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# NUMERICAL ANALYSIS OF VARIATION AMONG BASMATI RICE MUTANTS

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## Abstract

In order to identify the major characters which account for variation among Basmati rice mutants, 11 mutants developed from Basmati-370 and 2 from Basmati-Pak along with parents and three standard checks were studied using Single Linkage Cluster Analysis (SLCA) and Principal Component Analysis (PCA). Seven characters were studied. The first three PCs with eigen-values > 1 contributed 78.7% of the variability among the genotypes. Four characters were positive to $PC_3$ than $PC_2$ and $PC_1$. Productive tillers/plant and panicle fertility contributed maximum in $PC_3$. Thus this principal component is a weighted average of the characters. Results of SLCA agreed with that of PCA ordination on axis II and I. Three groups of mutants were revealed. The discrimination between groups and description of differences between groups were more strongly marked from SLCA than in the PCA. The promising genotypes from particular groups or clusters may be chosen for hybridization programs. Clusters with superior agronomic types identified, may be exploited for genetic potential to transfer the desirable genes to improve yield potential of the rice crop.

## 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 (Anon[a]., 2004) About 90% of the world's rice is produced and consumed by small-scale farmers in low-income developing countries (Anon., 2004). In Pakistan rice is considered as the stuff of life and covers more than 2.58 million hectares of cropped area with total yield of 5.44 million tons It accounts for 5.7% of the total value added in agriculture and 1.2% of G.D.P. (Anon[b]., 2006-07).

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). Dwarfism and earliness are the most common induce mutations of the released rice mutant cultivars world over. The study was under taken to run a multivariate analysis on the rice genotypes, which will enable us to classify the available germplasm into distinct clusters on the basis of their morphological diversity. The information thus obtained will be helpful to develop an effective rice-breeding programme.

## Materials and Methods

Thirteen mutants originated from different doses of $^{60}$Co gamma rays and their respective parents used in advanced yield trial were grown at NIAB, Faisalabad during

2004-05. 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 was collected on seven characters viz., days to 50% flowering, plant height (cm), productive tillers/plant, panicle length (cm), panicle fertility %, 1000-seed weight (g) and yield (kg/ha). Observations were recorded on 10 randomly selected plants from 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). The average data was analyzed by numerical taxonomic techniques using the procedure of cluster and principal component analysis (Sneath & Sokal 1973). The data matrix of 7 x 18 was prepared for the analysis. The data was standardized and transformed to SLCA and PCA by using a computer programme MINITAB 13.2. Using character variations, the SLCA summarized the position of accessions into dendrogram. The character loading was used to calculate the accession component scores. The first two components were extracted for a two dimensional ordinations of accessions.

## Results and Discussion

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. 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.

**Principal component analysis:** The first three components, with eigen-values >1 contributed 78.7 % of the variability among genotypes evaluated for morphological and yield components (Table 2). Other PCs (4-7) had eigen-values less than 1. The first PC was more related to 50% heading days, plant height and panicle length whereas the second PC relates to productive tillers/plant, panicle length and yield. The third PC exhibited positive effects for plant height, productive tillers/plant, panicle length and panicle fertility. The variation for panicle length was distributed among all the components. Four characters contributed positively to $PC_3$: thus this component is the weighted average of the characters. In $PC_3$ the panicle fertility exhibited the greatest positive weight. The characters with positive weight on $PC_2$ were panicle length, followed by yield and productive tillers/plant. This finding suggests that this component reflects tendency of each accession to emphasize on vegetative phase along with long panicle to get the higher yield.

$PC_1$ exhibited positive effects for panicle length followed by plant height and 50% heading days. This suggests that the genotypes that emphasize on flowering complete their stem elongation earlier with more panicle length. The first two PCs contributed to 58.3 % of variability, hence these were plotted to observe the relationship between the clusters (Fig. 1). The mutants of Basmati-370 fall in the same cluster which consists of Super Basmati, which is high yielding and adaptive variety. The mutants of Basmati-Pak clustered into a different group.

**Table 1. Mean squares for the analysis of variance for quantitative traits among 18 genotypes of Basmati rice.**

| S.O.V | df | 50% heading days | Plant height (cm) | Productive tillers/ plant | Panicle length (cm) | 1000-seed weight (g) | Fertility % | Yield (kg/ha) |
|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 5.62 | 0.99 | 4.17 | 1.57 | 0.01 | 1.59 | 2356.35 |
| Genotypes | 17 | 136.58** | 433.63** | 25.35** | 11.01** | 6.75** | 10.66** | 788196.7** |
| Error | 34 | 1.23 | 0.75 | 3.02 | 0.73 | 0.060 | 2.49 | 21599.0 |

* Significant at p=0.05, ** Highly significant at p=0.01

**Table 2. Principal Components (PCs) for 7 quantitative characters in 18 genotypes of Basmati rice.**

| | $PC_1$ | $PC_2$ | $PC_3$ |
|---|---|---|---|
| Eigen-values | 2.2509 | 1.8271 | 1.4309 |
| Proportion of $\sigma^2$ | 32.2 | 26.1 | 20.4 |
| Cumulative $\sigma^2$ | 32.2 | 58.3 | 78.7 |
| Variables | **Eigen vectors** | | |
| 50% Heading Days | 0.225 | -0.269 | -0.633 |
| Plant Height (cm) | 0.268 | -0.525 | 0.398 |
| Productive tillers/plant | -0.379 | 0.185 | 0.115 |
| Panicle length (cm) | 0.510 | 0.292 | 0.223 |
| Panicle fertility % | -0.344 | -0.411 | 0.500 |
| 1000-seed weight (g) | -0.195 | -0.559 | -0.334 |
| Yield (kg/ha) | -0.564 | 0.227 | -0.129 |

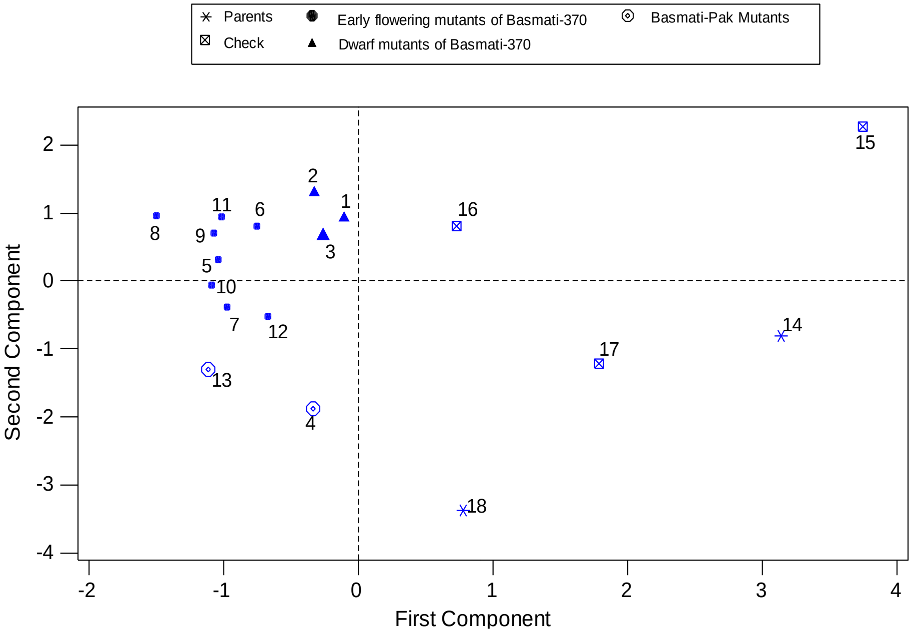

Fig. 1. Two dimensional ordination of 18 accessions of Basmati rice on Principal Component axis I and II.

**Table 3. Thirteen mutants of Basmati rice with mutant number and Pedigree.**

| Code No. | Genotypes | | Pedigree | Dose (Gy) |
|---|---|---|---|---|
| 1. | DM-1-20-7-99 | (M) | Basmati-370 | 200 |
| 2. | DM-1-30-3-99 | (M) | Basmati-370 | 300 |
| 3. | DM-1-30-34-99 | (M) | Basmati-370 | 300 |
| 4. | DM-2-25-9-02 | (M) | Basmati-Pak | 250 |
| 5. | EF-1-20-119-02 | (M) | Basmati-370 | 200 |
| 6. | EF-1-30-54-02 | (M) | Basmati-370 | 300 |
| 7. | EF-1-20-2-1-04 | (M) | Basmati-370 | 200 |
| 8. | EF-1-20-15-1-04 | (M) | Basmati-370 | 200 |
| 9. | EF-1-20-51-1-04 | (M) | Basmati-370 | 200 |
| 10. | EF-1-20-52-1-04 | (M) | Basmati-370 | 200 |
| 11. | EF-1-20-59-1-04 | (M) | Basmati-370 | 200 |
| 12. | EF-1-20-119-1-04 | (M) | Basmati-370 | 200 |
| 13. | DM-2-20-11-3-04 | (M) | Basmati-Pak | 200 |
| 14. | Basmati-370 | (P) | | |
| 15. | Basmati-385 | (C) | | |
| 16. | Super Basmati | (C) | | |
| 17. | Basmati-2000 | (C) | | |
| 18. | Basmati-Pak | (P) | | |

(P): Parent (M): Mutant (C): Check

**Table 4. Mean, and standard deviation for 3 clusters based on 7 quantitative characters in 18 accessions of rice.**

| Variables | Cluster-I | Cluster-II-a | Cluster-II-b | Cluster-III |
|---|---|---|---|---|
| 50% Heading days | 119.14 ± 1.26 | 118.84 ± 0.58 | 105.92 ± 2.35 | 112.17 ±2.60 |
| Plant height (cm) | 146.16 ± 7.22 | 115.87 ± 4.84 | 128.78 ± 2.55 | 143.50 ± 15.41 |
| Productive tillers/plant | 19.76 ± 2.38 | 18.13 ± 1.07 | 19.43 ± 3.29 | 15.60 ± 0.85 |
| Panicle length (cm) | 27.36 ± 1.00 | 28.76 ± 0.46 | 29.30 ± 0.63 | 33.22 ± 2.28 |
| Panicle fertility % | 94.38 ± 1.57 | 91.36 ± 0.98 | 94.54 ± 0.44 | 91.21 ± 3.35 |
| 1000-seed weight (g) | 23.0 ± 0.61 | 21.25 ± 0.44 | 20.94 ± 1.25 | 18.97 ± 0.42 |
| Yield (kg/ha) | 4697 ± 532 | 5183 ± 277 | 5322 ± 245 | 3999 ± 272 |

**Cluster analysis:** The letters 1-18 corresponds to the genotypes as in Table 3. Matrixes (7 x 18) exhibited the dendrogram in as in Fig. 2. At the 40.37% level of similarity 3 clusters were observed where cluster-II-a and cluster-II-b united to form one cluster. Moreover a middle cluster made up of Basmati-2000 is also formed. Two mutants were grouped together with parent (Basmati-Pak) in cluster-I. The cluster-II consists of three dwarf and eight early flowering mutants of Basmati-370 including the standard and high yielding variety Super Basmati. Cluster-III consists of Basmati-370 and Basmati-385.

Mean values along with standard deviation for each cluster presented in Table 4 revealed that mutants derived from Basmati-Pak are late in flowering and taller in height whereas the mutants clubbed together in cluster-II-b are early in flowering and were short statured. The mutants in cluster-II-a are dwarf in height than all the three clusters. The genotypes in cluster-III exhibited more panicle length than all the clusters. For yield cluster-II-b is high yielder followed by cluster-II-a and cluster-I whereas cluster-III is lower in yield. Results reported by Ghafoor *et al.*, (2001, 2003) showed multivariate analyses to be a valid system to deal with germplasm collection.

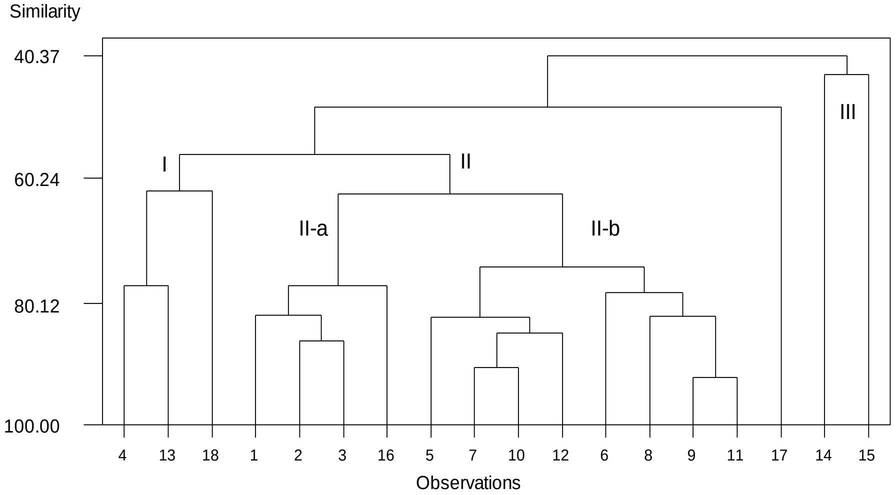

Fig. 2. Dendrogram resulting from Single Linkage Cluster Analysis (SLCA) of 18 mutants of Basmati Rice.

Cluster analysis grouped together mutants with greater genetic similarity and the clusters include the mutants from same parent in one group. The desirable accessions may be chosen from particular group for hybridization programme. Clusters with superior agronomic types have been identified which might be exploited for genetic potential and then could be used to transfer the desirable genes to improve yield potential of the crop.

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