



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.211>

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN WILD AND CULTIVATED ACCESSIONS OF RICE (*Oryza sativa* L.)

Uma Bharti¹, Daisy Basandrai^{2*} and Ashwani Basandrai³

¹Department of Genetics and Plant Breeding, CSK HPKV, Palampur (HP)-176062, India

²ICAR- National Institute of Biotic Stress Management, Baronda (Chhattisgarh)-493225, India

³Department of Plant Pathology, CSK HPKV, Palampur (HP)-176062, India

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

(Date of Receiving : 27-03-2026; Date of Revision : 13-05-2026; Date of Acceptance : 03-06-2026)

ABSTRACT

The present investigation was conducted during *Kharif* 2021 to assess the magnitude of genetic variability, heritability and genetic advance in 30 accessions of wild and cultivated rice. Analysis of variance revealed significant differences among accessions for the majority of the traits studied except kernel length, kernel breadth and L: B ratio, indicating the presence of considerable genetic diversity in the test material. High phenotypic (PCV) and genotypic (GCV) coefficients of variation were recorded for grain yield/plant (38.44% and 37.00%) and harvest index (37.02% and 35.69%), while low PCV and GCV values were recorded for milling (%) and head rice recovery (%). High broad-sense heritability ($h^2_{bs} > 80\%$) was observed for 17 traits, with the highest values recorded for biological yield/plant (98.41%), days to 75% maturity (98.21%) and plant height (97.97%). High heritability coupled with high genetic advance as a percentage of mean was observed for grain yield/plant (92.62%; 73.35%), harvest index (92.96%; 70.88%) and number of spikelets/panicle (93.65%; 52.57%), indicating predominance of additive gene action and the effectiveness of direct selection for these traits. The results highlight the potential of wild rice accessions as rich sources of genetic diversity for rice improvement programmes.

Keywords : Additive, Genetic advance, Genetic variability, Heritability, PCV.

Introduction

Rice (*Oryza sativa* L.) is one of the most important staple crops, serving as the primary food source for more than half of the global population, especially in Asia, Africa and Latin America. It contributes about 23% of per capita energy intake and 16% of per capita protein intake worldwide (FAO, 2022). With the global population expected to reach 9.7 billion by 2050, rice production must rise substantially to ensure food security, making the identification of high-yielding and genetically diverse germplasm a priority.

The genus *Oryza* includes 24 species, of which *O. sativa* L. and *O. glaberrima* are cultivated. Wild rice accessions harbours novel alleles for yield, stress tolerance and grain quality traits that were largely eroded from elite cultivars during the domestication process (Sweeney and McCouch, 2007; Khush, 2005).

Genetic variability is the cornerstone of any successful plant breeding programme. The evaluation of variability parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2_{bs}) and genetic advance (GA) as a percentage of mean is essential for the selection of desirable genotypes [Johnson *et al.*, 1955; Burton and De Vane, 1953]. While PCV reflects the total variation observed in a trait, GCV represents only the portion attributable to genetic differences among genotypes. The ratio of genetic to phenotypic variance, expressed as heritability, indicates the reliability of a trait's phenotypic value as a guide to its breeding value. Genetic advance, in combination with heritability, helps determine whether the observed variation is mainly due to additive or non-additive gene action (Falconer and Mackay, 1996).

Several workers have assessed genetic diversity in cultivated and wild rice germplasm and reported a

wide range of variability for economic traits [Swain *et al.*, 2017; Koli *et al.*, 2020; Bhargavi *et al.*, 2021]. However, comprehensive studies encompassing both wild and cultivated accessions under the same agro-climatic conditions and covering phenological, yield-contributing and grain quality traits simultaneously, remain relatively scarce. Such integrated evaluations are necessary to identify donor parents possessing superior alleles for pyramiding through conventional or marker-assisted breeding.

The present study was therefore undertaken to estimate the extent of genetic variability, heritability and genetic advance for 19 agronomic and quality traits in 30 accessions of *Oryza* spp. (including wild and cultivated ones), with a view to identifying promising genotypes for use in rice improvement.

Materials and Methods

Plant Material and Experimental Design

Thirty accessions representing wild and cultivated (*O. sativa*) rice species were evaluated during the *Kharif* 2021 growing season. The experiment was laid out in a Randomized Block Design (RBD) with two replications. Each accession was transplanted in a plot of two rows, 5 m in length, with row-to-row and plant-to-plant spacing of 20 cm × 15 cm. Recommended agronomic practices and plant protection measures were followed throughout the crop growing period.

Traits Recorded

Data were recorded on 19 traits viz., days to 50% flowering, days to 75% maturity, plant height (cm), total tillers/plant, flag leaf length (cm), panicle length (cm), number of branches/panicle, number of spikelets/panicle, spikelet fertility (%), biological yield/plant (g), 1000-grain weight (g), grain yield/plant (g), harvest index (%), kernel length (mm), kernel breadth (mm), L: B ratio, hulling (%), milling (%) and head rice recovery (%). Observations were recorded on five randomly selected plants per accession per replication.

Statistical Analysis

Analysis of variance (ANOVA) was performed following the standard procedure of Panse and Sukhatme (1985) at 5% level of significance. Parameters of genetic variability i.e., PCV, GCV, h^2_{bs} and GA as % of mean, were estimated following the methods of Burton and De Vane (1953) and Johnson *et al.*, (1955). PCV and GCV values were categorised as high (>30%), moderate (15-30%) or low (<15%); heritability values as high (>80%), moderate (50-80%) or low (<50%) and GA as % of mean as high (>50%), moderate (25-50%) or low (<25%).

Results and Discussions

Analysis of Variance

The analysis of variance for 19 yield and yield-contributing traits in 30 accessions of *Oryza* spp. are presented in Table 1. Significant differences ($p \leq 0.05$) were recorded among accessions for various traits viz., days to 50% flowering, days to 75% maturity, plant height, total tillers/plant, flag leaf length, panicle length, number of branches/panicle, number of spikelets/panicle, spikelet fertility (%), biological yield/plant, 1000-grain weight, grain yield/plant, harvest index, hulling (%), milling (%) and head rice recovery (%), whereas kernel length, kernel breadth and L: B ratio were found non-significant. The significant differences among the accessions for the traits inferred wide and huge genetic variability among the test material studied. Swain *et al.*, (2017) observed significant differences for all the traits studied among different accessions of *O. nivara* and *O. rufipogon*. The present results of significant differences for various traits viz., days to 50% flowering, days to maturity, effective tillers, plant height, panicle length, panicle weight, filled grain, unfilled grain, number of grains/panicle, spikelet fertility, 1000-grain weight and total grain weight, etc. were corroborated by earlier workers (Koli *et al.*, 2020). These results were also in close conformity with similar findings of Devi *et al.* (2016); Jan *et al.* (2020); Bhargavi *et al.* (2021) and Gupta *et al.* (2022).

Table 1: Analysis of variance for 19 traits in 30 accessions of *Oryza* spp. (*Kharif* 2021)

Source of variation	Mean sum of squares		
	Replication	Treatment	Error
Df	1	29	29
Days to 50% flowering	3.27	125.86*	1.65
Days to 75% maturity	1.35	138.16*	1.25
Plant height (cm)	0.01	394.92*	4.06
Total tillers/plant	0.20	5.38*	0.33
Flag leaf length (cm)	2.09	21.38*	3.11
Panicle length (cm)	0.13	14.65*	1.46

Number of branches/panicle	0.04	3.54*	0.44
Number of spikelets/panicle	236.02	5433.61*	178.33
Spikelet fertility (%)	15.01	253.20*	7.52
Biological yield/plant (g)	40.11	225.34*	1.81
1000-grain weight (g)	2.27	30.36*	0.84
Grain yield/plant (g)	0.11	24.77*	0.94
Harvest index (%)	4.68	119.67*	4.37
Kernel length (mm)	0.00	0.54	0.02
Kernel breadth (mm)	0.00	0.09	0.00
L: B ratio	0.00	0.34	0.02
Hulling (%)	0.28	71.15*	2.04
Milling (%)	1.02	27.59*	2.11
Head rice recovery (%)	0.21	28.41*	2.36

*Significant at 5% level of significance

Estimation of parameters of variability

The estimates of mean performance, range, PCV, GCV, h^2_{bs} and GA as % of mean for all 19 traits are presented in Table 2. In all cases, PCV exceeded GCV, confirming that phenotypic expression of quantitative traits is mostly influenced by environmental factors (Singh *et al.*, 2011; Aditya *et al.*, 2016). Crucially, the difference between PCV and GCV was small for most of the traits studied, implying that observed phenotypic variation had a genetic rather than an environmental basis and supporting the reliability of phenotypic selection.

Phenotypic and genotypic coefficient of variation

High PCV (>30%) was recorded for harvest index (37.02%) and grain yield/plant (38.44%), indicating that the substantial variation was influenced by both genotype and environment. Grain yield in rice is a complex, polygenic trait shaped by various developmental and physiological processes, and a high coefficient of variation indicates that the accessions cover a broad phenotypic spectrum, which is a prerequisite for successful selection and hybridization (Eberhart and Russell, 1966). Moderate PCV (15-30%) was recorded for plant height (15.47%), total tillers/plant (23.88%), panicle length (15.19%), number of branches/panicle (18.57%), number of spikelets/panicle (27.25%), spikelet fertility (%) (15.95%), biological yield/plant (23.77%) and 1000-grain weight (19.07%). Low PCV (<15%) was recorded for days to 50% flowering (8.60%), days to 75% maturity (7.25%), flag leaf length (13.00%), kernel length (9.12%), kernel breadth (12.18%), L: B ratio (11.86%), hulling (%) (8.46%), milling (%) (6.07%), and head rice recovery (%) (6.74 %). Similar patterns of PCV distribution were reported by Chouhan *et al.* (2014) in 35 wild rice accessions and by Bhati *et al.* (2015) in elite rice genotypes.

The genotypic coefficient of variation (GCV) pattern closely paralleled that of phenotypic coefficient of variation (PCV). High GCV (>30%) was confined to grain yield/plant (37.00%) and harvest index (35.69%), while moderate GCV (15-30%) was recorded for plant height (15.31%), total tillers/plant (22.48%), number of branches/panicle (16.40%), number of spikelets/panicle (26.37%), spikelet fertility (%) (15.49%), biological yield/plant (23.57%) and 1000-grain weight (18.55%). Low GCV (<15%) was recorded for days to 50% flowering (8.49%), days to 75% maturity (7.18%), flag leaf length (11.23%), panicle length (13.74%), kernel length (8.87%), kernel breadth (11.69%), L: B ratio (11.22%), hulling (%) (8.34%), milling (%) (5.62%) and head rice recovery (%) (6.20%). The notably small difference between PCV and GCV values, especially for yield-contributing traits, indicates low environmental influence on these traits and thus suggests phenotypic selection, a conclusion corroborated by Singh *et al.*, (2011) and Aditya *et al.*, (2016).

Broad-sense heritability (h^2_{bs})

Broad-sense heritability (h^2_{bs}) estimates ranged from 75.49% (flag leaf length) to 98.41% (biological yield/plant). High heritability (>80%) was recorded in 17 traits out of 19 traits viz., days to 50% flowering (97.42%), days to 75% maturity (98.21%), plant height (97.97%), total tillers/plant (88.60%), panicle length (81.84%), number of spikelets/panicle (93.65%), spikelet fertility (94.23%), biological yield/plant (98.41%), 1000-grain weight (94.60%), grain yield/plant (92.62%), harvest index (92.96%), kernel length (94.56%), kernel breadth (92.06%), L: B ratio (89.45%), hulling (97.10%), milling (85.81%) and head rice recovery (84.68%). Moderate heritability (50–80%) was recorded only for flag leaf length (75.49%) and number of branches/panicle (77.89%),

while none of the traits exhibited low heritability (<50%).

High heritability indicates that a large proportion of observed phenotypic variation is genetically determined, which indicates that the selection based on phenotypic performance will lead to the identification of genetically superior individuals. These results align with Devi *et al.* (2016), who observed high heritability for effective tillers/plant, plant height, flag leaf length and grain yield/plant in 27 rice genotypes and with Nath *et al.*, (2021), who reported similarly high heritability for days to 50% flowering, plant height and test weight in 26 diverse rice genotypes. Comparable findings were also reported by Sarker *et al.* (2020), Bhargavi *et al.* (2021) and Gupta *et al.* (2022). However, it is important to note that heritability alone is an incomplete guide to selection response, so genetic advance must be studied along with heritability to determine the true effectiveness of selection.

Genetic Advance as Percentage of Mean

Genetic advance as a percentage of mean (GA%) ranged from 10.73% (milling %) to 73.35% (grain yield/plant). High GA% (>50%) was recorded for grain yield/plant (73.35%), harvest index (70.88%) and number of spikelets/panicle (52.57%). A high value of GA% is indicative of predominantly additive gene effects governing trait expression, meaning that selection would be useful and rewarding for the improvement of such traits (Johnson *et al.*, (1955); Singh and Chaudhary, 1985).

Moderate GA% (25-50%) was observed for plant height (31.22%), total tillers/plant (43.58%), panicle length (25.61%), number of branches/panicle (29.80%), spikelet fertility (30.97%), biological yield/plant (48.19%) and 1000-grain weight (37.17%), suggesting involvement of both additive and non-additive effects and indicating that moderate genetic improvement through selection is achievable. Low GA (<25%) was observed for days to 50% flowering (17.25%), days to 75% maturity (14.66%), flag leaf length (19.98%), kernel length (17.77%), kernel breadth (23.10%), L: B ratio (22.85%), hulling (%) (16.93%), milling (%) (10.73%) and head rice recovery (%) (11.75%), reflecting the predominance of non-additive gene effects or a narrow range of actual genetic variation, which would limit the effectiveness of simple directional selection (Lingaiah *et al.*, (2014); Shrivastava *et al.* (2015)).

Heritability and Genetic Advance: Combined Interpretation and Implications

The combined analysis of heritability and genetic advance provides a far more reliable framework for

guiding selection programmes. Three distinct patterns emerged from the present data.

High heritability (>80%) coupled with high GA% (>50%) was recorded for the number of spikelets/panicle, harvest index and grain yield/plant. This combination is the most favourable for a plant breeder, as it determines the additive gene effects and phenotypic selection will lead to efficient improvement (Panse and Sukhatme, 1985). Mass selection, pedigree selection and recurrent selection schemes are therefore expected to be more useful in future for the improvement of these traits. These findings are in agreement with Chouhan *et al.* (2014), who reported the same pattern for fertile spikelets/panicle and grain yield/plant in 35 wild rice accessions and with Yadav *et al.* (2022) for various yield-contributing traits. Corroborating results were also reported by Sarker *et al.* (2020) and Chamar *et al.* (2021).

High heritability coupled with moderate GA% (25-50%) was observed for plant height, total tillers/plant, panicle length, spikelet fertility, biological yield/plant and 1000-grain weight. Although heritability is high for these traits, the moderate GA% suggests that both additive and non-additive gene effects contribute meaningfully to their variance. Hybridization strategies that capture both additive and dominance effects, such as single-seed descent in biparental populations, may be particularly effective (Kearsey and Pooni, 1996).

High heritability coupled with low GA% (<25%) was recorded for kernel length, kernel breadth, L: B ratio, hulling (%), milling (%) and head rice recovery (%). This pattern shows involvement of non-additive genetic variance (dominance and epistasis) rather than the additive component that responds to selection. For such traits, exploitation of heterosis through hybrid breeding or generation mean analysis would be a more informative approach before designing selection schemes. Grain yield/plant, harvest index and number of spikelets/panicle emerge as the primary targets for direct phenotypic selection among the 30 accessions of *Oryza* spp., while plant height, total tillers/plant, biological yield/plant and 1000-grain weight also offer reasonable selection prospects. Wild rice accessions in particular represent largely untapped repositories of favourable alleles that can be strategically introgressed into elite cultivated backgrounds to broaden the genetic base and enhance yield potential, provided that appropriate pre-breeding strategies are employed to overcome barriers associated with interspecific hybridisation.

Conclusion

The present study revealed wide genetic variability among 30 accessions of *Oryza* spp. for most of the 19 traits studied. High heritability coupled with high genetic advance as a percentage of mean was recorded for grain yield/plant, harvest index and number of spikelets/panicle, confirming the role of additive gene effects and indicating the effectiveness of direct selection for these characters. Traits such as days to maturity, kernel length, kernel breadth, L: B ratio, milling (%), hulling (%) and head rice recovery (%)

exhibited high heritability with low genetic advance and are likely to be governed by non-additive gene action. The study underlines the importance of wild rice accessions as valuable sources of genetic diversity for incorporation into rice improvement programmes. Accessions exhibiting high grain yield/plant, spikelet fertility and harvest index merit priority attention in hybridization and selection schemes aimed at developing high-yielding and broad genetic-based rice varieties.

Table 2: Estimates of parameters of variability for 19 yield and yield-contributing traits in 30 accessions of *Oryza* spp. (Kharif 2021)

Traits	Mean $\pm$ SE	Range	PCV %	GCV %	h^2_{bs} (%)	GA as % of mean
Days to 50% flowering	92.87 $\pm$ 0.91	83.00-121.00	8.60	8.49	97.42	17.25
Days to 75% maturity	115.22 $\pm$ 0.79	101.00-140.00	7.25	7.18	98.21	14.66
Plant height (cm)	91.31 $\pm$ 1.42	60.64-117.81	15.47	15.31	97.97	31.22
Total tillers /plant	7.08 $\pm$ 0.40	4.40-11.00	23.88	22.48	88.60	43.58
Flag leaf length (cm)	26.92 $\pm$ 1.25	20.95-34.45	13.00	11.23	75.49	19.98
Panicle length (cm)	18.69 $\pm$ 0.86	13.45-24.85	15.19	13.74	81.84	25.61
Number of branches/panicle	7.59 $\pm$ 0.47	5.30-11.25	18.57	16.40	77.89	29.80
Number of spikelets/panicle	194.38 $\pm$ 9.44	131.00-320.00	27.25	26.37	93.65	52.57
Spikelet fertility (%)	71.58 $\pm$ 1.94	46.75-90.67	15.95	15.49	94.23	30.97
Biological yield/plant (g)	44.86 $\pm$ 0.95	29.13-71.09	23.77	23.57	98.41	48.19
1000-grain weight (g)	20.71 $\pm$ 0.65	12.49-29.78	19.07	18.55	94.60	37.17
Harvest index (%)	21.28 $\pm$ 1.48	10.04-44.59	37.02	35.69	92.96	70.88
Kernel length (mm)	5.78 $\pm$ 0.09	4.86-6.79	9.12	8.87	94.56	17.77
Kernel breadth (mm)	1.64 $\pm$ 0.04	1.22-2.32	12.18	11.69	92.06	23.10
L: B ratio	3.56 $\pm$ 0.10	2.63-4.43	11.86	11.22	89.45	22.85
Hulling (%)	70.48 $\pm$ 1.01	60.66-82.63	8.46	8.34	97.10	16.93
Milling (%)	63.46 $\pm$ 1.03	56.79-72.98	6.07	5.62	85.81	10.73
Head rice recovery (%)	58.24 $\pm$ 1.09	51.24-68.38	6.74	6.20	84.68	11.75
Grain yield/plant (g)	9.33 $\pm$ 0.69	5.41-17.74	38.44	37.00	92.62	73.35

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