancarae, Pennisetum hohenackeri, Setaria palmifolia, Setaria pumila, Dimeria ornithopoda, Eriochloa procera, Themeda tremula, Zoysia matrella* etc. The temperate species having similarity in the Himalayan flora are not available in Orissa grasses. The grasses are mostly tropical and sub-tropical in nature. The important forage grasses are *Dichanthium, Chrysopogon, Brachiaria, Panicum, Pennisetum, Setaria, Chloris* etc. The diversity of these genus is very much in Orissa and availale in different eco-climatic regions with maximum variability.

Rare/Threatened/Endemic Species

Due to human interference and lack of proper protection, the vegetation have been ruthlessly degraded which had resulted in the extinction of many species. This is mainly due to habitat destruction and operation of many biotic factors. Due to these activities most of the species are under rare/endemic/threatened category. The details are given in Table 2 (Saxena and Brahmam, 1983 and Nayar *et al*, 1984). These species need immediate protection and conservation. Strategies should be developed for protection of these species.

Table 2. List of rare/threatened/endemic speices in Orissa

Name of Species	Family	Status
Acacia donaldii Haines	*Mimosaceae*	*Threatened*
Acacia tomentosa Willd.	*Mimosaceae*	Threatened
Albizia orissensis Sahni et Bennet	*Mimosaceae*	Threatened
Atylosia cajanifolia Haines	*Fabaceae*	*Threatened*
Desmodium ritchiei Sanjappa	*Fabaceae*	Threatened
Eleiotis sororia (L.) DC.	*Fabaceae*	Threatened
Erythrina resupinata Roxb.	Caesalpiniaceae	*Threatened*
Intsia bijuga (Colebr.) Kuntze	Caesalpiniaceae	*Threatened*
Mucuna minima Haines	Fabaceae	Endemic
Rhynchosia hainesiana Satyam. & Thoth.	Fabaceae	Endemic
Rhynchosia suaveolens (L.f) DC	Fabaceae	Threatened
Tephrosia roxburghiana Drumm.	Fabaceae	Threatened
Tephrosia purpurea (L.) Pers. Var. *maritima* Haines	Fabaceae	Endemic
Dimeria acutipes Bor	Poaceae	Threatened
Dimeria lehmanii (nees Ex Steud) Hack.	Poaceae	Threatened
Dimeria mahendragiriensis (Ravi) Saxena et Brahmam	Poaceae	Threatened
Dimeria mooney Raizada & Mooney	Poaceae	Threatened
Dimeria orissae Bor	Poaceae	Endemic
Dimeria trimenii Hook. f.	Poaceae	Threatened
Oryza Jeyporensis Govind & Krishnan	Poaceae	Endemic
Themeda mooneyi Bor	Poaceae	Endemic
Themeda saxicola Bor	Poaceae	Endemic

Conservation :

It is envisaged from the observation that many of the plant species have been vanished and some are on the verge of extinction due to interference of human civilization. This has resulted some plant to be under rare/threatened/endemic categories. Hence, it is the high time to conserve our forage genetic resources before further genetic erosion. Conservation should be *in situ* or *ex-situ* depending on the nature of species. Species viz, *Cajanus cajanifolia, Oryza jeyporenis, Rhynchosia hainesiana, Rhynchosia suaveolens, Dimeria mooney, Dimeria orissae, Themeda mooneyi, Mucuna minima, Desmodium ritchiei* etc should be conserved in *in situ* because lot of variability are also met with in these species. Conservation of genetic resources will help future plant improvement programme. Among the Legumes, the genus like *Crotalaria, Desmodium, Indigofera, and Vigna* have larger number of species with lot of variation. Similarly among the grasses *Panicum, Dimeria, Eragostris brachiaria* etc have maximum number of species. These species need maximum priority for conservation. *Stylosanthes* are the important pasture legume and forage crop also. Lot of work have been done in temperate countries where maximum species are available. In India, only *Stylosanthes fruitcosa* is found proper attention for conservation and domestication. Besides attention should be given for conservation of the threatened/endemic species. There are many important forage genus viz. *Desmodium tortuosum, Macrotyloma ciliatum, Canavalia maritima, Canavalia gladiata,* and many species of Sesbanias, should be conserved and domesticated to meet the fodder demand. Besides the threatened/ endemic species listed in the table 2 are to be conserved for posterity.

REFERENCES

Bairiganjan, G. C., P. C. Pand, B. P. Choudhury & S. N. Patnaik. 1985. Fabaceae in Orissa. *J. Econ. Tax. Bot.* 7(2): 249-275.

Bor N.L. 1960. The Grasses of Burma, Ceylon, India and Pakistan, Pergamon Press, London.

Choudhury, B. P. and S. N. Patnaik. 1980. Flora of Bhubaneswar and adjoining region III. New records of plants for the state of Orissa. *J. Orissa. Bot. Soc.* 2: 19-26.

Haines, H. H. (1921-25). The botany of Bihar and Orissa, 6 parts, London. (Rep. Edn. BSI, 1961)

Hudrad, C. E. 1954. Grasses, Pelican Books. A295, U.K.

Hussain, T. and S. L. Kapoor. 1990. Enumeration of Legumes in India (Indigenous and introduced). National Botanical Research Institute, Lucknow.

Mehra, K. L. and M. L. Magoon. 1974. Collection conservation, and exchange of genepool of forage grasses. *Indian J. Genet.* 34A: 26-32.

Mehra, K. L. and M. L. Magoon. 1974. Gene centre of tropical and sub-tropical pasture legumes and their significance in plant introduction. Proc. XII Internat. Grassld. Cong. Moscow, p 251-256.

Mooney, H. F. 1950. Supplement to the Botany of Bihar and Orissa. Catholic Press, Ranchi.

Nayar, M. P., M. Ahmed and D. C. S. Raju. 1984. Endemic and Rare plants of Eastern ghats. *Ind. J. Forestry* 7(1): 35-42.

Saxena, H. O., M. Brahmam and M. B. Raizada. 1980. Annonated list of vascular plants of Bhubaneswar. *Ind. J. Forestry* 3(I): 87-90.

Saxena, H. O. and M. Brahmam. 1983. Rare and endemic flowering plants of Orissa. pp 80-90. *In*: S.K. Jain and R. R. Rao (Editors): An assessment of threatened plants in Inida Botanical Survey of India. Calcutta, India.

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Short Communication

WILD JASMINES OF THE BAY ISLANDS

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A brief description of occurance and availability of *Jasminum* species in Andaman and Nicobar Group of Islands has been enumerated in this paper.

Key words : *Jasminum*, wild species, Andaman and Nicobar Islands, occurance

Jasmine (*Jasminum spp.*) is one of the most fragrant flowers cultivated by man since time immemorial. The flowers and buds are used for making garlands, venis used for adorning hair of women and for religious offerings. The flowers are highly valued in the perfumery industry for its concrete and absolute. Among the scented species, those widely grown are *J. grandiflorum, J. auriculatum, J. sambac, J. angustifolium, J. officinale, J. humile* and *J. pubescens.* In Malaysia, the flowers are used for scenting coconut hair oil. In China, Arabian jasmine is reported to be used for flavouring tea. The flowers and other parts of the plants are used for medicinal purposes as well.

Jasmines are native to tropical and subtropical regions. The genus *Jasminum* belongs to the family Oleaceae. A large number of species are centered around the regions comprising India, China and Malaysia (Wlth India., 1959). Among these, about 40 species are reported to occur in India. The distribution pattern of *Jasminum* species provides a strong base to the claim that India may be one of the principal centres of origin. The references to the three cultivated species, viz., *J. auriculatum, J. grandiflorum* and *J. sambac* in ancient Tamil literature belonging to the period of Sangam era prior to 500 BC suggests that South India may possibly be the home of atleast some of these species which occur only in wild forms. About 90 species of Jasmine have so far been identified. The Andaman and Nicobar Group of Islands, about 1,200 km away from the Indian mainland in the South-East Bay of Bengal are situated between 6°45' N and 13°41' N latitudes and 92°12' E and 93°57' longitudes. The islands enjoy a true maritine climate with the temperature ranging between 23°C and 32°C. Annual rainfall is more than 3000 mm, distributed over nine months and the relative humidity varies between 68 to 85 per cent. The climatic conditions prevailing in these islands are conducive for the luxuriant growth and development of various ornamental species, including flowering and foliage plants. A number of flowering trees, creepers, ferns, orchids and other ornamentals are found growing in the wild.

The tropical rain forests of Andaman and Nicobar Islands harbour eight species of Jasmine having horticultural and perfurmery value, and mostly grow wild in the forests and are staggling scandent shrubs having very attractive fragrant flowers. Some of these jasmine species can be grown as ornamental and decorative climbers in

the home gardens. Few of these species can also be used for making garlands and venis. Some of the wild *Jasminum* species present in the Bay islands are listed below along with the botanical description, distribution and status.

Jasminum andamanicum Bl. & Nair

The plant is a straggling and scandent shrub having pinnately trifoliate leaves and is endemic to these islands. The common petiole is about an inch long having swollen base, leaflets 1-4 inches long 1.5-2.0 inches broad, ovate to elliptic, round at the base dark green, flowers white, present in clusters very fragrant in axillary pendulous cyme, corolla tube - 1-1 1/4 inches long, flowering mostly in January-March. This species is rare and found only in South and Middle Andaman Islands.

Jasminum caudatum Wall.

A scandent shrub, leaves pinately trifoliate, the common petiole about an inch long, swollen at the base, leaflets 2-4 inches length, 1-21/2 inches broad, ovate to elliptic and often broadly so, the central leaflet largest and on long petioles, flowers handsome fragrant, borne in axillary cymes, corolla, tube 1-1 1/4 inches long, the limb 1/2-1 inches acros. Flowering in November-January.

Jasminum cordifolium Wall. ex. G. Don spp. *andamanicum* Srivast. & Kapoor

The plants are straggling and scandent climbers, leaves 2-4 1/2 inches long 1-2 inches broad ovate, finely acuminate, narrowed at the rounded base, dark green and glabrous, with lateral nerves boldly interarching at the margin. Petiole 1/1 to 1/2 inch long, flowers 1 inch in diameter in axillary or terminal trichotomous cymes, corolla tube 1/1 inch long, lobes 6-8, 1/2 inches long. Flowering is in January. Grows wild in South Andaman island (Baratang island). It is endemic to Andaman islands (Lakshminarasimhan and Rao, 1996).

Jasminum unifololatum Alakr & N.G. Nair

Scandent shrub with unifoliolate leaves and white flowers in paniculate cymes. It is rare (Nayar, 1994) and found in the North Andaman island (Saddle peak)

Jasminum multiflorum (Burn. f.) Andr

This is a very ornamental plant producing slightly fragrant white flowers and is in bloom through out the year. Found wild in the Great Nicobar island.

Jasminum ritchiei C.B. Clarke

A climbing scandent shrub found in the rain forests of Middle Andamans. The leaves are ovate, accuminate, glaborous, flowers white borne in 3-9 flowered often subpaniculate cymes. The leaves are used as a remedy for tooth-ache, wood for pipes tubes and flowers for treatment of piles.

Jasminum mauritianum Boj.

Scandent leaves pinnately trifoliate, the common petiole 1-1 1/2 inch long; leaflets 1-3 inch long and about half as broad, broadly elliptic to ovate, somewhat shortly and bluntly apiculate, lateral nerves fine, interarching rather far from the margin. Flowers white, in ample terminal corymbose glandular cymes; corolla tube 1-1 1/4 inch long, the limb about 1/2 inch across. Found wild in Long Island (Khader and Kumar, 1995).

REFERENCES

Khader, JBM M.A. and N. Kumar. 1995. Genetic Resources of Jasmine. *In: Advances in Horticulture.* Vol. 12, Eds K.L. Chadha and S. K. Bhattacherjee, Malhotra Publishing House, New Delhi, p 121-132.

Lakshminarasimhan, P. and P.S.N. Rao. 1996. A supplementary list of angiosperms recorded (1983-19993) from Andaman & Nicobar islands. *J. Econ. Tax. Bot.*, **20** (1): 175-185.

Nayar, M.P. 1994. Andaman & Nicobar Islands Death - traps of Endemic plant species. *Zoos' Print* 9(6): 5-11.

Wlth India. 1959. The Wealth of India. Council of Scientific and Industrial Research, New Delhi, p 279-292.

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Short Communication

MANAGING OF PLANT GENETIC RESOURCES IN RAJASTHAN

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Rajasthan being very diverse in relation to agroclimatic conditions has been divided in nine agroclimatic zones and has a very rich diversity in mothbean, pearlmillet, clusterbean, cowpea, sorghum, greengram, blackgram, sesame, brassicas etc. A great diversity has also been observed in chickpea, groundnut, cotton, tumba, cumin, coriander, fennel, fenugreek, chillies, medicinal plants and horticultural crops like ber, pomegranate, citrus, ker, salvadora, karonda, *Prosopis* etc.

Key words: Plant genetic resources, management, diversity

Some efforts have been made for the collection of germplasm by Rajasthan Agricultural University and the NBPGR but still major areas remains unexplored for various important crops. Explorations need to be conducted for exploiting the biological diversity in Rajasthan for pulses, oilseeds, spices, medicinal plants in particular and fibre crops, wheat, barley, sorghum, maize and agri-horticultural crops in general. Special efforts are required to collect, identify and analyse chemically, number of wild medicinal plants which are being used in interiors by the *Adivasi* in southern part of Rajasthan and local habitat of Great Indian Thar Desert.

A germplasm repository is being established with the World Bank aid under Agricultural Development Project at University headquarters Bikaner. After establishment, the germplasm of various crops being maintained in various agro-climatic zones will be shifted to this unit. The facilities for long and short term conservation will consequently be developed and the value added genotypes of various crops will be registered at the NBPGR.

Rajasthan is situated in the North-western part of India located between 23°30' N and 30° 12' N latitude and 69° 30' E and 78° 17' E longitude. It is the second largest state in India with a geographical area of 3.42 lac km^2 and represents 10.4 per cent area of the country. The state has a great variability in relation to soils i.e. poor sand dunes to rich clay and loamy soils, rainfall 100 mm to 1000 mm per annum, temperature 0° to 49° C and topography gangetic plains to Aravali hill ranges. On the basis of soil types, rainfall distribution and other climatic components the state has been divided into nine agro-climatic zones viz. Arid Western Plain Zone, Irrigated North Western Plain Zone, Transitional Plain of Inland Drainage, Transitional Plain of Luni Basin, Semi Arid Eastern Plain Zone, Flood Prone Eastern Zone, Humid Southern Plain Zone, Humid South Eastern Plain Zone and Sub Humid Southern and Aravali Hills Zone. Rajasthan represents the three agroclimatic zones of the national level i.e. Agro-ecological Zone (2), Hot arid agro-ecological Zone (4) and Agro-ecological Zone (5) out of 20 agro-ecological zones (Sharma, 1998) divided on the basis of microclimate has

a very rich diversity in mothbean, pearlmillet, clusterbean, cowpea, sorghum, greengram, blackgram, sesame, brassicas etc. A great diversity has also been observed in chickpea, groundnut, cotton, tumba, cumin, coriander, fennel, fenugreek, isabgol, chillies, medicinal plants and horticultural crops like ber, pomegranate, citrus, ker, salvadora, karonda, *Prosopis* etc. As no special efforts have been made to collect the variability from these crops hence in the present changing global trends it becomes imparative to complete this task for claiming our sovereign rights on the value added germplasm. Keeping the above points in view a case study on the plant genetic resources in Rajasthan has been carried out with the following objectives : (i) Current status of plant genetic resources in various agro-climatic zones of Rajasthan and (ii) Future plans for identification, collection, evaluation, conservation, documentation and registration of germplasm.

The genetic diversity for different crops has been reviewed in various agroclimatic zones of Rajasthan. The major crops being grown in various agro-climatic zones are being presented zonewise in Table 1

Table 1. Zonewise crops being grown in Rajasthan

No.	Zone	Major crops
1.	Arid Western Plain Zone - 1 a ARS, Mandore (Jodhpur)	Pearlmillet, mungbean, sesame, mothbean, clusterbean, chickpea, rapeseed & mustard, wheat, ,cumin, chilli, *Psyllium*, datepalm, tumba, ker, castor
2.	Irrigated North western Plain Zone - I b ARS, Sriganganagar	Cotton, chickpea, rapeseed & mustard, wheat, sugarbeet, clusterbean, mungbean, mothbean, groundnut, paddy, sugarcane, sesame, citrus, temperate fruits (peach, plum etc.), mango, grape
3.	Transitional Plain of inland Drainage - II a ARS, Fatehpur (Sikkar)	Chickpea, mustard, fenugreek, fennel, mungbean, mothbean, cowpea, clusterbean, sesame, groundnut, chilli, ber, pomegranate, cumin
4.	Transitional Plain of Luni Basin - II b ARS, Jalore	Cumin, *Psyllium*, sesame, chilli, fennel, tomato, mustard, pearlmillet, cotton, mungbean, wheat, chickpea, clusterbean, henna, ker, piloo
5.	Semi-arid Eastern Plain Zone - III a ARS, Durgapura (Jaipur)	Wheat, barley, groundnut, chickpea, taramira, pearlmillet, clusterbean, mothbean, mungbean, cotton, maize, fenugreek, fennel, onion, brinjal, ber, pomegranate, desi rose.
6.	Flood Prone Eastern Plain zone - III b ARS, Navgaon (Alwar)	Rapeseed & mustard, pearlmillet, pigeonpea, barley, clusterbean, wheat, chickpea, fieldpea, fodder sorghum, ber guava,mango, lemon, papaya
7.	Sub-humid Southern Plain and Aravali Hills Zone-IV a ARS, Udaipur	Maize, sorghum, medicinal and aeromatic plants, wheat, barley, mustard, sugarcane, blackgram, cotton, bunch groundnut, soybean, garlic, safflower, niger, ginger, sesame, pigeonpea, castor, guava, aonla
8.	Humid Southern Plain Zone - IV b ARS, Bansawara	Paddy, maize, urdbean, mango, minor millets, chickpea, wheat, barley, pigeonpea, soybean, mustard, caster, cotton, sowa, aijwain, garlic, sapota, papaya, lemon, guava
9.	Humid South Eastern Plain Zone - V ARS, Kota	Soybean, paddy, durum wheat, sorghum, linseed, lentil, blackgram, chickpea, mustard, sugarcane, sunflower, coriander, potato, orange

Arora (1991) has reported a rich diversity in mothbean, pearlmillet, clusterbean, cowpea, sorghum, mungbean, blackgram, sesame, brassicas, cucurbits, forage legumes and grasses. A huge diversity is also present in the field crops like cotton, groundnut; economic crops like cumin, isabgol, coriander, *Cucumis*, tumba, fennel, fenugreek, chillies, and horticultural crops like ber, pomegranate, citrus, *Salvadora*, Karonda, *Prosopis* spp. in Rajasthan which is also evident from the Table 1. The table also confirms wide diversity in relation to climatic conditions and diverse crops being grown in various zones. The germplasm of major field crops is being maintained

at different locations in the state is being listed in table 2 zone wise.

Table 2. Germplasm lines of various crops maintained in various agro-climatic zones in Rajasthan

	Crop	Zone
1.	Cotton	Ib
2.	Rapeseed mustard	III b,II b
3.	Groundnut	III a
4.	Wheat	III a
5.	Mothbean	I a
6.	Clusterbean	III a
7.	Chickpea	I b,III a
8.	Mungbean	III a
9.	Urdbean	IV b
10.	Barley	III a
11.	Rice	V
12.	Pearlmillet	III a
13.	Maize	IV a
14.	Sorghum	IV a

In addition to the above, there are a large number of life support species of which various parts are being used by the local habitat of the Great Indian Thar Desert and the *advasis* are being listed as under :

Type	Name of species	Plant part being used
Grasses	*Cenchrus* spp., *Penicum* spp., *Brachiaria* spp., *Lasiurus* spp., *Elusine* spp. and Dactyloctenium	Seeds are used by mixing with flour
Shrubs	*Haloxylon salicornicum*, Kumut (*Acacia senegal*), Matira (*Citrullus lanatus*)	Seeds are being used
Leguminous weeds	*Indigofera* spp., *Vigna trilobata*	-do-
Trees	Bordi (*Zizyphus nummularia*), Ker (*Capparis decidua*), Dansri (*Rhus mysorensis*), Gangeran (*Grewia tenax*) Gangeti (*Grewai villosa*) Gunda (*Cordia myxa*), Sainjna (*Moringa oleifera*), Kachra (*Cucumis* spp.), Khejri (*Prosopis cineraria*)	
	Guar patha (*Aloe vera*), Khejri (*Prosopis cineraria*)	Stem bark and leaf pulp
Rotts and tubers	Safed mushli (*Chlorophytum*), Dhak (*Butea monosperma*), Khadula (*Ceropegia tuberosa*), Semul (*Bombax malabarcum*)	Roots and tubers

These life support species need to be chemically analysed and their medicinal and nutritional values will be established and recognised and registered to avoid further complications regarding the ownership at the global level in future. A large number of germplasm lines of various crops are being maintained in the different agroclimatic zones in the state. For making the work more systematic and well planned, these lines need to be collected and maintained at one location under the Biodiversity Centre being built in the state whose mandate and functions are being mentioned here.

Germplasm Repository

A plant biodiversity centre is being established in the Rajasthan Agricultural University, Bikaner with the World Bank aid under the Agricultural Development Project which will be looking after collection, evaluation, conservation and value identification aspects of various unidentified plant species of economic, medicinal and nutritional importance. The germplasm repository is being constructed such that it meets the modern specifications required for storage and maintenance of plant material. This will be supplied with supplemental source of power in order to assure that all plant material will be well maintained at all times. The collection of clonal material will be sent to the national clonal repository operated by the Indian Government rather than being stored in Rajasthan because of costs and logical requirements associated with such facility.

The number of accessions of the germplasm collections are meagre in the state and are being maintained in scarted stages. Therefore, there is an urgent need for acquisition of more diverse

germplasm from various sources. Greater emphasis needs to be given for explorations and collection of agri-horticultural plants, medicinal, aeromatic and underutilised plant and life support species in the areas of diversity. The salient points on which immediate attention is to be given for the success of plant genetic resources in the state are as under : (i) Pooling and proper maintenance and documentation of the existing field crop germplasm and colelction of more diverse lines, (ii) Exploration and collection of diverse germplasm of agri-horticultural, medicinal, aeromatic, under utilised and life support species from the Great Indian Thar Desert, (iii) The detailed evaluation of germplasm by including as many as possible characters over years at different locations and Study of chemical nature of the rare and unknown species which are being used by the tribal people since very long and their importance should be recognised scientifically.

REFERENCES

Anonymous. 1996. Research Highlights. Directorate of Research, Rajasthan Agricultural University, Bikaner 334 006 (India).

Arora, R. K. 1998. Plant Diversity in the Indian Gene Centre. *In*: Plant Genetic Resources, Conservation and Management. Concepts and Approaches. (Eds. R. S. Paroda and R. K. Arora) IBPGR, Regional Office for Southeast Asia, New Delhi p. 25-44.

Gautam, P. L. 1998. Agro-biodiversity and Intellectual Property Rights (IPR) related issues. Presented in the Summer Institute on "Plant Genetic resources : Principles, Procedures and Approaches in Collection, Evaluation and Conservation" held from 27th July - 6th August, 1998 at NBPGR, New Delhi 110 012.

Vinod Shankar. 1988. Life support species in the Indian Thar Desert. Life support species : Diversity and conservation (eds. R. S. Paroda, Promila Kapoor, R. K. Arora and Bhag Mal). NBPGR, New Delhi 110 012. pp 34-37.

Sharma, B. D. 1998. Phytogeographical and agro-ecological zones of India. *In*: Plant Germplasm Collecting : Principles and Procedures (eds. P. L. Gautam, B. S. Dabas, Umesh Srivastava, S. S. Duhoon). NBPGR, New Delhi 110 012. p 40-43.

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Short Communication

SOURCES OF RESISTANCE IN CHILLI GERMPLASM AGAINST BACTERIAL WILT AND ANTHRACNOSE

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Sources of resistant genetic stocks are of great importance to the plant breeders for exploitation in crop improvement programme. Extensive screening for sources of resistance in chilli against anthracnose disease caused by *Colletotrichum* spp. resulted in different degrees of resistance in different genetic stocks of chilli. Sources of resistance against bacterial wilt and anthracnose disease so far identified have been listed in this article.

Key words: Chilli, *Capsicum annuum*, resistance, *Pseudomonas solanacearum*, *Colletotrichum* spp.

Bacterial wilt caused by *Ralstonia solanacearum* and anthracnose caused by *Colletotrichum* spp. are two severe and devastating diseases of chilli. They create a great havoc in commercial cultivation of chilli and limit the production. In India 50-100 per cent incidence of bacterial wilt disease has been reported (Das and Chottopadhyay, 1955; Khan *et al.*, 1979). In Assam, bacterial wilt occurs in all the six agro-climatic zones and becomes most severe when environmental factors favours the disease (Addy *et al.*, 1980; Bora, 1996). On the other hand, the anthracnose is present throughout India but more common and aggressive in Assam, North Bihar, Andhra Pradesh and parts of UP (Singh, 1992). It appears season after season as the pathogen continues to survive by vegetative mycelium or resting spores. In India, it is known to cause 12-32 per cent fruit rot in Assam (Choudhury, 1957), 10-30 per cent reduction in yield in Punjab (Bansal and Grover, 1969) and 10-35 per cent reduction in yield in Punjab and Haryana (Bansal and Grover, 1969). Both the diseases may occur simultaneously in the field causing tremendous loss in yield of the crop. (Fugro *et al.*, 1989). Moreover application of only chemicals cannot serve our purpose in the present day context of sustainable agriculture. Moreover, host plant resistance has assumed greater importance in integrated disease management strategies.

RESISTANT OR TOLERANT GENETIC STOCKS

a. Bacterial wilt

Different experiments have been conducted to screen and evaluate varieties of chilli against bacterial wilt caused by *P. solanacearum* (Table 1). Walker and Manser (1980) isolated the bacteria from bacterial wilt of an exotic capsicum cv. Asgrow Long Green and found susceptible. Local cultivars of capsicum were found resistant or tolerant to the pathogen. It appeared that the bacterial wilt pathogen was present in the soil and indigenous lines of solanaceous crops have developed some tolerance against it.

Baruah (1994) also appraised by presentation of data that local chillies of Assam were significantly

more resistant to bacterial wilt than introduced ones from other parts of India. This can be attributed to the climato-geographical peculiarities of the region where indigenous germplasm have attained inherent survival capacity. Nath (1996) tested the relative reaction of seven different varieties against bacterial wilt in Assam. But no variety was found resistant to bacterial wilt. California Wonder was found to be moderately susceptible showing 22.22 per cent wilt incidence while Pusa Jwala and Indo American Hybrid chillies were found to be susceptible. Four varieties Kharika (local), Gagan (local), Krishna and NP464 were found highly susceptible showing more than 40 per cent wilt incidence. This disease has also become a major constraint in capsicum production in Kerala (Jyothi *et al.*, 1993).

In Central and South America, pepper was found consistently susceptible to the wilt causing bacterial isolates of 70, 163, 130 isolated by French and Sequeira (1970). Most plants inoculated with these isolates died within 6-12 days. Other isolates caused wilting only in the inoculated leaf with slight inhibition of internode elongation. However, most pepper varieties had been considered to be moderatly or highly resistant to racel isolates in the past. In Brazil, fifty genotypes were grown under green house and inoculated at the 2 leaf stage with a mixture of 2 cultures of *P. solanacearum.* Six genotypes (with 1.8-2.8 scores) in 1-4 scale were rated resistant and the remaining were found susceptible (Matos *et al.*, 1990).

b. Anthracnose disease

From time to time different workers have screened and evaluated various genotypes of chilli (Table 2).

Chang and Chung (1985) from Korea reported that among 21 capsicum cvs. Kumchang No. 2, Bulamhouse, Pakistan and Hongilpam were found resistant. Another five were moderately resistant and other twelve (all these were sweet tasting cultivars) were susceptible. Pearson *et al.*, (1984) in Papua New Guinea found that among 23 CVs. assesed the sweet bell varieties were generally found more susceptible than long pungent ones (Red pepper, Pretty Red, Long Red Cayenne, Ilimo, Anaheim, NG7238, Hot Spike). Choi and Pae (1987) reported from Korea that six varieties of chilli showed differences in lesion size from 3-7 days after inoculation with *C. gloeosporioides* (*Glomerella cingulata*) or *C. ematium.* None was found immune out of ten cvs screened by Basak (1997) against *Colletotrichum capsici*, *G. cingulata* and *Fusarium semitectum* in Chittagong, Bangala Desh.

In Maharastra, it was found that cv. CA 960 suffered less from (Jieback and fruit rot than cvs. Bhiwarpur local followed by Musalwadi L, Jwala and Pant C-1. The variety CA 960 also gave significantly higher yield. It was noticed that variety with large fruit and thick pericarp were less affected and gave higher yield compared to variety with smaller fruits and thin pericarp (Patil *et al.*, 1993). Pusadhakar and Moghe (1991-92) reported that all the cvs. grown in the field produced fruit rot and dieback symptom, but M.G. Katol, Washim-30, Akolkhed, Warangal have shown some tolerance to fruit rot and dieback. Three varieties viz. Ceictio no.2, Sewal and Patna chilli were found least susceptible (Singh and Thakur, 1979). While searching for field tolerance to fungal and viral diseases in Punjab conditions the genotypes CH-1, Punjab Lal, ELS-2, Indonesia Sel, LLS and Pusa Jwala were found to be promising by Kaur *et al.* (1994) in addition to acceptable horticultural characters. The reaction of 21 varieties or selections to die back and fruit rot after infection with the fungus with or without previous or subsequent inoculation with TMV was studied. Selection of 34-13

Table 1. List of some chilli genotype showing resistant reaction against bacterial wilt

Germplasm	Reaction	Worker(s)	Year
KAU cluster,White Kandari and Pant C-1	R	Hibberd *et al.*	1984
Pant-C	R	Peter *et al.*	1984
Cholo	R	Jimenej *et al.*	1988
17245	FR	Jimenej *et al.*	1988
LCA-304,BC-24,BC-14-2	I	Fugro *et al.*	1988
Arka Lohit,Jayant,Phule-6-5 and X -235	MR	Fugro *et al.*	1988
Sel-2,HC-203 and Nath Heera	R	Fugro *et al.*	1988
Manjeri	MR	Jyothi *et al.*	1993
Ranche Khorsani (*C. chinense*) Heiser 6240, LS 2390,LS1840 (*C. frutescens*), LS1716, Casali BGH 1761 and Pickersgill 277 (*C. baccatum*)	R	Matsunga and Monma	1995
Capsicum annuum: CNPH 143 (MCA), CNPH 144 (MC5) and CNPH 145 (HC10)	HR	Matos *et al.*	
Selections CA219 and CA33	I	Gopalkrisna and Peter	1991
MC-4	R	Quezdo-Soares and Lopes	1995
MC4,MC5,PBC631,P1322727,Pi358812,PBC066,Kerting,P1369994,P136 9998,P1377688,OMS-B,P1322728 and Jatilaba	HR	KimByungSoo *et al.*	1998

I = Immune, HR = Highly resistant, R = resistant, FR = Fairly resistant, MR = Moderately resistant

showed acquired resistance to the fungus when first inoculated with TMV (Bansal *et al.*,1982). Such acquired resistance has great implications in biological control of disease. Chouhan and Duhan (1986) also studied reactions of different strains/varieties of capsicum against anthracnose under Haryana condition. Fugro *et al*, (1989) found that varieties LCA-304, BC-24, BC-14-2 were completely free from bacterial wilt and showed moderate resistance to die-back. The varieties Arka, Lohit, Jayant, Phule-6-5 and X-235 were found resistant to die back, but showed moderate resistance to bacterial wilt. The varieties Konkon Kirti were found moderately resistant to both the diseases. In an another experiment, they found that Sel-2, HC-203 and Nath Heera were resistant to both the diseases.

Out of 60 germplasms screened at AAV, Jorhat only one variety 'Balijuri' found to be resistant to both the diseases. Varieties C-1, C-3 and Kolajalakia (long) were found moderately resistant to both the diseases. Again varieties Ou Jalakia-II, Tupura Jalakia, Thupa Jalakia, Ugda Jalakia, Paharia Bhot and Dhan Marish resistant to anthracnose found moderately resistant to bacterial wilt.

REFERENCES

Bansal, R.D. and R.K. Grover. 1969. Reaction of chilli varieties to *Colletotrichum capsici*. *J. Res.* 6: 345-348.

Bansal, R.D., H. L. Khatri and O.P. Sharma. 1982. Interaction between Tobacco Mosaic Virus and *Colletotrichum capsici* in *Capsicum annuum* L. varietal reaction. *Joumal of Research, Punjab Agricultural University* 19(1): 39-43.

Baruah, S.J.N. 1994. Relative resistance expression of Assam type and introduced varieties in Jorhat condition. Proceedings of the ZREAC and DTCM (Plant Breeding & Horticulture), held in August, 1994.

Baruah, S.J.N. and B. Deka.1995-96. Annual Report. AICVIP, Jorhat centre, Assam p. 8-9

Basak, A.B. 1997. Reaction of sc,i-ne chilli germplasm to major fruit rotting fungal pathogen. *Chittagong University Studies, Science* 21(l): 123-125.

Table 2. The list of some chilli genotypes showing different reactions to anthracnose

Genotype Place/Country	Reactions	Worker(s)		Year
NP hybrid,Kashmir Yellow,Kalyanpur No1	R	Singh *et al.*	1977	Punjab
C-22-A.R. Larm,VIP-45-A,B-8-A-Hydarabad, C.A. 1047,C15-A-Mexico,CH-113,C.A.960, K-Surkh,745-Achalpur,745-America,I.C. 13277,724-Guntur,CH-107,B-29-A-Bihar, B-2-A-Dharwar,No. 762,Sel-14,Hy-No-8-Self,Chamatkar,G-2-A-Mexico				Local, G-5
Bengal Green,H-1,H-4,S20-1,H-6	R	Singh and Thind	1980	Punjab
520-l,H-1,H-A,H-6	HR	Singh and Thind	1980	Punjab
Capsicum annuum CVs. Artakis,August,Chinese Giant,Yolo-Y,Hungarian Wax,Sparton Emerald,Pimiento Paprika,Kalinkov-805,D-103,Ukrainskij Gorkij,Zlanten Medal,Wonder Top,Malaquetta,Paprika C. sinensis var. panca C. fasciculatum	R	Ullasa *et al.*	1981	
C. annuum cvs. Chinese Giant,Floriyis,Kapija,Szentesi,Maidova-118	MR	Ullasa *et al.*	1981	
NG7236,NG7239 Kumchang No 2,Bulamhouse	DE	Pearson *et al.*	1984	Papua New Guinea
Pakistan,Hongilpam	R	Chang and Chung	1985	Korea
Lorai,Perennial	R	Kaur and Singh	1985	Punjab
7262,Deglur,B79A,LIC24 764 Guntur,574 Thirumalapuram	MR	Perane and Joi	1986	Maharashtra
Pant C1,B7-9 self	R	Perane and Joi	1986	Maharashtra
Janghong	R	Choi *et al.*	1990	Korea
BG-1,Lorai,Perennial	R	Singh *et al.*	1980	Punjab
MS-13,MS-12,Surjamani,Laichi -IV-3,Tiwari-II,Laichi IV-4,Anheim Thick,Bharat Hybrid,ET-Late,MY 13-1-1,Laichi-1,MS4-MF3,Tiwari,X-200,Punjab Lal,MY 10-2,Anheim,Laichi-III,MF-11-1	R	Singh *et al.*	1980	Punjab
K Swekh, Ch 107,Chamatkar,Safer yellow, G4	MR	Singh *et al.*	1980	Punjab
Punjab Lal	R	Sokhi	1994	Punjab
HC28,HC44	R	Pandita *et al.*	1995	Haryana
Jati Cluti,Jati Small,Kharika,KC1,Round Chilli,Jati Long,Krishna,Nagabat,Karanga,Bhot	R	Baruah and Deka	1996	Assam
IC 99910,IC 99912,IC92150,P-1718,P- 1939,N-1015,EC 362901,EC 362910 EC 362913,EC 362925,EC 362934,EC 362935,EEC 3637	T	Muneem *et al.*	1995	Uttar Pradesh
DC1,DC2,DC3,DC4,DC5,DC6	MR	Roy *et al.*	1998	Assam
Longamiri,Latabih-1,Ou Jalakia-2,Chakma,Garofingi,Latabih-2,Firingi Jalakia,Tupura Jalakia,Kola Jalakia,Thupuka Jalakia,Balijuri,Nadharia, Kola Jalakia (uper mukhia),Ugda Jalakia,Khoti Jalakia,Bogori Jalakia,Sahab Jalakia,Pahari firingi,Pahiri bhot,Dhan marish	R	Unpublished data project, ICAR- Adhoc	1999	Assam
Rangulul,C-1,C-3,C-5,Refugi(AP),Singhasan,OuJalakia-1, Kolajalakia(L),SJNB,Mihi Firingi,Thupa jalakia, Assamia jalakia,Uparmukhia, Pavaria,Goswami-1 Andhra Pradesh	MR	Do	1999	Assam

Note: HR=highly resistant, R=resistant, MR=moderately resistant, T= tolerant, DE= disease escaping

Bora, L.C., P.K. Gogoi and B.C. Das. 1996. Bacterial wilt of tomato in relation to few environmental parameters in Assam. *Joumal of the Agril. Sc. Society of North East India* 8(2).

Chang, S.H. and B.K. Chung. 1985. Studies on the varietal resistance and effect of nutrients for fungal growth of pepper anthracnose disease caused by *Colletotrichum dernatium* fsp. Capsicum. *Korean J, of Mycology,* 13(4): 227-233.

Chauhan, M.S. and J.C. Duhan. 1986. Reaction of genetic stock entries of chillies against important diseases in Haryana State. *Indian J. of Plant Pathology* 4(2): 146-149.

Choi, J.K., D.Y. Park, Y.H. Woo and J. M. Sung.1990. Studies on the resistance of red pepper varieties to *Phytophthora* blight and Anthracnose. Researcli Report of Rural Development Administrative Horticulture, Korea Republic (Suweon) 32(2 Hortic): 29(l): 33-34

Choi, K.S. and D.H. Pae.1987. Studies on the breeding of resistant varieties of pepper 3. On the inoculation methods for resistant varieties of pepper to anthracnose. Research Report of the Rural Development Administrative Horticulture, Korea Republic. 29(l): 16-23.

Choudhury, S. 1957. Studies on development and control of fruit rot of chillies. *Indian Phytopath.* 10: 56-62.

Das, C.R. and A. Chottopathyay. 1955. Bacterial wilt of egg plant. *Indian Phytopath.* 8: 130-135.

Fugro, P.A., V.A. Patil and U.K. Sawant. 1989. Evaluation of chilli germplasm for resistance to Bacterial wilt and Die back diseases. 24(30): 45-48.

French, E. R. and L. Sequeira.1970. Strains of *Pseudomonas solanacearum* from Central and South America, a comparative studies. *Phytopathology* 60: 506-510.

Gopalkrishnan, T. R. and K.V. Peter. 1991. Screening and selection of bacterial wilt resistance in chilli. *Indian J. Genet.* 51(3): 332-334.

Hibberd, A. M., R.E. Stall and M.J. Basset. 1984. The resistance system to bacterial spot of pepper in a plant introduction. *Phytopathology* 74(7): 791.

Jimenez, J. M., E. Bustamante, W. Bermudez and A. Gamboa. 1988. Response of four cultivars of sweet pepper to bacterial wilt in Costa Rica. Manejo Integrado de Plagas No.7, 19-28.

Jyothi, A.R., A. Koshy and J. Alathew. 1993. Bacterial wilt of chillies in Kerala and reaction of certain chilli accession to *Pseudomonas solanacearum* (smith). *Bacterial wilt Newsletter* No. 6. 9.

Kadu, I. K., B.B. More and P.G. Utikar. 1978. Field reaction of chilli germplasm to anthracnose. *Indian Phytopath.* 31(3): 540.

Khan, A.N.A., K.S. Shetty and R.B. Patil. 1979. Occurrence of bacterial wilt of chillies in Karnataka 3nd its relationship to the wilt of solanaceous crops. *Indian Phytopath.* 32(4): 507-512.

Kim ByungSoo, Cheung JongDo, Cha YuSun and Hwang HeeSuk. 1998. Resistance to bacterial wilt of introduced peppers. *Korean J. of Pl. Path.* 14(3): 217-219.

Kaur, S., J.S. Hundal. and D.S. Khurana. 1994. Search for tolerance to fungal and virusdisease in chillies. *Indian J. Pl. Genet. Resources* 7(2): 223-226.

Kaur, S. and J. Singh. 1985, Resistance to fruit rot diseases under field conditions in pepper (*Capsicum annum* L.) *Capsicum Newsletter* 4.p. 67.

Matos, F. S. A., C.A. Lopes and Jakatsu. 1990. Identification of source of resistance to *Pseudomonas solanacearum* in *Capsicum* Spp. *Horticulture Brasileira* 8: 22-23.

Matsunaga, H. and S. Monma. 1995. Varietal differences in resistance to bacterial wilt in related species of Capsicum annuum. *Capsicum and Eggplant Newsletter* No. 14, 60-61.

Muneem, K.C., S.K. Verma and K.C. Pant. 1995. Performance of some chillies against leafspot, powdery mildew and fruit rot in Kumaon Hills. *Indian Phytopath.* 48(2): 206.

Nath, G. 1996. 'Management of Bacterial wilt of solanaceous crops caused by *Pseudomonas solanacearum.*' M.Sc.(Agri.) Thesis. A.A.U. Jorhat.

Pandita, M.L., S.K. Arora, P.S. Partap, M.S. Dahya and S.K. Poonan Dhawan. 1995. New Chillies 'HC28' and 'HC44'. *Indian Horticulture* p. 10-11.

Patil, C.U., U.B. Karekar and N.I. Peshney 1993. Effect of die back and fruit rot on the yield of chilli. *PKV Research Jounal* 17(l): 60-63.

Pearson, M. N., P.B. Bull and H. Speke. 1984. Anthracnose of Capsicum in Papua New Guinea, varietal reactions and associated fungi. *Tropical Pest Management* 30(3): 230-233.

Perane, R.R. and M.B. Joi. 1986. Reactions of chilli cultivars to fruit rot and die back of chilli infected by *Colletotrichum capsici. Current Research Reporter,* Mahatma Phule Agril. Univ. 2(l): 52-54.

Peter, K.V., R. W. Goth and R.E. Webb. 1984. Indian hot peppers as new sources of resistance to bacterial wilt, Phytophthora root rot, root knot nematode. *Hort Science* 19(2): 277-278.

Pusadhakar, G.K. and P.G. Moghe. 1991-92. Field performance of chilli cultivars under natural infection if die back and fruit rot disease. *Indian Phytopath.* 44&45 (Proc. a Meet, Indian Phytopath. Soc. Bhavnagar, 1991-92, 43-44), 114.

Quenzdo-Soares, A.M. and C.A. Lopes. 1995. Stability of resistance to bacterial wilt of sweet pepper. 'MC-4' challenged with strains of *Pseudomonas solanacearum Fitopatologia Brasileira* 20(4): 638-641.

Roy, A., D.K. Bordoloi and S.R. Paul. 1998. *PKV Research Joumal* 22(l): 155.

Singh, H., J. Singh and S. Kaur. 1980. Resistance sources to fruit rot (*Colletotrichum capsici*) in pepper. *J. Res.* 27(3): 419-420.

Singh, R.P., P.N. Singh and D.R Singh. 1977. Note on fruit rot disease of chillies. *Indian J. Agric. Res.* 11(3): 188-190.

Singh, S.A. and D.P. Thakur. 1979. Reaction of chilli varieties to *Colletotrichum capsici. Curr. Sci.* 48(11): 512-513.

Singh, J and T.S. Thind. 1980. Search for anthracnose and die back resistant varieties of chilli in Purijab. *The Punjab Veg Germs.* 15: 37-39.

Singh, R.S. 1992. Diseases cf Vegetable crops (2nd Ed) Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, p-362.

Sokhi, S.S. 1994. Integrated ipproaches in the management of vegetable diseases in India. *Indian Phytopath.* 47: 371-376.

Ullasa, B.A., R.D. Rawal, H.S. Sohi, D.P. Singh and M. C. Joshi. 1981. Reaction of sweet pepper genotypes to anthracnose, cercospora leaf spot and powdery miltiew disease. *Plant disease* 65(5): 600-601.

Walker, J. M. and P.D. Mansar. 1980. Bacterial wilt of capsicum. *FAO Plant Protection Bulletin* 28(3): 115-116.

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PLANT GERMPLASM REGISTRATION NOTICE*

Germplasm registration committee in its VIth meeting held on 10th May 2000 approved the registration of 19 germplasm/genetic stocks out of 76 proposals considered.

INGR 00001 is a high yielding (207.95 q/ha) genotype of sweet pepper (*Capsicum annuum* var *grossum*) with maturity, export quality, superior shelf life and high nutritive value. It is designated as Capsicum Selection 2 (Nishat -1) and developed from a cross between Oskash x World Beater Pedigree 8625-2-8-5-2 by Nazeer Ahmed and M.I. Tanki at SKUAST Srinagar.

INGR 00002 is a cytoplasmic genic male sterile line of til (*Sesamum indicum*) designated as CMS-C1. CMS-T3, CMS-T4, CMS-T6. It is developed from a cross between *S. malabaricum* x *S. indicum* by R. Sethupati Ramalingam K.A.A.J. Prabakaran, Jayanta Bhuyan, M. Kavitha, and S. Kirija at TNAU Coimbatore.

INGR 00003 is a bold grained genetic stock of wheat (*Triticum aestivum*) with high bread score (9.0), high chapati score (8.5), high protein content (14.28 %), high grain appearance (9.0) and designated as WH423. It is developed from a cross (WL 371- M164), Raj 842 by S. C. Sharma, Mohd. Yunus, Iqbal Singh, R. K. Rana and Sashi Madan at CCC HAU, Hisar.

INGR 00004 is a cytoplasmic male sterile fine of paddy (*Oryza sativa*) with basmati quality designated as Pusa 3A.It is developed from cross IR58025-A/ Pusa Basmati-1 through back crossing using Pusa Basmati-1 as recurrent parent by F.U. Zaman, A. R. Sadananda, M. J. Abraham, U. S. Natrajan, A. Mahendru, A. K. Singh, F. Mohammad and R. A. Singh at IARI, New Delhi.

INGR 00005 is a cytoplasmic male sterile line of paddy (*Oryza sativa*) designated as Pusa 5A. It is developed from the cross Pusa 150-21-1-1-2 as recurrent parent by F.U. Zaman, A. R. Sadananda, M. J. Abraham, U. S. Natrajan, A. Mahendru, A. K. Singh, F. Mohammad and R. A. Singh at IARI, New Delhi.

INGR 00006 is a GMS female parent of cotton hybrid VCHH-32 designated as VCMS2. It is a semi-erect, with yellow petals, dark green less hairy leaves. It is a re-selection from Supriya which is converted to GMS. This material was developed by Vijay Seed Company Jalna.

INGR 00007 is a germplasm of paddy (*Oryza sativa*) with less tiller number, low spikelet sterlity designated as KHO-CHI. It is a collection from Crane Basti, Mayabunder, N. Andaman and developed by Asit B. Mandal and R. Elanchezhian, CARI, Port Blair, A&N Islands.

INGR 00008 is a germplasm of paddy (*Oryza sativa*) with high nutritive value, bold grain with striped husk, black voilet in colour. Dehusked rice is voliet in colour. The germplasm is designated as Red Burma. It can be used to improve amylose content. It is a collection from Mayabunder, N. Andaman made by Asit B. Mandal and R. Elanchezbian, CARI, Port Blair, A&N Islands

INGR 00009 is a germplasm of paddy (*Oryza sativa*) with small slender, scented grains with black stripes on husk. It is designated as Black Jeera. It is collected from Dighpur, N. Andaman made by Asit B. Mandal and R. Elanchezhian, CARI, Port Blair, A&N Islands.

*Communicated by Dr. B. B. Singh, Member Secretaiy, ICAR Committee on Germplasm Registration

INGR 00010 is a genetic stock of cotton (*Gossypium hirsutum*) with high percentage of seed oil and seed oil index, early maturity (130-140 days) and thus escapes major pests. It is high yielding (19.50q/ha) with medium boll size and synchronous maturity. It is designated as CNO 131 and is developed by R. G. Dani, CICR, Nagpur from IC 491-Bobssshaw, an exotic accession from USA.

INGR 00011 is a genetic mungbean (*Vigna radiata*) stock with very high seed weight (6.2g/ 100 seed), very long pod (8.4 cm) and very high protein content (27.8%). It is designated as BSN-1. It is a selection from Nagpuri local made by B. S. Naik, Babita Singh, C. Kole, OUAT, Bhubaneswar, Orissa.

INGR 00012 is the first stable cytoplasmic genic male sterile line in pigeonpea (*Cajanus cajan*), designated as GT288A and GTB288B. It is a result of a cross *C. scarabaeoides* x *C. cajan* made by S. S. S. Tikka, L. D. Parmar and K. M. Chauhan at GAU, Sardar Krushinagar, Gujarat.

INGR 00013 is a hybrid *Gladiolus* with capsicum red (RHS-33A) flowers with charetreuse yellow (RHS-2D) on lip petals, petals ruffled and average spike length 138cm, mean number of florets 18.5 and flowers 10.2 cm in diameter It is designated as IHBT-G-1 and is a result of hybridisation between Green Woodpecker x Oscar made by D. Mukherjee, D. Dhyani and H. C. Rana at IHBT Palampur, Himachal Pradesh.

INGR 00014 is a hybrid Gladiolus with brick red (petals having Dresden yellow (RHS-5D) on lip petals, lip petals are nicely ruffled and average spike length 115cm, mean number of florets 18.3 and flowers 11.8 cm in diameter. It is designated as MTG-2 and is a result of hybridisation between Vink's GIory x Eurovision made by D. Mukhedee, D. Dhyani and H. C. Rana at IHBT Palampur, Himachal Pradesh.

INGR 00015 is a hybrid Gladiolus with white petals having deep purple voilet (RHS80A) edges, average spike length 125.4cm, mean number of florets 17.1 and flowers 10.5cm in diameter. It is designated as IHBT-G-3 and is a result of hybridisation between Snow Princess x Her Majesty made by D. Mukhedee, D. Dhyani and H. C. Rana at IHBT Palampur, Himachal Pradesh.

INGR 00016 is a hybrid Gladiolus with reddish purple (RHS-74D) petals and dark reddish purple (RHS-66A) blotches on the edges of both sides of the petal, lip petal magenta coloured with white stripes. Average spike length 120cm, mean number of florets 16.1 and flowers 11.3 cm in diameter. It is designated as IHBT-G-4 and is a result of hybridisation between Snow Princess x Her Majesty made by D. Mukhedee, D. Dhyani and H. C. Rana at IHBT Palampur, Himachal Pradesh.

INGR 00017 is a germplasm of cotton (*Gossypium arboreum*) immune to *Ramularia areola* the grey mildew disease of cotton. It is designated as G-135-491 *G. arboreum* L. race *bengalense* and is a collection from Jalgaon, Maharashtra by Punit Mohan, P. M. Mukewar, V. V. Singh and M. S. Kairon at CICR Nagpur, Maharashtra.

INGR 00018 is a germplasm of cotton (*Gossypium arboreum*) immune to *Ramularia areola*, the grey mildew disease of cotton. It is designated as 30805 *G. arboreum* L. race *cernuum* and is a collection from Assam by Punit Mohan, P. M. Mukewar, V. V. Singh and M. S. Kairon at CICR Nagpur, Maharashtra.

INGR 00019 is an amber grained genetic stock of wheat (*Triticum aestivum*) designated as ISD 215. It is 2% superior over the amber grained check Sonalika, protein content at par with the check variety Pusa 5 - (red grained). It is developed from K.S./*T.turgidum*// H38/3/Ska// *T.carthlicum*//3/Ska/Bluebird//Hd 2122 by Bhanwar Singh and N. K. Upadahaya at IARI, New Delhi.

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OBITUARY

Sir Otto Frankel (1900-1998)

A founder of the genetic resources movement, Sir Otto Frankel coined the phrase "genetic resources" with Erna Bennett and described genetic material of plants, animals, other organisms which is so crucial now-a-days. He couldn't celebrate his birth centenary. The cruel destiny snatched him on 21st November 1998 at the age of 98 years, while he was in Australia. In 1965, a panel of experts on crop germplasm exploration was set up with Sir Otto Frankel as chair. FAO Technical conference on plant genetic resources took place in 1967, 1973 and 1981 wherein Sir Otto Frankel, Erna Bennett, R.O. Whyte, Jack R Harlan, T.T. Chang, Jack G. Hawkes played an important role. In 1972, Sir Otto Frankel's address to first United Nations Conference on Human Environment in Stockholm alarmed policy makers to establish international forum in order to save depleting genetic resources world wide. After several meetings, International Biological Programme (IBP) was evolved. Dr. Frankel published a document "FAO/IBP Survey of Crop Genetic Resources in their centres of origin" in 1973.

In 1974, International Board for Plant Genetic Resources (IBPGR, now IPGRI) was established. He was closely associated with IPGRI till the end of his life. In a special function, organized in his honour, IPGRI paid tribute to him. His two monographs "Conservation and Evolution (1981) and the "Conservation of Plant Genetic Diversity (1995) developed the scientific basis for protection and conservation of both domesticated/cultivated and wild diversity of crop. Dr. Frankel argued a great deal that humanity may take responsibility of protection of these resources. His concept solely was for free exchange of germplasm material for the benefit of humankind.

Dr. Frankel was born in Vienna in the year 1900. His love to agriculture led him to work all over the world. In 1935, he visited Russia and met great Russian geneticist N.I. Vavilov. In 1951, he became Chief of Commonwealth Scientific and Industrial Research Organization (CSIRO) in Canberra, Australia. He was recipient of several awards. He was 'Fellow' of Royal Society of New Zealand, British Royal Society and the Australian Academy of Science. He was a Foreign Associate of the US National Academy of Sciences also.

Sir Otto Frankel is immortal. This doyen of PGR will remain with us for all the time to come. We owe our gratitude to the PGR visionary.

Jack R. Harlan (1917-1998)

The author of centres and non-centres of agricultural origins, Jack Harlan died on 26th August, 1998. No one with even a passing interest in plant genetic resources will ever forget him. The author of "Crops and Man", geneticist, plant explorer, plant breeders and archaeobotanist was a towering personality in the field of plant genetic resources for the last 50 years. With his work "Our vanishing genetic resources and genetics of disaster" in the 1970s, Dr. Harlan helped alert the world to the dangers of the loss of genetic diversity and alarmed the existing conservation system. With JMJ de Wet, he developed the concept of primary, secondary and tertiary gene pools and for their use in crop improvement work.

He established Crop Evolution Laboratory in the University of Illinois, USA. Prior to this, he spent most of his professional career at Oklahawa State University. There is a debate among plant genetic resources workers that no person ever knew as much about PGR diversity and its origin as Dr. Harlan. Probably this may remain true for future also.

Dr. Jack Harlan was recipient of number of recognitions and award. He was member of US National Academy of Sciences. He also served as President of Crop Science Society of USA and was Secretary of FAO Third International Technical Conference on Plant Genetic Resources in the year 1981.

We salute him for his stewardship in the field of plant genetic resources.

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