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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND MORPHO-PHYSIOLOGICAL TRAITS IN RICE (*Oryza sativa* L.)

Rahul T. Gahane[1], S.T. Burhade[1]*, M.G. Palshetkar[1], S.S. Desai[2], R.S. Shinge[3] and D.N. Mahind[1]

[1]Department of Agricultural Botany, College of Agriculture, DBSKKV, Dapoli - 415 712, Maharashtra, India.

[2]AICRP (Agroforestry), College of Forestry, DBSKKV, Dapoli - 415 712, Maharashtra, India.

[3]Plant Biotechnology Centre, College of Agriculture, DBSKKV, Dapoli - 415 712, Maharashtra, India.

*Corresponding author E-mail : sanketburhade77@gmail.com

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ABSTRACT

Assessment of genetic variability is a fundamental prerequisite for any systematic plant breeding program. The present field experiment was conducted during *Kharif* 2022 at the Research and Educational Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, District-Ratnagiri, Maharashtra, India; to quantify the magnitude of genetic variability, heritability and genetic advance for yield and yield-attributing components in twenty-five rice (*Oryza sativa* L.) genotypes. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Analysis of variance revealed highly significant ($p < 0.01$) variation among all genotypes for all nineteen quantitative traits examined. Phenotypic coefficients of variation (PCV) were marginally higher than their corresponding genotypic coefficients of variation (GCV), denoting minimal environmental influence on trait expression. High PCV and GCV were observed for number of filled grains per panicle (28.12% and 27.94%), grain yield per plant (26.42% and 24.33%), number of total spikelets per panicle (26.35% and 26.13%), and plant height (22.53% and 22.28%). Broad-sense heritability (h^2_b) was consistently high across all traits, ranging from 65.37% for straw yield per plant to 99.10% for days to 50% flowering. High heritability coupled with high genetic advance as a percentage of the mean (GAM) was recorded for number of filled grains per panicle (h^2_b = 98.71%, GAM = 57.18%), number of total spikelets per panicle (h^2_b = 98.38%, GAM = 53.39%), grain yield per plant (h^2_b = 84.82%, GAM = 46.16%), plant height (h^2_b = 97.78%, GAM = 45.38%), test weight (h^2_b = 98.79%, GAM = 37.96%) and number of productive tillers per plant (h^2_b = 89.51%, GAM = 33.94%). These results demonstrate the predominance of additive gene action governing these traits, suggesting that simple phenotypic selection would be effective for genetic improvement. Genotypes DPL-19, DPL-11, DPL-1, DPL-23 and DPL-4 were identified as superior yielders with desirable agronomic characteristics.

Key words : Rice (*Oryza sativa* L.), Genetic variability, Heritability, Genetic advance, Additive gene action, Grain yield, GCV, PCV.

Introduction

Rice (*Oryza sativa* L.) is a premier cereal crop that serves as the staple food for more than half of the global population, notably in Asia and Africa. Recognising its critical role in human sustenance, cultural heritage and poverty eradication, the United Nations designated 2004 as the 'International Year of Rice' under the theme "Rice is life". Globally, rice ranks third in agricultural output after sugarcane and maize. Approximately 80% of dietary calories consumed in Asia and 20% worldwide are supplied by rice, which contains 87% carbohydrates, 7–8% protein and minimal fat.

India is the largest producer and consumer of rice globally. During 2021, global rice cultivation covered 165.25 million hectares, producing 787.29 million tonnes with an average productivity of 4.76 t/ha. In India, rice is cultivated on 46.00 million hectares with an annual production of 130.84 million tonnes and a productivity of 2.607 t/ha. In Maharashtra state, rice occupies 14.65 lakh hectares with a total harvest of 32.76 lakh tonnes (productivity 2.180 t/ha). Within Maharashtra, the coastal Konkan region represents a major rice pocket, cultivating 3.69 lakh hectares with a total yield of 12.94 lakh tonnes and a productivity of 2.93 t/ha.

Despite historic yield increases driven by modern agricultural technologies, productivity growth in modern high-yielding varieties (HYVs) is plateauing. With global population expansions and changing consumer demands, global rice production must expand by an estimated 40% by 2030 to ensure sustainable food security. Developing varieties with superior yield potential and adaptation stability requires exploiting genetic variability present in indigenous landraces and uncharacterized germplasm.

The success of any plant breeding program depends fundamentally on the magnitude and nature of genetic variability in the initial breeding stock. Phenotypic variation combines genotypic variation and environmental effects. Partitioning phenotypic variance into genotypic and environmental components through genotypic (GCV) and phenotypic (PCV) coefficients of variation provides an accurate index of available variation. Heritability in a broad sense indicates the proportion of phenotypic variation attributable to genetic differences. However, heritability estimates alone do not indicate the expected genetic progress in segregating generations; predicting genetic gain requires coupling heritability with genetic advance. High heritability accompanied by high genetic advance as a percentage of the mean indicates the predominance of additive gene action, whereas high heritability paired with low genetic advance denotes non-additive gene effects.

The present investigation was undertaken to evaluate the extent of genetic variability, phenotypic and genotypic coefficients of variation, broad-sense heritability and genetic advance as a percentage of the mean for yield and twelve morpho-physiological traits among twenty-five rice genotypes.

Materials and Methods

The field evaluation was carried out at the Research and Educational Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, District Ratnagiri, Maharashtra, during the *Kharif* season of 2022. Dapoli is situated in the South Konkan Coastal Agro-Climatic Zone at 17°45’32" N latitude and 73°11’8" E longitude, with an elevation of 243.84 meters above mean sea level. The local climate is warm and humid tropical, receiving an average annual rainfall of 3,500 mm concentrated between June and October. The experimental soil was lateritic. The plant material consisted of twenty-five rice genotypes (twenty-four advanced lines/landraces designated DPL-2 to DPL-25 and one standard check cultivar, Ratnagiri-7 / DPL-1) maintained by the Department of Agricultural Botany, College of Agriculture, Dapoli.

The experiment was laid out in a Randomized Block Design (RBD) with three replications. Seeds were sown on raised nursery beds on June 10, 2022. Thirty-day old seedlings were transplanted into the main field on July 11, 2022, with a spacing of 20 cm between rows and 15 cm between plants. The net plot size was 3.0 m × 0.06 m, accommodating three rows of twenty plants per genotype per replication (60 plants total per genotype per replication). Data were recorded from five randomly selected competitive plants per genotype per replication (excluding border rows) for nineteen quantitative traits *viz*., Days to 50% flowering (Recorded on a plot basis when half the plants had flowered), Days to maturity (Recorded when over 80–90% of the grains matured), Plant height {cm} (Measured from ground level to the tip of the main panicle), Number of productive tillers per plant (Total number of panicle-bearing tillers on the sampled plants), Panicle length {cm}(Measured from the panicle base (ciliate ring) to the tip of the topmost spikelet), Number of total spikelets per panicle (Total grain loci (filled plus unfilled) per panicle), Number of filled grains per panicle (Well-developed, fully fertile grains per panicle), Spikelet fertility{%}(Proportion of filled grains to total spikelets per panicle), Test weight {g} (Weight of 1,000 well-developed, matured grains), Grain yield per plant {g} (Cleaned and dried grain harvest weight per plant), Straw yield per plant {g} (Sun-dried vegetative biomass weight per plant after threshing), Harvest index {%} (Ratio of economic (grain) yield to total biological yield (grain + straw) expressed as a percentage), Protein content {%} (Estimated using the Micro-Kjeldahl digestion and distillation method (AOAC, 2000), multiplying total nitrogen by the specific conversion factor of 5.95), Amylose content {%} (Quantified using the simplified colorimetric iodine absorption method (Juliano, 1971) at an absorbance wavelength of 620 nm), Carbohydrate content {%} (Determined through the Anthrone colorimetric method (Hedge and Hofreiter, 1962) at an absorbance of 630 nm against a D-glucose standard), Fat content {%} (Analyzed via solvent extraction using petroleum ether in a Soxhlet extraction apparatus), Iron (Fe) content (Measured by aspirating the di-acid digested extract into an Atomic Absorption Spectrophotometer (AAS) at 248.3 nm), Zinc (Zn) content (Analyzed using Atomic Absorption Spectrophotometry (AAS) at a wavelength of 213.9 nm), Calcium (Ca) content (Determined using Atomic Absorption Spectrophotometry (AAS) at 422.7 nm).

Mean data were analyzed using the standard RBD ANOVA model of Panse and Sukhatme (1985) to test for significant genotypic differences. Components of

variance- environmental, genotypic and phenotypic were computed from expected mean squares. Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated using the formulae of Burton and De Vane (1953) and classified per Sivasubramanian and Menon (1973). Broad-sense heritability, expected genetic advance, and genetic advance as a percentage of the mean were calculated and categorized according to Johnson *et al*. (1955).

Results and Discussion

Analysis of Variance

The analysis of variance revealed highly significant differences ($p < 0.01$) among the twenty-five genotypes for all twelve quantitative traits (Table 1). This demonstrates substantial genetic diversity within the evaluated material, providing scope for phenotypic selection. Similar findings of significant genotypic variation in rice germplasm have been reported by Adhikari *et al*. (2018), Tiwari *et al*. (2019), and Yadav *et al*. (2022).

Table 1 : Analysis of variance for yield contributing components in rice.

S. no.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	2	24	48
1	Days to fifty percent flowering	3.453	461.581**	1.398
2	Days to maturity	1.693	484.141**	2.054
3	Number of productive tillers per plant	0.257	4.534**	0.17
4	Panicle length (cm)	4.297	17.979**	1.995
5	Plant height (cm)	25.429	2023.653**	15.215
6	Grain yield per plant (g)	0.131	45.219**	2.547
7	Straw yield per plant (g)	0.113	43.589**	6.543
8	Harvest index (%)	0.279	36.608**	4.166
9	Test weight (g)	0.059	54.542**	0.221
10	Number of filled grains per panicle	27.012	2960.489**	12.806
11	Number of total spikelets per panicle	11.105	4397.669**	24.089
12	Spike fertility (%)	9.128	93.398**	5.437
13	Protein (%)	0.007	6.465**	0.058
14	Amylose (%)	0.059	5.572**	0.454
15	Carbohydrate (%)	3.007	51.011**	3.685
16	Fat content (%)	2.836	5.301**	1.429
17	Iron (ppm)	0.072	20.509**	0.908
18	Zinc (ppm)	1.069	23.626**	0.678
19	Calcium (ppm)	31.271	958.584**	44.366

The mean performance across genotypes showed the following patterns:

Days to 50% flowering and maturity: Days to 50% flowering averaged 97 days, ranging from 76 days in DPL-2 to 123 days in DPL-3. Days to maturity ranged from 104 days in DPL-2 to 152 days in DPL-8, with a population mean of 127 days. Genotypes DPL-2 (76 and 104 days), DPL-21 (77 and 109 days), DPL-14 (84 and 113 days) and DPL-13 (85 and 113 days) were the earliest, making them suitable donors for developing early-maturing cultivars. Genotypes DPL-3 (123 and 150 days), DPL-8 (119 and 152 days), and DPL-5 (119 and 148 days) were late-maturing.

Plant height : Plant height ranged from 80.00 cm in DPL-23 to 164.00 cm in DPL-5, with a general mean of 116.00 cm. Dwarf to semi-dwarf genotypes, including DPL-23 (80 cm), DPL-10 (85 cm), DPL-22 (87 cm), and DPL-7 (88 cm) are potential donors for reducing lodging susceptibility.

Number of productive tillers per plant: Productive tillers per plant averaged 6.93, ranging from 4.13 (DPL-20) to 9.13 (DPL-23). Higher tiller counts were recorded in DPL-23 (9.13), DPL-14 (9.07), DPL-25 (8.47), and DPL-2 (8.33).

Panicle length : Panicle length averaged 23.53 cm, ranging from 18.90 cm in DPL-21 to 29.06 cm in DPL-17. Long panicles were also observed in DPL-24 (28.43 cm), DPL-11 (26.97 cm) and DPL-19 (26.90 cm).

Spikelet characteristics and fertility : The number of total spikelets per panicle ranged from 84.00 in DPL-21 to 210.00 in DPL-19, with an overall mean of 146.00. Number of filled grains per panicle ranged between 66.00 (DPL-21) and 178.00 (DPL-19), averaging 112.00. Genotypes DPL-19 (210 total, 178 filled), DPL-11 (202 total, 151 filled), and DPL-1 (194 total, 165 filled) showed higher spikelet counts. Spikelet fertility ranged from 66.52% (DPL-17) to 85.32% (DPL-14), averaging 76.78%.

Test weight : 1,000-grain weight ranged from 14.31 g in DPL-3 to 33.09 g in DPL-22, with a mean of 22.95 g. High test weights were also recorded in DPL-4 (30.23 g), DPL-15 (27.71 g), and DPL-12 (27.05 g).

Grain yield, straw yield, and harvest index : Grain yield per plant averaged 15.50 g, varying from 11.67 g in DPL-13 to 25.69 g in DPL-19. The top-yielding genotypes were DPL-19 (25.69 g), DPL-11 (22.43 g), DPL-1 (21.93 g), DPL-23 (20.05 g), and DPL-4 (19.53 g). Straw yield per plant ranged from 18.35 g (DPL-2) to 31.19 g (DPL-19), averaging 23.40 g. Harvest index averaged 39.58%, with values ranging from 32.09% in DPL-9 to 45.24% in DPL-19.

Number of filled grains per panicle : Exhibited a wide range from 66 (DPL-21) to 178 (DPL-19) with a general mean of 112. High grain numbers per panicle were produced by DPL-19 (178) and DPL-1 (165).

Number of total spikelets per panicle : Ranged from 84 (DPL-21) to 210 (DPL-19) with a mean value of 146. DPL-19 (210) followed by DPL-11 (202) produced the highest total spikelet count.

Crude protein content (%) : Varied from 3.26% (DPL-24) to 8.68% (DPL-3) around a mean of 6.31%. Genotypes DPL-3 (8.68%), DPL-11 (8.54%), and DPL-1 (8.54%) were superior donors for protein improvement.

Amylose content (%) : Ranged between 17.58% (DPL-16) and 22.37% (DPL-2) with an average mean of 19.88%. Values spanned from low (<20%) to intermediate (20–25%) amylose classes.

Total carbohydrate content (%) : Ranged from 70.38% (DPL-4) to 88.00% (DPL-19) with a general mean of 81.01%. Maximum carbohydrate concentration was recorded in DPL-19 (88.00%) and DPL-14 (87.39%).

Fat content (%) : Varied from 14.11% (DPL-5) to 18.87% (DPL-15) with an overall mean of 15.80%. Highest fat accumulation was observed in DPL-15 (18.87%) and DPL-19 (17.83%).

Iron (Fe) content (ppm) : Ranged between 10.20 ppm (DPL-25) and 20.60 ppm (DPL-14) with a general mean of 16.19 ppm. DPL-14 (20.60 ppm) and DPL-9 (19.45 ppm) were identified as rich sources of iron.

Zinc (Zn) content (ppm) : Varied from 6.80 ppm (DPL-6) to 18.70 ppm (DPL-16) with a population mean of 11.18 ppm. Promising zinc donors were DPL-16 (18.70 ppm) and DPL-11 (15.30 ppm).

Calcium (Ca) content (ppm) : Exhibited a wide spectrum from 52.38 ppm (DPL-4) to 113.02 ppm (DPL-1) around a mean of 86.41 ppm. Highest calcium levels were documented in DPL-1 (113.02 ppm) and DPL-17 (110.20 ppm).

Components of variation

Phenotypic, genotypic and environmental variance constituted the entire populations variation. The estimations of these three variance components for nineteen characters provided in Table 2.

Table 2 : Estimates of Components of variation for yield contributing components.

S. no.	Characters	σ^2p	σ^2g	σ^2e
1	Days to fifty percent flowering	154.79	153.39	1.40
2	Days to maturity	162.75	160.70	2.05
3	Number of productive tillers per plant	1.63	1.45	0.17
4	Panicle length (cm)	7.32	5.33	2.00
5	Plant height (cm)	684.70	669.48	15.22
6	Grain yield per plant (g)	16.77	14.22	2.55
7	Straw yield per plant (g)	18.89	12.35	6.54
8	Harvest Index (%)	14.98	10.81	4.17
9	Test weight (g)	18.33	18.11	0.22
10	Number of filled grains per panicle	995.37	982.56	12.81
11	Number of total spikelets per panicle	1481.95	1457.86	24.09
12	Spikelet fertility (%)	34.76	29.32	5.44
13	Protein (%)	2.19	2.14	0.06
14	Amylose (%)	2.16	1.71	0.45
15	Carbohydrate (%)	19.46	15.78	3.69
16	Fat (%)	2.72	1.29	1.43
17	Iron (ppm)	7.44	6.53	0.91
18	Zinc (ppm)	8.33	7.65	0.68
19	Calcium (ppm)	349.11	304.74	44.37

For various yield attributing traits, the phenotypic, genotypic, and environmental variations varied from 1.62 to 1481.95, 1.29 to 1457.86 and 0.17 to 44.37 respectively. Typically, phenotypic variations were higher in magnitude than genotypic and environmental variances. The phenotypic variance was higher for number of total spikelets per panicle (1481.95) followed by number of filled grains per panicle (995.37), plant height (684.70), calcium (ppm) (349.11) and days to maturity (162.75). The genotypic variance was higher for number of total spikelets per panicle (1457.86) followed by number of filled grains per panicle (982.56), plant height (669.48), calcium content (304.74) and days to maturity (160.70). The environmental variance was maximum for calcium content (44.37) followed by number of total spikelets per panicle (24.09) followed by number of filled grains per panicle (12.81) and plant height (15.22). For each of the

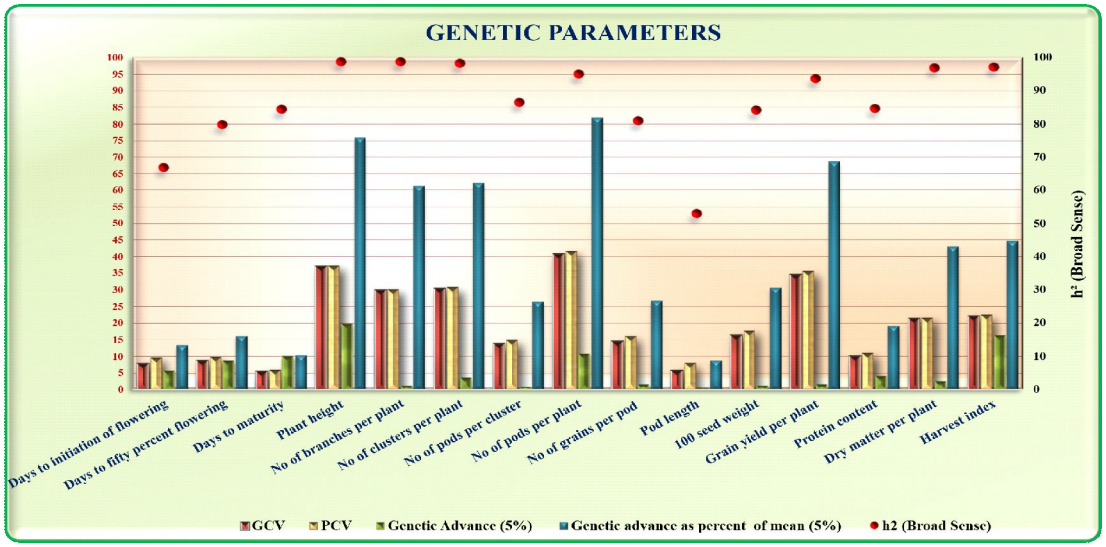


Fig. 1 : GCV, PCV, Genetic advancement 5%, Gen. Adv as % of mean 5% and Heritability (h^2bs) in green gram.

nineteen characters, the environmental variation was smaller than the genotypic variances. This showed that environmental variables compared to genotypic variables were more important for the expression of these traits. Khaire *et al.* (2017), Rashid *et al. (*2017), Saha *et al.* (2019) and Sadimantara *et al.* (2021) recorded the similar type of results but Chuchert *et al.* (2018) observed higher phenotypic and genotypic variance in yield per plant followed by number of total spikelets per panicle.

Coefficient of variation

The estimates of the coefficient of variation at the phenotypic (PCV), genotypic (GCV), and environmental levels are provided in Table 3.

Normally, phenotypic coefficients of variation (PCV) were greater in magnitude than the corresponding genotypic coefficients of variation (GCV) and environmental coefficients of variation (ECV). The phenotypic coefficient of variation (PCV) was observed highest in the trait number of filled grains per panicle (28.12) followed by grain yield per plant (26.42), number of total spikelets per panicle (26.35), zinc content (25.81), protein content (23.46), plant height (22.53) and calcium content (21.62). whereas the characters carbohydrate content (5.45) recorded minimum phenotypic coefficient of variation followed by amylose content (7.39), spikelet fertility (7.68) and harvest index (9.78).

Genotypic coefficient of variation (GCV) is a quantitative measure of the level of genetic variation exists within a population. The genotypic coefficient of variation was observed highest in number of filled grains per panicle (27.94) followed by number of total spikelets per panicle (26.13), zinc content (24.74), grain yield per plant (24.33), protein content (23.14), plant height (22.28) and calcium content (20.20), while the characters carbohydrate content (4.90) recorded minimum genotypic coefficient of variation followed by amylose content (6.57), spikelet fertility (7.05), fat content (7.19) harvest index (8.31), panicle length (9.81) and days to maturity (9.97).

Similar type of findings for both phenotypic and genotypic coefficient of variation were observed by Khaire *et al.* (2017), Srivastava *et al.* (2017), Rashid *et al.* (2017) and Saha *et al.* (2019), but in contrast Nayak *et al.* (2016) reported higher PCV and GCV in number of productive tillers per plant followed by number of filled grains per panicle. Adhikari *et al.* (2018), Chuchert *et al.* (2018) and Yadav *et al.* (2022) observed higher PCV and GCV in grain yield per plant.

Heritability and Genetic advance

The estimates of broad sense heritability, genetic advance and genetic advance as percent of mean is given in Table 3.

The heritability in a broad sense varied from 47.67 (fat %) to 99.10 (days to fifty percent flowering), indicate that the currently studied characters showed significant high heritability except for fat (%), which showed moderate heritability (47.67%). Similar results were obtained by Rashid *et al.* (2017) and Chuchert *et al.* (2018). Sadimantara *et al.* (2021) reported highest heritability in days to maturity followed by total spikelets per panicle. Khaire *et al.* (2017) and Srivastava *et al.* (2017) observed highest heritability in number of total spikelets per panicle followed by number of filled grains per panicle. Srinivas *et al.* (2016) and Saha *et al.* (2019) reported highest heritability in test weight.

The genetic advance was ranged from 1.61 for fat % to 78.01 for number of total spikelets per panicle. The

Table 3 : Estimates of coefficient of variation, heritability and genetic advance for yield contributing components in rice.

S. no.	Characters	ECV	GCV	PCV	h^2b	GA	GAM%
1	Days to fifty percent flowering	1.22	12.77	12.83	99.10	25.40	26.19
2	Days to maturity	1.13	9.97	10.03	98.74	25.95	20.41
3	Number of productive tillers perplant	5.96	17.41	18.41	89.51	2.35	33.94
4	Panicle length (cm)	6.00	9.81	11.50	72.76	4.06	17.24
5	Plant height (cm)	3.36	22.28	22.53	97.78	52.71	45.38
6	Grain yield per plant (g)	10.29	24.33	26.42	84.82	7.16	46.16
7	Straw yield per plant (g)	10.93	15.02	18.57	65.37	5.85	25.01
8	Harvest Index (%)	5.16	8.31	9.78	72.19	5.76	14.54
9	Test weight (g)	2.05	18.54	18.65	98.79	8.71	37.96
10	Number of filled grains perpanicle	3.19	27.94	28.12	98.71	64.16	57.18
11	Number of total spikelets perpanicle	3.36	26.13	26.35	98.38	78.01	53.39
12	Spikelet fertility (%)	3.04	7.05	7.68	84.36	10.25	13.34
13	Protein (%)	3.82	23.14	23.46	97.35	2.97	47.04
14	Amylose (%)	3.39	6.57	7.39	78.99	2.39	12.03
15	Carbohydrate (%)	2.37	4.90	5.45	81.06	7.37	9.09
16	Fat (%)	7.57	7.19	10.44	47.47	1.61	10.21
17	Iron (ppm)	5.89	15.79	16.85	87.80	4.93	30.47
18	Zinc (ppm)	7.37	24.74	25.81	91.86	5.46	48.85
19	Calcium (ppm)	7.71	20.20	21.62	87.29	33.60	38.88

magnitude of genetic advance was observed highest for the characters number of total spikelets per panicle (78.01), number of filled grains per panicle (64.16), plant height (52.71), calcium content (33.60), days to maturity (25.95) and days to fifty percent flowering (25.40), while moderate magnitude of genetic advance was observed by the spikelet fertility (10.25) and rest characters recorded low estimates of genetic advance. Khaire *et al.* (2017), Srivastava *et al.* (2017) and Saha *et al.* (2019) observed similar results which support the present results, but Chuchert *et al.* (2018) recorded higher genetic advance in grain yield per plant.

The genetic advance as percent of mean was varied from 9.09 for the carbohydrate % to57.18 for number of filled grains per panicle indicating low to high genetic advance as percent of mean for all the characters under study. The genetic advance as percent of mean was recorded low by carbohydrate content (9.09) and moderate by the characters fat content (10.21), amylose content (12.03), spikelet fertility (13.34), harvest index (14.54) and panicle length (17.24), while the rest characters show high genetic advance as per cent of mean. Same kind of results for genetic advance as percent of mean were found by Rashid *et al.* (2017), Srivastava *et al.* (2017) and Saha *et al.* (2019), which support the current results.

Broad sense heritability provides information on the portion of reported variability that can be linked to genetic variations. Heritability by itself cannot tell us how much of anything is inherited. In current study, high heritability coupled with high genetic advance were recorded for all the characters excepts for amylose %, spikelet fertility, harvest index, panicle length, fat % and carbohydrate %. Khaire *et al.* (2017), Srivastava *et al.* (2017), Sadimantara *et al.* (2021) observed similar results which support the present results.

High heritability coupled with low genetic advance as percent of mean was reported for carbohydrate content (81.06%, 9.09%, respectively) indicate the influence of non-additive gene action. Therefore, it is suggested to use suitable selection procedure for improvement of these characters since high heritability coupled with high genetic advance suggest the presence of less environmental influence and additive gene action in their expression.

Conclusion

In conclusion, it is noted that the genotypes investigated for the various quantitative characteristics showed a significant range of variability. The results of the current research experiment show the wide range of variability for different traits, high heritability coupled with high genetic advance as percentage of mean for all yield contributing traits except carbohydrate (%), fat (%), amylose (%), spikelet fertility, harvest index and panicle length. Selections based on the traits which exhibit high heritability with high genetic advance as percentage of

mean could directly increase productivity in rice.

The genotype DPL-19 found superior for the characters grain yield per plant, straw yield per plant, harvest index, number of filled grains per panicle, number of total spikelets per panicle and carbohydrate per cent among all the studied genotypes. The highest protein per cent and lowest test weight was observed in DPL-3. DPL-15 showed the highest Fat % among all the studied genotypes. DPL-14, DPL-16 and DPL-1 observed superior for the parameters iron content, zinc content and calcium content respectively. DPL-19, DPL-1, DPL-11, DPL-14, DPL-15, DPL-23, DPL-4, DPL-2, DPL-17, DPL-3, DPL-22 and DPL-16 were reported best for yield and yield contributing characters.

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