Original Research Article

Analysis ofgenetic variability and correlations in rice (*Oryza sativa* L.) recombinant inbred lines (F_6) for yield and its componenttraits

Abstract

An experiment was carried out to evaluate genetic variability and determine the correlation between grain yield and its component traits in 150rice recombinant inbred lines, their parents and six checksat ICAR-IIRR, Hyderabad and AHRS, Kathalagere in *wet* 2022. The experiments were laid out in anaugmented block design with five blocks. Phenotypic coefficients of variance were higher than genotypic coefficients of variance for all the traits across the locations. A joint consideration of high heritability in broad sense (h^2) and genetic advance as per cent mean estimates were obtained for plant height, number of tillers, number of productive tillers, panicle length, number of grains per panicle, test weight, grain yield per plant suggesting that the traits were primarily under genetic control. Furthermore, high heritability (h^2) and GAM recorded in these characters could be explained by additive gene action. However, high estimates (h^2) combined with moderate GAM recorded for days to 50% flowering could be due to non-additive gene effect. Grain yield per plant recorded positive and significant correlation with the total number of grains per panicle (0.32***, 0.30***) and number of productive tillers per plant (0.21***, 0.26***) at both the locations. This result indicates that selection based on these two traits will be highly effective for yield improvement in rice.

Keywords RILs, Variability, Heritability, Correlation

Introduction

Rice (*Oryza sativa* L.) is an important staple food in the world, it feeds more than half of the world's population (Oladosu *et al.* 2014). The geometric growth rate of the global population has called for yield improvement of this very important cereal. Genetic improvements in yield and its contributing traits are influenced and defined by the quantity and nature of genetic variability, which is polygenically controlled, environmentally influenced, and determined (Wright, 1935). Knowledge of genetic variability and genetic parameter estimates for desired traits of economic significance is important for plant breeders before the release of any variety. The presence and magnitude of genetic variability in a gene pool areprerequisitesfor breeding programs. Heritability estimates provide information on the proportion of variation transmissible to progenies in subsequent generations (Appalaswamy and Reddy, 2004). Knowledge of heritability plays a major role in selection-based improvement of crops because it indicates the extent to which traits can be passed on to future generations. Therefore, genetic variability is a prerequisite for progress in crop breeding programs, and strong genetic progress combined with high heritability provides the best conditions for selecting a specific trait. Understanding the nature and strength of the relationship between yield and its components also contributes to the efficiency of genetic selection in plant breeding programs. The correlation coefficient unravels characters of little or no importance in the selection program (Singh *et al.* 2014). On the other hand, genotypic correlation, which represents the genetic portion of the phenotypic correlation, is the only inheritable nature and is therefore used to orient breeding programs. The existence of a correlation may be attributed to the presence of linkage or pleiotropic effects of genes, physiological and developmental relationships, environmental effects, or a combination of all (Oad et al. 2022). In this study, we conducted a phenotypic evaluation of 150 Recombinant Inbred Lines (RILs) at two diverse locations to evaluate genetic variability and determine the correlation between grain yield with its related traits.

Methodology

The experimental material comprised of mapping population (150 lines, TB1 to TB150) developed through the crossing of selected female parent mutant line (TI-128) with better yield and the original male parent (BPT 5204). The Mapping population (F_6) comprised of 150 RILs were evaluated at two locations ICAR-IIRR, Hyderabad (E_1) and AHRS, Kathalagere, KSNUAHS Shivamogga (E_2), for yield and yield related traits under irrigated conditions during wet 2022.

To evaluate the lines for yield and yield related traits, the experiment was laid out in augmented block design with five blocks, wherein, each block consisted of 30 lines along with parents (TI-128 and BPT-5204) and five checks (*viz*., Rasi, GNV1109, DRR Dhan-41, CR Dhan 202 and MTU 1010) were randomized in each block. Each line was sown in one row of two-meter length at 20cm × 15cm spacing. Agronomic practices were followed as recommended for the irrigated rice cultivation. The seeds were direct sown in the nursery beds and 30 days after sowing, the plants were transplanted to main field. Timely weeding was performed, and the field was maintained as per the agronomic practices.

The following observations were recorded for three plants *viz.*,days to 50 per cent flowering (DFF), plant height (PH), number of tillers per plant (NT), number of productive tillers per plant (PT), panicle length (PL), number of grains per panicle (NGPP), grain yield per plant (YPP) and test weight (TW). The analysis of variance genetic variability parameters and correlation were carried out in R studio (version 3.5.2) using R-scripts for statistical analysis (Aravind *et al.*, 2019)

Results and Discussion

Analysis of variance (ANOVA) for yield and yield related traits

The Mean Sum of Squares (MSS) for the yield and yield-related traits under irrigated conditions in mapping population during *wet* 2022 are presented in Table 1. The ANOVA revealed that the MSS of test genotypes *versus* checks was highly significant at $p<0.01$ and $p<0.05$ for all the traits under investigation for *wet* 2022. The MSS due to test genotypes exhibited high significant difference at $p<0.01$ and $p<0.05$ for most of the traits under investigation for both the seasons. The results are in consistent with the results of Demeke *et al.* (2023), Kulsum *et al*. (2022) and Faysal *et al*. (2022), their study indicated that lines were highly variable for traits that showed existence of sufficient inherent genetic variation among the lines, The genetic variability in breeding is very important, especially for desirable traits so higher variability in a population provides an opportunity for crop improvement.

Genetic variability parameters

The results of genetic variability parameters *viz*., range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability and genetic advance as *per cent* mean were analyzed using augmented *RCBD* package in R studio (*version* 3.5.2) to estimate the extent and magnitude of genetic variation for yield and yield-related traits in mapping population.The mean performance for the traits showed a wide range of variation for most of the characters studied and the findings of the present experiment are given in Table 2.The genetic parameters are classified as following GCV and PCV were classified into (0-10%) low, (10-20%) moderate, >20% high. Heritability was classified as (0-30%) low, (30-60%)moderate, (>60%) high,the genetic advance as *per cent* of mean was categorized into (0-10%) low, (10-20%) moderate and (>20%) high.

Study on variability revealed that phenotypic and genotypic coefficients of variation were high for number of tillers, number of productive tillers per plant, number of grains per panicle, test weight and grain yield per plant during *wet* 2022at both the locations and very narrow range of difference between GCV and PCV was noticed for all the traits indicating that there is little influence of environment on the expression of characters. High heritability coupled with high genetic advance was recorded for traits such as plant height, number of tillers, number of productive tillers, panicle length, number of grains per panicle, test weight and grain yield per plant at both the locations. The characters with a high GCV and PCV, as well as a high heritability and GAM, indicate that the character is driven by additive gene action and the selection could be beneficial in improving it, similar results were observed by Demeke *et al.* (2023). The heritability estimates for a given feature determine the reliability of the phenotypic value. As a result, high heritability aids in the efficient selection of a specific trait and improvement of such characters would be beneficial. Similar results were obtained by Acharya *et al.* (2018) where high heritability coupled with high genetic advance was recorded for traits such as plant height, number of tillers, number of productive tillers, panicle length and number of grains per panicle, High broad-sense heritability coupled with high genetic advance *per cent* means were reported by Mamata *et al.* (2018), Abebe *et al.* (2017) and Shaikh *et al.* (2017).

Estimates of correlation coefficients

Correlation between yield and yield related traits were studied under irrigated conditions during *wet* 2022, the graphical representation is given in Fig. 1. Grain yield per plant exhibited positive significant correlation with the total number of grains per panicle (0.32***, 0.30***), total number of tillers per plant (0.26***, 0.24**) and the number of productive tillers per plant (0.26***,0.20***) considering under both locations. The inter-correlation among the traits, plant height showed significant positive correlation with the panicle length (0.32***& 0.20*); panicle length with test weight (0.27*** & 0.05*); total number of tillers per plant with the number of productive tillers per plant (0.88** & 0.93**) considering under both locations respectively.

The yield component traits *viz*., the number of tillers, productive tillers per plant, number of grains per panicleand test weight correlated with grain yield per plant and significantly correlated with increasing yield under irrigated condition. The results were in accordance with Kiranmayee *et al.* (2018), who obtained positive significant association of the trait yield per plant with number of productive tillers and panicle length, similarly Sreedhar and Reddy, (2019) observed significant positive correlation of the trait yield per plant with number of grains per panicle and test weight. The degree of correlation among characters is an important factor when dealing with yield trait as it is controlled by many genes and highly influenced by the environment. The significant positive correlations between yield and yield related traits indicated that selection in favor of these traits could lead to positive indirect selection for grain yield improvement.

Conclusion

The study on variability for yield and yield related traits revealed that phenotypic and genotypic coefficients of variation were high for number of tillers, number of productive tillers per plant, number of grains per panicle, test weight and grain yield per plant during *wet* 2022 at both the locationsrespectively and very narrow range of difference between GCV and PCV was noticed for all the traits indicates that there is little influence of environment on the expression of characters.Correlation analysis revealed that the component traits *viz.*, the number of tillers and productive tillers per plant, panicle length and number of grains per panicle correlated with grain yield per plant and significantly correlated with increasing yield under irrigated conditions.

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Table 1: Analysis of variance for yield and yield related traits in RILs under irrigated condition during *Kharif* 2022 and *Rabi* 2022 at ICAR-IIRR, Hyderabad

Source	Location	*d. f.*	DFF	PH	NT	PT	PL	NGPP	YPP	TW
Treatment	EI	156	11.46*	4.84**	3.82**	3.50**	2.58*	1083.25*	39.08**	4.00**
	EII		10.12*	21.69*	1.97**	1.56**	4.36*	1027.89**	41.36**	4.65*
Check	EI	6	1.34*	19.12	0.56*	0.50*	0.91**	140.67*	23.61**	4.63*
	EII		1.29*	19.08*	0.59*	0.52*	0.93*	141.28*	23.82*	4.63*
Test genotypes	EI	149	11.56*	3.73*	1.85*	1.51*	2.41*	1114.67**	39.34**	3.84**
	EII		10.12*	20.26*	1.88**	1.50**	3.91*	1057.34*	41.47*	4.50*
Test vs. Check	EI	1	37.34*	112.57*	2.30*	4.92**	34.65*	171.75**	61.69**	24.43*
	EII		44.43	244.76	20.48**	15.51**	84.78**	189.84	65.69*	26.76*
Block	EI	4	64.94	143.18	6.16	7.71	17.62	1633.94	44.53	10.40
	EII		64.82	143.18	6.16	7.71	17.62	1633.94	44.53	10.40
Residuals	EI	16	15.1	29.67	0.63	0.49	3.77	860.54	16.39	3.38
	EII		15.19	29.67	0.63	0.49	3.77	860.54	16.39	3.38

Significance levels: *P<0.05 and **P<0.01, *d. f.* degrees of freedom

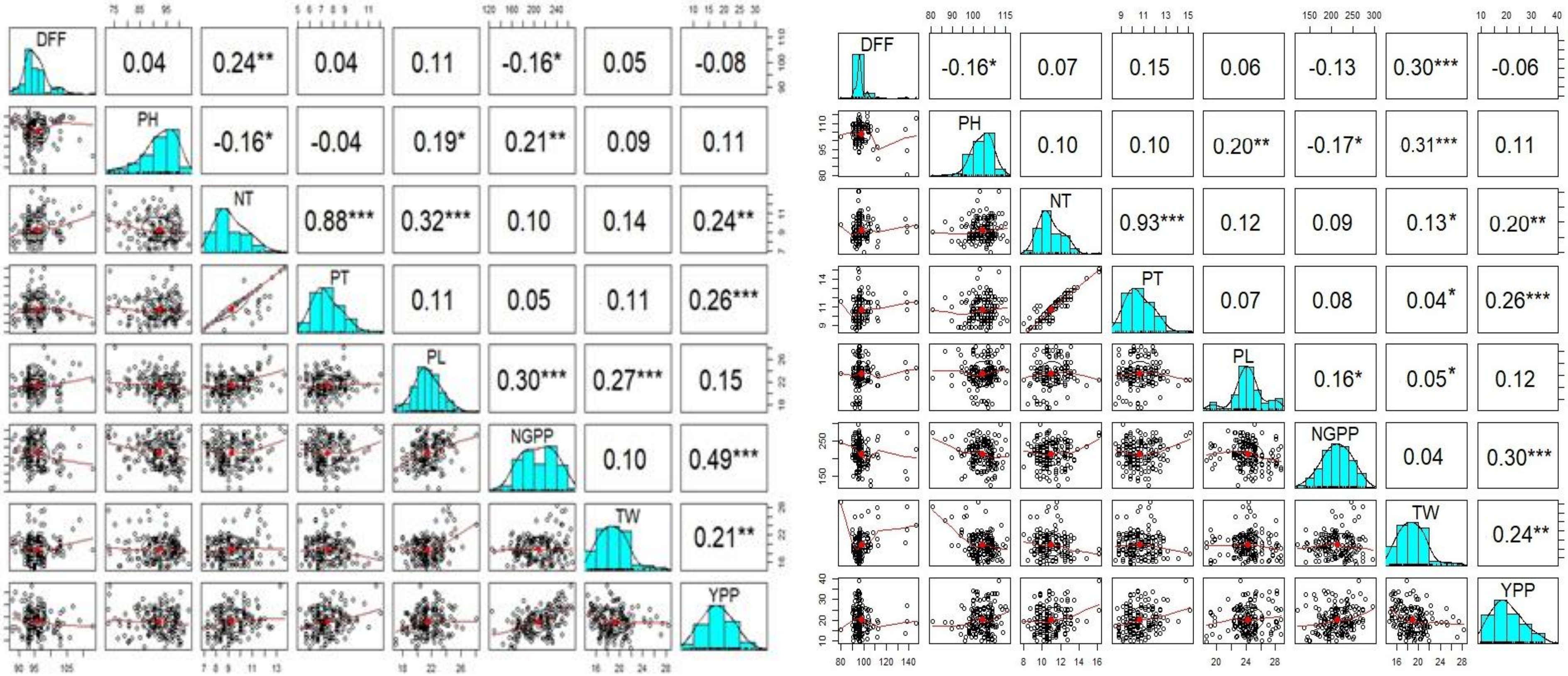
DFF- Days to 50 percent flowering, PH- Plant height, PL- Panicle length, NT- Number of tillers per plant, PT- Number of productive tillers per plant, NGPP-Total number of grains per plant, TW-Test weight (g), YPP- Grain yield per plant (g), SPAD- Soil Plant Analytical Development.

Table 2: Estimation of genetic variability parameters for yield and yield related traits in RILs under irrigated condition during *Kharif* 2022 and*Rabi*2022 at AHRS, Kathalagere

Traits	**Location**	**Range**		**Mean**	**CV (%)**	**Genetic variability**		**h^2(bs)** (%)	**GAM**	**Direction of selection**
		Min	**Max**			**GCV** (%)	**PCV** (%)			
DFF	EI	89.00	106.00	96.16	4.05	7.1	6.28	56.12	18.12	-
	EII	90.00	106.00	96.16	4.02	7.26	8.31	56.38	17.28	-
PH	EI	104.67	116.33	109.82	4.97	4.26	6.12	75.14	34.83	-
	EII	90.27	116.97	104.33	5.18	4.38	4.42	75.28	33.12	-
NT	EI	7.00	14.67	11.13	8.33	24.12	31.12	65.72	25.28	+
	EII	8.00	16.14	10.76	7.31	10.39	14.41	66.48	21.49	+
PT	EI	5.27	13.95	9.15	7.59	24.28	28.38	74.32	20.21	+
	EII	6.14	15.96	10.44	6.61	10.62	13.00	67.38	26.30	+
PL	EI	17.13	24.83	21.19	9.10	10.92	11.28	81.12	26.24	+
	EII	18.60	28.80	21.19	8.17	6.54	8.12	31.62	6.61	+
NGPP	EI	122	296	212.15	13.81	22.95	25.14	98.99	26.82	+
	EII	124	294	217.77	13.68	16.44	14.93	38.61	25.73	+
YPP	EI	12.64	34.35	20.31	20.12	23.92	31.21	97.68	34.18	+
	EII	12.46	33.42	20.31	20.25	24.18	31.09	60.47	38.06	+
TW	EI	14.68	22.48	18.53	9.86	24.12	21.14	93.24	23.42	+
	EII	14.68	22.48	18.53	9.84	15.74	11.57	26.84	21.38	+

PCV and GCV: Phenotypic and genotypic coefficient of variation,h^2(bs): Heritability (broad sense), GAM: Genetic advance as *per cent* of mean

DFF- Days to 50 percent flowering (days), PH- Plant height (cm),PL- Panicle length (cm),NT- Number of tillers per plant; PT- Number of productive tillers per plant, PL-Panicle length (cm),NGPP-Number of grains per panicle; TW-Test weight (g); YPP Grain yield per plant (g).



(a)

(b)

Fig. 1: Graphical representation of correlation coefficients for root architectural traits in RILs at 60 DAS stage under polyhouse condition during *Rabi* 2022 (a) ICAR-IIRR, Hyderabad, (b) AHRS, Kathalagere