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Genetic divergence analysis for yield and quality traits of local germplasm of rice of Himachal Pradesh

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Abstract

The present investigation was carried out with the forty five genotypes of rice including one check, to study the nature and magnitude of genetic divergence using D^2 statistics. Nineteen yield and quality traits were recorded on the genotypes in Randomized Block Design with three replications. The forty five genotypes were grouped into five clusters based on Tocher method of cluster analysis with cluster I containing the maximum of 34 genotypes. Maximum intra-cluster distance was observed in cluster I indicating greater genetic divergence between the genotypes belonging to this cluster. Gel consistency and amylose content contributed 78.79 per cent of total divergence. Maximum inter-cluster distance was recorded between clusters IV and V followed by clusters I and V indicating wide genetic diversity and it may be used in rice hybridization programme for improving the yield.

Key words: Genetic divergence, genetic distance, clusters, D^2 statistics, Tocher method.

Rice (*Oryza sativa* L.*)* is the world's second most important cereal crop and staple food for more than half of the global population providing about 75% of the calorie and 55% of the protein intake in their average daily diet. Knowledge on the nature and magnitude of genetic variability present in the plant material plays an important role in planning a sound breeding programme. It has been well established that genetically diverse parents are likely to yield desirable gene recombinants and or to produce high heterotic effect. Mohalanobis's D^2 statistic (1936) has proved to be powerful tool for quantifying genetic divergence in a given population. It is based on multivariate analysis and grouped into various cluster as given by Rao (1952). This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 45 rice genotypes and to identify the diverse genotypes for future breeding programme.

Materials and Methods

Forty five diverse genotypes of rice from different geographical origin in H.P. were transplanted in the with 3 replications with in RBD design at Rice and Wheat Research Station, Malan, College of Agriculture, CSK HP Krishi Vishvavidyalaya, Palampur, during Kharif 2018. In each replication, single seedling was transplanted per hill in 4 rows with 20 x 15 cm spacing. The observations were recorded on five randomly taken plants from each plot for days to 50 per cent flowering, days to 75 per cent maturity, plant height at maturity, total tillers/plant at maturity, effective tillers/plant at maturity, grain yield/plant, spikelets/panicle, grains/panicle, panicle length, 1000-grain weight, spikelet fertility, kernel elongation, grain length (L), grain breadth (B), length breadth ratio (L:B), gel consistency (GC), gelatinization temperature (GT) rating, protein content and amylose content. The analysis of genetic divergence was done using Mahalanobis (1936) D^2 statistics. The genotypes were grouped into different clusters by applying Tocher method (Rao 1952). Intra and inter-cluster distances and mean performance of the clusters for the characters were also computed.

Results and Discussion

On the basis of Mahalanobis D^2 statistic the forty five rice genotypes were grouped into five clusters (Table 1 and Fig 1) (Garg *et al.* 2011 and Allam *et al.* 2014). Thirty four genotypes were falling in cluster I, one genotype was falling in cluster II, IV and V, respectively. Eight genotypes were falling under cluster III.

Table 1. Distribution of 45 genotypes of rice among clusters on the basis of D^2-analysis

Clusters	No. of genotypes	Genotypes
I	34	Chari Basmati, IC 3131185, IC 3131182, IC 3131155, Debel, Harabagh, IC 3131159, Green apiculus, Tiyun, IC 3131173, RLC-1-P2, Kherwar Local, Matali-2, IC 3131175, LG-16-2, Palwala, Begmi, IC 3131166-2,Kala Dhan, HPR 2880 ©, Ramjawain (HPLC-77-1), IC 3131176, Chitti Zheeni, Kalijhini, Local-2, Sukara Dhan, KLC-4, KLC-6, IC 3131161, SLC-3, IC 3131180, IC 3131167, IC 3131172, Ram Jawain (HPLC-77-3)
II	1	IC 3131187-1
III	8	IC 3131174, IC 3131177, HPR 957, LG-14, Jhumka Parmal, Banogi Dhan, Local Ziri, LC-99-3B-2
IV	1	Totu Dhan
V	1	RJ 100

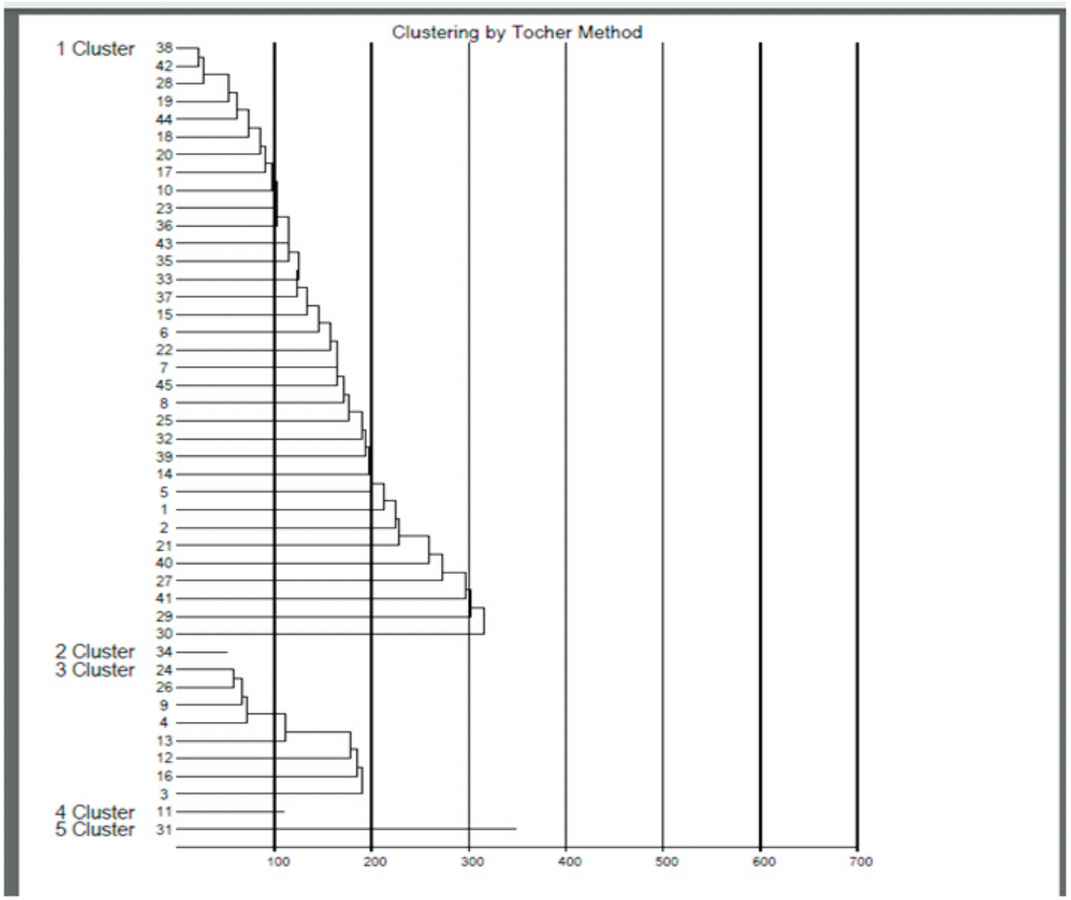

Fig 1. Distribution of rice genotypes among clusters on the basis of D^2 analysis by Tocher's Method

D^2 values between all possible pairs of forty five genotypes ranged from 0.00 to 37.51. Average, intra and inter-cluster distances are presented in Table 2. Highest intra-cluster distance was observed for cluster I (14.47) followed by cluster III (13.35). Highest inter cluster distance was observed between cluster IV and V (37.51). The lowest value for inter-cluster distance was observed between cluster II and III (13.35). The highest inter cluster distance was between cluster IV and cluster V emphasize the possibilities of getting high heterotic F_1 hybrid as well as transgressive segregants in the advanced generation for different traits when hybridization was carried out involving genotypes between these two divergent clusters contributed largely for total divergence in genotypes revealing ample scope for improvement of these traits through hybridization. (Souroush *et al.* 2004 and Singh *et al.* 1987).

Cluster IV and cluster V showed the maximum cluster means for grain length, L:B ratio, total tillers/plant, effective tillers/plant, 1000-grain weight, amylose content and protein content in cluster IV and plant height, grains/panicle, spikelets/panicle, grain yield/plant, spikelet fertility, GC and GT in cluster V, respectively. While, minimum cluster means observed for days to 50% flowering, days to 75% maturity, plant height, panicle length, grains/panicle, spikelets/panicle, spikelet fertility and GC in cluster IV. Contribution of individual trait to the divergence among genotypes was presented in Table 3. The data showed that GC (56.67%), contributed maximum towards divergence, followed by amylose content (22.12%), protein content (8.38%), plant height (5.66%), grains/panicle (2.83) and days to 50% flowering (2.12%). Similar results were reported by Garg *et al*. (2011); Sandhyakishore *et al.* (2007) and Rao (2015). Remaining traits had very little or no contribution towards genetic divergence and hence were of less importance. Since varieties with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programme become more important. Since days to maturity contributed maximum towards the genetic divergence, we may go for direct selection of this trait for diversity purpose.

Table 2. Average intra and inter-cluster values of D^2 among five clusters

Clusters	I	II	III	IV	V
I	**14.47**	19.49	23.25	20.35	33.32
II	-	**0.00**	13.24	28.22	19.04
III	-	-	**13.35**	33.2	21.99
IV	-	-	-	**0.00**	37.51
V	-	-	-	-	**0.00**

Bold values are intra-cluster distance

Table 3. Relative contribution (%) of individual trait to the divergence among genotypes

Traits	Number of times ranked first	Contribution (%)
Days to 50% flowering	21	2.12
Days to 75% maturity	0	0.00
Plant height (cm)	56	5.66
Total tillers/plant	0	0.00
Effective tillers/plant	0	0.00
Panicle length (cm)	6	0.61
Grains /panicle	28	2.83
Spikelets/panicle	0	0.00
Grain yield/plant (g)	1	0.10
1000 grain weight (g)	0	0.00
Grain length (mm)	2	0.20
Grain breadth (mm)	1	0.10
L:B ratio	3	0.30
Kernel elongation (mm)	2	0.20
Spikelet fertility (%)	0	0.00
Gel consistency (mm)	561	56.67
Gelatinization temperature (GT) rating	7	0.71
Amylose content (%)	219	22.12
Protein content (%)	83	8.38

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