

CLUSTERING OF BASMATI RICE MUTANTS BY METROGLYPH ANALYSIS

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Abstract

Deviations observed by Metroglyph method regarding the number of clusters formed, number of genotypes in each cluster and superimposition of the genotypes within the cluster pointed out the precision and refinement of the technique in studying the germplasm collection. It is noted that through induced mutation genetic improvement for yield and yield components is possible. Metroglyph scatter diagram provided the possibility of 11 clusters of rice genotypes. Cluster-I and cluster-II possessed the highest index scores i.e., 66 and 56 respectively on morphological basis. On the basis of this clustering, it can be interpreted that mutants between cluster-I and cluster-II is expected to give better types after hybridization.

Introduction

Rice is the staple food of almost half of the world's population, employs millions in jobs, and has enormous impact on the environment. About 90% of the world's rice is produced and consumed by small-scale farmers in low-income development countries (Anon., 2003). In Pakistan, rice is considered as the stuff of life and covers more than 2.5 million hectares of cropped area with an annual yield of 1994 kgs/hectare. It accounts for 5.7% of the total value added in agriculture and 1.3% of G.D.P. (Anon., 2004-05).

The fine grain aromatic Basmati rice is considered high quality rice and fetches high price in the national and international trade. However, yield per unit area of Basmati rice is very low due to tall plant habit and late maturity. Conventional techniques have not been able to resolve these problems due to its narrow genetic base. So, broadening the genetic base of rice is an essential requirement for rice improvement programme. The shortest possible method for the development of Basmati rice varieties/germplasm is induced mutation (Rashid *et al.*, 2003). Induced mutation has been used in rice more than any other crop as confirmed by more than 443 rice mutant varieties listed in the FAO/IAEA Mutant Varieties Database (Anon., 2004). Semidwarfism and earliness are the frequently induced mutations of the released rice mutant cultivars world over (Cheema & Awan, 1988; Awan, 1999).

Classificatory techniques are being used to quantify the genetic divergence in a given population of rice (Kotaiah *et al.*, 1986, Gomathinayagam & Natarajan 1988, Sinha *et al.*, 1991, Mahapatra *et al.*, 1995, Bharadwaj *et al.*, 2001, Cheema *et al.*, 2004). Roy & Sharma (1994) in pigeon pea and Ponitha & Raveendram (2000) in cotton. As such a quantification of the degree of divergence would be of help in choosing suitable genotypes for on-going rice breeding programme.

The study was undertaken to run a classificatory analysis on the rice genotypes by means of Metroglyph statistic, which will enable us to classify the available germplasm into distinct clusters on the basis of their genetic diversity. The information, thus obtained, will be helpful to develop an effective rice-breeding programme.

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Materials and Methods

Pure and dry dormant seeds of Basmati varieties viz., Basmati-370 and Basmati-Pak were treated with gamma rays with different doses by maintaining the moisture content of the seed about 12-14%. M₁ generation was planted in the same season at NIAB, Faisalabad, Pakistan with one seedling/hill by spacing 10 cm apart between and within rows. Main panicle from each M₁ plant was harvested at physiological maturity and was bulked dose wise for growing M₂ population next year as plant progeny rows (Rashid *et al.*, 2003). From M₂ population desirable mutants were isolated on the basis of early flowering, short stature, good plant type and other grain characteristics. The breeding behavior of the selected mutants was evaluated for stability in M₃ and M₄ progeny rows along with untreated control planted after every 10th M₂, M₃ and M₄ progeny. The homozygous lines with desired grain characteristics were evaluated in preliminary and advanced yield trials at the station along with parent and commercial varieties.

Twenty mutants and their respective parents originated from different doses of gamma rays used in advanced yield trial were grown at NIAB, Faisalabad during 2004-05 (Table 2). Basmati-385, Super Basmati and Basmati-2000 were used as check varieties. The experiment was laid out in randomized complete block design (RCBD) with three replications. Thirty days old seedlings were transplanted into a 1.50 x 2.50 (sq. m.) plot size with one seedling/hill. Standard agronomic practices and plant protection measures were adopted. The data were collected on six characters viz., days to 50% flowering, plant height (cm), productive tillers/plant, panicle length (cm), 1000-seed weight (gm) and yield (kg/ha). Observations were recorded on 10 randomly selected plants of the middle rows excluding the border plants. Their means were used for statistical analysis.

Analysis of variance for all the characters was carried out by following the procedure described by Steel & Torrie (1984). Clustering was done according to Metroglyph analysis proposed by Anderson (1957) and used by Singh & Chaudhary (1979) to study the pattern of morphological variation in crop species. The means over replications of the characters were used for this purpose. Two most variable characters which exhibited highest variance (highly significant values of F calculated) were selected and plotted on X and Y-axis using the values of each genotype. Besides the two characters which were taken on X and Y-axis, all the other characters were represented by rays on the glyph. Each ray represents a particular character obtained by dividing the range of variation into three equal classes giving the grades low, medium and high for each character. The length of ray assigned to the characters depends upon the index scores of genotypes for that character (1 for low value, 2 for medium and 3 for highest value). The performance of genotypes was indicated by total index scores of genotypes, which was the sum of the index values with regards to all characters. The clustering of the genotypes was carried out on the basis of sum of index scores of all the genotypes in that cluster.

Results and Discussions

The analysis of variance for means indicated that the differences among the genotypes were highly significant for all the characters studied (Table 1). Cheema *et al.*, (2004) found the significant mean squares results for 6 quantitative characters in 30 genotypes of rice. Kotaiah *et al.*, (1986) and Bharadwaj *et al.*, (2001) reported that the significant differences among the rice genotypes indicated the necessity to group them into clusters to identify the divergent groups. Mehdi & Asghar (1999) also classified the sorghum genotypes in 5 distinct groups.

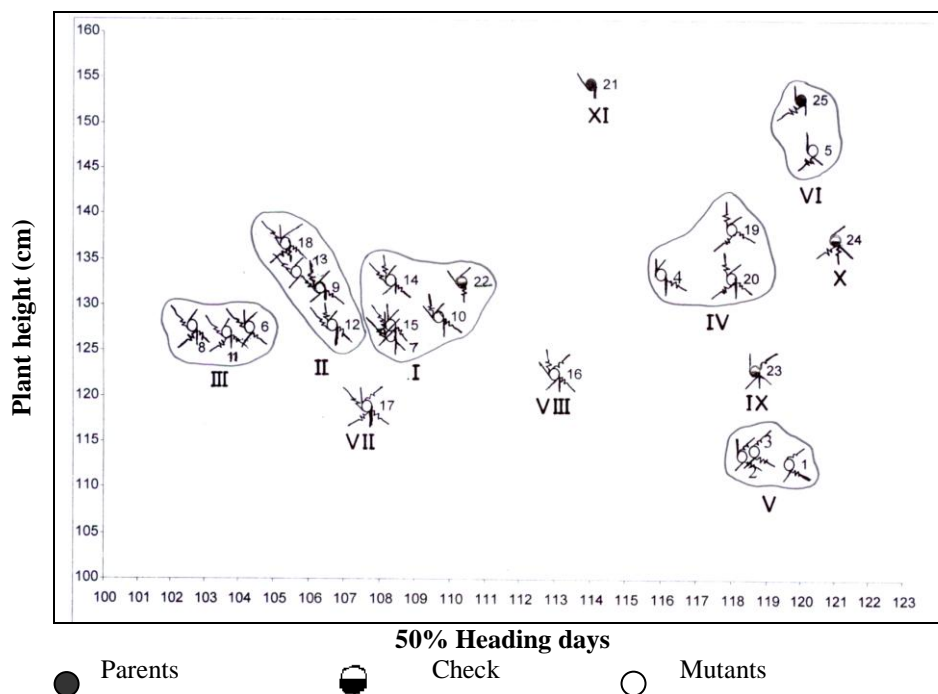


Fig. 1. Metroglyph scatter diagram illustrating distribution of various groups formed from 25 genotypes of Basmati rice

According to Anderson's Metroglyph technique (1957), the index score was allotted to each character of the 25 rice genotypes, which indicated the worth of the genotype regarding the character (Table 2 & 3). Similarly, Gomathinayagam & Natarajan (1988) used index scores for studying the morphological variations of 40 rice entries tested at the upland rice sites. The same thing is represented as rays on the glyph (Fig. 1), Ibrahim *et al.*, (1990) plotted a scatter diagram by using the glyph between plant height and single plant yield. The traits i.e., days to 50% heading and plant height are required for desirability in a lower magnitude. Das & Borthakur (1973) and Maurya & Singh (1977) observed that flowering time and plant height were the important contributors to genetic divergence in rice. Therefore, higher score was given to the genotypes, which showed a low magnitude of that character.

Among genotypes, genotypes number 9, 14, 16, 17 and 18 had the highest index scores as total and no genotype had 1 score (Table 2). Genotype number 21 and 25 scored the minimum index score of 8. The cluster with lowest of 8 index score was cluster number 11 which included a single genotype 21. Twenty five diverse rice genotypes formed 11 clusters (Fig. 1) on the basis of relative dispositioning of genotypes on the graph. The results suggested that the metroglyph analysis would be suitable for grouping the genotypes as reported by Chandra (1977). The number to each cluster was allotted on the basis of net index scores of the cluster in ascending order. The cluster number VII, VIII, IX, X and XI were formed by individual genotypes i.e., 17, 16, 23, 24 and 21 respectively (Table 4).

Cluster-I included 5 genotypes, cluster-II has 4 genotypes, likewise cluster-III, IV and V have 3 genotypes, respectively. This clustering can be used in the future hybrid-breeding programme for the improvement of rice population. Hybridization between cluster I and cluster II is expected to give better types.

From these results, one can foresee that those genotypes, which have high index scores and fell into different clusters, can be crossed to have maximum variability of good combinations of characters. Similarly induced mutation can effectively be used in improving a character, which is undesirable or otherwise weak on a genotype. This information will be helpful in identifying the cross (es) that could be attempted to obtain the desired results.

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(Received Publication for 9 February 2007)