Received: 18 Oct 2022 | Revised: 22 Dec 2022 | Accepted: 06 Jan 2023

Electronic Journal of Plant Breeding

Research Note

Multivariate analysis among advanced breeding lines of rice (*Oryza sativa* L.) under sub-tropical ecology of Jammu region of Jammu and Kashmir

Danish Mushtaq* and Bupesh Kumar

Division of Plant Breeding and Genetics, She-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Main Campus, Chatha, Jammu (J&K)-180009
***E-Mail:** khandayd2@gmail.com

Abstract
The present study aimed to determine the nature and extent of genetic divergence for agro-morphological and quality traits amongst advanced breeding lines of rice utilizing multivariate techniques. Based on the *inter se* D^2 values, breeding lines were grouped into six non-overlapping clusters, indicating presence of diversity amongst the lines. Cluster I and Cluster II were found to be the largest clusters consisting of 14 and 9 genotypes, respectively, while, the remaining four clusters were mono-genotypic. The maximum inter-cluster distance was observed between cluster II and VI, while the maximum intra-cluster distance was recorded for cluster II. Breeding lines present in cluster II were observed to have highest cluster means for traits *viz*., plant height, total number of tillers per plant, amylose content, grain yield per plant and grain yield per plot indicating its superiority over rest of the clusters. Traits including grain yield per plot, grain yield per plant, days to maturity, 1000-grain weight, total number of tillers per plant and panicle length were observed to be the major contributors to genetic divergence. Principal component analysis extracted six principal components of which first five components *viz*., PC-I to PC-IV had eigen scores greater than one. This suggested that traits within these axis were of importance. Principal component analysis revealed that the traits *viz.,* number of effective tillers per plant, grain yield per plot, plant height, panicle length and days to 50 per cent flowering contributed maximum towards genetic diversity.

Keywords: Rice, Genetic diversity and PCA analysis

Rice (*Oryza sativa* L.) is the principal cereal crop, next to wheat in terms of global cultivated area. It is the staple food of more than half of the world's population. In addition to calories, rice is a good source of magnesium, phosphorus, manganese, selenium, iron, folic acid, thiamine and niacin; but it is low in fibre and fat (Fukagawa and Ziska*,* 2019). In India, rice is cultivated over an area of about 45.07 million hectares with production and productivity of 122.27 million tonnes and 2.71 tonnes per hectare respectively (Anonymous, 2022), while in the Union Territory of Jammu and Kashmir, it is cultivated over an area of 267.58 thousand hectares with production and productivity of 5186 thousand quintals and 21.74 quintals per hectare respectively (Anonymous, 2022). Rice is unique in terms of variability and adaptability having multitude of forms of cultivated and wild relatives and which is cultivated from sea level to higher elevations in hills. The availability of significant genetic diversity in the parents is the most important pre-requisite for hybridization and a successful breeding programme which in turn helps in developing improved rice varieties having production potential and adapted to various agro-climatic situations. A quantitative assessment of genetic diversity directs breeders in selection of suitable parents

https://doi.org/10.37992/2022.1304.179

to get preferred recombinants in segregating generations. Hybrids with high heterosis are typically derived from parental genotypes differing in common ancestry, ecotype, geographic origin, and so on. Morphological, biochemical and DNA markers can be used to assess genetic diversity within breeding populations. However, traditionally it is assessed using the D^2 approach based on morphological features. This approach gives a measure of the proportional contribution of different traits to diversity both within and across clusters and genotypes selected from highly divergent clusters are likely to yield heterotic hybrids and considerable heterogeneity in segregating generations. While D^2 analysis provides the *inter se* genetic distance between any two genotypes, clustering by Tocher's method groups the genotypes into various clusters so that genotypes belonging to different clusters could be attributed to be diverse in nature. Present study attempted to quantify the genetic diversity among 27 advanced breeding lines of rice for agro-morphological and quality traits using D^2statistics (Mahalanobis, 1928), identify promising parents for hybridization and to have insight into the traits of importance based on principal component analysis.

Twenty seven advanced and stable breeding lines of rice available with the Division of Plant Breeding and Genetics were evaluated for agro-morphological and quality traits so as to assess diversity among them for planning a hybridization programme. Experimental material was evaluated in Randomized Complete Block Design with three replications at Research Farm of the Division of Plant Breeding and Genetics, Faculty of Agriculture, SKUAST-J, Main Campus, Chatha, Jammu during *kharif* 2020. The average rainfall recorded was rainfall.6 mm while, minimum and maximum temperatures ranged from 9.20°C (November) to 36.90°C (March and June). All the recommended cultural practices were followed as per schedule to provide a favorable environment for crop growth. Observations on different agro-morphological and quality characteristics *viz.*, plant height (cm), total number of tillers per plant, number of effective tillers per plant, panicle length (cm), 1000- grain weight (g) and grain yield per plant (g) were recorded on five random plants from each replication, while observations *viz.*, days to 50 *per cent* flowering, days to maturity and grain yield per plot (kg) were taken on plot basis. Grains of each line were dehulled for grain quality assessment such as length and breadth of kernel, length-breadth ratio and amylose content respectively.

Analysis of Variance (ANOVA) was conducted as per RCBD following Panse and Sukhatme (1967). Wilk's criterion was assessed before undertaking the analysis of diversity. Genetic diversity was determined by employing the D^2 statistic given by Mahalanobis (1928) and clustering of genotypes was done following Tocher's method as described by Rao (1952). Principal component analysis was done by the method explained by Harman (1976).

ANOVA (**Table 1**) revealed presence of significant genetic variability in the set of 27 advanced breeding lines for all the agro-morphological and quality traits. The presence of considerable amount of genetic variation within the advanced breeding lines might be due to the inherent differences in the parents. The findings of Sarwar *et al.* (2015); Konate *et al.*(2016) and Dhakal *et al.*(2021) are also in agreement with the findings of the present study.

On the basis of clustering pattern as revealed by Tocher's method (Rao, 1952) the 27 entries were grouped into six non-overlapping clusters (**Table 2 and Fig. 1**) indicating the presence of considerable amount of genetic diversity among the advanced breeding lines of rice. Similar clustering pattern was also reported by Manohara and Singh, (2013); Dubey *et al.* (2018); Ranjith *et al.* (2018) and Lakshmi *et al.* (2022). The diversity pattern revealed that out of the six clusters, the first two clusters were multi-genotypic consisting of 14 and nine genotypes respectively, while rest of the four clusters were mono-genotypic. The maximum number of lines were reported in clusters (I and II). On the other hand, it was also observed that some of the advanced breeding lines originating from a single source were dispersed through multiple clusters indicating the presence of a significant amount

Table 1. Analysis of variance for agro-morphological and quality traits in advanced breeding lines of rice

Source of variation	Degrees of freedom	Days to 50% flowering (no)	PH (cm)	Total number of tillers per plant	Number of effective tillers per plant	DTM	PL (cm)	1000 grain weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Amylose content (%)	Grain yield per plant (g)	Grain yield per plot (kg)
Replication	2	174.16	197.05	9.32	5.69	812.30	17.40	60.15	16.75	0.37	2.30	0.80	33.38	0.30
Breeding lines	26	140.73**	370.99**	33.67**	25.14**	131.37**	22.36**	12.88**	5.74**	0.22**	0.85*	58.80**	41.67**	0.36**
Error	52	37.23	21.82	4.60	3.78	43.38	3.97	4.10	2.03	0.09	0.46	0.08	9.02	0.07

** and * represents significance level at 1 % and 5 %

* PH: Plant height, DTM: Days to Maturity, PL: Panicle length

Table 2. Allocation of experimental material in various clusters

Cluster Number	Number of advanced breeding lines	Description of advanced breeding lines
I	14	SJR-103-2-2, SJR-103-2-2, SJR-103-4-1, SJR-103-4-1, SJR-108-1-2, SJR-120-2-1, SJR-121-2-2, SJR-121-6-1, SJR-122-1-1, SJR-122-2-1, SJR-123-2-1, SJR-103-2-3, SJR-92-2-1, SJR-82-2-3
II	9	SJR92-2-2, SJR-98-2-1, SJR-121-5-1, SJR-49-1-1-2, SJR-81-1-1, SJR-76-1-1, SJR-74-1-1, SJR-102-4-1, SJR-72-1-1
III	1	SJR-49-1-1-2
IV	1	SJR-82-4-1
V	1	SJR-121-6-2
VI	1	SJR-123-2-2

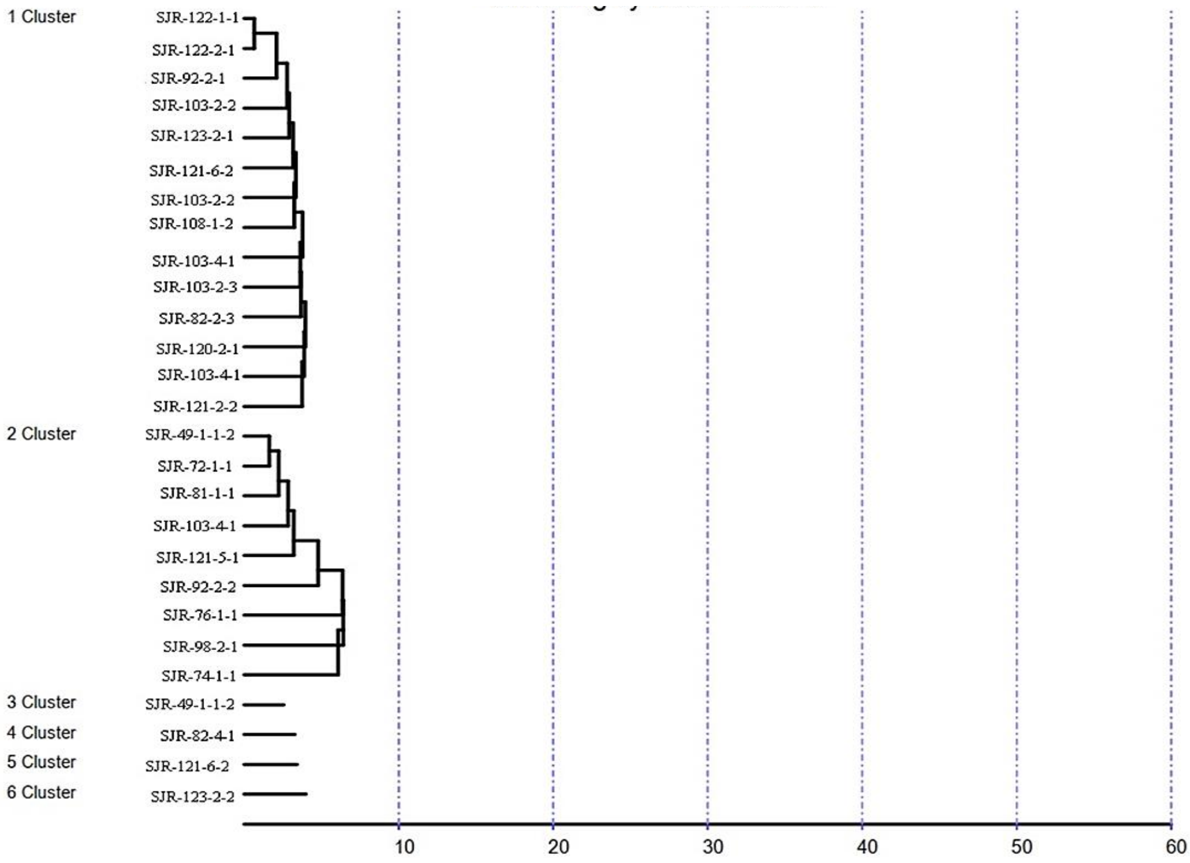

Fig. 1. Clustering behaviour among advanced breeding lines (Tocher's method)

of diversity within the segregants. The diversity among the advanced breeding lines of common origin may arise due to diversity of parents and selection pattern. The maximum inter-cluster distances (**Table 3 and Fig. 2**) were reported between cluster II and cluster VI (42.41), indicating the presence of highly diverse breeding lines in both the clusters, while a minimum inter-cluster distance was recorded between cluster III and cluster V (10.35) indicating genotypes in these clusters are relatively less diverse. The maximum intra-cluster distance was reported for cluster II (15.98) indicating the presence of a significant amount of diversity among the genotypes in this cluster. The advanced breeding lines of rice belonging to the most diverse clusters based inter-cluster distances can be utilized as parents in hybridization programmes to get a wide range of variability, transgressive

Table 3. Intra (diagonal) and inter cluster distances

Cluster	I	II	III	IV	V	VI
I	10.60	17.66	14.97	13.50	15.59	21.52
II		15.89	28.12	27.88	30.60	42.41
III			0.00	12.71	10.35	21.81
IV				0.00	14.60	24.71
V					0.00	10.69
VI						0.00

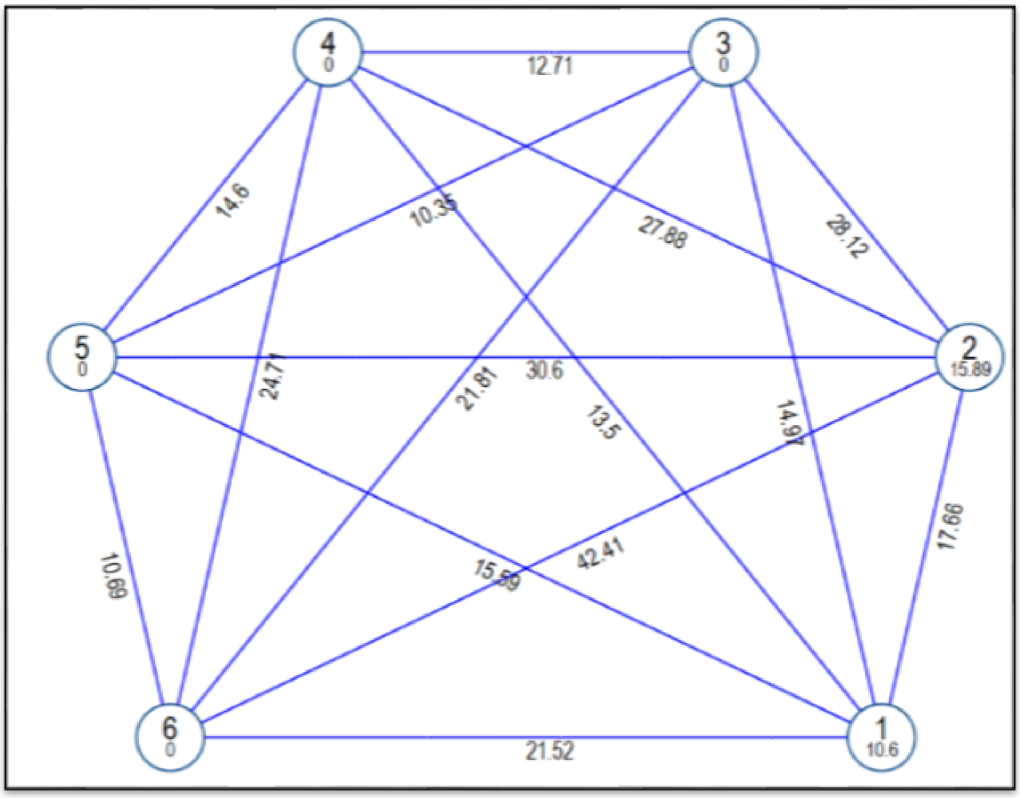

Fig. 2. Mahalanobis euclidean distance (Not to the scale)

segregants and desirable heterotic combinations. A similar recommendation was also proposed by Murthy and Arunachalam (1996) and Rahman, (1997). While selecting the parents for the hybridization programme based on the genetic distance, *per se* performance should not be overlooked. Cluster means for various traits are presented in (**Table 4**). The maximum cluster mean for characters *viz*., plant height (127.36), total number of tillers per plant (15.44), grain yield per plant (24.18) and grain yield per plot (1.78), were reported in cluster II, reflecting its superiority over rest of the clusters. Further perusal of experimental findings confirmed that traits *viz*., grain yield per plot, grain yield per plant, 1000 grain weight, days to maturity, total number of tillers per plant and panicle length contributed maximum toward genetic divergence (**Table 5**). The contribution of these traits in total towards genetic divergence is 84.92 %. The traits contributing maximum towards genetic divergence (D^2 value) need to be given top priority during selection and hybridization programmes (De *et al.,* 1988).

Principal component or canonical root analysis revealed the genetic divergence in advanced breeding lines of rice. The cumulative variance of 81.24 per cent (**Table 6 and Fig. 3**) was depicted by the first five vectors with eigen value greater than one, suggesting that identified agro-morphological and quality traits within the axis demonstrated potential effect on the development

Table 4. Cluster means among agro-morphological and quality traits

Cluster No.	Days to 50% flowering	PH (cm)	Total No. of tillers per plant	No. of effective tillers per plant	DTM	PL (cm)	1000 grain weight (g)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Amylose (%)	Grain yield per plant (g)	Grain yield per plot (kg)
Cluster I	93.83	113.86	12.54	11.22	133.07	27.26	27.54	10.06	2.31	6.03	19.05	23.18	1.68
Cluster 2	92.78	127.36	15.44	13.41	135.00	28.35	28.25	9.58	2.21	5.85	24.02	24.18	1.78
Cluster 3	85.67	100.56	8.40	6.33	131.67	22.77	22.77	9.61	1.84	5.58	22.31	18.79	1.25
Cluster 4	106.33	104.59	11.27	10.27	142.67	29.33	23.33	10.04	2.05	6.04	19.23	21.74	1.65
Cluster 5	91.00	97.02	13.53	12.37	125.00	25.30	28.27	11.00	2.00	6.50	21.25	18.55	1.73
Cluster 6	95.00	94.75	12.80	14.33	123.00	23.21	28.53	8.60	2.23	5.42	20.01	22.15	1.69

Table 5. Contribution by individual trait towards total genetic divergence

Agro-morphological and quality traits	Times ranked 1st	Contribution towards genetic divergence
Days to 50 % flowering	1	0.28 %
PH (cm)	11	1.98 %
Total number of tillers per plant	35	9.97 %
Number of effective tillers per plant	5	1.42 %
DTM	36	10.26 %
PL (cm)	29	8.26 %
1000 grain weight (g)	55	15.67 %
Kernel length (mm)	18	5.13 %
Kernel Breadth (mm)	17	4.84 %
L/B ratio	8	2.28 %
Amylose (%)	6	1.15 %
Grain yield per plant (g)	63	17.95 %
Grain yield per plot (kg)	75	20.81 %

Table 6. Contribution of first six component axis to total genetic variation in advanced breeding lines

Agro-morphological and quality traits	PC-I	PC-II	PC-III	PC-IV	PC-V	PC-VI
Days to 50 percent flowering	0.21	0.32	0.25	0.26	0.13	0.62
PH (cm)	-0.37	0.37	-0.15	-0.01	0.18	0.28
Total number of tillers per plant	0.26	-0.17	-0.37	0.07	0.58	0.02
Number of effective tillers per plant	0.45	-0.16	-0.09	-0.23	0.08	0.36
DTM	0.21	0.2	0.31	0.05	0.45	-0.51
PL(cm)	-0.23	0.16	0.55	-0.29	-0.04	0.04
1000 grain weight (g)	0.15	0.1	-0.29	-0.63	-0.29	0.005
Kernel length (mm)	0.03	-0.41	0.35	-0.29	0.18	-0.04
Kernel breadth (mm)	0.35	0.35	0.02	0.17	-0.2	-0.13
L/B ratio	0.13	-0.45	0.33	0.14	-0.15	0.26
Grain yield per plant (g)	0.22	0.31	0.15	-0.44	0.22	0.07
Grain yield per plot (Kg)	0.45	0.1	0.08	0.16	-0.38	-0.18
Eigene value (Root)	3.21	2.33	1.87	1.26	1.06	0.71
Variance (%)	26.75	19.49	15.6	10.55	8.89	5.93
Cummulative variance (%)	26.75	46.25	61.85	72.41	81.3	87.24

* PH: Plant height, DTM: Days to Maturity, PL: Panicle length

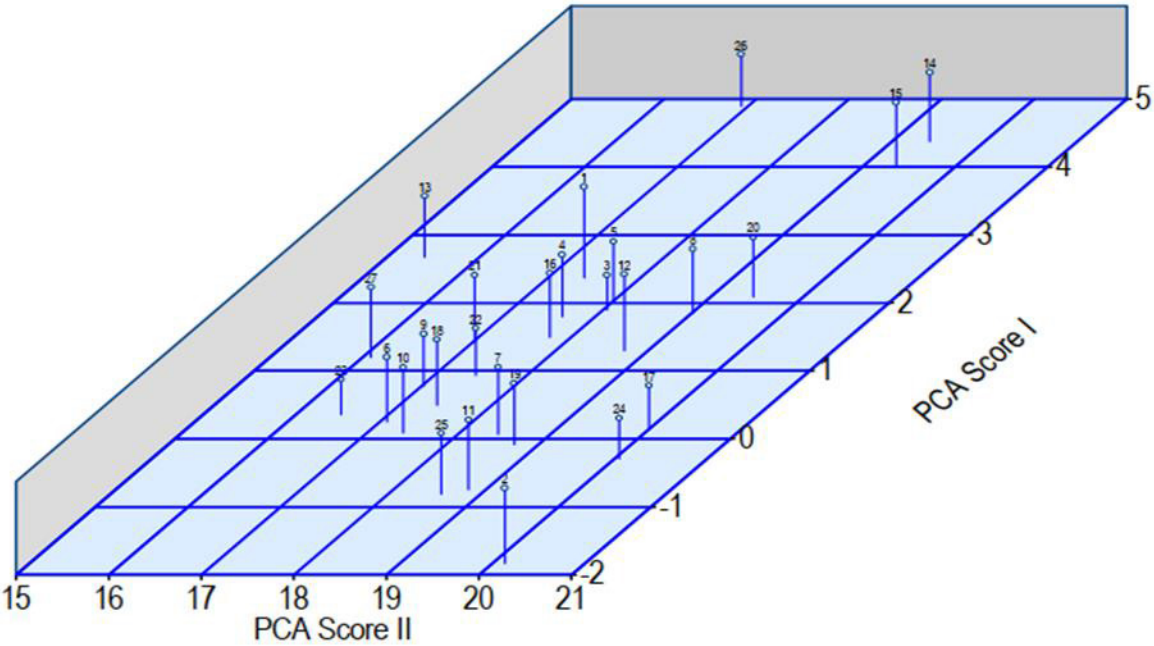

Fig. 3. Principal component scatter plot

of phenotype of the advanced breeding lines of rice. In the present study, Clifford and Stephenson's (1975) criterion was considered which suggested that only the first three canonical vectors or principle components play a crucial role in depicting the patterns of genetic variations among breeding material. Similar criteria were also adopted by Guei *et al.* (2005). Results of PCA revealed that the first three components accounted for 61.85 per cent of total genetic variation, portraying intrinsic structure of the variables being analysed. Similar trends in principal components were also observed by Vishnu *et al.* (2014); Ravi Kumar *et al.* (2015) ; Gour *et al.* (2017) and Sheela *et al.*(2020) for dissecting phenotypic variation within a breeding population and classifying genotypes based on potential morphological and quality traits. The first principal component (PC-I) accounted for 26.75 per cent of total genetic variation present with in the advanced breeding lines of rice (**Table 6**). Traits such as grain yield per plot and number of effective tillers per plant were reported to have maximum (0.45) contribution to genetic variation among all agro-morphological and quality traits under investigation followed by kernel breadth (0.35), total number of tillers per plant (0.26), grain yield per plant (0.22) and days to maturity (0.21). However, plant height (-0.37) and panicle length (-0.23) were reported to contribute to total genetic variation negatively in PC-1. The principal component second (PC-II) was reported to account for 19.49 per cent of total genetic variation. In PC-II, plant height (0.37) was reported to have maximum contribution towards genetic variation followed by kernel breadth (0.35), days to 50 per cent flowering (0.32) and grain yield per plant (0.31) respectively. However, traits *viz.,* number of effective tillers per plant (-0.16), total number of tillers per plant (0.17), kernel length (-0.41) and L/B ratio (-0.45) were reported to negatively add to total genetic variation in PC- II respectively. Principal component third (PC-III) accounted for 15.60 per cent of total genetic variation available within advanced breeding lines. In this component, traits *viz.,* panicle length (0.55), kernel length (0.35), L/B ratio (0.33) and days to maturity (0.311) were reported to have maximum contribution towards total genetic variation. However traits *viz.,* plant height (-0.15), total number of tillers per plant (-0.37) and number effective tillers per plant (-0.09) were reported to negatively contribute to total genetic variation. The fourth principal component was reported to account for 10.55 per cent of total genetic variation. In PC-IV traits which were reported to share maximum contribution to total genetic variation were, days to 50 *per cent* flowering (0.26) followed by kernel breadth (0.17), grain yield per plot (0.16) and L/B ratio (0.014). Traits *viz.,* plant height (-0.01), number of effective tillers per plant (-0.23), panicle length (-0.63), kernel length (-0.29) and grain yield per plant (-0.44). Principal component five (PC- V) was reported to account for 8.89 per cent of total genetic variation. In this component major contributors to total genetic variation were total number of tillers per plant (0.58) followed by days to maturity (0.45) and grain yield per plant (0.22). However, traits *viz.,* panicle length (-0.04), 1000 grain weight (-0.29), kernel breadth (-0.20) and grain yield per plot (-0.38) were reported to negatively contribute to the genetic variation accounted by this component. Among six principal components or vectors first five components together were reported to account for 81.30 per cent of total genetic variation. Sathish and Senapati (2017) also reported similar trends while investigating advanced breeding lines of rice grown in low land conditions of West Bengal. Mahendran *et al.* (2015) suggested that potential morphological and quality traits which remain side by side in various principal components and contributing maximum towards total available genetic variation with in breeding population have likelihood to remain together and provide ample scope and opportunity to be utilized in hybridization programmes.

From the foregoing discussion, it was apparent that there is possibility for utilizing the advanced breeding lines under study to obtain transgressive segregants and heterotic hybrids. Parents for hybridization should be chosen from different clusters based on their *inter se* distance as well as *per se* performances. From the present study it was observed that crosses between genotypes from cluster II and those from cluster III, IV, V and VI are likely to yield high heterosis and generate potential recombinants. Based on mean performance and their *inter se* distances, the promising breeding lines identified are SJR-92-2-2, SJR-98-2-1, SJR-121-5-1, SJR-49-1-1-2 from cluster II for total number of tillers per plant, number of effective tillers per plant, aroma and SJR-123-2-2 from cluster VI for earliness and grain yield per plant respectively. These breeding lines can be utilized in to multiple crossing programmes to yield desirable segregants as well as in bringing together different desirable traits into the common genetic background. Further results of the principal component or canonical vectors analysis indicated the potential traits in the group of genotypes explaining the variation were number of effective tillers per plant, grain yield per plot, plant height, panicle length and days to 50 per cent flowering. Consideration of these traits will ensure efficient and goal-oriented improvement based on the pool of genotypes under study.

REFERENCES

Anonymous, 2022. Digest of statistics. Directorate of economics and statistics, Govt. of Jammu and Kashmir.

Anonymous, 2022. ICAR-National Rice Research Institute Cuttack, India.

Clifford, H.T. and Stephenson, W. 1975. An Introduction to Numerical Classification. Academic Press, London, pp. 229. [Cross Ref]

De, R.N., Seetharaman, R., Sinha, M.K. and Banerjee, S.P. 1988. Genetic divergence in rice. *Indian Journal of Genetics and Plant Breeding*, **48**(2): 189-194.

Dhakal, K., Yadaw, R.B., Baral, B.R., Pokhrel, K.R. and Rasaily, S. 2021. Agro-morphological and genotypic diversity among rice germplasms under rainfed low land condition. *AGRIVITA, Journal of Agricultural Science*, **43**(3): 466-478. [Cross Ref]

Dubey, K., Dwivedi, D.K., Singh, A. and Rampreet. 2018. Genetic divergence studies among rice genotypes. *Journal of Pharmacognosy and Phytochemistry,***2**:153-155.

Fukagawa, N.K. and Ziska, L.H. 2019. Rice: Importance for global nutrition. *Journal of nutritional science and vitaminology*, **65**:2-3. [Cross Ref]

Gour, L., Maurya, S.B., Koutu, G.K., Singh, S.K., Shukla, S.S. and Mishra, D.K. 2017. Characterization of rice (*Oryza sativa* L.) genotypes using principal component analysis, including scree plot and rotated component matrix. *International Journal of Chemical Studies*, **5**(4): 975-983.

Guei, R.G., Sanni, K. A. and Fawole, A.F.J. 2005. Genetic diversity of rice (Oryza sativa). Agronomy Africaine, **5**:17–28.

Harman, H.H. 1976. Modern factor analysis. 3nd Ed. University of Chicago Press,Chicago, pp. 376.

Konate, A.K., Zongo, A., Kam, H., Sanni, A. and Audebert, A. 2016. Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits. *African Journal of Plant research,***11**(35): 3340-3346. [Cross Ref]

Lakshmi, M., Shanmuganathan, M., Jeyaprakash, P. and Ramesh, T. 2022. Genetic variability and diversity analysis in selected rice (*Oryza sativa* L.) varieties. *Electronic Journal of Plant Breeding,* **13**(3): 959-966. [Cross Ref]

Mahalanobis, P.C. 1928. On the need for standardisation in measurements on the living. *Biometrika*, **20**(2): 1-31. [Cross Ref]

Mahendran, R., Veerabadhiran, P., Robin, S. and Raveendran, M. 2015. Principal component analysis of rice germplasm accessions under high temperature stress. *International Journal of Agricultural Science and Research*, **5**(3), 355-359.

Manohara, K.K. and Singh, N.P. 2013. Genetic divergence among rice landraces of Goa. *ORYZA-An International Journal on Rice,* **5**(2):100-104.

Murthy, B.R. and Arunachalam,V. 1996. The nature of genetic divergence in relation to breeding system in some crop plants. *Indian Journal of Genetics*, **26**:188-198.

Panse V.G. and Sukhatme, P.V. 1967. Statistical methods for Agriculture workers. Indian council of Agriculture, New Delhi.

Rahman, M., Acharya, B., Sukla, S.N. and Pande, K. 1997. Genetic divergence in low land rice genotypes. *Oryza,* **34**(3): 209-212.

Ranjith, P., Sahu, S., Dash, S.K., Bastia, D.N. and Pradhan, B.D. 2018. Genetic diversity studies in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry,***7**(2): 2529-2531.

Rao, C.R. 1952. Advanced statistical methods in biometric research.

Ravikumar, B.N.V.S.R., Naga Lumari, P., Rao, V. R. M. P., Girija, R. P.V., Satyanarayana, N., Chamundeswari, K., Mohan V., Suryanarayana, Y., Bharathalakshmi, M. and Reddy, A.V. 2015. Principal component analysis and character association for yield components in rice (*Oryza sativa* L.) cultivars suitable for irrigated ecosystem. *Current Biotica*, **9**(1): 25-35.

Sarwar, G., Hossain, M.S., Harun-Ur-Rashid, M. and Parveen, S. 2015. Assessment of genetic variability for agro-morphological important traits in Aman rice (*Oryza sativa* L.). *International Journal of Applied Sciences and Biotechnology*, **3**(1):73-79. [Cross Ref]

Sathish, V. and Senapati, B. 2017. Principal component analysis of morphological and yield attributing traits in advanced breeding lines of rice grown at rainfed shallow lowland condition of West Bengal. International journal of biological research and *development,* **7**(3):1-6. [Cross Ref]

Sheela, K.S., Robin, S. and Manonmani, S. 2020. Principal component analysis for grain quality characters in rice germplasm. *Electronic Journal of Plant Breeding,* **11**(01):127-131. [Cross Ref]

Vishnu, V.N., Robin S., Sudhakar, D., Raveendran, M., Rajeswari, S. and Manonmani, S. 2014. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. *Indian Journal of Science and Technology*,**7**(10): 1555-1562. [Cross Ref]