Assessment of genetic variability, heritability, genetic advance and association analysis in elite lines of rice (*Oryza sativa* L.)

ABSTRACT

Experimental material consisted a total of 57 genotypes (including checks) of rice~~, which was~~ sown ~~using~~ randomized complete block design having 2 replications. For the 57 rice genotypes (including checks) for 12 quantitative characters. High magnitude of genotypic coefficient of variation and phenotypic coefficient of variation was obtained for ~~N~~umber of unfilled grains per panicle whereas, ~~G~~rain yield per plot showed high ~~value of~~ PCV and moderate ~~value of~~ GCV. High heritability along with high genetic advance as percentage of mean was observed for number of unfilled grains per panicle followed by number of filled grains per panicle, number of effective tillers per square meter, flag leaf length and hundred seed weight, suggesting more stable and less impacted by environment, controlled by additive gene action. Grain yield per plot showed highly positive and significant correlation at both genotypic and phenotypic level with harvest index followed by biological yield, number of filled grains per panicle and number of effective tillers per square meter. ~~The result on p~~ath coefficient analysis indicated that harvest index had maximum direct effect on grain yield per plot followed by days to maturity, biological yield, number of effective tillers per square meter, plant height, number of unfilled grains per panicle, 100 seed weight and flag leaf length. Favourable genotypes on the basis of preferred kernel length/ breadth ratio are characterized under medium slender range *viz*., IR18A1061, R-2322-180-1-169-1, R-RHZ-CC-162 and R-2485-PHD-SPS-15-1. Alkali Spread Value of genotypes having intermediate value are preferred viz., R-RHZ-RKC-212, R-RHZ-MI-95NS, IR18A1042, R2744-19-1, IR17A3050, R-RGY-IS-110, R-2485-PHD-SPS-15-1, IR18A1073 and R2744-118-1

Key words: Genetic variability, Heritability, Genetic advance, Gene action, Correlation and Path analysis.

Introduction

Rice belongs to the family Poaceae and genus *Oryza*. The tropics and subtropics of the globe are home to the genus *Oryza.* It comprises 25 species, 23 of which are wild and only two (*Oryza sativa* and *Oryza glaberrima*) are cultivated. *Oryza sativa* is primarily grown in Asia, but *O. glaberrima* is grown in Africa. There are diploid (2n = 24) and tetraploid (2n = 48) species in the genus~~.~~ (Roy *et.al*., 2013). Over 90% of the world's rice is produced and consumed in the Asia-Pacific area. Approximately 787 million tons of rice were produced worldwide on 165.25 million acres of land in crop year 2021. Asia has consistently produced and consumed the greatest amount of rice worldwide (Anonymous, 2021).

Chhattisgarh is known as the "Rice Bowl of India" because Chhattisgarh produces a significant portion of the nation's rice and covers the most area in rice during the *kharif* season. Of its 13.51 million hectares of land, 5.90 million are used for agriculture. With a yield of 7.16 million tonnes, rice is grown on 3.79 million hectares in Chhattisgarh (Anonymous, 2020). Increasing productivity is the key to increasing rice production. Numerous studies have shown that adopting advised rice technology increases farmers' revenue and yields (Singh *et al.,* 2014). Those place where rice is grown, new initiatives and technologies are being developed to raise yield per hectare in order to feed the growing population. The demand that is expected to arise by 2025 is staggering because, in the major Asian countries, rice consumption is increasing day by day but production rate is slower so new technique adoption is compulsory to expand faster than population growth. The Indian Rice Market size is estimated at USD 52.82 billion in 2024, and is expected to reach USD 59.46 billion by 2029, growing at a CAGR of 2.40% during the forecast period 2024-2029 (Anonymous 2023).

Material methods

The current experiment was carried out at the Research cum Instructional farm of Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.). Total of 57 elite lines of rice, ~~together with the~~ nine checks Samleshwari, Bastar Dhan, Danteshwari, Sahbhagi Dhan-1, Narendra 97, Annada, Vandana, Protezin and Zinco Rice-MS were used for the experiment. The experiment was set up in a Randomised Block Design with two replications during *kharif* 2023. days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of effective tillers per square meter, number of filled grains per panicle, number of unfilled grains per panicle, flag leaf length (cm), grain yield (g), biological yield per plot (g), harvest index (%) and 100 seed weight (g)~~.~~ using SPARS2.0 and XLSTAT.

RESULT

The Genotypic and phenotypic coefficient of variation was estimated which showed that values of PCV was slightly greater than the corresponding GCV values for most of the traits. Except for panicle length, biological yield, harvest index and grain yield per plot where the variation is double which indicates the impact of environment on that trait.

The highest value of PCV was recorded for number of unfilled grains per panicle (40.67%) followed by harvest index (32.87%) and number of filled grains per panicle (30.36%) while maximum GCV was recorded for number of unfilled grains per panicle (40.61%) followed by number of filled grains per panicle (30.35%) and number of effective tillers per square meter (18.70%). The lowest amount of PCV and GCV was recorded for days to maturity (7.18% and 7.03% respectively). In case of quality traits, high GCV and PCV were shown by head rice recovery (30.20% and 30.24% respectively) and alkali spread value (32.46% and 33.64% respectively). Lowest GCV and PCV were shown by hulling percentage (2.02% and 2.34% respectively), whereas, grain yield per plot shown high value of PCV (26.84%) and moderate value of GCV (13.56%). Similar results obtained by Sreeparvathy *et al.* (2010) and Islam *et al.* (2015) in case of high value of PCV for grain yield per plot and Seyoum *et al.* (2012) in case of both PCV and GCV for grain yield.

Characters which showed moderate (10-20%) value of GCV were Panicle length (12.04%), number of effective tillers per square meter (18.70%), Flag leaf length (10.23%), Harvest index (11.12%), Hundred Seed weight (14.29%), Grain yield per plot (13.56%). In case of quality traits moderate GCV and PCV were showed by kernel length/breadth ratio (10.62%, 12.88%), amylose content (10.52%, 11.05%) and gel consistency (12.60%, 12.94%)

Characters which showed low (<10%) value of GCV and PCV were days to maturity (7.03%, 7.18%), plant height (8.36%, 8.51%) and Days to 50% flowering (9.22%, 9.37%) while in case of quality traits these are hulling percentage (2.02%, 2.34%), milling percentage (5.03%, 5.08%), paddy length (8.05%, 8.33%), paddy width (7.94%, 9.23%), milled rice length (6.68%, 6.94%) and milled rice width (6.12%, 8.95%). Similar results were also obtained by Devi *et al.* (2016) for days to 50% flowering.

The yield characters for which highest and lowest heritability obtained were number of filled grains per panicle (99.93%) and harvest index (11.45%) respectively and in case of quality characters highest and moderate heritability were obtained by head rice recovery (99.75%) and milled rice width (46.83%).

The yield characters which showed high (>60%) heritability were days to 50%

flowering (99.77%), days to maturity (95.78%), plant height (96.49%), number of effective tillers per square meter (97.59%), number of filled grains per panicle (99.93%), number of unfilled grains per panicle (99.72%), flag leaf length (98.04%) and hundred seed weight (98.75%). In case of quality characters, head rice recovery (99.75%), gel consistency (94.84%), amylose content (90.56%), alkali spread value (93.10%), kernel length/breadth ratio (68.05%), milled rice length (92.63%), paddy width (74.02%), paddy length (93.34%), milling percentage (98.01%) and hulling percentage (74.54%). High heritability character traits are more resistant to environmental influences and more likely to undergo natural selection-driven genetic advancement. Similar results were also obtained by Nath *et al*. (2021) and Akshay *et al.* (2022) for plant height and Pravallika *et al.* (2023) for panicle length and plant height. Dhidhi *et al.* (2021) got similar result in plant height, number of filled grains per panicle, number of unfilled grains per panicle, 100 seed weight and days to 50% flowering.

Characters which showed low (0-30%) value of heritability were Panicle length (25.90%), Biological yield (22.14%), harvest index (11.45%) and grain yield per plot (25.33%). High heritability with high genetic advance was shown by trait number of unfilled grains per panicle followed by number of filled grains per panicle, number of effective tillers per square meter, flag leaf length and hundred seed weight suggesting that this character is more stable, controlled by additive gene action and less impacted by the environment. Similar results was also obtained by Verma *et al.* (2023) for traits like number of tillers per plant, 1000 seed weight, grain yield per plant, biological yield per plant and harvest index.

The yield characters which showed high heritability with moderate genetic advance was days to 50 % flowering, days to maturity, plant height, panicle length and grain yield per plot. High heritability and moderate genetic advance indicate the presence of non-additive gene action, making heterosis breeding effective for enhancing these traits.

Correlation

In table 1.1 grain yield per plot showed highly positive and significant correlation at both genotypic and phenotypic level with harvest index (0.719,0.627) followed by biological yield per plot (0.361,0.475), number of filled grain per panicle (0.510,0.260) and Number of effective tillers per square meters (0.939,0.578) and also showed positive and significant correlation with 100 seed weight (0.186) at genotypic level. Negative and significant correlated results with number of unfilled grains per panicle (-0.201) and flag leaf length (-0.198).

The character 100 seed weight showed highly negative and significant correlation at both genotypic and phenotypic level with days to 50% flowering (-0.330, -0.324), days to maturity (-0.354, -0.336) and showed negative and significant correlation with flag leaf length (-0.203, -0.199).

Harvest index showed highly positive and significant correlation at genotypic level with number of effective tillers per square meters (0.642) followed by number of filled grains per panicle (0.469) and showed positive and significant correlation at phenotypic level with number of effective tillers per square meters (0.239), whereas it showed highly negative and significant correlation at both genotypic and phenotypic level with biological yield (-0.373, -0.263). Negative and highly significant correlation coefficient was recorded for days to 50% flowering (-0.267), days to maturity (-0.271), plant height (-0.448), panicle length (-0.533), number of filled grains per panicle (-0.469), number of unfilled grains per panicle (-0.357) and flag leaf length (-0.539) at genotypic level.

Biological yield showed positive and highly significant values with plant height (0.790,0.346), number of effective tillers per square meters (0.709,0.379), flag leaf length (0.562,0.265) at both genotypic and phenotypic level and days to 50% flowering (0.557), plant height (0.790), panicle length (1.069), number of filled grain per panicle (0.247) at genotypic level. Its showed significant and positive correlation with days to 50% flowering (0.229) and days to maturity (0.234) at phenotypic level.

Flag leaf length showed highly significant value and positive coefficient of correlation with days to 50% flowering (0.496,0.481), days to maturity (0.472,0.453), plant height (0.311,0.302), number of filled grain per panicle (0.260,0.257) at both genotypic and phenotypic level. Number of unfilled grains per panicle showed highly significant value and positive coefficient of correlation at both genotypic and phenotypic level with days to maturity (0.286,0.281), number of filled grains per panicle (0.274,0.274) and showed significant and positive correlation with days to 50% flowering (0.206,0.206) at both genotypic and phenotypic level. Number of filled grains per panicle showed highly significant value and positive coefficient of correlation with panicle length (0.282) at genotypic level. Number of effective tillers per square meter showed highly significant value and negative coefficient of correlation at genotypic level with panicle length (-0.313). Panicle length showed highly significant value and positive coefficient of correlation with plant height (1.034,0.512) at both genotypic and phenotypic level. It showed positive and significant correlation with days to 50% flowering (0.225), days to maturity (0.217) at genotypic level. Plant height showed highly significant value and positive coefficient of correlation with days to 50% flowering (0.318,0.306) and days to maturity (0.310,0.297) at both genotypic and phenotypic level.

Days to maturity showed highly significant value and positive coefficient of correlation with days to 50% flowering (0.999,0.982) at both genotypic and phenotypic level.

The study revealed that grain yield per plot showed highly significant and positive association with harvest index, biological yield, number of filled grains per panicle and Number of effective tillers per square meter at both genotypic and phenotypic level, indicating increase in any of above characters would lead to increase in seed yield. Hence, these traits could be utilized in direct selection for improving grain yield per plot. Rajamadhan and Murugan (2011), Chandra *et al*. (2009) and Noatia *et al.* (2021) also reported positive significant correlation of grain yield per plot with number of effective tillers per square meter. Similarly, Prasad *et al.* (2017), Chandra *et al*. (2009), Nandan *et al.* (2010) and Sanghera *et al*. (2013) observed similar findings for number of filled grains per panicle. Hence, the seed yield can be improved if the characters namely harvest index, biological yield, number of filled grains per panicle and number of effective tillers per square meter were given importance during selection process.

Path coefficient analysis

The result on path coefficient analysis (table no. 2) indicated that harvest index had positive direct effect (0.808) on grain yield per plot followed by days to maturity (0.603), biological yield (0.379), number of effective tillers per square meter (0.261), plant height (0.255), number of unfilled grains per panicle (0.077), 100 seed weight (0.027) and flag leaf length (0.022) and negative direct effect on grain yield per plot by days to 50% flowering (-0.602), panicle length (-0.080) and number of filled grain per panicle (-0.010). Days to 50% flowering shows positive indirect effect via days to maturity (0.602), plant height (0.081), number of unfilled grains per panicle (0.016), flag leaf length (0.011) and biological yield (0.228).

Days to maturity shows positive indirect effect via plant height (0.079), number of unfilled grains per panicle (0.022), flag leaf length (0.010) and biological yield (0.211), whereas negative indirect effect via days to 50% flowering (-0.601), panicle length (-0.017), number of effective tillers per square meter (-0.005), number of filled grain per panicle (-0.001), harvest index (-0.219) and hundred seed weight (-0.010). Plant height shows positive indirect effect via days to maturity (0.187), number of unfilled grains per panicle (0.000), flag leaf length (0.007), biological yield (0.299), and hundred seed weight (0.004), whereas negative indirect effect via days to 50% flowering (-0.601), panicle length (-0.083), number of effective tillers per square meter (-0.025), number of filled grain per panicle (-0.001), harvest index (-0.362).

Panicle length shows positive indirect effect via days to maturity (0.131), plant height (0.264), number of unfilled grains per panicle (0.008), flag leaf length (0.008), biological yield (0.405), and hundred seed weight (0.004), whereas negative indirect effect via days to 50% flowering (-0.136), number of effective tillers per square meter (-0.082), number of filled grain per panicle (-0.003), harvest index (-0.431).

Number of effective tillers per square meters shows positive indirect effect via harvest index (0.544), biological yield (0.291), 100 seed weight (0.001), panicle length (0.050) and days to 50% flowering (0.040). However, negative indirect effect via flag leaf length (-0.003), number of filled grains per panicle (-0.001), number of unfilled grains per panicle (-0.006), plant height (-0.025) and days to maturity (-0.013). Number of filled grains per panicle shows positive indirect effect via biological yield (0.093), harvest index (0.379), flag leaf length (0.006), plant height (0.025), number of unfilled grains per panicle (0.021), number of effective tillers per square meters (0.025) and days to maturity (0.082), whereas negative indirect effect via 100 seed weight (- 0.002), panicle length (-0.023), days to 50% flowering (-0.086). Number of unfilled grains per panicle shows positive indirect effect via flag leaf length (0.003), plant height (0.001) and days to maturity (0.173). However, negative indirect effect via 100 seed weight (-0.004), harvest index (-0.288), biological yield (-0.008), Number of filled grains per panicle (-0.003), number of effective tillers per square meters (-0.019), panicle length (-0.009) and days to 50% flowering (-0.002). Flag leaf length shows positive indirect effect via number of unfilled grains per panicle (0.009), biological yield (0.214), plant height (0.079) and days to maturity (0.285), whereas negative effect of this trait on grain yield per plant was mainly via 100 seed weight (-0.006), harvest index (-0.435), number of filled grains per panicle (-0.003), number of effective tillers per square meters (-0.036), panicle length (-0.030) and days to 50% flowering (-0.009). Biological yield shows positive indirect effect via 100 seed weight (0.003), flag leaf length (0.012), number of effective tillers per square meters (0.183), plant height (0.202) and days to maturity (0.336). However, negative indirect effect via harvest index (-0.301), number of filled grains per panicle (-0.002), number of unfilled grains per panicle (-0.002), panicle length (-0.086) and days to 50% flowering (-0.362). Harvest index shows positive indirect effect via 100 seed weight (0.004), Number of effective tillers per square meters (0.167), panicle length (0.043) and days to 50% flowering (0.161), However, negative indirect effect via flag leaf length (-0.012), biological yield (-0.141), number of filled grains per panicle (-0.005), number of unfilled grains per panicle (-0.028), plant height (-0.114) and days to maturity (-0.164). Hundred seed weight shows positive indirect effect via harvest index (0.115), biological yield (0.035), number of filled grain per panicle (0.001), Number of effective tillers per square meters (0.008), plant height (0.040) and days to 50% flowering (0.199), However, negative indirect effect via flag leaf length (-0.004), number of unfilled grains per panicle (-0.010), panicle length (-0.011) and days to maturity (-0.213).

The results on path coefficient analysis indicated that highest positive direct effect on grain yield per plot was shown by harvest index, days to maturity and biological yield whereas, moderate direct effect was shown by plant height and number of effective tillers per square meter. Hence, selection based on these traits would be effective in increasing the grain yield per plot. The traits like number of filled grain per panicle and panicle length had negative direct effect on seed yield, however, large positive indirect effect *via* harvest index, days to maturity and biological yield had converted the correlation coefficient into highly significant positive. All the above facts, indicated clearly that harvest index should be given maximum importance with close consideration of number of filled grains per panicle and panicle length during the selection procedure aimed at important of rice crop.

Conclusion

Favourable genotypes on the basis of preferred kernel length/ breadth ratio are characterized under medium slender range *viz*., IR18A1061, R-2322-180-1-169-1, R-RHZ-CC-162 and R-2485-PHD-SPS-15-1. Alkali Spread Value of genotypes having intermediate value are preferred viz., R-RHZ-RKC-212, R-RHZ-MI-95NS, IR18A1042, R2744-19-1, IR17A3050, R-RGY-IS-110, R-2485-PHD-SPS-15-1, IR18A1073 and R2744-118-1 and genotypes having medium amylose content (20-25%) are R-2300-377-2-261-1, R-2297-6-1-3-1, R-1670-3269-2-3926, Vandana, Narendra-97, R-2321-154-1-94-1, R-2341-337-3-180-1, Danteshwari, R2744-19-1, IR17A3050, R2748--1-1, R-2307-46-1-24-1, R-RGY-IS-110, Sahbhagi-Dhan-1, R-2297-4-1-2-1, R2739-86-1, R-2485-PHD-SPS-15-1, R2739-43-1, IR18A1061, R2735-56-1, IR18A1073, IR17A3105, R2739-120-1, R-2341-281-2-332-1, R-RHZ-CC-162, R2744-118-1, R2744-119-1, IR18A1076, R2743-78-1, R2756-27-1, Bastar Dhan-1, R-1877-41-1-13-1, JDP-5925, R-2774-C-3-1-1, R2739-115-1 and R-2775-C6-2-3.

Table 1: Genotypic and Phenotypic association between yield and yield related traits

Characters		DF	DM	PH	PL	ET	NFG	NUFG	FL	BY	HI	HSW	GYP
DF	g												
	p												
DM	g	0.999**											
	p	0.982**											
PH	g	0.318**	0.310**										
	p	0.306**	0.297**										
PL	g	0.225*	0.217*	1.034**									
	p	0.108	0.111	0.512**									
ET	g	-0.025	-0.021	-0.097NS	-0.313**								
	p	-0.036	-0.024	-0.097NS	-0.130NS								
NFG	g	0.143	0.135	0.099NS	0.282**	0.095NS							
	p	0.140	0.131	0.096NS	0.146NS	0.095NS							
NUFG	g	0.206*	0.286**	0.005NS	0.107NS	-0.073NS	0.274**						
	p	0.206*	0.281**	0.004NS	0.057NS	-0.073NS	0.274**						
FL	g	0.496**	0.472**	0.311**	0.371**	-0.139NS	0.260**	0.119NS					
	p	0.481**	0.453**	0.302**	0.197*	-0.136NS	0.257**	0.118NS					
BY	g	0.602**	0.557**	0.790**	1.069**	0.701**	0.247**	-0.022NS	0.565**				
	p	0.229*	0.234*	0.346**	0.141NS	0.379**	0.123NS	-0.004NS	0.265**				
HI	g	-0.267**	-0.271**	-0.448**	-0.533**	0.642**	0.469**	-0.357**	-0.539**	-0.373**			
	p	-0.128	-0.141	-0.165NS	-0.059NS	0.239*	0.155NS	-0.132NS	-0.172NS	-0.263**			
HSW	g	-0.330**	-0.354**	0.156NS	0.136NS	0.029NS	-0.074NS	-0.130NS	-0.203*	0.092NS	0.143NS		
	p	-0.324**	-0.336**	0.147NS	0.066NS	0.029NS	-0.074NS	-0.128NS	-0.199*	0.048NS	0.036NS		
GYP	g	0.085	0.072	0.091NS	0.089NS	0.939**	0.510**	-0.201*	-0.198*	0.361**	0.719**	0.186*	
	p	-0.027	-0.023	0.011NS	0.002NS	0.578**	0.260**	-0.106NS	-0.096NS	0.475**	0.627**	0.094NS	

* and ** significant at 5% and 1% probability level

DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Number of effective tillers per sq. m; NFG = Number of filled grains per panicle; NUFG = Number of unfilled grains per panicle; FLL = Flag leaf length (cm); BY = Biological yield (g); HI = harvest index; HSW = Hundred seed weight (g); GYP = Grain yield per plot (g)

Table 2: Genotypic path coefficient analysis matrix of direct and indirect effects on its contributing traits in rice

Traits	DF	DM	PH	PL	ET	NFG	NUFG	FLL	BY	HI	HSW	r_g corr
DTF	**-0.602**	0.602	0.081	-0.018	-0.007	-0.001	0.016	0.011	0.228	-0.216	-0.009	0.085
DM	-0.601	**0.603**	0.079	-0.017	-0.005	-0.001	0.022	0.010	0.211	-0.219	-0.010	0.072
PH	-0.191	0.187	**0.255**	-0.083	-0.025	-0.001	0.000	0.007	0.299	-0.362	0.004	0.091
PL	-0.136	0.131	0.264	**-0.080**	-0.082	-0.003	0.008	0.008	0.405	-0.431	0.004	0.089
ET	0.040	-0.013	-0.025	0.050	**0.261**	-0.001	-0.006	-0.003	0.291	0.544	0.001	0.939
NFG	-0.086	0.082	0.025	-0.023	0.025	**-0.010**	0.021	0.006	0.093	0.379	-0.002	0.510
NUFG	-0.124	0.173	0.001	-0.009	-0.019	-0.003	**0.077**	0.003	-0.008	-0.288	-0.004	-0.201
FLL	-0.298	0.285	0.079	-0.030	-0.036	-0.003	0.009	**0.022**	0.214	-0.435	-0.006	-0.198
BY	-0.362	0.336	0.202	-0.086	0.183	-0.002	-0.002	0.012	**0.379**	-0.301	0.003	0.361
HI	0.161	-0.164	-0.114	0.043	0.167	-0.005	-0.028	-0.012	-0.141	**0.808**	0.004	0.719
HSW	0.199	-0.213	0.040	-0.011	0.008	0.001	-0.010	-0.004	0.035	0.115	**0.027**	0.186

Bold (diagonal) figures depicts direct path values; Residual = 0.023

DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Effective tillers; NFG = Number of filled grains per panicle; NUFG = Number of unfilled grains per panicle; FLL = Flag leaf length (cm); BY = Biological yield (g); HI = harvest index; HSW = Hundred seed weight (g); GYP = Grain yield per plot (g)

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