Genetic Attributes for Selection and Assessment of Yield Enhancement in Paddy (*Oryza sativa* L.)

Abstract

The present investigation was conducted in the Agricultural and Horticultural Research Station, Kathalagere. The experiment comprised sixty-seven advanced breeding lines of paddy. The experiment was conducted in three replications with 4mx3m of plot size. The observations are recorded on days to fifty per cent flowering, Days to maturity, Plant Height(cm), Panicles per sqm, Grain yield per plot(kg) and Grain yield per hectare(Kg). The data is subjected to analysis for genetic variability and diversity parameters (Key factors of plant breeding).Higher Genetic coefficient of variability (GCV) and Phenotypic coefficient of variability (PCV)are Days to fifty per cent flowering, Days to maturity, Plant height(cm), Panicles per square meter and grain yield per plot (Kgs) should be considered at the time of selecting the genotypes/varieties/breeding lines for progressing and prosperingin the yield and yield contribution towards the varietal performance. Genetic diversity studies proved that the traits viz., days to 50 per cent flowering, Days to maturity, Panicles per square meter, Plant height and Grain yield per plot are prompt traits that contributed maximum divergence to the genotypes.Some clusters are composed of superior genotypes that may contribute to the several crossing studies to improvethrough transgressive segregants with high genetic yield potential and early maturity.

Keywords:GCV,PCV, Diversity, Variability

Introduction:

"Rice (*Oryza sativa* L.) is a cultivated crop belonging to the family Gramineae, sub-family Bamboosoideae and tribe Oryzeae" [1]. "It is diploid with twelve chromosomes (2n=24). In Nepal and Bhutan, rice is grown as low as three meters below sea level" [2]. For a significant portion of the global population, particularly in the Asian region, it is the most commonly consumed staple food and one of the main food crops in the globe. After sugarcane and maize, it is the agricultural product whose output ranked third globally in 2014 with 741.5 million tons. However, it is the most significant grain in terms of nutrient and calorie intake, providing more than one-fifth around the globe [3]. According to Hossain *et al*. (2015), rice comprises 75% protein, 12% water, and 75–80% starch [4]. Furthermore, animal feed is produced using rice in a large number of nations worldwide [5].

For over half the world's population, rice is the primary food. Rice, also known as the "grain of life," is a staple cereal consumed by almost 90% of people in Asia. Nearly 94% of the world's rice is produced in Asia, where the majority of the crop is grown. During 2020–21, India produced 124.37 million tonnes of rice, covering an area of around 45.8 million hectares. About 2.04 million hectares and 6.9 million tonnes of rice were produced and grown in Tamil Nadu, respectively [6]. The growing population requires rice fields to be more productive, and high-yielding cultivars can help achieve this goal.For the study, specific cultivars with varying origins were used, and variability was evaluated to facilitate trait selection for increased production.

Because offspring from various parents exhibit higher heterosis and offer a wide range of variability in subsequent generations, genetic diversity is more significant in plant breeding. In addition to causing genetic variation, diversity allows for fresh gene recombination within the gene pool. Gaining further insight into the genetic diversity of closely related crop types is essential to ensuring the efficient use of genetic resources. To determine the genotypes that differ genetically, the current investigation was conducted with the aforementioned goals in mind.

Material and Methods: The experimental material comprised sixty-sevenadvanced breeding lines of rice (*Oryza sativa* L.) grown in RCBD at Agricultural and Horticultural Research Station, Kathalagere, Chennagiri, Davanagere, Karnataka, India, during Kharif-2019. “The recommended package of practice and plant protection measures are followed to raise a normal crop. Observations on six different quantitative characters viz., days to 50% flowering, days to maturity, plant height, number of tillers per square meter, grain yield per plot and grain yield per hectare were recorded for each replication of each genotype except for days to 50% flowering and days to maturity where data is recorded based on plot basis during various phenophase of the crop. Mean values of 5 randomly selected plants of 3 replications for each genotype were averaged and expressed as the mean of the respective character and considered by RCBD for each of the characters separately as per standard statistical procedure” given by [7]. Heritability (h2) in the broad sense was calculated according to the formula given by [8] for all the characters. Phenotypic and genotypic coefficient of variation (PCV and GCV) were computed according to [9].“Analysis of variance and variability parameters were calculated by R studio software was used for D^2 statistics analysed as per the method” suggested by Mahalanobis (1936) [10].

Results and Discussion:

The mean sum of squares of genotypes was found to be significant for all the traits under study indicating the presence of significant differences in the traits across the genotypes (Table 1). Of all the traits, the grain yield per hectare showed the highest mean sum of squares for the genotypes (810707) followed by the panicles per square meter area trait recorded (4702.6) second highest MSS in ANOVA. The third day to maturity recorded the 129.36 mean sum of squares. The trait days to fifty per cent flowering recorded the 127.81 mean sum of square. The plant height trait concerned the sum of squares recorded the 115.17.

Similarly, there is a significant mean sum of squares of replication for all the traits under study.The error sum of the square is also recorded as significant for all the characters under investigation.

The highest and lowest days to fifty per cent flowering were observed about `120 days and 87 days respectively. The maximum and minimum days to maturity were recorded as 145 and 112 days respectively. The plant height trait concerned the maximum height was observed at 124cm and the minimum height observed at 80 cm. The panicle per square meter recorded the 499 highest number of panicles and 302 lowest number of panicles per square meter. The grain yield per plot recorded the 8.26 kg maximum yield and 4.05 kg per plot lower yield. Grain yield per plot is converted to grain yield per hectare the proportionate highest grain yield per hectare observed was 6883kgs/ha and the lowest yield was 3375kgs/ha.

The present investigation analyzed the observations recorded in field experimentsand showed that the PCV was found to be marginally higher than the GCV for all the charactersunder investigation which indicates the environmental influence on the expression of characters. PCV and GCV were high for the traits viz., the number of panicles per square meter (10.01 %, 9.45 %), grain yield per plot and grain yield per hectare (9.24 %, 8.39 %), the plant height (6.97 %, 5.68 %),the days to 50% flowering (6.64 %, 6.46 %) and days to maturity (5.31% and 5.17%) (Table 2). The results found in this studyare corroborated with the findings of Manjunath *et al.* (2019), Fathima *et al.* (2021), Bhargava *et al*. (2021) and Nikhitha *et al*. (2020) [11,12,13,14] for plant height and the panicles per square meter as well as days to maturity. For the grain yield per plot and grain yield per hectare in rice by Manjunatha B *et al.* (2020) and Singh*et al.* (2021) [15,16]. The amount of genetic variability that is transferred from parents to offspring is mirrored by heritability [17]. High heritability with high Genetic advance as percent of mean (GAM) was observed for days to 50 per cent flowering (96.0%, 94.00%), Panicles per square meter (75.5%, 89.0%), the days to maturity (12.96%, 94.7%), plant height(96.1%, 66.0%) and grain yield per plot(1.12%, 82.6%) the scientific findings in this genetic investigation are correlated to findings were reported in rice by Bhargava *et al.* (2021)[13] and Fathima *et al.* (2021)[12] for plant height, panicle per square meter the grain yield per plot and grain yield per hectare; Nikhitha *et al.* (2020) and Singh *et al.*(2021)[14,16] for days to fifty percent flowering and plant height and panicle per square meter exhibited high heritability with high GAMthese findings are in corroborated with the Nikhitha *et al.* (2020), Bhargava *et al.* (2021) and Singh *et al.* (2021)[13,16,14] in rice.The genetic improvement of a trait for a genotype is not only consented with high heritability through selection with genetic advance [18]. According to Johnson *et al.* (1955)[19], the selection of phenotypic expression of a trait by the genotype is strictly based on the heritability and genetic advance calculation must be together would be more advantageous in the selection process of diverse genetic material for advanced breeding activities. The heritability estimates along with genetic advances can be useful in predictingthe effect of selection in selection programs. The traits like days to fifty percent flowering, yield and plant height exhibited a high magnitude of genetic advance as a percent of the meansuggesting that the majorly additive gene action in the expression of these traits. Therefore, the selection may be operative through these traits. The traits associated with high heritability coupled with moderate genetic advance as percent of mean was observed and some traits are recorded with high heritability and low genetic advance as percent of mean which indicated the non-additive gene action in the expression of the traits in their pedigree, hence it will not permit the selection of the genotypes on phenotypic expression of the traits.

The genetic material that has to be assessed for genetic diversity may comprise of advanced genotypes, germplasms, strains, and varieties. The breeding materials are commonly selected based on phenotypic variability along with the germplasms or geographical origin [20]. “Based on the existing/significant variability in the tested lines, a D^2 analysis is done. Based on Euclidean distances using Tocher’s method, sixty-seven genotypes were grouped into fourcluster groups (Table 4). Out of four clusters, cluster I was the largest which comprises thirty-eight genotypes followed by cluster II which had twenty-seven genotypes. Clusters III and IV had one genotype each” Singh and Chaudhary (1977), Behera *et al.* (2018), Devi *et al.* (2019) and Singh *et al.* (2020)Lakshmi*et al.* (2022) [20,22,20,23,25]. “Maximum inter-cluster distances were between clusters III andcluster VI (1203.59) indicating the genotypes falling in these clusters exhibited the highest genetic diversity whereas, minimum inter-cluster distances were observed between clusters II and IV (268.41) indicating the close association and similarity between the genotypes for most of the characters. Similarly, cluster I showed the highest intra-cluster distance (75.54), whereas clustersIII and IV showed the lowest intra-cluster distance (0.0)”. Vennela *et al.* (2017) and

Behera *et al.* (2018) [26,22]. The inter-cluster distances were recorded as higher than the intra-cluster distanceswhichindicates that the parental linesof ethnicfamiliesspeckled significantly (Table 4).The origin of the genotypes is not only responsible for the clustering pattern of the genotypes in clustering tendency. The spreading frequency of genotypes is quite natural it indicates/shows that the primary center of origin of genotypes is from various states clubbed together into the same cluster and vice versa (Genotypes from the same state grouped into the different clusters). Therefore, the selection of genotypes for a trait completely depends on breeding behaviours like selection criteria, Adaptation,Selection pressure and Genotype environment interactions are major activities to exist the diversity among the genotypes belonging to the same geographic origin [27].

Apart from divergence, the traits and genotypes that lead the most to divergence should also be considered for crop improvement due to their apparent benefits. Genetic diversity was assessed using data gathered for six yield and yield-attributing characteristics in 67 genotypes using Mahalanobis D2 analysis. Among all the six traits, Days to fifty per cent flowering exhibited the maximum contribution (41.8%) towards the diversity by taking the first rank followed by days to maturity (38.8%), Panicles per square meter (10.2%), Grain yield per hectare (6.3%) and Plant height trait contributed the 3.6% towards the diversity of the genotypes (Fig 1).Usha-Kumari and Rangasamy (1997) [28] also recorded that the traits grain yield per plot and plant height contributed the maximum to divergence and the selection progress or planned on these traits of the genotypes only.Many plant breeders have adopted the Mahalanobis D^2 statistic for multivariate analysis, including analyses of the degree of divergence in plant breeding germplasm collections and varieties. The efficacy of this statistic tool for examining genetic divergence in rice crop breeding was explained by Singh *et al.* (2006), Kuchanur *et al.* (2009), Shahidullah *et al*. (2009), Vennela *et al.* (2017), Meena *et al*. (2017) and Behera *et al.*2018) [29,30,31,26,31,22].

Conclusion: The current investigation concluded that based on the traits that showed the higher genetic and phenotypic coefficient are kept for standard indicators the traits shown the higher GCV and PCV should be considered at the time of selecting the genotypes/varieties/breeding lines for progressing and prosperingin the yield and yield contribution towards the varietal performance. Genetic diversity studies proved that the traits viz., days to 50 per cent flowering, Days to maturity, Panicles per square meter, Plant height and Grain yield per plot are prompt traits that contributed maximum divergence to the genotypes. As anoutcome of the current field experiment/investigation can be utilized to recognize the differences/variables that contribute to the variability and select the germplasms/varieties to use as donors for the heightening of yield component traits in the further upcomingrice breeding activities/program.

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Table.1 Analysis of variance for five characters of 67 rice genotypes during kharif-2019

	Mean Sum of Squares		
Characters	**Replication**	**Treatments**	**Error**
Days to 50% flowering	6.475	127.817	2.316
Days to maturity	6.37	129.36	2.46
Plant height (Cm)	7.446	115.179	16.660
Panicles per sqm	12.0	4702.6	182.1
Grain yield per plot	0.061	1.167	0.076
Grain yield per hectare	42679	810707	53178

Table.2 Estimation of genetic parameters for grain yield and other components in rice.

Characters	Max.	Min.	Vg	Vp	GCV	PCV	H(BS)	GA	GA as % mean
Days to 50% flowering	120.0	87.0	41.83	44.14	6.46	6.64	0.94	0.9607	0.96
Days to maturity	145	112	41.83	44.14	5.1715	5.3127	0.947	12.96	10.37
Plant height(Cm)	124	80	32.83	49.49	5.680	6.97	0.66	9.61	9.53
Panicles per sqm	499	302	1506.83	1688.97	9.45	10.01	0.89	75.53	18.39
Grain yield per plot (Kg)	8.26	4.05	0.3636	0.4402	8.39	9.24	0.82	1.12	15.72
Grain yield per hectare (Kg)	6883	3375	252509.81	305687.76	8.40	9.25	0.82	940.81	15.7

Vg = genotypic variance, Vp = phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance
H(BS): Heritability(Broad Sense)

Table 3: Cluster groups

Clusters	Genotypes
Cluster 1	16 26 5 15 3 25 6 11 21 17 33 4 45 34 18 27 9 307 10 31 53 1 68 13 23 28 12 44 32 66 49 20 50 8 59 19 29 40
Cluster 2	48 65 61 63 64 62 35 57 37 58 51 36 41 54 56 39 2 14 24 55 52 43 42 38 60 47 67
Cluster 3	22
Cluster 4	46

Table 4: Cluster distances (D2) - torcher method:

Diagonal values are intra-cluster distances.

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**
Cluster 1	**75.54**	280.46	406.02	446.36
Cluster 2	280.46	**49.07**	1141.07	192.31
Cluster 3	406.02	1141.07	**0**	1203.59
Cluster 4	446.36	192.315	1203.59	**0**

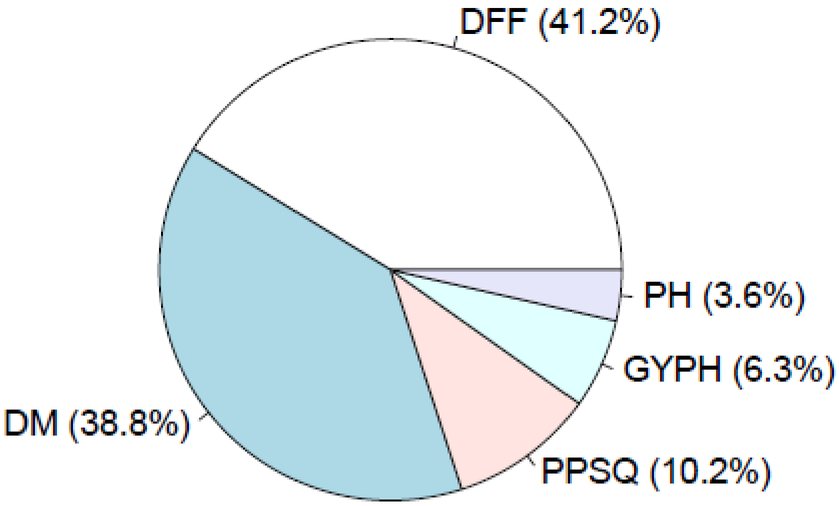

Fig.1 Per cent contribution of each traits towards the diversity