

Review Paper

GENETIC DIVERGENCE – A REVIEW

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Introduction

The knowledge of available genetic diversity is an important factor for any heritable improvement and its nature and degree useful for selecting desirable parents from a germplasm for any successful breeding programme. Several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives of which, Mahalanobis's generalized distance (Mahalanobis, 1936) occupy a unique place in plant breeding. It is a very sensitive and potent biometrical tool in quantifying the degree of divergence between biological populations and also to assess the relative contribution of different components to the total divergence both at inter and intra cluster levels.

Keywords: Genetic divergence, Clustering pattern, D^2 analysis

The relative studies on the analysis of genetic divergence are countable and those which have been published are reported here under.

Ramanujam *et al.* (1974) observed that a cross involving genetically diverse parents is more likely to produce high heterotic effects as compared with lines which are more closely related with each other.

Singh and Prasad (1991) revealed that the hybrids involved in different clusters may produce greater heterotic effects by giving transgressive segregants and may be advanced to the segregating generations for superior high yielding lines.

38 strains of tomato for genetic diversity were grouped into 8 clusters irrespective of geographical divergence, indicating no parallelism between geographical and genetic diversity. The characters like plant height, number of branches plant⁻¹, single fruit weight and number of fruits plant⁻¹, number of seeds fruit⁻¹ and fruit yield plant⁻¹ played an important role in divergence between the populations (Gadekar *et al.*, 1992).

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Pramanick *et al.* (1992) studied 38 lines of eggplant and were grouped in nine clusters which were homogenous within and heterogeneous between clusters. Minimum intra cluster divergence was between genotypes falling in cluster VI and maximum divergence was in cluster III. The maximum inter-cluster divergence was observed between clusters I and IX.

Clustering behavior of entries and mean yield performance of genotypes of individual clusters were not consistent over environment because of larger genotypes and environment interaction. Therefore, for effective hybridization and desired improvement the genotypes can be selected randomly from divergent clusters processing higher number of fruits and mean yield (Yadav *et al.*, 1996).

The thirty seven genotypes of different geographical origin were assessed to know the nature and magnitude of genetic divergence for yield and its contributing characters by Rai *et al.*, 1998. The clustering pattern indicates that there was no association between geographical distribution of genotypes and genetic divergence. The characters namely, number of primary branches, longitudinal fruit length, days to flowering, pericarp thickness, plant height and average fruit weight were contributing maximum divergence and play more role in the improvement of tomato yield.

Dharmatti *et al.* (2001) studied genetic divergence in a population of 402 tomato lines. They observed that cluster II was the most divergent consisting of 51 genotypes/hybrids with potato leaf types and pink fruits which exhibited field tolerance to TLCV. Considerable diversity within and between the cluster were noted and it was observed that the characters like tomato leaf curl virus, fruit yield plant⁻¹ and number of white flies plant⁻¹ contributed maximum to the divergence.

The clustering methods, from the morphoagronomical traits, presented more similar results in the autumn/winter than the summer season. Owing to the inconsistent behavior of the accessions in reaction to the genotype-season interaction, the similarity in the group composition of the environments was reduced. Crosses between accessions 4 (UENF 1469) and 9 (UENF 1488) and accessions 4 (UENF 1469) and 6 (UENF 1486); as well as the use of their F₁ in combination with access 9 (UENF 1488), are recommended to obtain superior segregates in advanced generations. Accessions 6 (UENF 1486 - 'Alessa'), 8 (UENF 1487 - 'Andra'), 9 (UENF 1488 - 'Cota'), 12 (UENF 1483 - 'Isla'), and 14 (UENF 1579) are indicated for the use by regional producers, in an experimental state, as a new option for crop rotation (Teixeira *et al.*, 2004).

The hybrid involved in cluster III and V exhibited maximum genetic divergence from other clusters and between them. The hybrid involved in these clusters may produce greater heterotic effects by giving transgressive segregants and hybrids may be bred to advanced to the generations for selection of superior high yielding lines. (Kushwah *et al.*, 2005).

Gogate *et al.* (2006) reported existence of large variability among the genotypes for all characters in chilli. The intra cluster distance ranged from 0.00 to 875.95. Number of fruits per plant, chlorophyll content, green fruit yield and ascorbic acid content largely influenced genetic discrimination of genotypes. Genotypes RHRC 16-5, ACG 349 were identified as promising parents for future breeding programme.

Singh *et al.* (2006) studied 29 brinjal genotypes on geographical diversity and observed that among characters distribution study, number of fruits per plant, plant height, average fruit yield per plant, number of branches per plant contributed maximum divergence and have a major role in improvement of fruit yield in brinjal.

Mehta *et al.* (2007) concluded from their experiment that cluster I topped with maximum number of genotypes among clusters formed, while maximum inter cluster distance was noticed between cluster V and VII followed by cluster III and VII. Cluster II and V stepped as important clusters with respect to ideotypic plant characters including fruit yield which could be utilized for breeding programme.

Shashi Kamal *et al.* (2007) revealed that cluster II had maximum eight genotypes, while cluster VI and VII had one genotype each for nine quality traits in twenty five genotypes of potato. The study also revealed that crosses between genotypes of different clusters may be used for developing the high yielding and superior genotypes.

Sherly and Shanthi (2007) evaluated that maximum inter cluster distance was observed between cluster II and IV (43.45) while minimum was recorded between cluster I and III (24.39). Thus, considering cluster means and genetic distance the genotypes of cluster IV with genotypes of cluster III were likely to recombine the genes for high yields.

Mehta and Asati (2008) studied genetic divergence analysis using Mahalanobis D^2 statistic in twenty two tomato determinate genotypes. These genotypes were grouped into six clusters based on sixteen important fruit characteristics. The cluster I was the largest containing seven genotypes followed by cluster III with six genotypes. The diversity among the cultivars was measured by inter-cluster distance. The higher order of divergence was

recorded between cluster II and V which was adequate for improvement of tomato by hybridization and selection.

An experiment was carried out to assess the value and magnitude of genetic divergence among sixty seven tomato genotypes of different geographical origin. Wide genetic diversity among the genotypes was observed and grouped into seven clusters. The maximum inter cluster distance was observed between cluster V and VI, closely followed by cluster III and V, cluster IV and V, cluster IV and VII, cluster VI and VII and cluster V and VII. The cluster II revealed the least distance relationship with the cluster III (Prashanth *et al.*, 2008).

Clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The characters like number of fruits plant⁻¹, average fruit weight, plant height and fruit yield (qha⁻¹) contributed maximum to genetic divergence (Singh *et al.*, 2008).

From the D² statistics and canonical analysis, the genotypes were grouped into 5 clusters irrespective of geographical diversity by Ara *et al.* (2009), indicating no parallelism between geographic and genetic diversity. The maximum inter cluster distance was noticed between cluster III and V (19316.55) followed by cluster III and IV (13336.55), cluster II and V (10659.36), cluster I and III (7013.87) and cluster II and IV (6396.41). Among characters studied, fruit yield plant⁻¹, number of fruits plant⁻¹, plant height and fruit weight, fruit size and number of primary branches plant⁻¹ contributed maximum to divergence and have a major role in improvement of fruit yield in tomato. Crossing between genotypes belonging to cluster III and V as well as cluster III and IV and cluster II and V were expected to give maximum heterosis.

Medium to high genetic diversity for radish, turnip and coriander, whereas in the case of fenugreek, the level of genetic diversity was low. Among all the vegetables desirable agronomic traits were identified which could be exploited for vegetable improvement. Greater environmental stresses represented high biodiversity even in the same vicinity as the case of Attock and TT Singh (radish), Sahiwal (turnip) and DG Khan (coriander), whereas in some areas low diversity might be associated with vegetable growing culture in the area (Qureshi *et al.*, 2009).

The clustering pattern of germplasm usually did not follow the geographical distribution. Appreciable diversity within and between 11 clusters was observed Reddy *et al.*, 2012. The characters fruit length, internodal length and number of marketable fruits per plant

were the potent factors in differentiating the germplasm of okra under study. The use of diverse genotypes from the clusters with high intercluster distance in hybridization is expected to result in high heterosis and throw desirable transgressive segregants.

The extent of distribution of genotypes from diverse geographical region into different clusters was random. It might be due to free and frequent exchange of genetic materials among the farmers and breeders of different regions. Differential selection pressure according to regional preference also produced greater uniformity in germplasm. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin such as exchange of genetic stock, genetic drift, spontaneous mutation, natural and artificial selection are responsible for diversity. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity (Chattopadhyay *et al.*, 2013).

A study was conducted using nineteen exotic collections of tomato by Reddy *et al.* (2013). Considerable genetic diversity was observed among 19 genotypes of tomato. Fruit weight, plant height and number of fruits plant⁻¹ contributed 92.40% to the total divergence. Five clusters were fanned from the D² analysis using Tocher's method. Cluster II topped with maximum number of genotypes among cluster fanned, while maximum inter-cluster distance was observed between cluster III and IV followed by cluster IV and V.

Genetic divergence for seedling traits in tomato was studied by Rizvi *et al.* (2013). The scatter diagram partially indicated the clustering pattern and the clusters 3, 4 and 5 intermixed. Sub clustering of individual clusters revealed 5 sub clusters of cluster 1, three of cluster 2 and 5 in each case, six in cluster 3, 4 and 7 and cluster 6 and 8 had 4 each. The cluster 2, 3, 4 and 6 joined at higher genetic linkage with induction of single genotype in the cluster 2, 4 and 6, whereas in cluster 3, two main groups joined at higher distance including one group comprising of the 41 genotypes and the second comprising 19 genotypes, which joined at 80% linkage distance.

A Study carried out by Rathod *et al.* in 2015 revealed considerable genetic diversity among 43 genotypes of tomato for all the twenty characters which was pertaining to growth, earliness, yield and quality. Appreciable diversity within and between the clusters was observed. Seven clusters were fanned from the D² analysis using Tocher's method. Cluster I topped with maximum number of genotypes among cluster fanned, while maximum inter-cluster distance was observed between cluster III and VI followed by cluster V and VI.

Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a great heterosis than those between closely related strains. Geographical diversity may not be the only factor responsible for causing genetic diversification, thus focus should be laid on selecting the parents based on genetic diversity rather on geographical diversity (Kumar *et al.*, 2017).

Intrapopulational genetic diversity was 67% while interpopulational genetic diversity was only 33%. The dendrogram obtained, using genetic distances among taxa, showed three different groups. With the exception of *B. incana*, they agree to the already accepted relationships among the 14 taxa studied: the West Mediterranean group, with *B. oleracea*, *B. alboglabra*, *B. bourgeauii* and *B. incana*; another group of species growing in the central Mediterranean area, which includes *B. illosa*, *B. illosa* subsp. *drepanensis*, *B. rupestris*, *B. macrocarpa* (the four taxa together with *B. incana* are considered the *B. rupestris* group) and *B. montana*; and finally the Aegean group, which includes the three subspecies of *B. cretica*. Clearly separated were *B. insularis* and *B. hilarionis*, showing the maximum genetic distance. Separate dendrograms were also obtained for *B. oleracea*, *B. montana*, *B. cretica* and *B. rupestris* group, and genetic diversity parameters were estimated. Genetic distances among *B. oleracea* populations are in the same range as populations of the *B. cretica* subspecies. Highest genetic distances were found among populations of the *B. rupestris* group (La'zaro *et al.*, 1998).

Conclusions

The clustering pattern of the genotypes was independent of their geographical distribution. Genetic drift and selection in different environment could cause greater diversity than geographical distance. On the basis of inter cluster distances, the genotypes belonging to more divergent clusters should be inter-crossed in order to generate more variability and improving fruit yield. In heterosis breeding, genotypes of diverse cluster are known to play an important role of potential parents and when each genotypes of different cluster are inter crossed they are likely to produce heterotic combinations.

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