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Genetic study of yield variation in medium to early duration irrigated rice (*Oryza sativa* L.) genotypes

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Abstract

An experiment was conducted during Kharif 2024 at BTC College of Agriculture and Research Station, Bilaspur, under IGKV, Raipur, to evaluate fourteen medium to early duration irrigated rice genotypes along with four checks (MTU-1010, US-312, CHANDRAHASINI, and Gontra Bidhan-3). Significant variability was observed for yield and yield-contributing traits, with high GCV, PCV, heritability, and genetic advance recorded for number of fertile spikelet's per panicle, biological yield, grain yield, and number of effective tillers per plant, indicating the predominance of additive gene action and their suitability for selection. Grain yield showed strong positive correlations with panicle length, effective tillers, biological yield, 1000-grain weight, spikelet's per panicle, flowering, maturity, L/B ratio, and plant height, suggesting their utility as selection criteria. Path analysis revealed that fertile spikelet's per panicle, days to maturity, biological yield, L/B ratio, and plant height exerted the highest positive direct effects on grain yield. Overall, genotypes HRI-216, RNC-0992, HRI-217, RRX-3341, and YNPK-7258 were superior in yield performance over all checks, indicating their promise for future improvement of medium to early duration irrigated rice.

Keywords: Rice (*Oryza sativa* L.), genetic variability, heritability, correlation coefficient and path analysis

1. Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world, belonging to the genus Oryza and family Poaceae. The genus Oryza comprises two cultivated and 22 wild species, of which *Oryza sativa* and *Oryza glaberrima* are grown commercially. Rice is primarily a self-pollinated crop with a remarkable adaptation to diverse ecological conditions, ranging from irrigated lowlands to upland rainfed systems. Globally, rice is considered the staple food for more than half of the world's population, serving as the cheapest and most accessible source of dietary carbohydrates. In many rice-growing countries, it contributes over 70% of daily caloric intake, underscoring its critical role in ensuring food and nutritional security.

In India, rice contributes significantly to both dietary energy and agricultural economy, providing nearly 43% of the caloric requirement of the human diet and generating about 20-25% of agricultural income due to its large-scale and intensive cultivation. Medium to early duration rice varieties are particularly important as they mature within 115-120 days, fitting well into multiple cropping systems and ensuring timely harvest with reduced risk of exposure to biotic and abiotic stresses. During 2023-24, global rice production was estimated at 521.52 million metric tonnes, with India ranking first in production. The country recorded an area of 49 million hectares under rice cultivation, producing nearly 147 million metric tonnes, which marked an increase of 16.17 million tonnes compared to the previous year (Anonymous, 2023-24) [2]. At the regional level, Chhattisgarh, known as the "Rice Bowl of India," plays a crucial role in national rice production. In 2023-24, the state reported about 3.91 million hectares under rice cultivation with a total production of 14.7 million tonnes (Anonymous, 2023-24) [2]. Given its dominance in the agrarian economy and daily diet, rice remains not only a vital staple food but also a strategic crop for addressing challenges of food security, livelihood improvement, and sustainable agricultural growth in India and beyond.

2. Materials and methods

The present investigation was conducted during Kharif 2024 at the Research Farm of Barrister Thakur Chhedilal College of Agriculture and Research Station, Bilaspur, under Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. The experiment comprised fourteen rice genotypes along with four standard checks, namely MTU-1010, US-312, CHANDRAHASINI, and Gontra Bidhan-3. Seedlings of all genotypes were first raised in a nursery bed and subsequently transplanted in the main field. Each genotype was grown in a plot size of 1.20 m × 9.50 m = 11.40 m^2 per entry per replication. The crop was managed with the recommended package of practices, including fertilizer application and intercultural operations, to ensure uniform growth. Observations were recorded on twelve quantitative traits using five competitive plants selected from each replication, and the averaged data were subjected to statistical analysis.

The variability among genotypes was assessed through analysis of variance following the procedure of Singh and Chaudhary (1985) [25]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Falconer (1964) [8]. Heritability (broad sense) was estimated using the method of Allard (1960) [1], and from these estimates, genetic advance (GA) was calculated following Burton and Devane (1953) [5]. Genetic advance as a percentage of mean was further classified into categories as suggested by Johnson *et al.* (1955) [12]. Correlation coefficients were estimated according to the formula proposed by Miller *et al.* (1958) [15], while path coefficient analysis was carried out based on the method suggested by Wright (1921) [28] and later elaborated by Dewey and Lu (1959) [7].

3. Results and discussion

3.1 Analysis of variance

The Analysis of variance of fourteen genotypes of rice with respect to twelve quantitative characters is presented in the Table 1. The analysis of variance for twelve characters revealed significant differences among the genotypes for all the traits studied. ANOVA was done based on mean values of twelve quantitative traits in fourteen rice genotypes. The ANOVA analysis (Table 1) indicated that the material used in the study possesses inherent variability among themselves. The range of variability indicated that biological yield (q/ha), number of fertile spikelet's per panicle, grain yield (q/ha), plant height (cm), days to 50% flowering and days to maturity had highly significant variability, indicating that parents should be of diverse origin and that these characteristics should be used for further selection.

3.2 Genetic parameter of variation

In this study, the PCV values were greater than GCV values with minimal differences for all the characters studied, indicating less effect on the expression of all studied traits. The high to moderate PCV and GCV (Table 2) were recorded for number of effective tillers per plant, biological yield (q/ha) and 1000 grains weight (g) respectively indicating that these traits were under the major influence of genetic control and less variable due to environmental factors. In the present experimental set, high heritability coupled with high genetic advance as percentage of mean was recorded for number of fertile spikelet's per panicle followed by biological yield (q/ha), number of effective tillers per plant and grain yield (q/ha). The above results indicated that these characters had additive gene effect indicating effectiveness of selection for the improvement of these traits in medium to early duration irrigated rice genotypes. Similar findings were revealed by Saran *et al.* (2023) [20], Faysal *et al.* (2022) [9], Jasmine *et al,* (2022) [11], Sheera *et al.* (2021) [22], Gupta *et al.* (2020) [10], Sravan *et al.* (2012) [26].

3.3 Correlation coefficient analysis

The correlation study (Table 3) revealed that Grain yield (q/ha) had strong positive association with plant height (r_g = 0.996** r_p = 0.321**), panicle length (r_g = 0.996** r_p = 0.687**), number of effective tillers per plant(r_g = 0.972** r_p = 0.680**), number of fertile spikelet's per panicle (r_g = 0.930** r_p = 0.840**),1000 grains weight (r_g = 0.932** r_p = 0.643**), biological yield(r_g = 0.935** r_p = 0.854**), paddy grain L/B ratio(r_g = 0.202 r_p = 0.129), paddy grain length(r_g = 0.448** r_p = 0.364), paddy grain width (r_g = 0.504** r_p = 0.36**) and days to 50% flowering (r_g = 0.372* r_p = 0.266) Similar findings were revealed by Singh *et al.* (2023) [23] for plant height, number of effective tillers per plant and number of fertile spikelet's per plant ; Katkani *et al.* (2019) [13] for panicle length, 1000 grains weight and number of fertile spikelet's per panicle, paddy grain L/B ratio; Bhujel *et al.*(2018) [3], for days to maturity, biological yield; Rathore *et al.* (2016) [19]; Bitew *et al.* (2018) [4] for days to 50% flowering, days to maturity and 1000 grains weight; Khare *et al.* (2014) [14] for days to 50% flowering, panicle length, number of fertile spikelet's per panicle; Singh *et al.* (2014) [24] for days to 50% flowering, number of fertile spikelet's per panicle, paddy grain length, paddy grain width.

3.4 Path coefficient analysis

Path coefficient analysis (Table 4 and Table 5) of the present material for twelve characters revealed that highest positive direct effect on grain yield at genotypic level was exhibited by number of fertile spikelet's per panicle followed by days to maturity, biological yield, paddy L/B ratio and plant height. Similar findings were revealed by Sudeepthi *et al.* (2020) [27] for test weight; Devi *et al.* (2019) [6] for panicle length, test weight, plant height and spikelet fertility(%); Katkani *et al.* (2019) [13] for days to 50% flowering, panicle length, test weight and total number of grains per panicle; Naseem *et al.* (2014) [16] for days to maturity and total number of grains per panicle; Nayak *et al.* (2016) [17] for panicle length, plant height and days to 50% flowering; Patil *et al.*(2016) [18] for days to 50% flowering, test weight, filled grains per panicle; Seyoum *et al.*(2012) [21] for total number of grains per panicle, days to 50% flowering, panicle length, spikelet fertility and test weight.

Table 1: Values of mean sum of squares of analysis of variance for grains yield and its components character in medium to early duration irrigated rice genotypes

S. No	Source of variation	Mean sum of square (MSS)		
		Replication	**Treatment**	**Error**
	Degree of freedom	**2**	**13**	**26**
1.	Days to 50% flowering	5.786	92.383**	5.35
2.	Days to maturity	0.881	56.535**	5.419
3.	Plant height (cm)	9.424	212.754**	60.697
4.	Panicle Length (cm)	0.5	20.434**	3.5
5.	Number of effective tillers per plant	0.31	3.179**	0.438
6.	Number of fertile spikelet's per panicle	4.952	788.082**	17.824
7.	1000 grains weight (g)	0.802	23.737**	2.407
8.	Grain yield (q/ha)	386.36	368.14**	52.57
9.	Biological yield (q/ha)	702.069	1067.536**	96.178
10.	Paddy L/B ratio	0.215	0.318**	0.043
11.	Paddy grain length(mm)	0.002	0.92**	0.052
12.	Paddy grain width(mm)	0.109	0.144**	0.029

**Significant at 1% probability level

Table 2: Genetic parameters of variation for grain yield and its component in early duration irrigated rice genotypes

S.No	Traits	Mean	CD	CV%	Coefficient of variance		h^2 (bs)	GA	GA as% of mean
					PCV	**GCV**			
1.	Days to 50% flowering	92.357	3.903	2.504	6.347	5.832	84.43	10.195	11.039
2.	Days to maturity	129.238	3.929	1.801	3.667	3.194	75.869	7.407	5.731
3.	Plant height (cm)	123.479	4.498	6.31	8.547	5.766	45.506	9.893	8.012
4.	Panicle Length (cm)	25.643	3.157	7.296	11.793	9.265	61.726	3.845	14.995
5.	Number of effective tillers per plant	5.333	1.117	12.405	21.799	17.925	67.615	1.619	30.363
6.	Number of fertile spikelet's per panicle	86.119	7.125	4.902	19.241	18.606	93.508	31.919	37.064
7.	1000 grains weight (g)	25.035	2.618	6.197	12.323	10.651	74.706	4.747	18.964
8..	Grain yield (q/ha)	62.467	12.236	11.607	20.107	16.419	66.677	17.25	27.618
9	Biological yield (q/ha)	146.658	16.551	6.687	13.97	12.26	77.099	32.548	22.193
10.	Paddy L/B ratio	3.254	0.349	6.363	11.27	9.302	68.121	0.515	15.815
11.	Paddy grain length(mm)	8.526	0.386	2.686	6.854	6.306	84.645	1.019	11.951
12.	Paddy grain width(mm)	2.631	0.285	6.423	9.837	7.451	57.369	0.306	11.625

**Significant at 1% probability level

NOTE- GCV=Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2 (bs)= Heritability broad sense, GA= Genetic advance, GAM= Genetic advance as percentage of mean

Table 3: Genotypic and phenotypic correlation matrix. (Above diagonal Phenotypic and below diagonal Genotypic)

	DFF	DM	PH	PL	ETPP	FSPP	TW	BY	L/B Ratio	Ple	PW	GY
DFF	1	0.809**	-0.236	0.113	0.162	0.161	0.026	0.397**	0.261**	0.210	-0.151	0.266**
DM	0.893**	1	-0.323*	-0.046	0.202	0.088	0.009	0.354*	0.010	-0.049	-0.103	0.184**
PH	-0.304	-0.599**	1	0.320*	0.205	0.249	0.289	0.270	0.150	0.195	-0.052	0.321**
PL	0.228	0.098	0.512**	1	0.592**	0.738**	0.602**	0.629**	0.155	0.425**	0.300	0.687**
ETPP	0.167	0.178	0.400**	0.896**	1	0.790**	0.648**	0.673**	0.062	0.166	0.243	0.680**
FSPP	0.133	0.072	0.280	0.972**	0.958**	1	0.838**	0.789**	0.069	0.411**	0.534**	0.840**
TW	0.036	-0.027	0.404**	0.909**	0.845**	0.938**	1	0.574	0.118	0.442**	0.364*	0.643**
BY	0.539**	0.391*	0.139	0.959**	0.918**	0.898**	0.757**	1	0.157	0.307	0.309	0.854**
L/B RATIO	0.344*	0.103	0.473**	0.211	0.063	0.074	0.143	0.223	1	0.654	-0.463	0.129**
Ple	0.225	-0.076	0.454**	0.605**	0.262	0.461**	0.575**	0.347*	0.723**	1	0.112	0.364**
PW	-0.181	-0.146	-0.191	0.593**	0.455**	0.650**	0.591**	0.298	-0.585**	0.138	1	0.360**
GY	0.372**	0.304**	0.141**	0.996**	0.972**	0.930**	0.932**	0.935**	0.202**	0.448**	0.504**	1

** Significant at 1% probability level

NOTE, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), PL= Panicle length (cm), NETPP =Number of effective tillers per plant, NFSPP=Number of fertile spikelet's per panicle, TW=1000 grains weight(g), GY = Grain yield (q/ha),BY= Biological yield (q/ha), L/B Ratio= Paddy grain length and breadth ratio, Ple=Paddy grain length(mm), PW=Paddy grain width(mm)

Table 4: Genotypic path coefficient analysis showing direct effect (bold and diagonal values) and indirect effect (non-bold and off diagonal)

	DFF	DM	PH	PL	NETPP	NFSPP	TW	BY	L/B RATIO	Ple	PW	Yield correlation
DFF	-0.367	0.484	-0.043	0.008	0.074	0.197	-0.009	0.142	0.051	-0.027	0.010	0.372**
DM	-0.327	0.542	-0.085	0.003	0.079	0.106	0.007	0.103	0.015	0.009	0.008	0.304**
PH	0.111	-0.324	0.142	0.019	-0.179	0.417	-0.107	0.036	0.071	-0.056	0.011	0.141**
PL	0.083	0.053	0.072	0.038	-0.402	1.448	-0.241	0.279	0.031	-0.075	-0.034	0.996**
NETPP	-0.061	0.096	0.056	0.034	-0.449	1.426	-0.224	0.242	0.009	-0.032	-0.026	0.972**
NFSPP	-0.048	0.038	0.039	0.037	-0.430	1.489	-0.249	0.236	0.011	-0.057	-0.038	0.930**
TW	-0.013	-0.014	0.057	0.035	-0.379	1.397	-0.266	0.199	0.021	-0.071	-0.034	0.932**
BY	-0.197	0.211	0.019	0.040	-0.412	1.337	-0.201	0.263	0.033	-0.043	-0.017	0.935**
L/B RATIO	-0.126	0.055	0.067	0.008	-0.028	0.109	-0.038	0.058	0.150	-0.089	0.034	0.202**
Pe	0.082	-0.041	0.064	0.023	-0.117	0.686	-0.152	0.091	0.109	-0.124	-0.008	0.448**
PW	0.066	-0.079	-0.027	0.022	-0.204	0.968	-0.157	0.078	-0.088	-0.017	-0.058	0.504**

Residual effect: 0.1133

** Significant at 1% probability level

Table 5: Phenotypic path coefficient analysis showing direct effect (bold and diagonal values) and indirect effect (non-bold and off diagonal values)

	DF	DM	PH	PL	NETPP	NFSPP	TW	BY	L/B RATIO	PLe	PW	Yield correlation
DF	0.011	-0.007	-0.017	0.006	-0.006	0.092	-0.003	0.181	-0.017	0.012	0.012	0.266**
DM	0.009	-0.008	-0.023	-0.002	-0.007	0.050	-0.001	0.162	-0.000	-0.002	0.008	0.184**
PH	-0.002	0.002	0.072	0.017	-0.007	0.142	-0.034	0.123	-0.010	0.011	0.004	0.321**
PL	0.001	0.000	0.023	0.055	-0.022	0.422	-0.070	0.288	-0.010	0.025	-0.025	0.687**
NETPP	0.001	-0.001	0.014	0.032	-0.037	0.452	-0.076	0.308	-0.004	0.009	-0.020	0.680**
NFSPP	0.001	-0.000	0.018	0.040	-0.029	0.572	-0.098	0.361	-0.004	0.024	-0.045	0.840**
TW	0.000	-0.000	0.021	0.033	-0.024	0.479	-0.117	0.263	-0.007	0.026	-0.031	0.643**
BY	0.004	-0.003	0.019	0.034	-0.025	0.451	-0.067	0.458	-0.010	0.018	-0.026	0.854**
L/B RATIO	0.002	-0.000	0.010	0.008	-0.002	0.039	-0.013	0.072	-0.067	0.038	0.039	0.129**
PLe	0.002	0.000	0.014	0.023	-0.006	0.235	-0.052	0.140	-0.044	0.059	-0.009	0.364**
PW	-0.001	0.000	-0.003	0.016	-0.009	0.305	-0.042	0.141	0.031	0.006	-0.085	0.360**

Residual effect: 0.1845

** Significant at 1% probability level

NOTE - DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), PL= Panicle length (cm), NETPP =Number of effective tillers per plant, NFSPP=Number of fertile spikelet's per panicle, TW=1000 grains weight(g), GY = Grain yield (q/ha),BY= Biological yield (q/ha), L/B Ratio= Paddy grain length and breadth ratio, Ple=Paddy grain length(mm), PW=Paddy grain width(mm)

4. Conclusion

The genotypes evaluated in the present study exhibited significant variation among themselves. High heritability coupled with high genetic advance as a percentage of mean was recorded for the number of fertile spikelet's per panicle, followed by biological yield (q/ha), number of effective tillers per plant, and grain yield (q/ha), indicating the predominance of additive gene action for these traits. Path coefficient analysis further revealed that the number of fertile spikelet's per panicle and days to maturity were the most influential traits contributing to grain yield, highlighting their importance in selection programmes aimed at improving yield in medium to early duration irrigated rice genotypes. Among the tested entries, five genotypes- HRI-216, RNC-099, HRI-217, RRX-3341, and YNPK-7258—demonstrated superior performance for grain yield over the standard checks MTU-1010, US-312, CHANDRAHASINI, and Gontra Bidhan-3. These promising genotypes may therefore be recommended for advancement to further multi-location and advanced yield trials.

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6. Conflict of Study

The authors declare that there is **no conflict of interest** regarding the publication of this research work.

7. Future Scope

1. The identified superior genotypes can be further validated through multi-location and multi-season trials to assess their stability and adaptability.
2. Genotypes showing desirable traits may be utilized in hybridization and breeding programs to develop high-yielding and stress-tolerant varieties.
3. Integration of molecular marker-assisted selection with traditional breeding can accelerate the development of improved cultivars.
4. Further studies on genotype × environment interactions will help in identifying location-specific high-performing rice genotypes.
5. Advanced genomic tools can be applied to explore the genetic basis of yield and yield-attributing traits for more precise selection.

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