

Study of genetic diversity in rice (*Oryza sativa* L.) genotypes under direct seeded condition by using principal component analysis

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ABSTRACT

The present investigation was carried out to assess the genetic diversity by using principal component analysis for yield and yield contributing traits in thirty-two genotypes of rice under direct seeded condition (DSR). The experiment was conducted at Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar in randomized block design with three replications. The results revealed that first four component axes had eigen values ≥ 1.0 , representing a cumulative variability of 76.86 %. Principal component analysis (PCA) indicate that four components (PC1 to PC4) accounted for about 76.86% of the total variation present among all the traits. Out of total principal components PC1, PC2, PC3 and PC4 with values 33.781%, 19.02%, 13.859% and 10.206% respectively, contributed more to the total variation. The first principal component had high positive loading for 15 traits out of 17. Similarly, second and third principal component had 7 traits each, fourth component with 6 traits had high positive loadings which contributed more to the diversity. Genotypes in cluster V showed higher mean performance for most of the yield attributing traits. Therefore, selection of parents for different traits would be effective from this cluster. Thus, result of the present study could be exploited in planning and execution of future breeding programme in rice under direct seeded condition.

Key words: PCA, genetic diversity, K-clustering, DSR

Introduction

Any crop improvement program depends on the utilization of germplasm stock available in different research organization or institutes. Due to rapid growth of the population, rice yield is urgently required to increase to meet the food demand. In order to meet the requirement of food demand there is a necessity for development of high yielding varieties along with having good yielding attribute traits. Genetic diversity represents the heritable variation

present within and between populations of organisms. The success of plant breeding depends on the availability of genetic variation, knowledge about desired traits and efficient selection strategies that make it possible to exploit existing genetic resources. Rice is a major agricultural crop in India grown under diverse ecological conditions with varied phenology and yield.

Before exploiting any population for trait improvement, it is essential to understand the magnitude of variability present in the population and

which is fundamental too for genetic improvement in all the crop species. The success of any crop improvement programme is also dependent on the efficient manipulation of the genetic variability present in the germplasm and the selection of genotypes with all possible desirable yield contributing traits (Ravi *et al.*, 2018).

Grain yield is a complex polygenic character with great genetic, physio-morphological, ecological and pathological dependence. The hereditary potential of a genotype depends upon its stability and yielding ability of the traits. Genetically, yield attributing traits, their genetic nature and magnitude of their association with other traits are responsible for realizing yield potential influenced by changing edaphic, agro-climatic condition. Therefore, it is highly important to investigate the genetic variation of the varieties and lines of this crop in breeding programme. One of the important approaches for rice breeding is hybridization and subsequent selection. Parent's choice is the first step in plant breeding program through hybridization. In order to benefit transgressive segregation, understanding of genetic distance between parents is necessary (Joshi *et al.* 2004). Higher the genetic distance between parents, higher heterosis can be observed in progeny. Estimation of genetic distance is one of appropriate tool for parental selection in rice hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004). Principal Component Analysis (PCA), Cluster analysis and discriminate analysis are the important multivariate analysis methods which helps in parental selection and identification of genetic diversity (Nachimuthu *et al.*, 2014).

Principal component analysis helps researchers to distinguish significant relationship between traits and facilitate the choice of genitors for rice plant breeding programs. It may be used to disclose the pattern and eradicate redundancy in data sets as variation regularly arises in crop species for yield (Mazi and Shaibu, 2012). PCA can be used to uncover similarities between variable and classify the cases (genotypes), while cluster analysis on the other hand is concerned with classifying previously unclassified materials. Statistical method of classification is usually by multivariate methods as it has extensive use in summarizing and describing the inherent variation among crop genotypes. This multivariate analysis method aims to explain the correla-

tion between a large set of variables in terms of a small number of underlying independent factors. PCA condense the magnitude of a multivariate data to a small number of principal axes, generates an eigen vector for every axis and produces component (PC) scores for the traits (Ariyo and Odulaja, 1991). The Principal Component was used to determine the extent of genetic variation. Eigen values were obtained from PC, which were used to determine the relative discriminative power of the axes and their associated characters (Pradhan *et al.* 2011). The cluster analysis is an appropriate method for determining family relationship but the main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002). This approach is especially valuable for screening large number of genetic resources by a large number of descriptor variables (Beiragi *et al.*, 2011 and Golbashy *et al.*, 2010). PCA has been used by many researchers like Gana *et al.* (2013), Asfaq *et al.* (2014) and Ravikumar *et al.* (2015) for characterization of different rice germplasm lines.

Keeping in view of this fact, the main objective of this study was to assess the potential genetic diversity and correlation among rice genotypes by using cluster analysis and cluster analysis-based methods for selection of parents in hybridization programme. The aim of present study was to identify better combinations as selection criteria for developing high yielding rice genotypes. Such type of findings may help rice breeders and could provide new opportunities for promoting the production of rice with better yield.

Materials and Methods

The experimental material comprised of thirty-two genotypes of rice including one check *i.e.* Rajendra bhagwati (Table 2) were procured from Dr. Rajendra Prasad agricultural university, Pusa, Bihar. The experiment was laid out in randomized block design (RBD) with three replications at the rice research farm of Department of Plant Breeding and Genetics, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar during *kharif* season, 2017. Each genotype was sown in plot of 1.80 x 2.50 square meters with the spacing 20x15 cm row to row and plant to plant distance, respectively. Standard agronomic package of practices and plant protection measures were taken as per schedule to raise good

crop. The data was recorded on seventeen quantitative traits which include ten morpho-physiological traits and seven agrometeorological indices, the observations were recorded on plot basis for days to 50 % flowering, days to physiological maturity and grain yield per plant. For rest of the morphological traits, the data were recorded on five randomly selected plants from each genotype in each replication *viz.* plant height (cm), number of tillers per plant, panicle length (cm), number of panicles per plant, spikelet fertility (%), relative water content (%), 1000-grain weight (g). Observations for seven agrometeorological indices *viz.* growing degree days, helio-thermal unit, photo-thermal unit, photo-thermal index, heat use efficiency, relative temperature depression and critical temperature for reproductive stage ($^{\circ}\text{C}$) were calculated. The recorded morphological traits and calculated agrometeorological indices data were averaged and analyzed for simple statistics *i.e.* mean, variance, range, frequency distribution, coefficient of variance and standard deviation using computer software (MS-Excel 2007). Cluster and principal component analysis (PCA) were performed on the recorded data for quantitative traits. Before to cluster and PCA, mean of each parameter was standardized to avoid scaling differences effects. The data were analyzed using INDOSTAT version 9.1.

Growing degree days (GDD) was calculated by taking 10°C as base temperature on the basis of daily mean temperature with the help of following formula suggested by Nuttonson (1995).

$$\text{GDD} = \frac{\sum(T_{\text{max}} + T_{\text{min}})}{2} - T_b$$

Where,

T_{max} and T_{min} are daily maximum and minimum temperature, T_b is the base temperature.

Photo-thermal unit (PTU) was calculated on the basis of GDD and day length with the formula:

$$\text{PTU} = \text{GDD} \times \text{Day length (degree-days hours)}$$

Helio-thermal unit (HTU) was calculated using GDD and sunshine hours by the following formula:

$$\text{HTU} = \text{GDD} \times \text{Duration of sun shine hours (degree-days hours)}$$

Photo-thermal index (PTI) was calculated using the following equation:

$$\text{PTI} = \text{GDD} / \text{Growth days (degree-days day}^{-1}\text{)}$$

Heat use efficiency (HUE) was calculated with the help of seed yield (kg ha^{-1}) per GDD with the help of following equation:

$$\text{HUE} = \text{Seed yield (kg ha}^{-1}\text{)} / \text{GDD (kg ha}^{-1}\text{ degree-days)}$$

Relative temperature depression was calculated using the formula

$$\text{RTD} = \frac{\sum T_{\text{max}} - T_{\text{min}}}{T_{\text{max}}} \times 100$$

Critical temperature for reproductive stage (CT) was measured by recording accumulated daily temperature till flowering and accumulated daily temperature till maturity and calculated using equation as proposed Arnold (1960):

$$\frac{\text{Accumulated daily temperature till maturity (}^{\circ}\text{C)} - \text{Accumulated daily temperature till flowering (}^{\circ}\text{C)}}{\text{No of days to maturity} - \text{No. of days to flowering}}$$

Where,

Accumulated daily temp. till maturity = Sum of daily average temperature \times Number of days till maturity

Accumulated daily temp. till flowering = Sum of daily average temperature \times Number of days till flowering

Relative water content (RWC) of the flag leaves was determined using the equation given by Barr and Weatherley (1962):

$$\text{RWC} = \frac{F.W - D.W}{T.W - D.W} \times 100$$

Where,

F.W. = Fresh Weight of flag leaf (g)

D.W. = Dry Weight of flag leaf (g)

T.W. = Turgid Weight of flag leaf (g)

Results and Discussion

Principal component analysis is a form of multivariate analysis utilized in the present study, where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for each such axes, respectively (Sharma *et al.*, 1996). The variations were identified for seventeen characters and most of the variation was accounted for the first four canonical vectors represent the primary, secondary, tertiary and fourth axes of differentiation in thirty-two genotypes of rice (Table 1). These four vectors were used to obtain means of canonical variates and three dimensional (3D) pictorial representations of all the thirty-two genotypes. Genetic divergence was measured between variates in terms of spatial distance. According to Chahal and Ghosal (2002), characters with largest absolute

value closure to unity within the first principal component influence the clustering more than those with lowest absolute value closer to zero. Therefore, in the present study, differentiation of the genotypes into different clusters was due to relatively high contribution by few traits rather than small contribution from each trait. The results of PCA explained the genetic variation among the genotypes for all morphological and agrometeorological indices under study. Data were considered in each component with Eigen values more than 1 as per the suggestions given by Brejda *et al.* (2000), which determines a minimum 10% of the variation. The factors with eigen values less than 1 were ignored by following "Guttman's lower bound Principle" (Kaiser, 1958). The eigenvalues are often used to determine how many factors to retain. The sum of the eigenvalues is usually equal to the number of variables. Superior Eigen values are considered as best attributes in principal components. In our study, four components exhibited Eigen values of >1 and showed 76.86% of cumulative variation of the total variation among the genotypes for all the traits. It indicates that the identified characters within these components exhibited immense influence on the phenotypes of the genotypes. Table 1 presents principal components, Eigen values and percentage contribution of each component to the total variation in the rice genotypes.

The four components *viz.* PC1, PC2, PC3 and PC4 showed 33.78%, 19.02%, 13.86% and 10.21% of variations among the traits, respectively. Similar results were reported by Ojha *et al.* (2017) and Ravi *et al.* (2018). The first principal component (PC1) with Eigen value 5.743 explained 33.781 % of the variation and highly loaded with traits such as heat use efficiency (0.340), plant height (0.326), tillers per plant (0.318), panicles per plant (0.309), panicle length (0.305), days to physiological maturity (0.280), days to 50% flowering (0.267) and helio-thermal unit (0.252) contributed in positive direction whereas agro-meteorological indices like photo thermal index (-0.331) and critical temperature for reproductive stage (-0.143) contributed in negative direction. It clearly indicates that the variations in PC1 are mainly contributed by yield traits and heat unit. The second Principal component (PC2) with Eigen value 3.234 accounted for 19.023 % of the total variation and loaded with the traits *viz.* days to physiological maturity (0.250), days to 50% flowering (0.225), growing degree days (0.363), panicle length (0.152), panicles per plant (0.148), photo thermal index (0.144), plant height (0.116) contributed in positive direction while spikelet fertility (-0.476), grain yield per plant (-0.395), critical temperature for reproductive stage (-0.348), helio-thermal unit (-0.330), photo-thermal unit (-0.165), heat use efficiency (-0.124) contributed negatively to the total

Table 1. Vector loadings and percent variation for different traits contributed by Principal Components

| Characters | Vector1 | Vector2 | Vector3 | Vector4 |
|---|---------------|---------------|---------------|---------------|
| Days to 50% Flowering | 0.267 | 0.225 | 0.153 | 0.363 |
| Days to Physiological maturity | 0.280 | 0.250 | -0.029 | 0.265 |
| Plant height (cm) | 0.326 | 0.116 | 0.125 | 0.017 |
| Panicle length (cm) | 0.305 | 0.152 | 0.065 | -0.088 |
| Number of tillers per Plant | 0.318 | 0.038 | -0.122 | -0.393 |
| Number of panicles per Plant | 0.309 | 0.148 | -0.176 | -0.141 |
| Spikelet fertility (%) | 0.171 | -0.476 | 0.056 | 0.128 |
| 1000 grain weight (g) | 0.072 | -0.053 | -0.471 | 0.250 |
| Growing degree days (Degree days) | 0.143 | 0.363 | -0.293 | -0.202 |
| Helio-thermal unit (Degree-days hours) | 0.252 | -0.330 | 0.190 | 0.212 |
| Photo-thermal unit (Degree-days hours) | 0.154 | -0.165 | -0.212 | 0.485 |
| Photo-thermal index (Degree-days day ¹) | -0.331 | 0.144 | 0.228 | 0.002 |
| Heat use efficiency (Kg/ha) Degree-days | 0.340 | -0.124 | 0.088 | -0.204 |
| Relative Temperature depression | 0.083 | -0.085 | 0.516 | 0.036 |
| Critical temperature for reproductive stage (°C) | -0.143 | -0.348 | -0.241 | -0.217 |
| Relative water content (%) | 0.178 | -0.094 | 0.303 | -0.307 |
| Grain yield per plant (g) | 0.168 | -0.395 | -0.206 | -0.177 |
| Eigene Value (Root) | 5.743 | 3.234 | 2.356 | 1.735 |
| % Var. Exp. | 33.781 | 19.023 | 13.859 | 10.206 |
| Cum. Var. Exp. | 33.781 | 52.804 | 66.663 | 76.869 |

variation. These findings were in agreement with Nachimuthu *et al.* (2014). PC3 with Eigen value 2.356 which accounted for 13.859 % of total variation has contribution from the traits like relative temperature depression (0.516), relative water content (0.303), days to 50% flowering (0.153), plant height (0.125), helio-thermal unit (0.190) and photo thermal index (0.228) in positive direction whereas, 1000 grain weight (-0.471), growing degree days (-0.293), critical temperature for reproductive stage (-0.241), photo-thermal unit (-0.212), grain yield per plant (-0.206), panicles per plant (-0.176) and tillers per plant (-0.122) contributed negatively. Morphological and agrometeorological traits like days to 50% flowering (0.363) spikelet fertility (0.128), 1000 grain weight (0.250), days to physiological maturity (0.265), helio-thermal unit (0.212), photo-thermal unit (0.485) in positive direction and characters like

tillers per plant (-0.393), panicles per plant (-0.141), growing degree days (-0.202), heat use efficiency (-0.204), critical temperature for reproductive stage (-0.217), relative water content (-0.307), grain yield per plant (-0.177) contributed in negative direction and contribution was 10.206 % of the total variation in PC4. The prominent traits which come together in different principal components and contributed maximum towards the diversity explain the variability, as the tendency to remain together and may be kept into consideration during utilization of these traits in breeding programme. Through PCA we could identify the number of plant characters, which are responsible for the observed genotypic variation within a group. So, a breeder has to go for positive selection for those traits which showed positive contribution towards yield. These findings revealed that first four principal components relate various mor-

Table 2. Means of Canonical variate

| Genotypes | Vector 1 | Vector 2 | Vector 3 | Vector 4 |
|---------------------------|----------|----------|----------|----------|
| RAU1417-2-1-5-7-7 | 7.709 | -13.293 | 39.375 | 5.305 |
| RAU1421-12-1-7-4-3 | 10.946 | -16.017 | 41.305 | 2.454 |
| RAU1415-35-76-9-5-3-4 | 9.346 | -13.438 | 39.935 | 3.875 |
| RAU1401-18-1-1 | 8.549 | -13.963 | 40.154 | 3.726 |
| RAU1401-18-1-1-5 | 13.377 | -13.884 | 42.455 | -0.084 |
| RAU1428-543-35-5-5 | 9.213 | -12.326 | 40.389 | 2.816 |
| RAU1421-12-1-7-4-4 | 11.112 | -15.094 | 40.764 | 2.081 |
| RAU1421-15-3-2-5-3-7 | 10.079 | -13.607 | 39.948 | 1.355 |
| RAU1417-9-7-22-5-7-3 | 9.335 | -12.828 | 40.530 | 1.114 |
| RAU1451-66-1-1-5-1 | 9.492 | -14.226 | 41.930 | 1.634 |
| RAU1451-66-1-1-5-2 | 9.754 | -13.444 | 41.534 | 3.174 |
| RAU1416-4-2-5-2-2 | 9.868 | -13.380 | 39.224 | 2.983 |
| RAU1397-25-8-1-2-5-4 | 5.839 | -6.041 | 38.326 | 3.726 |
| RAU1417-11-1-74-3-2 | 5.578 | -5.072 | 43.409 | 2.143 |
| RAU1421-15-3-2-5-7-3 | 9.800 | -14.406 | 42.495 | 4.104 |
| RAU1415-35-7-6-9-5-1 | 9.163 | -14.107 | 41.032 | 4.922 |
| RAU1426-43-2-5-4 | 7.978 | -11.684 | 41.968 | 4.914 |
| RAU1463-16 | 9.159 | -13.085 | 39.645 | 3.120 |
| RAU1415-8-6-4-3-3 | 7.843 | -13.190 | 38.420 | 6.115 |
| RAU1397-18-3-7-9-4-7 | 9.432 | -11.938 | 40.634 | 2.942 |
| RAU1428-7-3-6 | 8.211 | -13.754 | 41.519 | 3.376 |
| RAU1421-12-1-7-3 | 9.068 | -14.149 | 41.890 | 3.048 |
| RAU96-P-1-2 | 13.645 | -9.780 | 44.892 | 6.543 |
| MTU-1010 | 8.305 | -7.396 | 39.227 | 3.340 |
| Sahbhagi | 14.829 | -11.939 | 39.290 | 5.149 |
| Prabhat | 8.733 | -13.880 | 35.873 | 5.878 |
| Richaria | 8.422 | -9.860 | 41.104 | 3.935 |
| Rasi | 9.914 | -15.069 | 39.522 | 4.450 |
| Vandana | 16.497 | -11.332 | 39.970 | 4.932 |
| Turanta | 10.458 | -14.577 | 36.881 | 3.753 |
| Rajendra Nilam | 14.896 | -13.846 | 39.922 | 1.395 |
| Rajendra Bhagwati (Check) | 14.809 | -14.635 | 39.706 | 2.216 |

phological characters and agrometeorological indices in rice, mostly associated with early genotypes and agrometeorological indices *i.e.* heat unit requirement can identify the diverse genotypes which could be employed in hybridization programme. Comparable studies and results in rice were obtained by the researchers like Das *et al.*, 2014 and Jakhar *et al.* (2018).

Table 3 showed that thirty-two genotypes of rice were grouped into six clusters using K-means non-hierarchical clustering. Cluster III was the biggest one and comprised of 14 genotypes namely, RAU 1417-2-1-5-7-7, RAU 1415-35-76-9-5-3-4, RAU 1401-18-1-1, RAU 1421-15-3-2-5-3-7, RAU 1417-9-7-22-5-7-3, RAU 1451-66-1-1-5-1, RAU 1451-66-1-1-5-2, RAU 1416-4-2-5-2-2, RAU 1415-35-7-6-9-5-1, RAU 1463-16, RAU 1415-8-6-4-3-3, RAU 1428-7-3-6, RAU 1421-12-1-7-3, Prabhat followed by cluster VI contain 5 genotypes *viz.*, RAU 1421-12-1-7-4-3, RAU 1421-12-1-7-4-4, RAU 1421-15-3-2-5-7-3, Rasi and Vandana. Cluster II had 4 genotypes namely, RAU 1428-543-35-5-5, RAU 1426-43-2-5-4, RAU 1397-18-3-7-9-4-7 and Richaria whereas, cluster I, IV and V each comprised of 3 genotypes namely, RAU 1401-18-1-1-5, Rajendra Nilam and Rajendra Bhagwati (Cluster I), RAU 1397-25-8-1-2-5-4, RAU 1417-11-1-74-3-2 and MTU-1010 (Cluster IV) and RAU 96-P-1-2, Sahbhagi and Vandana (Cluster V).

Means of canonical variate (mean value of Z_1 , Z_2 , Z_3 and Z_4) have been presented in Table 2. The PCA scores for 32 genotypes plotted in graph to get the 2D (PCA I as X axis and PCA II as Y axis) and 3D (PCA I as X axis, PCA II as Y axis and PCA III as Z axis) scatter diagram (Fig. 1 and Fig. 2). The figure depicts spatial distance between genotypes as a measure for genetic divergence between them. Inter and intra cluster distances between different genotypes were shown in Table 4. Genetic divergence was found maximum between cluster V and VI followed by cluster IV and VI, cluster III and VI, cluster I and VI, cluster III and IV. On the basis of cluster distance from diversity study the genotypes which showed maximum divergence are Sahbhagi and RAU 1421-12-1-7-4-3. This suggest that genotypes belonging to clusters separated by high statistical distance should be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. Similar results were obtained in the findings of Thippani *et al.*, 2017.

K-cluster mean of principal component analysis for all the morphological characters and agrometeorological indices obtained are presented in Table 5. The individual cluster reflected superiority for various traits. Cluster I showed highest mean for number of tillers per plant (13.889), number of panicles per plant (10.556), heat use efficiency

Table 3. Distribution of thirty-two genotypes into different clusters based on K-mean cluster analysis

| Group K | Number of genotypes | Cluster Members |
|---------|---------------------|---|
| 1 | 3 | RAU 1401-18-1-1-5, Rajendra Nilam, Rajendra Bhagwati |
| 2 | 4 | RAU 1428-543-35-5-5, RAU 1426-43-2-5-4, RAU 1397-18-3-7-9-4-7, Richaria |
| 3 | 14 | RAU 1417-2-1-5-7-7, RAU 1415-35-76-9-5-3-4, RAU 1401-18-1-1, RAU 1421-15-3-2-5-3-7, RAU 1417-9-7-22-5-7-3, RAU 1451-66-1-1-5-1, RAU 1451-66-1-1-5-2, RAU 1416-4-2-5-2-2, RAU 1415-35-7-6-9-5-1, RAU 1463-16, RAU 1415-8-6-4-3-3, RAU 1428-7-3-6, RAU 1421-12-1-7-3, Prabhat |
| 4 | 3 | RAU 1397-25-8-1-2-5-4, RAU 1417-11-1-74-3-2, MTU-1010 |
| 5 | 3 | RAU 96-P-1-2, Sahbhagi, Vandana |
| 6 | 5 | RAU 1421-12-1-7-4-3, RAU 1421-12-1-7-4-4, RAU 1421-15-3-2-5-7-3, Rasi, Turanta |

Table 4. Intra and inter-cluster distances between different clusters

| | 1 Cluster | 2 Cluster | 3 Cluster | 4 Cluster | 5 Cluster | 6 Cluster |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| 1 Cluster | 55.271 | 73.23 | 134.088 | 236.084 | 147.265 | 360.826 |
| 2 Cluster | | 53.945 | 134.609 | 226.33 | 156.93 | 245.207 |
| 3 Cluster | | | 71.189 | 293.519 | 258.393 | 385.660 |
| 4 Cluster | | | | 126.563 | 163.918 | 488.990 |
| 5 Cluster | | | | | 44.157 | 513.979 |
| 6 Cluster | | | | | | 108.271 |

(1.761), relative water content (82.082) and grain yield per plant (16.138). Cluster II showed highest mean for photo-thermal index (29.797) whereas lowest mean value was observed for plant height (cm), number of tillers per plant (9.083), heat use efficiency (1.298) and grain yield per plant (11.273). Cluster III showed lowest mean value for traits viz., days to 50% flowering (71.714), days to physiological maturity (92.357), number of panicles per plant (6.905), growing degree days (2749.266), helio-thermal unit (14272.720), photo-thermal unit (35388.079) and relative temperature depression (20.590). Cluster IV showed highest mean for Critical temperature for reproductive stage (21.118) whereas, spikelet fertility (58.444) and 1000 grain weight (21.650) showed

lowest mean value. Cluster V showed highest mean for most of the traits viz., days to 50% flowering (98.111), days to physiological maturity (120.778), plant height (101.697), panicle length (24.651), 1000 grain weight (26.207), Growing degree days (3581.984), Helio-thermal unit (18666.206), Photo-thermal unit (45592.928), relative temperature depression (21.118) and lowest mean for critical temperature for reproductive stage (29.543). Cluster VI showed highest mean for spikelet fertility (87.333) whereas, lowest mean was observed for panicle length (21.483), photo-thermal index (29.382) and

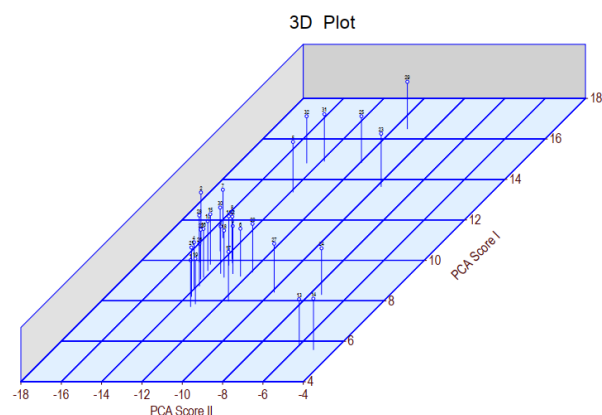


Fig. 1. Three-dimensional representation of rice genotypes showing divergence based on Principal Component Analysis

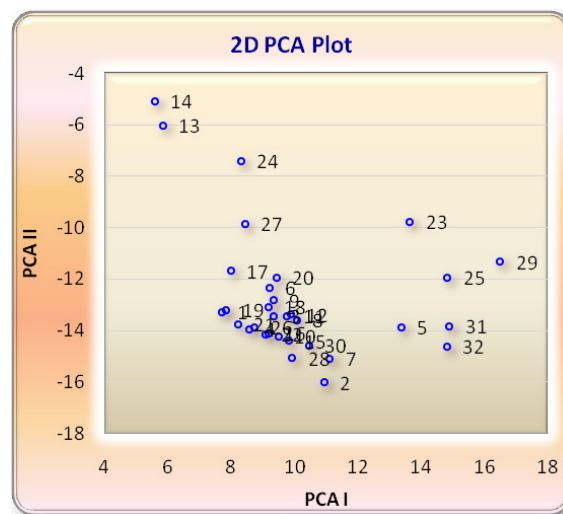


Fig. 2. Scatter diagram of PC I and PC II for morphological and agrometeorological traits of promising rice genotypes

Table 5. Cluster means of seventeen characters based on K-mean cluster analysis

| Clusters characters | I | II | III | IV | V | VI |
|---|-----------|-----------|-----------|-----------|-----------|-----------|
| Days to 50% Flowering | 81.778 | 76.000 | 71.714 | 78.111 | 98.111 | 74.333 |
| Days to Physiological maturity | 103.222 | 97.250 | 92.357 | 99.667 | 120.778 | 94.667 |
| Plant height (cm) | 96.982 | 85.995 | 86.851 | 86.099 | 101.697 | 87.768 |
| Panicle length (cm) | 24.480 | 21.839 | 21.968 | 22.457 | 24.651 | 21.483 |
| Number of tillers per Plant | 13.889 | 9.083 | 9.119 | 9.889 | 12.778 | 10.267 |
| Number of panicles per Plant | 10.556 | 7.167 | 6.905 | 7.556 | 9.556 | 7.733 |
| Spikelet fertility (%) | 83.778 | 78.000 | 82.952 | 58.444 | 83.222 | 87.333 |
| 1000 grain weight (g) | 24.211 | 23.113 | 24.542 | 21.650 | 26.207 | 24.164 |
| Growing degree days (Degree days) | 3059.770 | 2897.833 | 2749.266 | 2930.986 | 3581.984 | 2804.381 |
| Helio-thermal unit (Degree-days hours) | 15943.217 | 15105.963 | 14272.720 | 15293.876 | 18666.206 | 14569.065 |
| Photo-thermal unit (Degree-days hours) | 38997.960 | 37058.452 | 35388.079 | 37433.456 | 45592.928 | 35966.477 |
| Photo-thermal index (Degree-days day ¹) | 29.641 | 29.797 | 29.762 | 29.419 | 29.659 | 29.382 |
| Heat use efficiency (Kg ha ⁻¹ Degree-days) | 1.761 | 1.298 | 1.509 | 1.319 | 1.372 | 1.535 |
| Relative Temperature depression | 20.707 | 20.632 | 20.590 | 20.680 | 21.118 | 20.600 |
| Critical temperature for reproductive stage (° C) | 30.017 | 29.815 | 30.035 | 30.483 | 29.543 | 29.960 |
| Relative water content (%) | 82.082 | 72.556 | 67.212 | 66.619 | 75.497 | 66.328 |
| Grain yield per plant (g) | 16.138 | 11.273 | 12.350 | 11.584 | 14.752 | 12.917 |

relative water content (66.328). Clusters with desired mean may be used in hybridization segregants (Saraswathi *et al.*, 1996).

For the improvement of rice genotypes under direct seeded condition diverse parents could be selected based on genetic distance, K-cluster mean for different characters is presented in Table 5. Based on cluster mean, genotypes from cluster I can be selected for a greater number of tillers per plant, number of panicles per plant, heat use efficiency, relative water content and grain yield per plant. Cluster II can be selected for high photo-thermal index as well as genotypes from this cluster can be used for development of semi dwarf variety suitable under lodging conditions and excessive application of nitrogenous fertilizers. For development of early maturity cultivars with a greater number of panicles per plant genotypes from cluster IV can be selected. Similarly, Cluster V can be selected for high panicle length, 1000 grain weight, growing degree days, helio-thermal unit, Photo-thermal unit, relative temperature depression and low critical temperature at reproductive stage. Cluster VI is best suited for selection of genotypes for spikelet fertility.

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