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Estimation of genetic variability, heritability and genetic advance in germplasm of rice (*Oryza sativa* L.) for yield and yield attributing traits under agro-climatic conditions of Chhattisgarh

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Abstract

Rice underpins global food security, feeding over four billion people and remaining central to livelihoods across Asia (IRRI 2023). This study evaluated genetic variability among the 45 rice germplasm genotypes, including three checks (ANJALI, IR64, MTU1010) during *Kharif* 2024 at IGKV, Raipur. A randomized complete block design with three replications assessed eleven yield-related traits. ANOVA revealed significant variability for all traits. PCV exceeded GCV across all traits, indicating environmental influence; Highest GCV (22.8) and PCV (26.78) is recorded for number of filled grains per panicle, while grain yield per plot showed the GCV (19.88) and PCV (23.57). The traits that exhibited both high heritability (>60%) and high genetic advance as% of mean (>20%) were days to 50% flowering (98.18, 29.06), number of filled grains per panicle (72.60, 40.05), number of total grains per panicle (70.38, 35.17), 100 seed weight (g) (94.44, 26.17), biological yield per plot (g) (69.76, 26.40), grain yield per plot(g) (71.14, 34.53), harvest index (62.68, 33.27) suggesting predominance of additive gene action and suitability for direct selection.

Keywords: Rice, genetic variability, heritability, genetic advance, yield traits, germplasm

Introduction

Rice (*Oryza sativa* L.), belonging to the grass family Poaceae, is a self-pollinating cereal crop with a diploid genome comprising $2n = 24$ chromosomes (*Oryza sativa* 2025) ^[11].

In 2023, global rice production reached approximately 800 million tonnes, with China and India together contributing over 50%, underlining the crop's central role in global food security (Rice 2025) ^[12].

Rice (*Oryza sativa* L.) is a global staple food that plays a vital role in ensuring food security and nutritional requirements for billions of people. Historically, Asian countries have dominated rice cultivation, with China contributing 27.99% of global rice production, followed by India with 23.56%. Other major producers include Bangladesh (7.25%), Indonesia (7.22%), Vietnam (5.65%), Thailand (3.99%), Myanmar (3.31%), Philippines (2.54%), Brazil (1.46%) and Cambodia (1.44%), together accounting for about 85% of global rice output (FAO 2024). Asia remains the epicenter of rice agriculture, contributing nearly 89.6% of global production (IRRI 2023) ^[5]. The global consumption of milled rice was estimated at 520.4 million tonnes in 2022-23, highlighting the crop's indispensable role in sustaining livelihoods worldwide (USDA-ERS 2023) ^[10].

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world, serving as the primary source of calories for more than half of the global population (IRRI 2023) ^[5]. It contributes significantly to food security, employment and income generation, especially in Asia where nearly 90% of the global rice is produced and consumed (FAO 2024). In developing countries, rice provides 20-50% of daily dietary energy, making it indispensable for nutrition and livelihood security (GRiSP 2013) ^[3].

In India, rice occupies about 44 million hectares, contributing over 40% of national food grain production and remains central to the agricultural economy and rural livelihoods (DA&FW 2025) ^[11]. Given its socio-economic importance, enhancing rice productivity through exploitation of genetic variability and adoption of improved cultivars is crucial to

meet the demands of a growing population under changing climate scenarios (Khush 2013) [6]. Understanding the genetic variability and heritable components in rice germplasm is crucial for effective selection and yield improvement (Singh *et al.*, 2021) [8]. Estimating genetic parameters like genotypic variance, heritability and genetic advance in rice germplasm is critical for identifying traits with strong additive genetic control and forecasting selection gains (Heera *et al.*, 2023) [4]. Recent studies in 2024 have not only confirmed substantial genetic variability in aus rice germplasm but also highlighted its use in breeding programs targeting yield and adaptation (Sar *et al.*, 2024) [7].

Materials and Methods

The investigation was conducted during Kharif-2024 at the Research-cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur,

Chhattisgarh, situated at 21°16' N Latitude, 81°37' E longitude and 289.6 m above mean sea level, under the Chhattisgarh plains agro-climatic zone. The experimental material comprised 45 germplasm accessions including three checks (ANJALI, IR64, MTU1010) sourced from 3k panel, IRRI Philippines. The experiment was laid out in Randomized Block Design using 48 genotypes or treatments in 2 replications during Kharif, 2024. The sowing was on 8th June, 2024.

Observations were recorded on ten quantitative traits: days to 50% flowering, plant height (cm), panicle length (cm), number of filled grains per panicle, total number of grains per panicle, spikelet fertility%, harvest index%, 100 seed weight (g), biological yield per plot (g), grain yield per plot (g). Data for genetic variability parameters including GCV, PCV, heritability (H^2) and genetic advance were computed following standard biometrical procedures.

Table 1: List of Experimental materials

Entry No.	Designation	Entry No.	Designation
1	KATUNG: IRGC 71536-1	25	NEANG AN: IRGC 81315-1
2	MANGSUR: IRGC 18187-1	26	IR 19746-28-2-2: IRGC 78072-C1
3	TAISEN GLUTINOUS YU 1157: IRGC 78750-1	27	FORTUNA BLANCO (SAN MARCOS): IRGC 50764-1
4	PICO NEGRO: IRGC 55849-1	28	NEANG LAU: IRGC 81328-1
5	KHAU TRA BONG: IRGC 78342-1	29	NIRA PRIETO: IRGC 51145-1
6	TJERE MANGGA: IRGC 19116-2	30	LAWANGAI: IRGC 49850-2
7	P PEY SIQAT: IRGC 8129-1	31	MAUNG NYO: IRGC 33351-2
8	TV 30: IRGC 55221-1	32	GADABUNG (GUNDIL): IRGC 17569-2
9	ZO: IRGC 56914-1	33	KALALAN: IRGC 33154-2
10	MALASAY: IRGC 19456-1	34	CHAN LEUY: IRGC 81223-1
11	PULUT CENRANA: IRGC 27400-2	35	C 1016-1: IRGC 50368-1
12	MEDUSA: GERVEX 323-C1	36	ARC 18001: IRGC 42195-2
13	CR 157-392-4: IRGC 39247-2	37	PAMPANGON (H): IRGC 60392-1
14	ARC 7263: IRGC 20570-2	38	C 662083: IRGC 62101-1
15	IR 57514-PMI 5-B-1-2: IRGC 117372-1	39	REMOL: IRGC 18624-1
16	DL 5: IRGC 8593-1	40	SADAJIRA 19-317: IRGC 38344-2
17	IR 31142-14-1-1-3-1-1-2: IRGC 117378-1	41	IR 63295-AC 209-7: IRGC 117365-1
18	IR 9560-2-6-3: IRGC 40451-1	42	MAE YEU: IRGC 64509-1
19	AUS 177: IRGC 29009-1	43	SICAN: IRGC 117029-1
20	TAUNGDI: IRGC 33746-2	44	GINAYANGGANG: IRGC 87131-1
21	THAKADE THEEDAT: IRGC 33772-2	45	CT 9506-18-7-1T-2: IRGC 116973-1
22	KAYANGYA D 402: IRGC 7927-2	46	Anjali
23	KUNENG: IRGC 71545-1	47	IR64
24	LUA CHAN HUONG: IRGC 16800-1	48	MTU1010

Results and Discussions

Genetic variability

Analysis of variance (ANOVA) revealed highly significant differences among the 48 rice genotypes for all the ten quantitative characters (Table 2), confirming substantial genetic variability. The wide range of genetic variability was observed for the traits like days to 50% flowering (74-138), plant height in cm (86.8-199.59), panicle length in cm (18.3-31.9), number of filled grains per panicle (72-282), total number of grains per Panicle (86-346), spikelet fertility (68.47-96.22), 100 seed weight (90.56-3.10), biological yield per plot (g) (602.51-1351.5), harvest index (20.63-55.90), grain yield per plot (g) (210-484.7) indicating ample scope for selection.

Among all the traits, the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation

(GCV), pointing to environmental influence on trait expression. Following the classification of Sivasubramanian and Madhavamenon (1973) [9], high PCV coupled high GCV was recorded for number of filled grains per panicle (GCV 22.8%, PCV 26.78%), total number of grains per panicle (GCV 20.35%, PCV 24.26%), harvest index (GCV 20.40%, PCV 25.77%) and seed yield per plant (GCV 20.00%, PCV 23.57%). Traits such as days to 50% flowering (GCV 14.24%, PCV 14.37%), plant height (GCV 10.76%, PCV 16.41%), 100 seed weight (GCV 13.07%, PCV 13.45) and biological yield per plot (g) (GCV 15.35%, PCV 18.38) exhibited moderate variability, in agreement with Yadav *et al.* (2022). Low variability was noted for panicle length (10.00% PCV, 8.38% GCV) and spikelet fertility (7.09% PCV, 6.80% GCV).

Table 2: Variability Assessment for Rice Traits Using ANOVA

S. No	Sources of variance	Mean sum of squares		
		Replication (df = 1)	Genotypes (df = 47)	Error (df = 47)
1.	Days to 50% flowering	78.84	393.98**	3.61
2.	Plant height (cm)	868.3300	821.49**	327.54
3.	Panicle length (cm)	10.940	12.24**	2.531
4.	Filled grains per panicle	173.3400	2783**	441.87
5.	Total grains per panicle	283.594	3096.95**	538.50
6.	Spikelet fertility percent	0.2800	67.76**	2.23
7.	100 seed weight (g)	0.0100	0.2**	0.006
8.	Biological yield per plant (g)	16970.54	47247.88**	8415.81
9.	Harvest Index (%)	5.8400	128.72**	29.540
10.	Grain yield per plant (g)	58.6600	8953.23**	1509.70

** Significance at 1% level of probability

High heritability was observed for days to 50% flowering (98.19%), panicle length (65.72%), number of filled grains per panicle (72.59%), total number of grains per panicle (70.38%), spikelet fertility percentage (93.62%), 100-seed weight (94.44%), biological yield per plot (g) (69.76%), harvest index percentage (62.68%) and grain yield per plot (71.14%), indicating these traits are predominantly governed by additive gene effects and less influenced by environmental factors, consistent with Aman *et al.* (2022). Moderate heritability was recorded for plant height (42.98%) suggesting partial environmental influence. Among yield traits, High levels of genetic advance as

percentage of the mean were noted for the traits including number of filled grains per panicle (40.05%), total number of grains per panicle (35.17%), days to 50% flowering, 100 seed weight (26.16%), biological yield per plot (26.40%), Harvest index (33.27%) and grain yield per plot (34.53%) among yield attributing traits, highlighting their potential for effective improvement through selection. Moderate genetic advances as% of the mean were found in traits such as plant height (14.53%), panicle length (13.99%), spikelet fertility percent (13.67%) indicating moderate selection response. No traits were recorded with low genetic advance as% of mean.

Table 3: Genetic variability parameters for yield attributing traits in rice genotypes

S. No	Traits	Mean	Range		Coefficient of Variation		h ²	GA as % of mean
			Max	Min	GCV	PCV		
1.	Days to 50% flowering	98.11	138.00	74.00	14.23	14.37	98.18	29.06
2.	Plant height (cm)	146.04	199.59	86.80	10.76	16.41	42.98	14.53
3.	Panicle length (cm)	26.29	31.90	18.30	8.38	10.33	65.72	13.99
5.	Number of filled grains per panicle	149.92	282	72.00	22.80	26.78	72.59	40.05
6.	Total number of grains per panicle	175.69	346	86.00	20.35	24.26	70.37	35.17
7.	Spikelet fertility percent	83.39	96.22	68.47	6.80	7.09	93.61	13.67
8.	100 seed weight (g)	2.40	3.10	1.56	13.07	13.45	94.43	26.16
9.	Biological yield per plot (g)	907.8	1351	602.5	15.34	18.37	69.76	26.40
10.	Harvest Index (%)	34.52	55.90	20.63	20.40	25.76	62.67	33.27
11.	Grain yield per plant (g)	306.93	484.70	210.0	19.87	23.56	71.14	34.53

Max = Maximum, Min = Minimum, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation, h² = Heritability in Broadsense, GA as% of mean = Genetic Advance as percent of mean

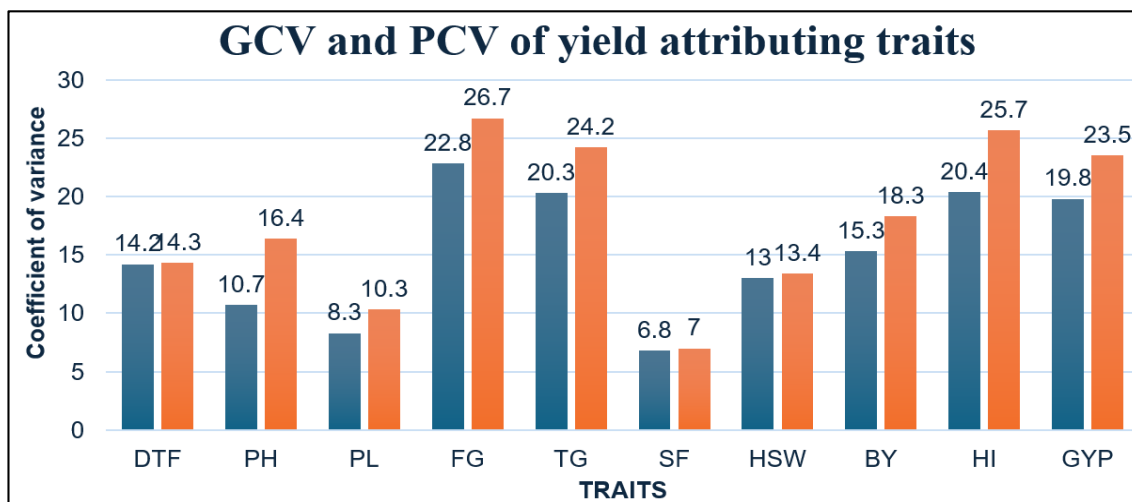


Fig 1: Graphical presentation of phenotypic and genotypic coefficient of variability for yield and its contributing traits

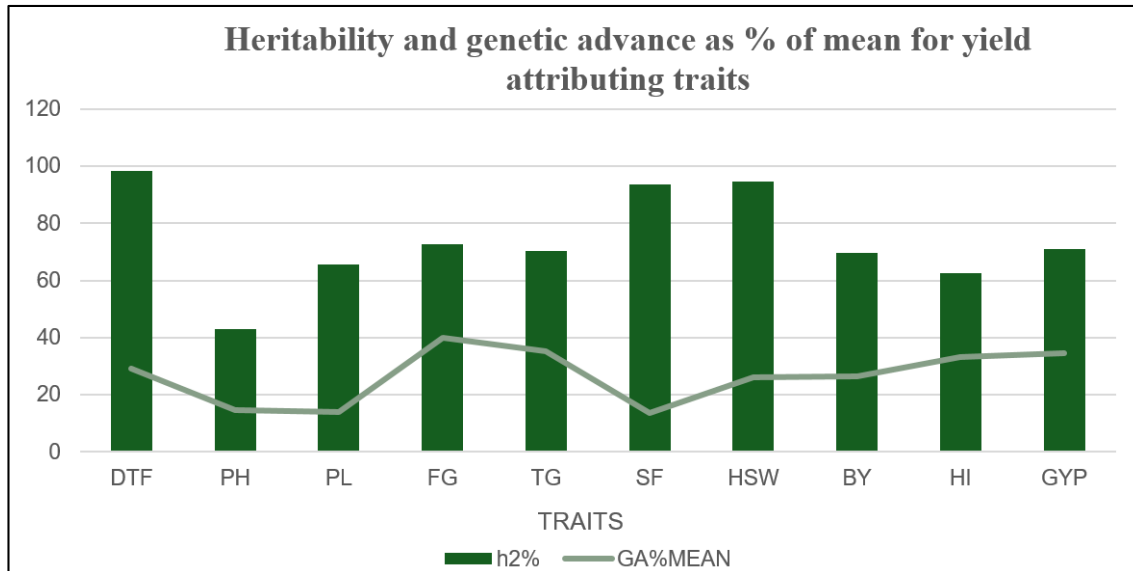


Fig 2: Graphical presentation of heritability and genetic advance as percent of means for yield and contributing traits

The traits that exhibited both high heritability and high genetic advance as% of mean were days to 50% flowering (98.18%, 29.06%), number of filled grains per panicle (72.59%, 40.05%), number of total grains per panicle (70.37%, 35.17%), 100 seed weight (g) (94.44%, 26.16%), biological yield per plot (g) (69.76%, 26.40%), grain yield per plot (g) (71.14%, 34.53%), harvest index percentage (62.67%, 33.27%) suggesting additive gene action and suitability for direct selection. Overall, grain yield per plot, harvest index, number of filled grains per panicle and total number of grains per panicle demonstrate substantial genetic variability, heritability and genetic advance, making them reliable selection indices for yield enhancement in rice.

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