ARAVS

REVIEW ARTICLE

Importance of Genetic diversity in Plant breeding

1. **B. Hari vara prasad 2. T. Anjaneyulu and 3. L.K.Verma**
1 & 2. Teaching associates in college of Horticulture, Dr. Y. S. R. H. U; 3. Ph.D scholar UAS
Dharwad.

Genetic diversity is the total number of genetic characteristics in the genetic makeup of a species. It is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary.

Genetic diversity serves as a way for populations to adapt to changing environments. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Those individuals are more likely to survive to produce offspring bearing that allele. The population will continue for more generations because of the success of these individuals.

When humans initially started farming, they used selective breeding to pass on desirable traits of the crops while omitting the undesirable ones. Selective breeding leads to monocultures: entire farms of nearly genetically identical plants. Little to no genetic diversity makes crops extremely susceptible to widespread disease; bacteria morph and change constantly and when a disease-causing bacterium changes to attack a specific genetic variation, it can easily wipe out vast quantities of the species. If the genetic variation that the bacterium is best at attacking happens to be that which humans have selectively bred to use for harvest, the entire crop will be wiped out.

In plant breeding for varietal or hybrid development diverse parents are to be preferred. To say morphologically genetic diverse nature is nothing but the complementary characters between the two parents. In terms of genetic basis the combining ability of the two parents should be high enough in giving high yielding progeny. When you say about biochemical basis the two parents should produce different kind of proteins which has ability to survive under normal and stress conditions also. In terms of molecular basis the two parents should contain favourable it's distributed complementarily for each trait. An individual genotype is said to be highly diverse when it has high general combining ability. General assumption is when you make a cross between two high general combiners such combination will give good hybrid.

The hybridization programme also requires two diverse parents which could give transgressive progenies in segregating generations. In same way heterosis in F1 will be maximum when there is maximum diversity between the parents. According to Falconer $HF1 = dy^2$ heterosis in F1 progeny depends upon the degree of dominance and genetic diversity between the two parents. Here the degree of dominance includes it could be of partial/incomplete/co dominance/complete dominance/over dominance. The genetic diversity here says about the allelic differences between the parents for the different yield contributing traits.

Heterosis is due to a high degree of heterozygosity in the genome, that is, the presence of different alleles at many gene loci in the homologous chromosomes. Heterozygosity can be increased by crossing genetically distinct parental materials, i.e. materials belonging to distinct heterotic groups. So heterotic grouping means identifying germplasm groups that are genetically distinct from each other and that produce superior hybrids when crossed. Heterotic pools, once detected, need to be maintained separately to ensure they remain unrelated by descent. Crossing representatives of different heterotic pools will maximize heterozygosity, hybrid vigour and yield stability of the new cultivars. The enhanced yield stability is due to enhanced capacity for individual buffering in heterozygous genotypes. This concept can be applied to both self and cross pollinated crops. The most common approach in developing heterotic

pool is reciprocal recurrent selection method where simultaneously two opposite populations are developed.

Heterotic groups identified via diversity analysis are validated through multi-location evaluation of intra-pool and inter-pool crosses. This enables identification of the optimal genetic distance among parental materials for attaining maximal hybrid vigour. At the same time, superior crosses can be directly employed as new experimental cultivars and then tested on farms. In the allogamous (outcrossing) pearl millet, the detection and use of heterotic pools provides a basis for sustainable breeding of both open-pollinated and hybrid cultivars, as both types profit from heterozygosity and hybrid vigour. Results from the project are being employed in the development of highly heterozygous open-pollinated population varieties by crossing representatives of the heterotic pools. Such variety structures have wider potential for adoption at the moment in the absence of viable seed systems. The way is also being cleared for hybrid breeding. In the predominantly autogamous (self-pollinating) sorghum, the heterotic groups will be directly implemented in the development of new hybrids based on available male-sterile lines.

There are different biometrical tools where genetically diverse genotypes can be selected for crossing programme. They are D^2 statistics, cluster analysis, Metroglyph analysis, Principal component analysis and factor analysis.

REFERENCES

1. Ashok Kumar Meena, Deshraj Gurjar, S.S. Patil and Bheru Lal Kumhar, 2017, Concept of Heterotic Group and its Exploitation in Hybrid Breeding. *Int.J.Curr.Microbiol.App.Sci* 6(6): 61-73.
2. Betran, F.J., Ribaut, J.M., Beck, D. and de Leon D.G. (2003) Genetic diversity, specific combining ability, and heterosis in tropical maize under stress and nonstress environments. Crop Sci. 43:797-806.