



Genetic parameters and association analysis for grain yield and yield attributing traits in rice (*Oryza sativa* L.) germplasm lines

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ABSTRACT

The intensity of trait association and genetic variability of yield attributing variables in 217 rice genotypes was investigated during *kharif* 2018. The existence of genetic variability among the genotypes was demonstrated by analysis of variance, which recorded significant differences for all the seven studied parameters. The estimation of variability indicated that The full grain number per panicle (37.2 % and 34.1 %) & single plant yield (24.7 % and 20.55 %) had the highest intensity of phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV), and High heritability along with high genetic advance as a per cent of mean (GAM) was found in Plant height (98.9 % and 20.8 %), panicle number per plant (95.4 % and 36 %), panicle length (96.8 % and 35.9 %), full grain number per panicle (99.5 % and 61.6 %), thousand seed weight (98.1 % and 40.25 %) and single plant yield (69.2 % and 35.2 %) , depicting additive gene action in inheritance of these parameters. A simple selection procedure can help to enhance these characteristics even further. Correlation and regression coefficient findings indicated that plant height (0.193**) and the full grain number per panicle (0.177**) had a significant impact on single plant yield. The full grain number per panicle (0.265**), followed by thousand seed weight (0.194**) and plant height (0.110**), had the maximum direct positive effect on single plant yield, as per path coefficient analysis. As a result, accessions with a higher full grain number per panicle, thousand seed weight and plant height would be suitable for yield enhancement programme.

Introduction

The world's population is expected to exceed nine billion and food insecurity might become a major issue worldwide by 2050 (Alexandratos and Bruinsma 2012). As a consequence, increasing the output of essential cereal crops such as rice is critical to meet expanding population need (Fitzgerald *et al.*, 2009). Rice accounts for roughly 20 % of the calories consumed by humans. It is known in India as "Prana," which means "breath of life." Rice, like other cereal grains, has a high

biological value and substantial protein content. Successful parent selection necessitates knowledge of the kind and degree of population diversity, trait conglomeration with yield and its attributes, as well as the degree of the environmental effect on the manifestation of the attributes. Correlation and path coefficient analysis may be one of the useful strategies in accurately assessing cause and conglomeration between yield and agronomic traits (Khan *et al.*, 2003). Seed yield is a multifaceted

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parameter that is influenced by a wide range of factors that can have favorable or negative consequences. Assessing each trait's contribution is essential in order to place greater attention on those that have the greatest impact on seed yield. As a result, data on the confederation between characteristics and seed production is critical for defining yield-based selection criteria for rice breeding. Genetic advancement is another term for the predicted response to selection (GA). Significant genetic advancement paired with high heritability estimates is the most successful selection condition (Shalini *et al.*, 2000). The focus of this research was to identify rice germplasm with high yielding potential and to see the conglomeration between morphological traits and yield. This morphological analysis will aid in discovering the relationships between these traits, which will ultimately assist in the production of a desirable plant type that combines the expression of numerous desired traits.

Material and Methods

The germplasm used in this investigation consisted of 210 accessions of *O. sativa*. The trial was conducted in *kharif* 2018 at Rice Research Centre, Agriculture Research Institute, Rajendranagar, Hyderabad, Telangana State, by utilizing Federer's (1956, 1961, 1991) augmented design with seven checks. Thirty-one days old seedlings were placed into a well prepared main field after establishing a healthy nursery. Each genotype has two rows of 4m length, consisting 25 plants in each row. For each genotype, plant height, panicle number per plant, panicle length, full grain number per panicle, thousand seed weight, and single plant yield, were all determined on randomly selected five plants. On a full plot basis, days to 50% heading was recorded. ANOVA was used to compare the mean data of each character. Burton (1952) and Shafique, *et al.*, (2016) approach was used to quantify the genotypic and phenotypic variances, as well as the genotypic (GCV) and phenotypic (PCV) coefficients of variation. The genetic advance (GA) being determined using Johnson *et al.* (1955) method and heritability in the broad sense [h^2 (b)] was estimated utilising the formulae provided by Lush (1940). correlations as per Singh and Chaudhary (1985) and path analysis as outlined by Dewey and

Lu (1959), and INDOSTAT software ver 9.2 was used to perform regression analysis.

Results and Discussion

Genetic variation among parameters is vital for breeding and selecting desirable types, an investigation of the correlation between seed yield and yield components is critical for determining selection criteria. Since seed yield is a polygenic and complex trait that is influenced by a huge range of other factors, direct selection based solely on an association pattern between two variables may occasionally mislead the breeder; therefore, direct and indirect effects should be differentiated for effective selection. (Awol and Alise, 2018).

The correlation coefficient reflects the degree of relationship of various yield component characteristics among themselves and with the yield. Correlation studies between various yield attributes and yield provide a foundation for future breeding programmes. Path coefficient analysis determines the direct effect of one variable on another and allows the correlation coefficient to be divided into components of direct and indirect effects (Swetha *et al.*, 2019). Information on the variability and correlation studies among the economic characters of the crop. is of great value to plant breeders (Shedje *et al.*, 2019). It will not only, help to understand the desirable and undesirable relationship of economic characters but also help in assessing the scope of simultaneous improvement of two or more attributes (Shanmugam and Kalaimagal, 2019).

Genetic parameters: variability, heritability, and genetic advance

All the seven parameters in the current investigation showed significant differences between the genotypes as illustrated in the ANOVA (Table 1). The minimal genotypic coefficient of variation (GCV) (5.59 %) and phenotypic coefficient of variation (PCV) (5.69 %) were observed for the days to 50 % heading. The estimated heritability for this parameter was high (96.5%), while GA (genetic advance as per cent of mean) was moderate (11.7%) (Table 2). These results were akin to the findings of Prasannakumari *et al.* (2020) for minimal GCV and PCV, Pragnya *et al.* (2018) for high heritability and Sandeep *et al.* (2018) for moderate GA. For plant height, the GCV and PCV estimates were moderate, 10.19 and 10.24

Table 1: ANOVA for yield and its attributing parameters in rice (*Oryza sativa* L.)

	DF	DFF	PH	PNP	PL	NFGP	TW	SPY
Entries (ignoring Blocks)	216	51.171**	154.589**	7.432**	25.646**	7031.833 **	26.252**	77.007**
Checks	6	151.581**	300.224**	2.77**	11.252**	28421.38 **	265.643**	119.537**
Varieties	209	47.989 **	144.046**	7.42**	25.635**	6120.859 **	19.466**	62.848**
Checks vs.Germplasm	1	113.668**	1484.308**	36.567**	114.206**	69088.190 **	8.318**	2781.070**
ERROR	54	1.285	1.139	0.262	0.639	22.477	0.283	16.097

DFF: Days to 50% flowering, PH: Plant height (cm), PNP: Panicle number per plant, PL: Panicle length (cm), NFGP: Full grain number per panicle, TW: 1000-seed weight, SPY; single plant yield(g).

** Significant at 1 level of probability

Table 2: Amplitude of variability, heritability and genetic advance for yield and its component parameters in rice

S N	Characters	Phenotypic Variance	Genotypic Variance	Environmental variance	PCV (%)	GCV (%)	Heritability in broad sense (h ²) (%)	Genetic Advance as % mean
1	DFF	37.43	36.15	1.28	5.69	5.59	96.5	11.3
2	PH	111.75	110.62	1.13	10.24	10.19	98.9	20.8
3	PNP	5.80	5.54	0.26	18.82	17.86	95.4	36
4	PL	19.98	19.34	0.63	18.05	17.76	96.8	35.9
5	NFG/P	4743.0	4720.5	22.47	30.06	29.99	99.5	61.6
6	TSW	15.13	14.84	0.28	19.91	19.72	98.1	40.25
7	SPY	52.28	36.18	16.09	24.70	20.55	69.21	35.2

per cent, respectively. This character had a high heritability estimate (98.90%) and a high GA (20.8 %). Similar results have been reported by Prasannakumari *et al.* (2020) for high heritability, Rachana (2018) for high GA for plant height.

Panicle number per plant had moderate GCV and PCV *i.e.*, 17.86 % and 18.82% respectively. The recorded heritability was high for this trait (95.4 %) with high GA (36 %) which are in accordance with the reports of Edukondalu *et al.* (2017) for moderate GCV and PCV, Nikhitha *et al.* (2020) for high heritability and high GA. The moderate GCV and PCV were recorded (*i.e.*, 17.76% and 18.05% respectively) for panicle length (cm). The estimated heritability (96.8%) and GA (35.9 %) were high for this trait. The results are in agreement with findings of Mishu *et al.* (2016) for moderate GCV and PCV, Rachana (2018) for high GA and heritability.

High GCV (29.99%) and PCV (30.06%) were recorded for the full grain number per panicle. This trait's heritability was correspondingly high (99.5%), with a high GA (61.6 %) and these results were akin with the reports of Rukmini Devi *et al.* 2017 and Fathima *et al.* (2021). 1000-grain weight exhibited moderate GCV (19.72%) and PCV (19.91%) with high heritability estimate (98.1%), as well as high GA (40.25 %). Similar findings were reported by Hema *et al.* (2019) for

high heritability and GA. Single plant yield recorded high GCV (20.55%), PCV (24.70 %) heritability (69.2 %) and GA (35.2 %) as reported earlier by Dhurai *et al.* (2014). Similarly to our findings, the above-mentioned observations for high GCV and PCV estimates in various genotypes, including early segregating and advanced generation for important yield component traits, suggest the possibility of genetic improvement through direct selection for these traits.

Correlation analysis

If a plant having high vegetative growth or plant height, usually flowering is delayed, and excess vegetative growth / plant height, itself is an indication of translocating high amount of nutrients, which eventually lead to filling of grains and high exerting panicle. There was a substantial and positive interaction of days to 50 per cent flowering with the plant height (0.152*) and negative, significant interaction with panicle length (-0.185**) (Table 3 and Figure 1) Significant and positive interaction was shown by plant height with panicle length (0.275**) and full grain number per panicle (0.224*). Similar findings were reported by Begum *et al.* (2021). The conglomeration of full grain number per panicle revealed a significant and negative phenotypic interrelation with 1000seed weight (-0.571**). Positive and significant

Table 3: Phenotypic (P) correlation coefficients of yield and its component traits in rice

	DFE	PH	EBT	PL	NFG/ P	TW	SPY
DFE	1.000	0.152 *	-0.037	-0.185 **	0.086	-0.109	0.049
PH	0.152 *	1.000	-0.031	0.275 **	0.224 **	0.097	0.193**
PNP	-0.037	-0.031	1.000	-0.113	-0.072	-0.078	0.034
PL	-0.185 **	0.275**	-0.113	1.000	0.067	0.091	0.056
NG/P	0.086	0.224 ***	-0.072	0.067	1.000	-0.571 ***	0.177**
TSW	-0.109	0.097	-0.078	0.091	-0.571 ***	1.000	0.044

* Significant at 5 per cent level; ** Significant at 1 per cent level

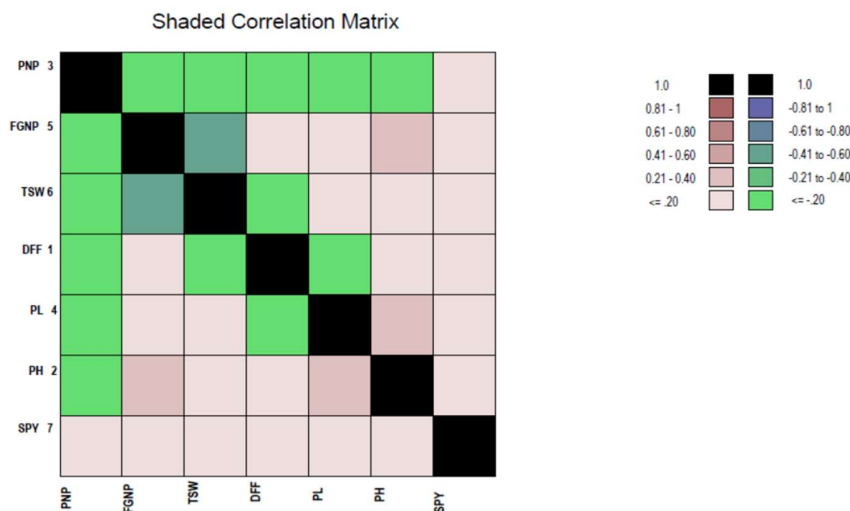


Figure 1: Correlogram visualizing the correlation in yield and its attributing traits rice

conglomeration of single plant yield with full grain number per panicle (0.193**) and plant height (0.177**), indicated that these two characteristics were essential for improvement of yield. Similar findings were found by Saleh *et al.* (2020) for full grain number per panicle.

Path coefficient analysis

The highest significant, positive direct phenotypic influence was exhibited by full grain number per panicle (0.265) on single plant yield (Table 4. and Fig.2) and it also contributed significant negative indirect effects *via* 1000-seed weight (-0.151). Saleh *et al.* (2020) found similar findings of positive direct effect of full grain number per panicle on single plant yield. Thousand seed weight (0.196) showed a greater direct phenotypic positive effect on single plant yield and this trait also contributed negative indirect effects through full grain number per panicle (-0.1108). Plant height (0.110) recorded a significant positive direct phenotypic influence on single plant yield. Other

traits i.e. days to 50% heading (0.034), panicle number per plant (0.074), and panicle length (0.005) had a negligible direct positive phenotypic effect on single plant yield. The full grain number per panicle had the greatest positive direct effect on single plant yield, followed by 1000-seed weight and plant height, according to path coefficient analysis. These characteristics should be emphasized in the selection process to isolate superior rice genotypes with higher yield potential.

Multiple linear regressions

Regression coefficients and the likelihood of the calculated variables in predicting single plant yield are displayed in table 3. Based on these findings, the following model equations for estimating grain yield/plant (Y) are developed.

$$Y = +0.06157x_1 DFE + 0.14020x_2 PH + 0.11325x_3 EBT + 0.10110x_4 PL + 0.01909x_5 NGP + 0.07731x_6 TW$$

The t-test for the parameters revealed that the plant height (0.5752) and full grain number per panicle, (0.7344) have contributed significantly to single plant yield as reported earlier by Begum *et al.*(2021).

Table 4: Phenotypic (P) path coefficients of yield and its component traits in rice

	DFE	PH	EBT	PL	NFG/ P	TW	SPY
DFE	0.034	0.005	-0.001	-0.006	0.003	-0.003	0.049
PH	0.016	0.110*	-0.003	0.030	0.024	0.010	0.193**
PNP	-0.002	-0.002	0.074	-0.008	-0.005	-0.005	0.034
PL	-0.001	0.001	-0.002	0.005	0.002	0.003	0.056
FGNP	0.022	0.059	-0.019	0.017	0.265**	-0.151	0.177**
TSW	-0.021	0.0188	-0.015	0.017	-0.1108	0.194**	0.0440

Phenotypic Residual effect = 0.365 Bold values are direct effects

Table 5: Multiple linear regression in predicting rice grain yield

	Beta Wt.	Simple R ²	Reg. Coeff.	Std.Err.	t-value	t Prob.	Partial R ²
INTERCEPT a		0.0000	1.90780	10.2164	0.8180	0.852	0.000
DFE	0.0344	0.0017	0.04318	0.0766	3.2793	0.4141	0.001
PH	0.1103	0.0213	0.08016	0.0476	0.5752	0.0012 **	0.010
PNP	0.0744	0.0026	0.24438	0.1946	0.9481	0.5656	0.006
PL	0.0057	0.0003	0.01010	0.1116	2.9995	0.3439	0.000
FGNP	0.2652	0.0469	0.02859	0.0082	0.7344	0.0029 **	0.043
TSW	0.1939	0.0085	0.34059	0.1320	0.8180	0.4633	0.024

* Significant at 5 per cent level; ** Significant at 1 per cent level

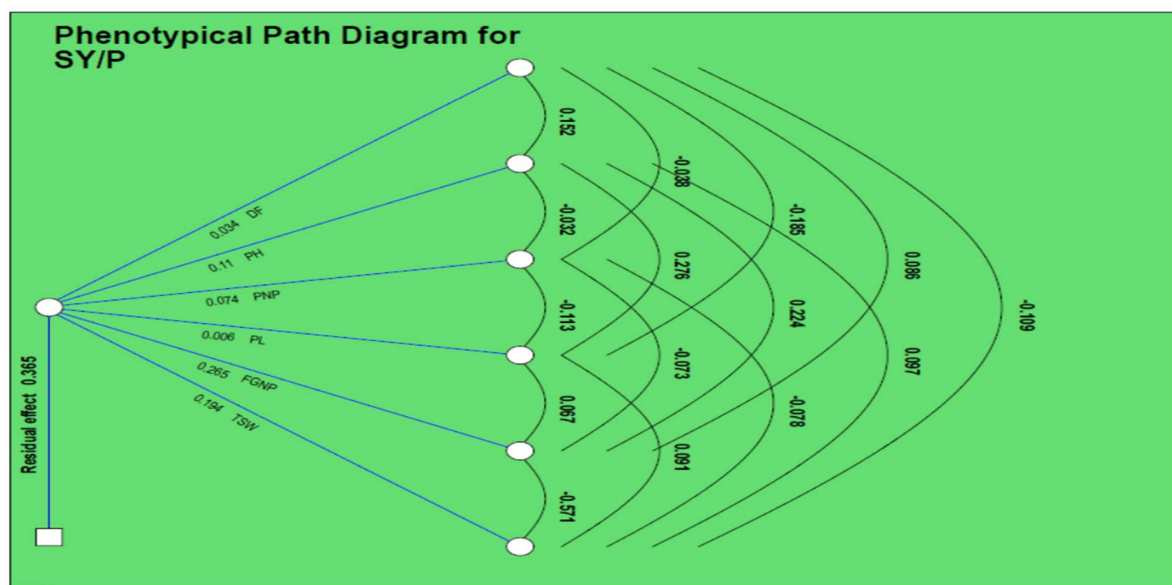


Figure 2: Phenotypic path diagram indicating direct and indirect effect of various traits on grain yield of rice.

Conclusion

The genetic organization of grain yield is the final net impact of multiple yield components interacting with one another. The present findings showed that the materials under investigation had substantial genetic variability. Plant height, panicle number per plant, panicle length, full grain number per panicle, 1000 seed weight, and single plant yield had high

heritability and genetic advance as per cent of mean, , showing that the characters were governed by additive gene effects, where selection can be practiced for these traits. High heritability estimates along with moderate genetic advance as per cent of mean for days to 50% heading, suggests the existence of non-additive gene effects, as well

as environmental influence. As per correlation and regression coefficient analysis, plant height and the full grain number per panicle contributed significantly to single plant yield. The full grain number per panicle had the greatest positive direct influence on single plant yield, followed by 1000-seed weight and plant height, according to path coefficient analysis. As a result, accessions with a larger full grain number per panicle with higher 1000-seed weight and plant height would be ideal for yield enhancement scheme.

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