Plant Archives Vol. 25, No. 1, 2025 pp. 2080-2088 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.1.302

UNLOCKING GENETIC VARIABILITY OF ADVANCED BREEDING LINES IN PADDY (*ORYZA SATIVA* L.)

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(Date of Receiving-25-01-2025; Date of Acceptance-01-04-2025)

ABSTRACT

The paddy production in India is influenced by the good varieties to anticipate with worlds average paddy production. India is still with lack of varieties with high yield potential with biotic and abiotic stress tolerance. Assessment of genetic variability is very much important criteria in the rice improvement program for the improvement/development of high yielding varieties. The investigation was conducted at Agricultural and Horticultural Research Station during *kharif*-2022. The study includes 32 genotypes of advanced breeding lines of paddy (*Oryza sativa* L.) to assess the genetic variability, heritability, and genetic advance among yield and yield attributing traits. Randomized Complete Block Design with two replications was used. There was a highly significant difference ($P < .001$) and high diversity among the genotypes for both quantitative and qualitative traits. The range of genotypic and phenotypic coefficient of variance was 4.0% to 23.06% and 3.65% to 17.89%, respectively. Broad sense heritability was high for all traits. Genetic advance as percent of the mean ranged from 6.55% to 28.59%. For Plant height, Number of tillers per plant, Number of productive tillers per plant, Number of spikelets per plant, Number of filled grains per panicle and grain yield per plant were with high heritability and high genetic advance as percent of mean, indicating the presence of additive gene effects for these traits. The research findings of the present investigation indicated the presence of sufficient variability across the genotypes; henceforth, there is an ample opportunity to identify the promising genotypes for further crop improvement programmes.

Key words : Variability, Heritability, GCV, PCV.

Introduction

Rice scientifically known as *Oryza sativa* L. having chromosome number 2n=24 is the most important cereal crop cultivated widely in many parts of the world. Genus Oryza belongs to the Oryzeae tribe in the Poaceae family. Out of 24 species of rice, 22 species are wild and only two species are cultivated, i.e., *Oryza sativa* and *Oryza glaberima*. It is a staple food for more than half of the world's population and is a major source of income in many Asian countries. It is grown in more than 100 countries in 154 million hectares with 90 percent of the total global production from Asia (Bista, 2018). Rice provides 21 per cent of global human per capita energy and 15 per cent of per capita protein. It is the primary source of food and protein (30%) providing 50-60 per cent of the total calories for about half of the mankind with an enormous nutritional and economic impact. The protein quality is around 0.55, which is also higher compared to other cereals. Apart from carbohydrates and proteins rice also provides essential amino acids, minerals (P, Mg, Ca), vitamins (Folic acid) and fibre. It is the crucial dietary and food security source of many Asian countries like China, India, Indonesia, Bangladesh and Vietnam. China and India are the largest producers and consumers of rice. India ranks the highest area of cultivation of rice in the world, next being China. In India, West Bengal has highest total rice production followed by Uttar Pradesh. The other major rice producing states in India are Punjab, Andhra Pradesh, Tamil Nadu, Bihar, Chhattisgarh, Odisha. In 2021-22, the rice area, production and productivity in India was 46.38 Mha, 130.29 mt and 2.81 t/ha, respectively. In Karnataka, rice occupies 1.39 million hectares with 4.29 million tonnes of production and 3.72 t/ha productivity (Anonymous, 2022). The existence of genetic variability is essential for selection in plant breeding as the significant amount of variability among the breeding materials will lead to effective selection. Rice shows an array of genetic variability which helps in effective selection for desirable traits. Yield improvement is the major objective in rice breeding programmes. The information about the extent of several genetic parameters *viz.*, Phenotypic Co-efficient of Variation (PCV), Genotypic Co-efficient of Variation (GCV), broad-sense heritability and genetic advance is essential for the successful genetic improvement of a genotype (Kishore *et al.,* 2015). Correlation is a very important factor for any selection program. Success in selection depends on the knowledge of the association of component traits with grain yield hence indirect selection for yield component traits are more reliable than selection for yield (Nath and Kole, 2021). Therefore, character association studies help to understand the nature of physical linkage and also provide information on the nature and direction of correlation which exists between the variables. Assessing genetic diversity is a fundamental aspect of the development of new genotypes with a desired combination of traits. Moreover, it hastens the revelation of promising genotypes without the need to evaluate all possible cross-combinations in breeding programs. Multivariate analysis tool like Mahalanobis D^2 statistic is functional for measuring genetic diversity by considering morphological and quantitative characteristics in a given population. It is utilized in detecting clustering patterns, to establish a link between genetic and environmental divergence, to study quantitative traits which determines maximum divergence and also to identify the characters which significantly contribute to divergence among the genotypes (Jangala *et al.*, 2022).

Materials and Methods

Description of study area: The field experiment was conducted in Agricultural and Horticultural Research Station (AHRS) during *kharif* season from June to November 2021/22 to assess existence and range of genetic variability among 32 rice genotypes and three check varieties. AHRS is found in the Chennagiri(T), Davanagere(D), Karnataka region, Annual maximum rainfall of 990 mm while the temperature ranges from 20.00°C to 36.00°C. The major soil types of the station are red sandy soils and the experiment was laid on red sandy soils.

Experimental materials : Thirty-two F5 advanced breeding lines of rice cross RNR-15048 × KPR-1 along with five check varieties *viz.*, RNR-15048, KPR-1, BPT-5204, JGL-1798, KHP-11, were collected from the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga to study genetic variabilit for yield and yield attributing traits under non-submergence.

Table 1 : List of materials used in the study.

R×K-1-4-3	R×K-12-2-6	R×K-2-2-14	RNR-15048 (Check I)
R×K-7-2-1	R×K-1-4-9	R×K-7-2-12	KPR-1 (Check I)
R×K-1-4-4	R×K-7-2-7	R×K-1-4-15	BPT-5204 (Check I)
R×K-7-2-2	R×K-1-6-10	R×K-4-2-13	JGL-1798 (Check I)
R×K-1-4-5	R×K-14-2-8	R×K-1-4-16	KHP 11 (Check I)
R×K-8-2-3	R×K-4-4-11	R×K-3-2-14	FR13A (Check II)
R×K-1-4-6	R×K-7-2-9	R×K-1-4-17	Swarna sub-1(Check II)
R×K-5-2-4	R×K-1-4-12	R×K-6-2-15	Jyothi (Check II)
R×K-1-4-7	R×K-8-2-10	R×K-1-4-18	BPT-5204 (Check II)
R×K-7-2-5	R×K-1-4-13	R×K-7-2-16	
R×K-1-4-8	R×K-7-2-11		

Experimental design and cultural practices: The experiment was laid out in Randomized Complete Block Design (RCBD) with two replications for testing 32 advanced breeding lines of rice with five checks. The seeds of 32 advanced breeding lines were sown to raise nursery bed during *Kharif* 2022 at AHRS, Kathalagere. Twenty-one days old seedlings were transplanted manually to the main field at the rate of one seedling per hill in RCBD with two replications by following spacing of 20 cm row to row and 15 cm plant to plant. The recommended package of practices was followed to maintain a healthy and good crop stand.

Data collection : The quantitative data are recorded on 12 traits *viz.*; Days to 50 per cent flowering, Days to maturity, Plant height (cm), Number of tillers per plant, Number of productive tillers per plant, Panicle length (cm), Number of spikelets per panicle, Number of filled grains per panicle, Spikelet fertility (%), Test weight (g), Length Breadth (L/B) ratio, Grain yield per plant (g). The data of mean value for all the characters were analyzed for their variance following Randomized Complete Block Design outlined by Cochran and Cox (1957).

Data analysis : Analysis was done using software WINDOSTAT version 9.2 and R software at Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga. Genotypic and phenotypic coefficients of correlation between all pairs of characters were determined by using variance and covariance components as suggested by Al Jibouri (1958). The analysis was done by using the WINDOSTAT version 9.2 software and R software.

Results and Discussion

The current study aimed to determine the type and extent of genetic diversity, variability and character association with regard to grain yield and attributes that contribute to yield among 32 advanced breeding lines of rice. Advanced breeding lines of rice demonstrated considerable population variability under the non-submergence condition, according to the analysis of variance (ANOVA), which found significant differences for all characters examined. Table 2 shows the analysis of variances for each of the 12 traits. Table 2 lists the genetic variability metrics for each of the 12 traits, including mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (in the broad sense) and genetic advance as per cent mean (GAM).

Analysis of variance : For all studied quantitative traits, the analysis of variance (ANOVA) revealed the presence of highly significant difference ($P < .001$) among 32 rice genotypes (Table 2) undr non-submergence which shows the existence of high and inherent variation among the genotypes for those traits. Therefore, there is high possibility for improvement of yield, yield attributing traits, and quality traits through the selection and hybridization of better parental genotypes. In agreement with this finding, Edukondalu *et al.* (2017), Manjunatha and Kumara (2019) and Katkani *et al.* (2023). Nikhil *et al.* (2014), Mulugeta Bitew *et al.* (2016), Adhikari *et al.* (2018), Tewachewu *et al.*(2018) and Brar *et al.* (2018) reported significant different for the above-mentioned traits.

Mean performance and range values

Looking only the performance of genotypes for yield is not effective to select genotypes which could be used as a parent material for further improvement activities since yield is influenced by different factors. Hence when performing variability activities, it is also recommended to look on the existence of variation for other yield attributing traits such as productive tiller, filled grain, maturity date, test weight, and plant height in order to use them as indirect selection criteria. As it is mentioned in the material and methodology part, all the materials were selected. Hence, prior to this experiment, all genotypes were subjected to nursery observation then pass to the evaluation due to their preferable phenotypic appearance, agronomic traits, and disease and pest resistance/tolerance. Therefore, in the present investigation, the best-performing advanced lines/ genotypes were selected and promoted for the further crop improvement stage using the corresponding quantitative traits as a indirect selection indices.

Days to fifty per cent flowering and maturity days Genotypes could be classified as earliest (105 days), early (106–119 days), medium (120–135 days) or late maturing (>135 days) genotypes (Tatsushi Tsuboi, 1992). The longest days to fifty per cent flowering recorded was 129 days (R×K-4-4-11) while the earliest was 101 days (KPR-1), while the grand mean for days to fifty per cent flowering is 116.78. KPR-1 was the earliest to mature at 131 days, while R×K-4-4-11 had late maturity at 159 days while the grand mean of day to 85 % maturity is 146.81 days. The 32 varieties/genotypes are fall under the late maturing (>135 days) class and KPR-1 reached 85% of maturity for 131 days.

Variation in days to fifty per cent flowering and maturity days may result due to differences in emergence dates. Genotype with the earliest emergence date might have the earliest flowering and the earliest days to maturity. However, this is mostly dependent on genotype genetic behavior (some genotypes took 30 days to mature after flowering, while others took up to 40 days) and environmental conditions (Harrell *et al.*, 2021). In AHRS, Kathalagere situation, genotypes with medium days to 50% flowering and maturity dates could be suitable for further breeding purpose and production to minimize growing period of genotypes with high yielding capacity and longest maturity date and minimize yield loss due to biotic and abiotic stresses. While early maturing genotypes could be used for further crop improvement of high yield and late maturing genotypes in water deficit or flooded agro ecologies of the country.

Plant height and panicle length : The panicle length is directly proportional to the plant height longer the panicle length higher will be the plant height, the lower the number of tillers or lower the number of productive tillers the lower the filled grain and grain yield. However, these yield parameters depend on the paddy subspecies type (Indica, Japonica, Javanica). From these studied genotypes, the highest plant height was 164 cm by R X K-7-2-5 while the lowest was 90 cm by KPR-1. The range for the plant height is between 90.00cm-164.80cm and grand mean value of 134.90 cm. There were 32 genotypes which scored higher plant height than all the checks. The range for panicle length was from lowest 13.20 cm by R×K- 7-2-12 to the longest 25.30 cm by R×K-1-4-16. Grand mean value for the panicle length was recorded is 21.89 cm. among 32 genotypes, 09 genotypes were with longer panicle than all the checks while, 23 genotypes scored shortest panicle length than all the checks. The variation that exists among the genotypes could be due to genetic variability or variation on growth behavior. Taller rice genotypes are mostly susceptible for lodging while short genotypes may submerge in highly water-logged areas and cause yield loss; hence, for the study area, genotypes with intermediate plant height could be suitable for breeding and crop improvement purpose. Gyawali *et al*. (2018) and Wangpan *et al*. (2018) reported range of 102.04 to 156.91 and 134.1 cm to 191 cm, respectively, for plant height while Kanushree *et al.* (2020) reported range of panicle length from 21.5 cm to 29.95 cm.

Number of tillers and productive tillers : The increase in the number of productive tillers will result in the increment of grain yield (Shankar *et al*., 2021). Low number of productive tillers could be resulted due to competition for assimilates during stem extension (Ambavaram *et al.*, 2014). Number of tillers per plant significantly differed among advanced breeding lines with a range of 10.20 to 23.00 and a mean value of 14.98. The lowest number of tillers per plant, *i.e.*, 10, were recorded by R×K-8-2-10 and the highest number of tillers was recorded by JGL-1798, with 23 tillers per plant. Number of productive tillers per plant significantly differed among advanced breeding lines of rice with a range of 9.50 to 23.00 and a mean value of 14.97. The lowest number of tillers of nine per plant was recorded by R×K-8-2-10 and the highest number of tillers was recorded by JGL-1798 with 23 tillers per plant.Prakash Poudel (2018) reported 97.5 to 266.5 per meter square; Brar *et al.* (2018) reported 14 to 27 productive tillers per plant.

Number of spikelets and filled grain per panicle : The paddy crop is composed of the panicles with spikelets is an important trait to identify the productive genotypes. The number of spikelets are directly proportional to the number of filled grains per panicle. In rice, the process of filling the grain depends on two main sources of carbon: assimilates produced during photosynthetic activity and carbohydrates transferred from vegetative tissues to the grain during pre-anthesis it called the source to sync relationship (Ambavaram *et al.*, 2014). The increase in the number of filled grains could be attributed to the photosynthesis-derived carbohydrates (Zing and Zang, 2010). For number of filled grains per panicle, the lowest and highest range were as followed mean value of 260.81 was recorded with the range of 175.80 to 392.00. The genotype R×K- 4-4-11 exhibited a minimum number of 176 grains per panicle, whereas JGL-1798 had a maximum number of 392 grains per panicle. Kanushree *et al.* (2020) reported range from 55 to 228 of filled grain among 48 germplasm accessions of rice. Osman *et al.* (2020) found significant difference and range of 4 to 24.5 for 21 rice double haploid lines. Variability was found more with the mean value of 233.98 recorded and the range of 144.00 to 337.62. The genotype R×K-3-2- 14 exhibited a minimum number of 144 filled grains per panicle, whereas JGL-1798 had a maximum number of 337 filled grains per panicle.

Thousand grain weight (Test weight in grams)

Grain weight is the measure of seed size that directly influence grain yield and reproductive efficiency. Test weight had a range from 15.60 to 29.50 grams, with a mean of 20.93 grams. R×K-6-2-15 had recorded the lowest test weight of 15.60 grams and KHP-11 recorded the highest test weight of 29.50 grams. Osundare *et al.* (2017) reported significant difference and range of 31.7 to 33 among six upland rice varieties.

Grain yield per plant

It is a complex trait incrementally interlinked by the nature of genotypes, environment, and the interaction of genotype and environment. It is primarily determined by its component traits; number of panicles (productive tillers), number of grains per panicle, and grain weight (Ambavaram *et al*., 2014). Grain yield per plant significantly varied, with the range of 21.20 grams to 41.85 grams with a mean of 29.32 grams. The lowest grain yield of 21.20 grams was recorded by R×K-1-4-12, and the highest grain yield of 41.85 grams was recorded by R×K-1-4-8. The observed yield difference could be due to differences in their genetic architecture for yield that is some genotypes being high yielder than others. The other reason could be difference in sensitivity rate of genotypes for environmental factors. Differences insensitivity rate cause genotypes to behave differently regarding yield or yield-related morphological traits (Mackill *et al.*, 1996). Additionally, the yield difference could arise due to the difference in yield related traits that influence yield directly like filled grain per panicle, thousand grain weight and productive tillers and/or indirectly like plant height, growing period, seed length, or panicle length (Shankar *et al*., 2021). Abebe *et al*. (2017) reported a yield range of 2.9 t/ha to 6.8 t/ha among 34 rice genotypes. Tewachewu *et al*. (2018) reported grain yield range from 4.28 t/ha to6.76 t/ha among 23 rice genotypes.

Estimation of variance components : One of the key targets of the rice breeding programme is yield improvement. For genetic improvement, it is crucial to have a thorough understanding of the types and degrees of genetic variation that affect quantitative heritable traits like yield and their corresponding attributes. Variability in the population is essential for any breeding programme and is vital for crop improvement for any desired character. Accordingly, determining level of diversity in the gene pool is perhaps the most crucial stage in every breeding effort. Critical evaluation of genetic variability measures including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as a per cent of mean are prerequisites for any crop improvement effort in plant breeding.

In the current investigation, phenotypic and genotypic coefficients of variation were recorded low for days to 50 per cent flowering (PCV: 4.94 and GCV:4.76) and days to maturity (PCV:4.00 and GCV:3.81). Similar findings were reported for both the traits by Edukondalu *et al.* (2017), Gour *et al.* (2017), Tiwari *et al.* (2019) and Katkani *et al.* (2023). Sumanth *et al.* (2017) obtained similar results for days to 50 per cent flowering and on par results were obtained for days to maturity by Prasad *et al.* (2017). Occurrence of low estimate value of phenotypic and genotypic coefficients of variation indicates that selection of these characters for crop improvement program will be inappropriate. Spikelet fertility was found to have low genotypic and phenotypic coefficient of variation (PCV:4.18 and GCV:3.95). The results obtained were parallel to the findings of Sravan *et al.* (2012), Nath and Kole (2021) and Niharika *et al.* (2022). Panicle length (PCV:10.39 and GCV:9.89) exhibited moderate PCV similar to the outcomes of Dhanwani *et al.* (2013) and Sandeep *et al.* (2018), low GCV in accordance with Singh *et al.* (2021) and Katkani *et al.* (2023). PCV and GCV obtained was moderate for plant height (PCV:15.10 and GCV:13.90). The findings for plant height were in accordance with Edukondalu *et al.* (2017), Gour *et al.* (2017), Chamar *et al.* (2021) and Katkani *et al.* (2023). Number of tillers per plant (PCV:16.92 and GCV:13.78) and number of productive tillers per plant (PCV:17.42 and GCV:14.52) were found to exhibit moderate PCV and GCV value and similar results were reported by Dhanwani *et al.* (2013), Devi *et al.* (2016), Srujana *et al.* (2017), Sumanth *et al.* (2017), Singh *et al.* (2021) and Katkani *et al.* (2023). Moderate estimates of GCV and PCV indicate that there is reasonable scope for enhancing crop yield through selection of these traits. Grain length and breadth ratio (PCV:9.45 and GCV:8.56) was found to exhibit low PCV and GCV, similar results were reported by Edukondalu *et al.* (2017) and Bandi *et al.* (2018). Grain yield per plant (PCV:23.06 and GCV:17.89) found to exhibit high PCV in accordance with Edukondalu *et al.* (2017), Ram *et al.* (2017) and Katkani *et al.* (2023). Moderate GCV in accordance with Bandi *et al.* (2018) and Tiwari *et al.* (2019). Results showed moderate PCV for test weight (PCV:11.42 and GCV:9.27) similar to results obtained from Singh *et al.* (2021) and Katkani *et al.* (2023). Low GCV for test weight were on par with the results Sravan *et al.* (2012). The traits *viz.*, number of spikelets per panicle (PCV:17.32 and GCV:14.15) and number of filled grains per panicle (PCV:16.17 and GCV:14.15) recorded moderate PCV and GCV. Identical results were observed by Niharika *et al.* (2022) and Katkani *et al.* (2023) for number of filled grains per panicle and number of spikelets per panicle. For all the characters studied, it was found that the phenotypic coefficients of variation values were more than the corresponding genotypic coefficients of variation. Chamar *et al.* (2021), Singh *et al.* (2021), Niharika *et al.* (2022) and Katkani *et al.* (2023) have reported the higher PCV estimates than GCV estimates for all the characters evaluated. A narrow difference of PCV and GCV was observed indicating that environmental influence is less and genetic factors contribute the most for variability in these characters. Although, information on the variability and its extent present in the advanced breeding lines studied, together with the influence of environment, can be obtained from phenotypic and genotypic coefficients of variation, an appropriate estimate of the extent of inheritance of the traits cannot be furnished. As a result, the heritability of a trait will give plant breeders the chance to decide how much selection pressure needs to be applied in the crop improvement programme for a specific environmental condition. High heritability in the broad sense combined with high genetic advance as a per cent of mean serve as direct selection criteria because they provide estimates of the traits' heritability, which depicts the efficacy of selection in improvement of the characters (Johnson *et al.*, 1955).

Estimation of heritability and genetic advance as percent of mean

Heritability (Broad sense) is classified into three classes as Low (30%), Medium (30-60%) and High (>60%) (Johnson *et al.*, 1955). Heritability is an important phenomenon of transmission of traits from generation to generation, the prediction of heritability can be applied for genetic gain and its estimative role to indicate the dependability of the phenotypic value as a base to breeding value (Lipi *et al.*, 2020). For all studied quantitative traits, the broad sense heritability in this study was high 60.19% to 93.12%, which directed that the phenotypic expression was largely determined by

Table 2 : Analysis of yield and its attributing characters in advanced breeding lines under non-submergence.

Source of variety	Degrees of freedom	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of tillers per plant	Number of productive tillers per plant	Panicle length (cm)
Replication	1	2.61	6.54	17.89	1.91	0.39	1.07
Genotype	36	63.34**	65.92**	767.22**	10.67**	11.54	9.89**
Error	36	2.29	3.09	63.18	2.17	2.08	0.48
CD (5%)		3.07	3.57	16.12	2.99	2.93	1.41
CD (1%)		4.12	4.79	21.62	4.01	3.92	1.89
CV%		1.23	1.19	5.89	9.83	9.63	3.17

Source of variety	Degrees of freedom	Number of spikelets per panicle	Number of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Length breadth ratio	Grain yield per plant (g)
Replication	1	66.46	83.42	14.06	4.06	0.01	17.22
Genotype	36	3404.82**	2301.55**	27.20**	9.48**	0.19**	73.21**
Error	36	680.34	561.99	3.71	1.94	0.02	18.19
CD (5%)		52.90	48.08	3.91	2.83	0.28	8.65
CD (1%)		70.93	64.47	5.24	3.79	0.37	11.60
CV%		10.00	10.13	2.05	6.67	4.00	14.55

**-Significant at 1% level.

Table 3 : Genetic Variability parameters for yield and yield related characters in advanced breeding lines under non-submergence.

S. no.	Characters	Mean	Range		PCV (%)	GCV (%)	H^2(bs) (%)	GAM (%)
			Min	Max				
1	Days to 50 % flowering	116.78	101.00	129.00	4.94	4.76	93.12	9.48
2	Days to maturity	146.81	131.00	159.00	4.00	3.81	91.02	7.50
3	Plant height (cm)	134.9	90.00	164.80	15.10	13.90	84.78	26.37
4	Panicle length (cm)	21.89	13.20	25.30	10.39	9.89	90.70	19.42
5	Number of tillers per plant	14.98	10.20	23.00	16.92	13.78	66.28	23.11
6	Number of productive tillers per plant	14.97	9.50	23.00	17.42	14.52	69.44	26.37
7	Number of spikelets per panicle	260.81	175.80	392.00	17.32	14.15	66.69	23.80
8	Number of filled grains per panicle	233.98	144.00	337.62	16.17	12.60	60.74	20.23
9	Spikelet (%)	93.98	81.13	98.50	4.18	3.65	75.97	6.55
10	Test weight (g)	20.93	15.60	29.50	11.42	9.27	65.97	15.52
11	Length breadth ratio	3.43	2.44	3.98	9.45	8.56	82.04	15.98
12	Grain yield per plant (g)	29.32	21.20	41.85	23.06	17.89	60.19	28.59

genotypic modifications, with minute effect from environmental influences. As a result, there is a good possibility of employing the progeny test and mass selection to modifying the expression of these phenotypic traits. Supporting this finding, Mulugeta Bitew *et al.* (2016) reported for maturity, thousand grain weight. Roy and Shil (2020) for panicle length and plant height; Tiwari *et al.* (2019) for days to 50% heading. Similarly, (Hossain *et al.*, 2018; Islam *et al.*, 2015; Prasad *et al.*, 2017) reported for number of productive tillers per plant, filled grain per panicle, and grain yield. The genetic advance is a valuable indicator of the progress that could be achieved as a result of selecting the relevant population (Islam *et al.*, 2015). In present study, there was no trait which can be categorized as trait with low genetic advance. The Genetic advance under mean percentage is classified into

Low (<10%), Moderate (10-20%) and High (>20%) (Johnson *et al.* 1955). The Low GAM was recorded by Spikelet per cent (6.55%), days to maturity (7.50%) and days to 50% flowering (9.48%) low GAM is low influence of additive and non-additive gene action on respective traits. Moderate percentage of genetic advance as percent of the mean was recorded by Test weight (15.52%), Length breadth ratio (15.98%) and panicle length (19.42%). Moderate GAM indicated that moderate action of both additive and non-additive genes on the control of those characteristics. Similar findings were reported by Roy and Shil (2020) for panicle length, Prasad *et al.* (2017) for days to 85% maturity and panicle length. A result of high GAM indicated the maximum control of characters by additive gene action and the high possibility of using this trait for genetic improvement through selection. In this study, high GAM was recorded for Plant height (26.37%), Number of tillers per plant (23.11%), productive tillers (26.37%), Number of spikelet per plant (23.80 %), Number of filled grains per panicle (20.23 %) and grain yield per plant (28.59%). Ajmera *et al.* (2017) and Abebe *et al.* (2017) reported similar result for these.

Understanding of the genetic phenomenon heritability coupled with genetic advance could be more useful than knowing only heritability of traits (Amegan *et al.*, 2020). In the present investigation, high heritability with high GAM was recorded for Plant height (84.78%, 26.37%), Number of tillers per plant (66.28% 23.11%), Number of productive tillers per plant (69.44 % 26.37%), Number of spikelets per plant (66.69 % 23.80%), Number of filled grains per panicle (60.74% 20.23%) and grain yield per plant (60.19% 28.59%). High heritability coupled with moderate GAM characters are Panicle length (90.70 % 19.42%), Test weight (65.97%, 15.52%) and Length to breadth ratio (82.04% 15.98%). This indicated that the control of additive genes was high on those traits while, the influence of non-additive genes was low (Table 2). This influences that these characters could be enhanced easily by simple selection. Similarly, Ajmera *et al.* (2017) reported for plant height, productive tillers, filled grain per panicle, and grain yield. Sandeep *et al.* (2018) reported for thousand grain weight, panicle length, Osman *et al.* (2020) reported for number of unfilled grain/ Panicles and biological yield, among 21 rice genotypes.

Conclusion and Recommendations

The present investigation found a highly significant difference (P < .001) for all quantitative traits and a high diversity for qualitative characters. Out of 32 advanced breeding lines the selection of promising genotypes based on their yield performance, better phenotypic appearance, medium maturity date, high filled grain per panicle, and productive tillers for further crop improvement/breeding purpose. All the studied quantitative traits were with high heritability percentage. For Plant height, Number of tillers per plant, Number of productive tillers per plant, Number of spikelets per plant, Number of filled grains per panicle and grain yield per plant were with high heritability and high genetic advance as percent of mean, indicating the presence of additive gene effects for these traits. Therefore, further crop improvement activity for incremental increase with respect to yield parameter through the indirect selection of genotypes with high filled grain, high productive tiller, high test weight and good physical quality. Regardless, the present study was conducted in one location for only one season. Hence, the materials should be tested in multi locations. In addition, even though variability based on agronomic traits is crucial in India, molecular characterization of those genotypes is required in order to discover the genetic variability and heritability of yield and yield related traits at molecular/ genomic level.

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