Multivariate approach to analyse genetic diversity in some basmati rice genotypes (*Oryza sativa* L.)

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Abstract

Twenty three genotypes of basmati representing the broad spectrum of variation were assessed for ten yield attributing characters and ten quality characters using principal component analysis and cluster analysis. Principal component analysis identified five principal components with eigen values more than one for four components which contributed 90.40 per cent of the cumulative variance. The genotypes were grouped into six clusters by using cluster analysis. Cluster II was the largest, consisting of six genotypes followed by five genotypes each in clusters III, IV and V, two genotypes each in clusters I and VI. The results indicated that there was some degree of similarity of genotypes clustered together on the basis of their origin. However, the pattern of distribution of some genotypes from different eco-geographical regions was found random, indicating that geographical diversity and genetic diversity were not related. The maximum intra cluster distance was observed for the cluster III. The highest genetic divergence was observed between the clusters IV and III exhibiting wide diversity. Among different traits, plant height, days to 50% flowering, spikelets per panicle, KLAC and amylose content had maximum contribution towards total divergence may be used as selection parameters in segregating generations. Judicious selection of genotypes from the clusters may be used as potential donors for future hybridization programmes to develop varieties and hybrids of high yield without much compromise on quality.

Key words

Basmati rice, genetic diversity, principle component analysis, cluster analysis, eigen value

Basmati Rice, indigenous to the Indian sub-continent and endowed with unique quality traits are palatal delights of the rice connoisseurs’ world over. These virtues of Basmati Rice command them premium price in domestic and international markets (Siddiq *et al.*, 2012). Improving productivity and quality traits of basmati rice always remain crucial. Traditional basmati rice varieties are very low yielding due to their poor harvest index, tendency to lodging and increasing susceptibility to foliar diseases, hence there is a need to develop new varieties combining the grain quality attributes of basmati with high yield potential (Amarawathi *et al.*, 2008).

Genetic variability is the pre requisite for any crop improvement programme. Improvement in any trait is solely depends on the amount of variability present in the base material of that trait. Accurate assessment of the levels and patterns of genetic diversity can be invaluable in crop breeding for diverse applications including, analysis of genetic variability in cultivars (Smith, 1984; Cox *et al.*, 1986), identifying diverse parental combinations to create segregating progenies with maximum genetic variability for further selection (Barett and Kidwell, 1998), and introgressing desirable genes from diverse germplasm into the available genetic base (Thompson *et al.*, 1998). An understanding of genetic relationships among inbred lines or pure lines can be particularly useful in planning crosses, in assigning lines to specific heterotic groups, and for precise identification with respect to plant varietal protection (Hallauer and Miranda, 1988). Significant emphasis is being paid to comprehensive analysis of genetic diversity in numerous field crops for long-term success of breeding program and maximum exploitation of the genetic resources (Belaj *et al.*, 2002). If the structure of the genetic diversity is known within a large collection of germplasm which may be of great help to make decisions on management procedures and breeding strategies to be used in breeding programs.

With the development of advanced biometrical techniques such as multivariate analysis, quantification of degree of divergence among the biological populations and assessing the relative contribution of different components to the total divergence at intra- and inter cluster levels have now become possible. Such a study also permits to select the genetically diverse parents to obtain the desirable recombinant in the segregating populations upon crossing. Multivariate statistical techniques which simultaneously analyze multiple measurements on each individual under investigation, are widely used in analysis of genetic diversity irrespective of whether it is morphological, biochemical or molecular marker-based and subsequently, classification of germplasm collections. Among the multivariate techniques, cluster analysis, principle component analysis (PCA), principal co-ordinate analysis...
(PCoA) and Multi-Dimensional Scaling (MDS) are at present, most commonly employed and appear particularly useful (Mohammadi and Prasanna, 2003). The present study was, therefore, undertaken to assess the extent of genetic diversity in 25 rice genotypes using multivariate analysis approaches like principle component analysis (PCA) and cluster analysis.

The experimental material used in the study comprised of twenty three basmati rice genotypes grown in different agro-ecological zones of India. Two non-basmati genotypes were also included in the study making a total of twenty five genotypes. Genotype name, parentage and origin details are presented in Table 1. All genotypes were evaluated for grain yield and its attributing characters following randomized complete block design (RBD) with three replications during kharif season of 2011 and 2012 at Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India, which is situated at 25° 18’ North latitude and 83° 03’ East longitude, at an altitude of 123.3m from mean sea level. The soil of the experimental plot was fertile, alluvial loam and was characterized as the type soil of Indo-Gangetic Plains. Transplanting was done 25 days after sowing of seeds in nursery bed in a 4m² plot. Plant to plant distance was 15cm, row to row distance was 20cm and the crop was raised as per recommended package of practices to ensure normal crop.

Observations were recorded on yield attributes viz., days to maturity, plant height (cm), panicle length (cm), effective panicles per plant (no.), spikelets per panicle (no.), spikelet fertility (%), test weight (gm) and yield per plant (gm) of ten randomly selected plants in each entry in a replication. Observations were also recorded to study grain quality characters viz., kernel length (mm), kernel breadth (mm), kernel L/B ratio, kernel length after cooking (mm), elongation ratio, alkali spread value (Little et al., 1958) and amylose content (Juliano 1971). For statistical analysis, INDOSTAT software version 8.6 was used. The mean of the twenty five genotypes were analyzed statistically by the method outlined by Ostle (1966). The analysis of variance for different characters was carried out in order to assess the genetic variability among genotypes as given by Cochran and Cox (1950). The level of significance was tested at 5% and 1% using F table values given by Fisher and Yates (1963). The data were statistically analyzed to study the genetic diversity by principal component analysis as described by Jackson (1991). The genetic diversity between the genotypes was worked out using Mahalanobis D² analysis (1936) and grouping of genotypes into clusters was carried out following Tocher’s method (Rao, 1948 and 1952).

The analysis of variance revealed a significant difference among twenty five genotypes for all ten yield characters indicating the existence of high variability among the genotypes (Table 2). However, there is little variation exist for quality traits since basmati quality traits are unique and should not vary (Table 3).

Principle component analysis identified five principle components with Eigen values which contributed 93.08 percent of cumulative variance (Table 4). The first principal component (PC1) contributed maximum towards variability (47.015) with high significant positive loading of number brown rice breadth (0.320) followed by kernel breadth (0.308), kernel length (0.288) and filled grains (0.287). The second principal component (PC 2) accounted 25.145 per cent of total variance and it reflected significant positive loading of days to 50% flowering (0.398) followed by spikelets per panicle (0.299), KLAC (0.222) and kernel L/B ratio (0.202). The third principle component (PC 3) accounted for 13.246 percent of total variation and was characterized conspicuously by high loading of test weight (0.543) followed by brown rice L/B ratio (0.299) and brown rice length (0.294). The fourth principle component (PC 4) accommodates only one character, days to maturity (1.000). The fifth principle component (PC 5) reflected highest contribution from alkali spread value (0.728). PC4 and PC5 accounted for 5 and 2.67 per cent total variation respectively. Based on the five principle components, mean genotypic scores or PCA score were computed (Table 5). The plot of PC 1, PC 2, PC 3 and PC 4 showed clear differentiation of genotypes according to their cluster membership of each cluster. Genotypes belonging to a common cluster have fallen nearer to each other and vice versa. Fig. 1 shows the two dimensional PCA plot with twenty five genotypes of rice clustered among themselves based on PCA scores. Thus the principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters.

Based on the relative magnitude of D² estimates, twenty five genotypes were grouped in to six clusters (Table 6). Cluster II was the largest, consisting of six genotypes followed by five genotypes each in clusters III, IV and V, two genotypes each in clusters I and VI. The clustering pattern indicated that there was some degree of similarity of genotypes clubbed together in a cluster on the basis of their origin. Similar findings were reported by Singh et al. (2008). However, some genotypes were placed in clusters independent of geographical origin. Similar kind of results were reported in other studies (Sharma et al., 2002; Datt and Mani, 2003; Pradhan and Mani, 2005; Sharma et al., 2008 and Sharma et al., 2011).
Average intra and inter cluster distance (D² and D) values among six clusters were presented in Table 7. The average intra cluster D values ranged from 0 to 51.294. The highest intra cluster distance (D=51.294) was observed in the cluster IV, indicating wide genetic variation among the genotypes included in the cluster. The inter cluster D values ranged from 19.44 to 110.013. The maximum genetic distance was between cluster IV and III (D=110.013) followed by cluster III and V (D=102.48), cluster III and VI (D=94.592) and cluster VI and I (D=85.810), revealing that genotypes included in these clusters are genetically diverse and may give rise to superior recombinants and high heterotic response. However, it was noted that cluster I and VI included two genotypes each which are traditional basmati genotypes. Emphasis should be given to this cluster while selections of parents for hybridization programme since traditional basmati cultivars are excellent in basmati cooking qualities.

Percentage contribution of the characters towards total divergence (Table 8) revealed that maximum percentage of contribution came from the trait amylase content (39.33%), followed by KLAC (10.67%), days to 50% flowering (10.67%), plant height (10 %), spikelets per panicle (10 %) and elongation ratio (5.33%). Relative importance of some of these characters in inter varietal divergence on basmati rice was reported in other study (Datt and Mani, 2003; Pradhan and Mani, 2005; and Singh et al., 2008). The other traits had very low contribution to genetic divergence. Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank (Table 8). Hence, amylase content, KLAC, days to 50% flowering, plant height, spikelets per panicle and elongation ratio may be used as selection parameters in the segregating generations.

The cluster mean values showed a wide range of variation for all the yield traits under study (Table 9) however, variation among quality traits was less (Table 10). Cluster means are helpful in selecting the desirable traits among clusters and it serves as a quick glance of clusters carrying desirable traits.

Considering the importance of principle components, Euclidean genetic distance, relative contributions of characters towards total divergence, the present investigation suggests that parental lines selected from cluster IV for plant height, panicle length and effective panicles; cluster I for spikelets/panicle, filled grains and alkali spread value; cluster II for cooking quality traits viz., brown rice L/B ratio, kernel length and kernel L/B ratio could be used in breeding programme to isolate superior recombinant genotypes with higher yield and best basmati quality. However, it was noted that, unlike the development of non-basmati hybrids, the task of developing basmati quality hybrids was challenging as the development of parental lines was required to be incorporated with the basmati quality traits in order to improve the yield potential without sacrificing the special quality features of basmati.

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### Table 1. Details of rice genotypes under study

| S. No. | Variety | Parentage | Origin       |
|--------|---------|-----------|--------------|
| 1      | TBD-1   | Mutant of Taroari Basmati | BHU          |
| 2      | TBD-2   | Mutant of Taroari Basmati | BHU          |
| 3      | TAROARI BASMATI | Pureline selection from local Basmati | Haryana     |
| 4      | BASMATI 370 | Pureline selection from local agro commercial group | Punjab     |
| 5      | KASTURI BASMATI | Basmati 370/CR 88-17-1-5 | DRR, Hyderabad |
| 6      | SONASAL BASMATI | - | Jammu & Kashmir |
| 7      | RANBIR BASMATI | Selection from Bas 370-90-95 | Jammu & Kashmir |
| 8      | PUSA 2517-2-51-1 | - | IARI, New Delhi |
| 9      | PUSA BASMATI-1 | Pusa 167/Karnal local | IARI, New Delhi |
| 10     | PUSA BASMATI-1S-97 | Selection from Pusa Basmati-1 | BHU          |
| 11     | PUSA 44 | IARI 5901-2/IR-8 | IARI, New Delhi |
| 12     | PUSA SUGANDHA-3 | - | IARI, New Delhi |
| 13     | PUSA SUGANDHA-5 | Pusa 3A/Haryana Basmati | IARI, New Delhi |
| 14     | HUBR-2-1 | HBR 92/Pusa Basmati-1/Kasturi | BHU          |
| 15     | BASMATI-24-1 | Local land race | Maharaj ganj, U.P |
| 16     | BASMATI-24-5 | Local land race | Partawal, U.P |
| 17     | BASMATI-24-7 | Local land race | Siddardh nagar, U.P |
| 18     | VASUMATI | - | IARI, New Delhi |
| 19     | PUSA SUGANDHA-2 | - | IARI, New Delhi |
| 20     | CSR-30(YAMINI) | Selection from Taroari Basmati | IARI, New Delhi |
| 21     | JP-2 | Collection from Basti | Uttar Pradesh |
| 22     | PUSA 1460 | Improved Pusa Basmati-1 | IARI, New Delhi |
| 23     | PUSA 1121(Pusa Sugandha-4) | Pusa 614-1-2/Pusa 614-2-4-3 | IARI, New Delhi |
| 24     | MAHI SUGANDHA | BK 79/Basmati 370 | Rajasthan |
| 25     | TYPE-3 | Selection from Dehradoon Basmati | Uttar Pradesh |
Table 2. Analysis of variance for yield attributing characters in Basmati rice

| Source        | d.f | Days to 50% Flowering | Days to maturity | Plant Height (cm) | Panicle Length (cm) | Effective Panicles (no.) | Spikelets/ Panicle (no.) | Filled Grains (no.) | Spikelet Fertility(%) | Test Weight (gms) | Yield per plant (gms) |
|---------------|-----|------------------------|------------------|-------------------|---------------------|--------------------------|--------------------------|---------------------|---------------------|------------------|------------------------|
| Replication   | 2   | 0.413                  | 0.093            | 0.982             | 1.279               | 0.213                    | 0.373                    | 25.120              | 0.492               | 0.010           | 0.538                  |
| Treatment     | 24  | 204.120**              | 202.396**        | 1117.06**         | 24.205**            | 11.264**                 | 2425.97**                | 1734.05**           | 23.470**            | 0.315           | 18.988**               |
| Error         | 48  | 0.705                  | 0.675            | 0.573             | 0.353               | 0.074                    | 5.901                    | 11.38               | 2.969               | 0.013           | 0.447                  |

*, ** significant at 5 and 1 per cent level, respectively

Table 3. Analysis of variance for quality characters in Basmati rice

| Source        | d.f | Brown Rice Length(mm) | Brown Rice Breadth(mm) | Brown Rice L/B Ratio | Kernel Length(mm) | Kernel Breadth(mm) | Kernel L/B Ratio | KLAC(mm) | Elongation Ratio | Alkali Spread Value | Amylose Content(%) |
|---------------|-----|------------------------|------------------------|---------------------|-------------------|-------------------|-----------------|----------|-----------------|---------------------|-------------------|
| Replication   | 2   | 0.005                  | 0.000                  | 0.000               | 0.003             | 0.042             | 0.036           | 0.000               | 0.053           | 0.108                  |
| Treatment     | 24  | 2.330**                | 0.005                  | 0.596               | 2.187*            | 0.034             | 0.606           | 6.048**             | 0.075           | 7.692**                 | 4.296**            |
| Error         | 48  | 0.004                  | 0.002                  | 0.000               | 0.001             | 0.016             | 0.025           | 0.000               | 0.025           | 0.083                  |

*, ** significant at 5 and 1 per cent level, respectively
Table 4. The eigen values, proportion of total variance, cumulative per cent variance and component loading of different characters for five principal components

| Character                      | PC 1     | PC 2     | PC 3     | PC 4     | PC 5     |
|-------------------------------|----------|----------|----------|----------|----------|
| Eigen Value (Root)            | 9.403    | 5.029    | 2.649    | 1.000    | 0.535    |
| % Var. Exp.                   | 47.015   | 25.145   | 13.246   | 5.000    | 2.675    |
| Cum. Var. Exp.                | 47.015   | 72.160   | 85.407   | 90.407   | 93.082   |
| Days to 50 % flowering        | 0.058    | 0.398    | 0.232    | 0.000    | 0.106    |
| Days to Maturity              | 0.000    | 0.000    | 0.000    | 1.000    | 0.000    |
| Plant Height (cm)             | -0.312   | -0.101   | 0.013    | 0.000    | -0.078   |
| Panicle Length (cm)           | -0.279   | -0.052   | 0.087    | 0.000    | 0.171    |
| Effective Panicles            | -0.295   | 0.142    | 0.048    | 0.000    | 0.164    |
| Spikelets/ Panicle            | -0.079   | 0.299    | -0.308   | 0.000    | -0.112   |
| Filled Grains                 | 0.287    | 0.173    | -0.006   | 0.000    | -0.007   |
| Spikelet Fertility %          | -0.241   | -0.219   | -0.089   | 0.000    | -0.302   |
| Test Weight (100 Grain Wt)    | 0.134    | 0.037    | 0.543    | 0.000    | 0.119    |
| Yield/ Plant (gms)            | 0.109    | 0.334    | -0.243   | 0.000    | 0.075    |
| Brown Rice Length (mm)        | -0.161   | -0.319   | 0.294    | 0.000    | -0.037   |
| Brown Rice Breadth (mm)       | 0.320    | -0.065   | 0.007    | 0.000    | 0.044    |
| Brown Rice L/B Ratio          | 0.155    | -0.297   | 0.299    | 0.000    | -0.077   |
| Kernel Length (mm)            | 0.288    | 0.185    | 0.050    | 0.000    | 0.050    |
| Kernel Breadth (mm)           | 0.308    | 0.022    | 0.178    | 0.000    | 0.011    |
| Kernel L/B Ratio              | -0.206   | 0.202    | 0.344    | 0.000    | 0.260    |
| KLAC (mm)                     | -0.227   | 0.222    | 0.281    | 0.000    | 0.040    |
| Elongation ratio              | 0.239    | -0.275   | 0.053    | 0.000    | -0.249   |
| Alkali Spread Value           | -0.053   | -0.313   | -0.249   | 0.000    | 0.728    |
| Amylose Content (%)           | -0.269   | 0.191    | 0.088    | 0.000    | -0.360   |

Fig. 1. Two dimensional graph showing relative position of 25 genotypes of basmati rice based on PCA scores (numbers 1 to 25 represent genotype serial number in table 1)
Table 5. The mean genotypic scores or PCA scores for 25 genotypes

| S. No. | Genotypes              | PC 1   | PC 2   | PC 3   | PC 4   | PC 5   |
|--------|------------------------|--------|--------|--------|--------|--------|
| 1      | TBD-1                  | -504.491 | 306.493 | 275.938 | 30.000  | -254.302 |
| 2      | TBD-2                  | -472.038 | 299.318 | 278.876 | 30.000  | -243.664 |
| 3      | TAROARI BASMATI        | -565.160 | 298.339 | 308.140 | 30.000  | -264.165 |
| 4      | BASMATI-370            | -579.919 | 305.398 | 274.454 | 30.000  | -263.387 |
| 5      | KASTURI BASMATI        | -519.428 | 251.318 | 274.685 | 30.000  | -253.576 |
| 6      | SONASAL BASMATI        | -537.372 | 261.984 | 261.822 | 30.000  | -256.246 |
| 7      | RANBIR BASMATI         | -530.121 | 264.733 | 278.470 | 30.000  | -259.070 |
| 8      | PUSA 2517-2-51-1       | -491.466 | 261.903 | 279.493 | 30.000  | -251.670 |
| 9      | PUSA BASMATI-1         | -502.865 | 297.430 | 286.575 | 30.000  | -241.822 |
| 10     | PUSA BASMATI-1S-97     | -505.831 | 300.189 | 283.441 | 30.000  | -243.822 |
| 11     | PUSA 44                | -497.798 | 300.651 | 280.324 | 30.000  | -256.101 |
| 12     | PUSA SUGANDH-3         | -489.697 | 254.544 | 278.112 | 30.000  | -246.098 |
| 13     | PUSA SUGANDH-5         | -478.902 | 252.547 | 276.249 | 30.000  | -246.630 |
| 14     | HUBR-2-1               | -490.089 | 268.136 | 279.444 | 30.000  | -236.767 |
| 15     | BASMATI 24-1           | -475.971 | 250.424 | 253.655 | 30.000  | -244.260 |
| 16     | BASMATI 24-5           | -516.905 | 287.454 | 287.130 | 30.000  | -268.020 |
| 17     | BASMATI 24-7           | -489.453 | 272.724 | 277.017 | 30.000  | -251.708 |
| 18     | VASUMATI               | -501.773 | 269.593 | 285.762 | 30.000  | -257.142 |
| 19     | PUSA SUGANDH-2         | -483.380 | 255.929 | 287.714 | 30.000  | -251.318 |
| 20     | CSR-30                 | -527.586 | 288.751 | 302.172 | 30.000  | -255.670 |
| 21     | JP-2                   | -473.352 | 232.515 | 279.038 | 30.000  | -240.247 |
| 22     | PUSA 1460              | -501.050 | 277.524 | 303.626 | 30.000  | -251.795 |
| 23     | PUSA 1121              | -479.981 | 270.450 | 301.648 | 30.000  | -249.227 |
| 24     | MAHI SUGANDHA          | -549.878 | 275.699 | 288.952 | 30.000  | -255.507 |
| 25     | TYPE-3                 | -566.055 | 281.030 | 294.936 | 30.000  | -250.313 |

Table 6. Distribution of 25 genotypes of Basmati rice in different clusters

| Cluster | Genotypes included                                                                 | No. of genotypes |
|---------|------------------------------------------------------------------------------------|------------------|
| I       | Taroari Basmati, Basmati 370.                                                      | 2                |
| II      | Pusa 2571-1-51-1, HUBR-2-1, Basmati 24-7, Vasumati, Pusa 1460, Pusa 1121.           | 6                |
| III     | Pusa Sugandha-3, Pusa Sugandha-5, Pusa Sugandha-2, Basmati 24-1, J.P-2.             | 5                |
| IV      | TBD-1, TBD-2, Pusa Basmati-1, Pusa Basmati-1S-97, Pusa 44.                          | 5                |
| V       | Kasturi Basmati, Ranbir Basmati, Sonasal Basmati, Basmati 24-5, CSR-30             | 5                |
| VI      | Mahi Sugandha, Type-3.                                                             | 2                |
Table 7. Average intra and Inter Cluster distance ($D_2$ and $D$) values among six clusters

| Cluster | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI |
|---------|-----------|------------|-------------|------------|-----------|------------|
| Cluster I | 378.103 (19.444) | 2523.309 (50.232) | 4299.450 (65.570) | 7363.450 (85.810) | 5343.192 (73.074) | 1570.968 (39.635) |
| Cluster II | 1163.680 (34.112) | 5970.428 (77.268) | 2560.090 (50.597) | 2311.110 (48.074) | 2656.271 (51.539) | 8947.732 (94.592) |
| Cluster III | 2631.606 (51.299) | 12102.923 (110.013) | 10502.781 (102.483) | 8947.732 (94.592) | 0.000 | 0.000 |
| Cluster IV | 0.000 | 1155.605 (33.994) | 5399.063 (73.478) | 0.000 | 3682.947 (60.687) | 0.000 |
| Cluster V | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| Cluster VI | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |

$D$ values are in parenthesis.

Table 8. Times ranked first and percentage contribution to total $D^2$

| S. No. | Characters | Times Ranked | $1^{ST}$ | Percentage contribution to total $D^2$ |
|--------|------------|--------------|----------|-------------------------------------|
| 1      | Days to 50% flowering | 44           | 10.67    | 10.67                               |
| 2      | Days to Maturity     | 0            | 0.00     | 0.00                                |
| 3      | Plant Height (cm)    | 41           | 10.00    | 10.00                               |
| 4      | Panicle Length (cm)  | 0            | 0.00     | 0.00                                |
| 5      | Effective Panicles  | 0            | 0.00     | 0.00                                |
| 6      | Spikelets/ Panicle   | 57           | 12.33    | 12.33                               |
| 7      | Filled Grains        | 0            | 0.00     | 0.00                                |
| 8      | Spikelet Fertility % | 0            | 0.00     | 0.00                                |
| 9      | Test Weight (100 Grain Wt) | 0 | 0.00 | 0.00 |
| 10     | Yield/ Plant (gms)   | 2            | 0.67     | 0.67                                |
| 11     | Brown Rice Length (mm) | 7       | 2.33     | 2.33                                |
| 12     | Brown Rice Breadth (mm) | 10      | 3.33     | 3.33                                |
| 13     | Brown Rice L/B Ratio | 0            | 0.00     | 0.00                                |
| 14     | Kernel Length (mm)   | 7            | 2.33     | 2.33                                |
| 15     | Kernel Breadth (mm)  | 9            | 3.00     | 3.00                                |
| 16     | Kernel L/B Ratio     | 0            | 0.00     | 0.00                                |
| 17     | KLAC (mm)            | 50           | 10.67    | 10.67                               |
| 18     | Elongation ratio     | 16           | 5.33     | 5.33                                |
| 19     | Alkali Spread Value  | 0            | 0.00     | 0.00                                |
| 20     | Amylose Content(%)   | 108          | 39.33    | 39.33                               |
Table 9. Mean values of different clusters with respect to ten yield traits

| Cluster | Days to 50% flowering | Days to Maturity | Plant Height (cm) | Panicle Length (cm) | Effective Panicles | Spikelets/ Panicle | Filled Grains | Spikelet Fertility % | Test Weight (100 Grain Wt) | Yield/ Plant (gms) |
|---------|-----------------------|------------------|-------------------|--------------------|-------------------|-------------------|---------------|---------------------|-----------------------------|------------------|
| I Cluster | 110.100** | 140.100** | 98.450* | 26.600 | 10.600 | 202.200** | 171.200** | 84.710* | 1.986 | 11.903 |
| II Cluster | 97.111 | 127.111 | 105.606 | 27.222 | 8.556 | 152.778* | 133.000* | 87.089 | 2.361 | 9.482 |
| III Cluster | 87.750 | 117.750 | 104.825 | 25.500* | 6.750* | 156.750 | 138.250 | 87.675 | 2.158 | 6.415* |
| IV Cluster | 98.625 | 128.625 | 149.000** | 30.875** | 10.875** | 175.500 | 152.750 | 86.813 | 2.310 | 12.586** |
| V Cluster | 85.667* | 115.667* | 131.017 | 30.667 | 9.333 | 163.167 | 145.500 | 89.017** | 1.875* | 8.563 |
| VI Cluster | 103.500 | 133.500 | 119.600 | 26.500 | 10.000 | 169.750 | 145.750 | 85.900 | 2.467** | 11.630 |

*lowest values; **highest values

Table 10. Mean values of different clusters with respect to ten quality traits

| Cluster | Brown Rice Length (mm) | Brown Rice Breadth (mm) | Brown Rice L/B Ratio | Kernel Length (mm) | Kernel Breadth (mm) | Kernel L/B Ratio | KLAC (mm) | Elongation ratio | Alkali Spread Value | Amylose Content (%) |
|---------|------------------------|-------------------------|----------------------|-------------------|-------------------|-----------------|-----------|------------------|---------------------|-------------------|
| I Cluster | 7.502 | 1.960* | 3.851 | 7.199 | 1.741 | 4.077 | 13.877 | 1.872 | 6.200** | 23.675 |
| II Cluster | 8.268** | 2.000 | 4.132** | 8.136** | 1.786 | 4.499** | 14.201 | 1.722 | 5.444 | 23.697 |
| III Cluster | 7.050* | 2.030** | 3.457* | 6.950* | 1.775 | 3.915* | 11.540* | 1.692* | 6.000 | 21.620* |
| IV Cluster | 7.609 | 1.995 | 3.825 | 7.400 | 1.760 | 4.229 | 14.667** | 1.920 | 3.625 | 24.170 |
| V Cluster | 7.582 | 1.988 | 3.708 | 7.160 | 1.693* | 4.148 | 14.053 | 1.955** | 2.833 | 24.327 |
| VI Cluster | 8.142 | 2.000 | 3.818 | 7.545 | 1.835** | 4.128 | 13.520 | 1.793 | 2.750* | 25.432** |

*lowest values; **highest values