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JIA 1037

Indian Journal of Agricultural Sciences 60 (12): 787-92, December 1990

Research review

World germplasm collections and their potential in crop productivity

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Received: 31 May 1990

ABSTRACT

Effective and imaginative utilization of the large variability assembled in the collection of genetic resources of cereals and legumes determines the potential and adaptation of future varieties. Modern methods of characterisation such as restricted fragment length polymorphism (RFLP), organelle deoxyribose nucleic acid (DNA) and nucleotide substitution rates should be used to classify germplasm and identify diverse types for use in crop improvement. To overcome the yield barrier and to achieve a quantum jump in yield and adaptation, it is necessary to diversify the genetic base, especially the male-sterile cytoplasm. To mobilize genetic resources, multi-locational testing is necessary. Use of intermediate weedy forms to confer resistance to biotic and abiotic stress factors, creation of gene pools, and selection under local conditions are desirable. Identification of specific genes and genotypes from the world collections offers genetic diversity for increased and sustainable crop productivity.

Concerted efforts during the past 25 years by the national and international organizations have resulted in the collection, evaluation and mobilization of world genetic resources mainly in cereals, legumes and oilseeds, and to some extent in other food crops, with timely prevention of their elimination by fast-spreading new varieties. Both International Bureau of Plant Genetic Resources (IBPGR) and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) with their co-operators, have prepared standard descriptor lists and documentation procedures. There is an on-going effort to make collection in priority crops and regions in spite of difficulties in the movement of material across continents

because of quarantine and other controls. The mobilization of world collections has greatly benefited the crops of the semi-arid tropics, which form the staple food in several developing countries. These crops are grown normally under marginal conditions and have high local adaptation. The Sorghum Conversion Programme in Puerto Rico, for example, helped sorghum production in the USA as much as in the tropics of Asia and Africa, and extended the range of adaptation of the varieties globally.

DWARFING GENES AND BIOMASS PRODUCTION

The utilization of genes for dwarfing and photoperiod-insensitivity from the local varieties, to restructure plant type in the major cereals, has enormously improved their productivity and range of adaptation, and has added stability to production, as evident in the

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national co-ordinated crop-improvement programmes (ICAR, New Delhi 1988). The next quantum jump in cereal yield for the 21st century would require a greater diversification of the genetic base, including cytoplasmic diversity, since only a small fraction of the world collections has actually entered the parentage of present-day advanced lines.

The Dee-gee-Woo-gen and Norin dwarfing genes in rice (*Oryza sativa* L.) and wheat (*Triticum aestivum* L. emend. Fiori & Paol.), and similar genes in sorghum [*Sorghum bicolor* (L.) Moench] and pearl millet [*Pennisetum glaucum* (L.) R. Br. emend. Stuntz] have complex functions influencing several characters. These genes improve the partitioning of dry matter from 17.0 to 34.1% and kernel weight fluctuating from 22 to 29% without significantly increasing the total biomass production of about 10 tonnes/ha in wheat during the last 100 years, as reported by Cox *et al.* (1988). Hence there is an urgent need to evaluate the world collections for higher biomass production to complement the superior harvest index and its stability. For example, in pearl millet, harvest index widely varied over locations (Table 1). Utilization of alternative sources of dwarfing with rapid biomass accumulation is essential.

For a planned transfer of these genes into advanced varieties, basic studies are needed

on adaptation mechanisms of genotypes to moisture, disease, soil and climatic stresses, and on the biochemical basis of their resistance to these biotic and abiotic factors. The adaptive mechanisms of genotypes with potentially high biomass under these stress conditions need special attention.

NEW TOOLS FROM FRONTIER SCIENCES

Frontier sciences like biotechnology now provide the tools for the transfer of specific DNAs into new varieties. Similarly, protoplast fusion can be utilized to reconstitute a new cytoplasmic base from the existing diverse cytoplasm and to produce more productive cytotosteriles. The sequencing of the DNA of the diverse sources of dwarfing, for example, to distinguish common and contrasting features, will help incorporation of multiple sources of efficient physiological mechanisms. Genetic analysis at the molecular level, as is being done for the basic processes of nodulation using non-nodulating, super-nodulating, and normal genotypes in soybean [*Glycine max* (L.) Merr.] can be applied to other leguminous crops. The inhibitors produced by the shoot in localizing nodulation in soybean helps in better understanding the transcription and translation mechanisms in the genetics of nodulation (Carroll *et al.* 1988). A similar evaluation in chickpea (*Cicer arietinum* L.), pigeonpea [*Cajanus cajan* (L.) Millsp.] and groundnut (*Arachis hypogaea* L.) is necessary.

Among the drought-tolerant land races, stage-specific resistance (rather than resistance during the entire growth period) is common at the seedling, mid-season or terminal stages, as in some of the upland rices in India. Since such stage-specific adaptations are due to diverse physiological mechanisms, integration of these genes into 1 genotype to face the random drought in SAT countries requires biotechnological expertise for specific DNA

Table 1 Stability of dry-matter partition in pearl millet

Genotype	Harvest index		Change (%) Pune over Hisar
	Pune	Hisar	
'WC-C75 (C)	39.9	9.7	76
'MBH 130 (C)	52.3	14.5	72
'K-560 = 230'	23.6	16.0	32
'AIB 16'	42.2	14.1	67
'AIB 18'	39.0	17.6	55
'ICMP 83401'	29.3	11.7	60

Source: Annual Report 1987-88, All-India Co-ordinated Millet Improvement Project. Indian Council of Agricultural Research, New Delhi

LAND RACES AS GENETIC COMPONENTS OF STABILITY

An analysis of the parentage of the widely

the pooling of the diverse gene blocks for adaptation from different land races contributed to their wider adaptation to various stresses. Such examples are in 'TR 60', 'TR 36' and 'TR 42' in rice; 'C 306', 'HD 2189', 'Chenab 70', 'Sholey' and 'Bijiga Yellow' in wheat; 'JG 62', 'BG 203', 'G 130' and 'K 850' in chickpea; 'CSH 5', 'CSH 9' and 'CSV 3541' in sorghum; 'BK 560', 'WC-C 75', 'Pusa 23' and 'ICMH 423' in pearl millet, to mention a few. In wheat these varieties were released during 1965-74, each having 3-8 land races in its parentage. In rice 'TR 36' (released in 1986) and 'TR 60' (recent) have 14 and 16 land races respectively in their parentage, whereas the other 3 varieties have 1-3 land races in their origin and were released during 1970-77. In sorghum, both the hybrids 'CSH 5' and 'CSH 9' were released in 1974 and 1981 respectively. These hybrids have 'CS 3541' as the common male parent, whereas they have closely related female parents, having the same cytoplasm. In pearl millet 'BK 560' (released in 1975) has only 1 land race in its parentage, whereas 'WC-C 75' (released in 1982) is derived from 7 land races. In chickpea, the varieties mentioned were released 12-20 years ago (1971-78) and have 1-5 land races in their parentage. Thus it appears that the varieties or hybrids popular even now were released long ago and have varying number of land races in their parentage, which could have conferred stability and wide range of adaptation. There is need for an in-depth study of these mechanisms of adaptation.

Stability of the cytoplasmic constituent is evident in the protoplast-fusion products and for only female parent in reciprocal crosses. The conversion programme needs to take this into consideration. The analysis of mt DNA δ isozyme pattern in land races will be

necessary to characterize more precisely these genetic stocks.

The genetics of characters associated with adaptation in land races needs to be studied in the crosses between land races and high yielding varieties, and the information shall be included in the documentation on the land races (Ehdaie *et al.* 1988). The sequencing of DNA of land races with specific adaptation, eg salt and drought tolerance, will be useful.

The genetic diversity in natural populations with specific or wide adaptation can be assessed by the Markov process of estimating nucleotide-substitution rates. Generally, natural mutation rates are very high under some specific ecological conditions. Such an analysis would be worthwhile in the Rajasthan (India) and Ghana collections of pearl millet, the sorghums of Sudan and Ethiopia, and the chickpeas of Ethiopia and south Iran, which have all adapted to severe environmental stress. Simulation studies using available data on specific isozyme loci will be useful in analysing adaptation in specific world collections.

GENETIC ANALYSIS OF REPRESENTATIVES OF WORLD COLLECTIONS

To understand the mechanisms of adaptation and evolution, particularly in land races, more genetic information needs to be obtained during the evaluation process:

- 1 It will be helpful to use RFLP as genetic markers and to analyse their polymorphism for assessment of diversity between location-specific and widely adapted accessions (Pring *et al.* 1982, Ehdaie *et al.* 1988, Hallden *et al.* 1988).
- 2 Cytoplasmic differentiation can be examined by analysing the organelle DNA with emphasis on mtDNA rather than ctDNA, and looking for unique types of mtDNA in indigenous races, as is being done in maize (*Zea mays* L.) (Weisinger *et al.* 1982, Escote-Carlson *et al.* 1988).

- 3 Simple and complex probes in RFLP studies to trace the contribution of different land races to the germplasm used in the breeding programme will be useful supplement for the analysis of organelle-DNA (Ehdaie *et al.* 1988, Hallden *et al.* 1988).
- 4 Work on protoplast fusion to produce cybrids from diverse cytoplasms needs to be strengthened. These cybrids can be examined for mtDNA and ctDNA recombinants if any (Pring *et al.* 1982, Figdore *et al.* 1988, Kemble *et al.* 1988). If these cytoplasmic constituents are stable, it is possible to maintain the functional diversity of the protoplast fusion products without disrupting the adaptative gene blocks in mtDNA.

DIVERSIFICATION OF GENETIC BASE IN PLANT-BREEDING PROGRAMMES

The diversity in the present-day advanced lines in regional trials indicates that the gains already realized by the limited use of genetic resources in the released varieties can be accelerated by sustained efforts for a wider genetic base. Although several varieties were released during the past 15 years (322 in rice, 167 in wheat, 46 in maize, 40 in sorghum, 32 in pearl millet, 68 in chickpea and 65 in groundnut), only a few are extensively grown by farmers and all these are releases of a decade or longer. For example, 'Sonalika', released in 1965, is still the most popular wheat variety, followed by 'HD 2285', 'HD 2329', 'HD 2189' and 'HD 2009' released during 1974-79. A similar situation exists in rice with 'IR 36', 'TET 1444', 'Mashore' and 'IR 20', released during 1966-81. 'Ratna', the upland rice released in 1970, is yet to be replaced by a better variety. In sorghum, 'CSH 5' and 'CSH 9' released in 1974 and 1981, are the ruling hybrids. In pearl millet, 'BK 560' released in 1975 is still popular, followed by 'WC-C 75' of 1982. In maize, 'Ganga 5' and some others, released

10-15 years ago, are still extensively grown. Though the stability of such varieties for long periods is commendable, their adaptation mechanisms are not adequately understood. The genetic structure of the subsequently released varieties must be studied if these are to contribute to a diversified genetic base. Some of the recent pearl millet hybrids, such as 'Pusa 23', 'ICMH 451' and 'ICMH 423' are the results of such a planned diversification based on studies of adaptation under stress. Utilization patterns of the large collections already available, and the limited and uneven field performance of the varieties released in the last decade, must be carefully studied. An analysis of their pedigree and selection methodology is necessary for the introduction of new genes from other sources in the world collection to remedy this situation.

An examination of the parentage of the advanced lines in the regional trials during 1987-88 indicated the genetic constraints limiting their productivity. Of the 620 wheat entries, a majority are based on 4 varieties, 'HD 2009', 'HD 2160', 'HD 2281' and 'S 308'—which too are of a complex parentage. It is necessary to further widen the base to break the present yield barrier and to use more winter wheats or intermediate forms in crossing. In rice too, a similar situation appears to exist. In 80 advanced lines of sorghum and 47 of pearl millet, all are based on the same cytoplasm. Hence further success will depend on the diversification of cytoplasmic base, because the present conversion of male-steriles as in pearl millet is restricted to A_1 cytoplasm only, which is susceptible to downy mildew. The post-rainy season sorghum-improvement programme is still to take off and the widely used material from Sudan, Ethiopia, Cameroon, Yemen and Nigeria should be considered along with Maldandi lines and central Indian materials. It is necessary to characterize the cytoplasm biochemically at molecular levels by

fractionating mitochondrial DNA for further manipulation of productive cytoasteriles.

Even among the legumes, eg chickpea, in which considerable hybridization has taken place during the past 15 years, the advanced lines under testing are based mainly on 5 varieties, viz 'G 130', 'C 214', 'BG 203', 'K 850' and 'C 235'. The best lines with consistent performance during the past 3 years are only 2, 'WBL 12' and 'GZ 769'. The yield difference in the Central Zone between the controls (1 300–1 500 kg/ha) and the advanced lines (950–1 665 kg/ha) is very small, much below the expectations based on a wide crossing programme. An analysis of their parental lines and an infusion of other genotypes from the world collection are called for.

It is interesting to compare the yield advances made in sorghum and pearl millet, wherein considerable effort was made to mobilize world collections with those of upland rice and rainfed wheat, where large collections are also available. In the IET trial under timely sowing, out of 25 entries of durum wheat (*Triticum durum* Desf.), the control, 'Meghdoot', yielded 1 620 kg/ha compared with the mean of 1 530 kg/ha of all the other entries. In the rainfed bread wheat trial in the Eastern Zone, 'C 306' (the control released 30 years ago) yielded 1 900 kg/ha and 'Sonalika' 1 950 kg/ha compared with 1 960 kg/ha—the mean of 6 entries; the difference was not significant. The rainfed regional trial revealed that 'NI 5439' (a control) yielded 1 600 kg/ha compared with 1 200–1 370 kg/ha of the other best 5 entries. The yield performance in the upland rice programme was similar to that of rainfed wheat. It would appear that a greater effort in rainfed wheat and upland rice can be effective only if the available genetic resources including the new collections are mobilized, as is being done in sorghum and millets.

OVERCOMING CONSTRAINTS IN MOBILIZING GENETIC RESOURCES

Greater attention by both national and

international genetic resource organizations may be considered on the following aspects of generation of material for regional problems, testing in contrasting environments, and emphasis on feedback on the evaluation of working collection in multi-locational testing.

1. Evidence is accumulating that stress to biotic and abiotic factors and high yield potential are probably due to independent mechanisms. Simultaneous screening of world collections for biomass yield potential and stress tolerance in specific stress environments is needed (Cox *et al.* 1988).
2. Intermediate forms, including natural and man-made introgression products, can be treated as genetic stocks for evaluation as revealed by the utility of forms such as *Pennisetum glaucum* × *P. villosum* R. Br. ex Fresen. in the sub-Saharan regions. These products retain their adaptation to stress, are far more useful to breeders, and complement the products of synthetic species hybrids and the introgression products.
3. Creation of complex hybridization products involving several land races and intermediate forms of introgression, and their supply to regional centres for selection in local conditions will accelerate the mobilization of germplasm. Feedback on this testing can be incorporated in the documentation.
4. Creation of gene pools for groups of important characters in cross-pollinated crops will permit easy management of the genetic material and its availability for ready use, which is difficult in individual accessions. Diverse sources of cytoplasm (cytoasteriles) can be used to create such gene pools in both self- and cross-pollinated crops. This will also promote recombination on a wider scale.
5. Regular exchange of information between users and genetic resource units on regional problems needing identification of suitable genotypes, decentralization of generation

of material, and testing of core collections in contrasting environments will accelerate the mobilization of several useful stocks already identified.

Though logistic difficulties exist in the evaluation of large collections at several locations, it is desirable to evaluate representative core collections, in multi-environmental testing to understand the mechanism of adaptation for a set of important variables like root activity, maturity growth pattern, duration of flowering or grain filling, disease and pest resistance, and related physiological parameters. This is necessary to comprehend the totality of genotype \times environment interactions of all these variables (taken together). This is possible using multivariate procedures like multi-dimensional scaling and principal component analysis combined with regression analyses, as were attempted recently on maize. Simulation studies using the existing data on character combinations in the world collections can be used to predict a plant type with higher production potential and adaptation, or to formulate a set of useful ideotypes in tropical legumes and oilseeds where the present efforts of restructuring the plant type are meeting with limited success.

The importance of genetic resources for the future of mankind cannot be minimized, as illustrated above, particularly with the fluctuating production of food crops in several semi-arid tropical regions, and even in the USA, where the recent drought attributed to the greenhouse effect has been devastating. With the identification of specific genes and genotypes after critical evaluation of the world collections and the utilization of the modern tools, it will not be difficult to transfer several useful genes into present-day and future varieties to achieve the next breakthrough in yield barrier. It must therefore be concluded that the available world collection offers genetic

diversity of great potential for increased and sustainable crop productivity.

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