Journal of Plant Genetics and Breeding Research Article

Open Access

Keywords: Rice breeding lines; Clusters and principal component analysis

Introduction

Rice (Oryza sativa L.) is a major and vital cereal grain, next only to wheat in terms of global cultivated area. It is the staple food of more than half of the population of world. 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 bre and fat (Fukagawa and Ziska, 2019). In India rice is cultivated over an area of about 45.07 million hectares in India with production and productivity of 122.27 million tons and 2.71 tons per hectare respectively (Anonymous, 2022), while in Union Territory of Jammu and Kashmir it was 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 one among few cereal crops with large amount of genetic variation and is being cultivated from sea level to higher elevations. e availability of signi cant genetic diversity for key characteristics in the parents being hybridized is the most important pre-requisite for starting a successful breeding operation which in turn helps in realizing the true production potential for developing improved rice varieties adapted to various agro-climatic zones [3-5].

A quantitative assessment of genetic diversity directs breeders towards speedy progress in breeding programs to get preferred recombinants in segregating generations. Hybrids with high heterosis are typically derived from parental genotypes di ering in common ancestry, ecotype, and geographic origin and so on. Morphological, biochemical and DNA markers can be used to assess genetic diversity and maximum temperature ranged from 9.20°C (November) to 36.90°C (March, June). All the recommended cultural practices were followed as per schedule to provide favorable environment for crop growth. Observations on di erent agro-morphological and quality characteristics viz., plant height (cm), total number of tillers per plant, number of e ective tillers per plant, panicle length (cm), 1000 grain weight(g) and grain yield per plant (g) were recorded on ve randomly chosen plants from each replication to identify the type and degree of genetic divergence in the experimental material, while as some of observations viz., days to 50 per cent owering (no), days to maturity (no) and grain yield per plot (kg) were taken on per plot basis [11]. Grains of each line were dehulled for grain quality assessment such as length and breadth of kernel, length-breadth ratio and amylose content respectively.

Genetic diversity among advanced breeding lines of rice was determined by employing the D^2 statistic given by Mahalanobis in the year 1936 and principal component analysis was determined by method explained by Harman (1976) [12] .

Results and discussions

Analysis of variance (Table 1) revealed presence of signi cant di erences among advanced breeding lines of all the agromorphological and quality traits viz., days to 50 per cent owering, plant height, total number of tillers per plant, number of e ective tillers per plant, days to maturity, panicle length, 1000 grain weight, kernel length, kernel breadth, length-breadth ratio, amylose, grain yield per plant and grain yield per plot. e presenceof enormous amount of genetic variation variability within advanced breeding lines may be due to inherent di erences in the parents being hybridized. Sarwar et al., 2015; Konate et al., 2016 and Dhakal et al., 2021 ndings are in agreement with the ndings of the present study [13].

On the basis of clustering pattern as revealed by Tocher's method (Rao, 1952) advanced breeding lines were categorized into six (6) non overlapping clusters (Table 2 and Figure 1) indicating presence of enormous amount genetic diversity among advanced breeding lines of rice, similar clustering pattern was reported by (Manohara et al., 2013; Dubey et al., 2018 and Ranjith et al., 2018). Tocher's approach was used to arrange the advanced breeding linesinto six clusters based on average D^2 values [14]. Further perusal of experimental results reported that out of six clusters, the rst two clusters were multi-genotypic consisting of fourteen (14) and nine (9) genotypes respectively, while rest four clusters were mono-genotypic consisting of single genotype only. e maximum number of advanced breeding lines were reported in clusters (I and II), because most these lines are sister lines of each other as depicted by their pedigree record. e advanced breeding lines came from single source and were dispersed through multiple

clusters indicating the presence of signi cant amount diversity within the genotypes. e diversity among the advanced breeding lines of common origin may arise due to factors like heterogeneity, genetic architecture and earlier selection for speci c trait [15]. e maximum inter-cluster distances (Table 3 & Figure 2) were reported between cluster II and cluster VI (42.41), indicating presence of highly diverse advanced breeding lines in both the clusters, while as minimum intercluster distance was recorded between cluster III and cluster V (10.35) indicating genotypes in these clusters are closely related. e maximum intra-cluster distance was reported for cluster II (15.98) indicating the presence of signi cant amount diversity among the genotypes in this cluster. e advanced breeding lines of rice belonging to most diverse clusters based on intra and inter cluster distances can be utilized as parents in hybridization programmes to get wide range of variability, transgressive segregants and desirable heterotic combinations. A similar recommendation was proposed by (Murthy and Arunachalam, 1996 and Rahman, 1997) [16]. Cluster means (Table 4) for various agromorphological and quality traits revealed the presence of enormous amount of the genetic variability for all the traits. e 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, re ecting its superiority over rest of the clusters. Further perusal of experimental ndings con rmed 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). e contribution of these traits in total towards genetic divergence is 84.92 %. ϵ 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 that the genetic divergence in advanced breeding lines of rice and cumulative variance of about 81.24 per cent (Table 6 & Figure 3) as depicted by the rst ve vectors with Eigen value greater than one, suggesting that identi ed agro-morphological and quality traits with in the axis demonstrated potential e ect on the development of phenotype of the advanced breeding lines of rice [17]. In present study Cli ord and Stephenson (1975) criterion was considered which suggests that only rst three canonical vectors or principle components play crucial role in depicting the patterns of genetic variations among breeding material, similar criterion was also adopted by Guei et al. (2005). Results of PCA revealed that rst three components accounted for 61.85 per cent of total genetic variation, portraying intansic structure of variables being analysed. Similar trends in principal components were also observed by Vishnu et al. (2014), Ravi Kumar et al. (2015) and Gour et al. (2017) respectively for dissecting phenotypic variation with in breeding population and classifying genotypes based on potential morphological

Cluster No.	Days to 50%	PH	Total No. οf	No. of	DTM	PL (cm)	1000	Kernel length	Kernel breadth	L/B	Amylose	Grain	Grain
	fowering	(cm)	tillers	efective			grain weight	(mm)	(mm)	ratio	(%)	vield per	vield per
			per plant	tillers per plant			(g)					plant	plot
												(g)	(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	28.35	28.25	9.58	2.21	5.85	24.02	24.18	1.78
Cluster 3	85.67	100.56	8.4	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	97.02	13.53	12.37	125	25.3	28.27	11	2	6.5	21.25	18.55	1.73
Cluster 6	95	94.75	12.8	14.33	123	23.21	28.53	8.6	2.23	5.42	20.01	22.15	1.69

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

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

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 vetors rst ve components all together were reported to account for 81.30 % total genetic variation. Sathish and Senapati (2017) also reorted similar trends while investigating advanced breeding lines of rice grown in low land conditions of West Bengal. Mahendran et al. (2013) 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 [20].

From the foregoing discussion, it is apparent that there is a possibility for transferring the genes available within these advanced breeding lines of rice to create transgressive segregants with desired traits through selection and hybridization. Parents for hybridization should be chosen from separate clusters with a large inter and intracluster distance and the chosen parents should perform exceptionally well for the characters that contribute the most to genetic divergence. Mono-genotypic clusters with a single genotype could be used in hybridization programmes to exploit heterosis predominantly as testers. However, it is clear from the present study that crosses between genotypes from cluster II and those from cluster III, IV, V and VI are likely to express or demonstrate a high percentage of heterosis and generate potential recombinants with desirable traits. Further results of principal component or canonical vectors analysis classi ed the total genetic variation within advanced breeding lines by considering potential traits such as number of e ective tillers per plant, grain yield per plot, plant height, panicle length and days to $\overline{50}$ per cent owering, because these agro-morphological traits account for maximum contribution towards genetic diversity among advanced breeding lines. Selection for these traits will ensure efficient and goal oriented improvement of rice cultivers.

References