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Genetic Variability and Correlation Studies on Yield and Yield-Related Traits in Rice (*Oryza sativa* L.) and their Implications in Selection

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ABSTRACT: Rice being a self pollinated crop suffers from reduced genetic diversity. The low heritability of yield trait is yet another problem in breeding which demands indirect selection *via* componental traits for its improvement. In this context, study of genetic variability and correlation forms the vital part of rice breeding programs. Twenty four rice genotypes including four popular checks were evaluated in a randomized complete block design with three replications, at Agricultural Research Station Gangavati, University of Agricultural Sciences Raichur, India. The experiment was carried out in *Kharif* 2018 to study the genetic variability and correlation between yield and yield attributing traits of rice crop. The analysis of variance indicated the presence of significant variability between the genotypes. The higher estimates of genetic parameters *viz.*, Vp and PCV as compared to the respective Vg and GCV revealed the influence of environment in the trait expression for all the characters studied. The results of correlation studies revealed the presence of positive genotypic correlation of grain yield per plant with other yield-related traits like the number of effective tillers per plant, length of panicles, panicle weight, number of grains per panicle and thousand seed weight. This showed that simultaneously selecting for these characteristics will result in an increase in grain yield; thus helps to breed high yielding rice genotypes.

Keywords: Rice; Grain yield per plant; Yield attributing traits; Genetic variability; Correlation.

INTRODUCTION

Rice is the predominant food crop in the world (Diwan and Shenoy, 2001). Being a valuable source of carbohydrates, it is the most consumed cereal grain at the global level. However, on one hand, the demand for rice production is increasing day by day with the expanding population; while on the other hand, the yield levels of most of the popular genotypes are stagnated. To satisfy the expanding population's food demands and attain food security, the current level of output must be raised. In this context, enhancing grain yield is the prime concern of any plant breeding program and it has become a challenge to the rice breeders. Rice varieties differ tremendously in terms of grain yield. The presence of sufficient genetic variability is critical for its further improvement by providing ways for the breeders to develop new hybrids and varieties. However, yield is a polygenic character with low heritability and is very much influenced by the environment. Hence, direct selection is not effective for its improvement (Zahid *et al*., 2006; Akhi *et al*., 2016; Aghaei *et al*., 2017, Li *et al*., 2019 and Gupta *et al*., 2020).

Karl Pearson's correlation coefficient (or simply, correlation coefficient) helps in identifying the nature of association between two distinct traits. The study of correlations enables plant breeders to understand how improving one trait will result in simultaneous improvement in other traits. Correlation studies, as a result, give improved ways for yield enhancement during selection programmes (Robinson *et al*., 1951 and Johnson *et al*., 1955). Simple phenotypic correlation, on the other hand, reveals the type of association which is seen between different attributes in a broader context. However, phenotypic correlations alone do not provide a valid basis for selection as they include all the observable associations which are the results of both genetic and environmental effects. As a result, genotypic correlations that are centered on the heritable portion of observed variation allow for the evaluation of the pattern of underlying link that exists between different traits. The present investigation was, therefore, undertaken to know the genetic variability and correlation among the yield and yield-related traits at both genotypic and phenotypic levels in a set of 24 rice genotypes.

MATERIAL AND METHODS

Description of the experimental material and layout

The experimental material for the present study comprised 24 rice genotypes that include both early and medium maturing advanced breeding lines and the information is furnished in Appendix I. The material for the investigation was obtained from ARS (Agricultural Research Station) Gangavati, University of Agricultural Sciences Raichur (UASR), Karnataka, India and the experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. The seeds were sown in the seedbed on 10th July 2018 and seedlings were transplanted to the main field in *Kharif* 2018 with a spacing of 20×15 cm. Standard agronomic practices were adopted for normal crop growth.

Appendix I: List of genotypes used in the study.

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	BPT-Mutant 1801	13	IABT-17
2.	BPT-Mutant 1802	14	Gangavati sanna
3.	Gontra Bidhan	15	IET-22066
4.	Rp-Bio-226 Mutant 614	16	IET-24767
5.	IET-25451	17	GNV-1108
6.	IET-27162	18	GNV-1602
7.	IET-25520	19	RNR-15048
8.	SMW-09-32	20	IET-25497
9.	Rp-Bio-226 Mutant 612	21	IET-26241
10.	BPT-Mutant 1808	22	GNV 1109
11.	Gangavati sona (Check)	23	GNV 10-89 (Check)
12.	BPT-5204 (Check)	24	MTU-1010 (Check)

Data collection: At the optimal plant development stage, five randomly selected plants from each treatment were harvested for data collection, leaving the first two border rows from across all four sides of the experimental plot. The data were recorded on 10 quantitative traits *viz.*, days to 50 percent flowering, plant height (cm), number of panicles (productive tillers) per plant, number of tillers per plant, length of flag leaf (cm), panicle length (cm), panicle weight (g), number of grains per panicle, test weight (1000 seeds weight in g) and grain yield per plant (g). Averages of the data from the sampled plants concerning different characters were used for statistical analyses using the software Windostat version 8.5.

RESULTS AND DISCUSSION

ANOVA (Analysis of Variance): Genetic variability is the cornerstone of any plant breeding program. Immense variability in the combinations of various yield-related traits owe to vast diversity in genetic composition. The ANOVA for different yield-related characters and their coefficients of variation are presented in Table 1. The ANOVA revealed the presence of significantly higher amount of variability among the genotypes for all the yield-related characters studied. The variability observed could be the result of the differential parentage/origin of the genotypes selected. Similar results were reported by Veni and Rani (2006); Kishore *et al.* (2015); Gupta *et al.* (2020).

Table 1: ANOVA for yield and yield-related traits in rice genotypes.

Source of variation	DF	DFF	PTH	TN	PN	FL	PL	PW	GN	TW	YPP
Treatment	23	106.98**	376.86**	7.31**	5.73**	45.59**	6.41**	0.83**	641.73**	18.71**	28.3**
Replication	2	0.13	114.97	2.48	3.02	38.01	1.26	0.21	194.8	1.05	29.74
Error	46	6.33	98.11	2.08	1.88	4.39	1.39	0.07	116.69	1.58	2.47
CV		2.45	9.98	11.08	12.30	7.27	5.26	9.89	8.61	6.00	6.26

Abbreviations: **- Significant @ 1% level; **DFF**- Days to 50% flowering; **PTH**- Plant height in centimetres; **TN**- Number of tillers per plant; **PN**- Number of panicles per plant; **FL**- Flag leaf length in cm; **PL**- Panicle length in cm; **PW**- Panicle weight in grams; **GN**- Number of grains per panicle; **TW**- Thousand seed weight in grams; **YPP**- Yield per plant in grams.

Genetic variability parameters for yield and yield related traits of rice genotypes

Coefficient of variation refers to the extent of variation in relation to the mean of the population whereas; heritability is an estimate of the heritable portion of the total or phenotypic variation. The variability and heritability of any trait is studied mainly to have an idea about the feasibility of selection. The estimates of genetic advance as per cent of mean (GAM) give more reliable information regarding the fruitfulness of selection programs. Thus, heritability values coupled with genetic advance would be more reliable and useful in operating selection as it indicates the presence of additive gene effects on heritability (Singh *et al.*, 2018 and Lingaiah *et al*., 2020). Genetic variability parameters for different yield and yield related traits *viz.*, range, phenotypic and genotypic variability, phenotypic and genotypic coefficients of variation, heritability, genetic advance (GA) and genetic advance as per cent mean (GAM) are presented in Table 2.

Table 2: Mean and other genetic parameters of yield and yield related traits of rice genotypes.

Sr. No.	Traits	Mean	Range		Variances		CV (%)		h^2 bs (%)	GA @ 5%	GAM
			Min.	Max.	Genotypic (Vg)	Phenotypic (Vp)	GCV	PCV			
1.	DFF	102.54	91.00	115.33	33.55	39.88	5.65	6.16	84.13	10.95	10.67
2.	PTH	99.21	73.53	118.60	92.92	191.03	9.72	13.93	48.64	13.85	13.96
3.	TN	13.03	10.33	17.80	1.74	3.83	10.13	15.02	45.53	1.835	14.08
4.	PN	11.16	8.57	15.73	1.28	3.17	10.14	15.94	40.49	1.48	13.26
6.	FL	28.81	23.20	35.44	13.73	18.12	12.86	14.78	75.78	6.65	23.08
7.	PL	22.44	19.53	25.20	1.67	3.07	5.76	7.80	54.57	1.97	8.77
8.	PW	2.72	1.73	3.63	0.25	0.32	18.42	20.91	77.63	0.91	33.45
9.	GN	125.42	99.87	160.60	175.02	291.70	10.55	13.62	60.00	21.11	16.83
10.	TW	20.95	17.27	28.27	5.71	7.29	11.41	12.89	78.29	4.36	20.81
11.	YPP	25.09	19.39	30.71	8.61	11.08	11.70	13.27	77.75	5.33	21.24

Abbreviations: **CV**- Coefficient of variation; **GCV**- Genotypic coefficient of variance; **PCV**- Phenotypic coefficient of variance; **H-** heritability in broad sense; **GA-** Genetic advance; **GAM**- Genetic advance as percent of mean.
(Other abbreviations are same as mentioned under Table 1).

For all of the traits studied, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV), showing the influence of environment in the phenotypic expression of traits (Table 2). GCV was the highest (18.42) for panicle weight followed by flag leaf length (12.86) and grain yield per plant (11.70) indicating a higher degree of genetic variability among the tested varieties for these traits. Higher heritability combined with high genetic advance as percent of mean was exhibited by flag leaf length, panicle weight, thousand seed weight, and grain yield per panicle indicating good scope for selection and thus help in yield improvement. The results are consistent with the reports of Bisne *et al.* (2009); Dhurai *et al.* (2014); Girma *et al.* (2018); Sudeepthi *et al.* (2020); Gupta *et al.* (2020). The trait panicle length recorded moderate heritability (54.57) coupled with low GAM (8.77) indicating the predominance of non-additive gene actions controlling the trait. Hence direct selection for this trait may not be fruitful. Similar results were also reported by Manjunatha *et al.* (2018) and Perera *et al.* (2014). On the contrary, Akinwale *et al.* (2011) and Seyoum *et al.* (2012) have earlier reported high heritability with low genetic advance for panicle length.

Estimation of genetic variability parameters revealed that the Plant height, effective tiller number per hill, panicle length and weight, number of grains per panicle, and thousand seed weight were shown to be the most dependable traits for yield enhancement in rice. As a result, while selecting for yield enhancement in rice, these characteristics should be prioritised.

Phenotypic Correlation. The inter-character associations estimated in terms correlation coefficients at both phenotypic and genotypic levels for different yield componential studied in the current investigation are presented in Table 3. All the yield-related traits *viz.*, plant height (0.4434), tiller number (0.4560), panicle number (0.4577), panicle length (0.2589), panicle weight (0.3249), grain number (0.2505) and test weight (0.3865) exhibited a positive significant association with grain yield per plant except days to 50% flowering and flag leaf length. This indicates that selection for tiller number, number of panicles per hill, panicle length and weight, number of grains per panicle, and test weight would help in grain yield enhancement of paddy varieties. Present results are on par with Wattoo *et al.* (2010) for correlation of grain yield per plant with grain number per panicle and panicle number per hill; Prasad *et al.* (2001); Agahi *et al.* (2007); Venkatalakshmi *et al.* (2014); Oladosu *et al.* (2018) for correlation with the number of productive tillers per hill; Kalyan *et al.* (2017) for correlation with plant height and days to fifty percent flowering; Adeyemi *et al.* (2011); Archana *et al.* (2018) for correlation with panicle weight; for correlation with thousand grain weight and Bhargava *et al.* (2021) for number of productive tillers per hill and panicle length.

The trait days to 50% flowering exhibited a negative significant correlation (-0.2788) with grain yield. This negative correlation might have arisen mainly from competition for a common factor like nutrient supply. The positive non-significant association of flag leaf length (0.1984) with grain yield might be the result of environmental effects masking the trait expression. Confirming results for correlation of flag leaf length with grain yield per plant were also reported by Hasan *et al.* (2011); Bhatt *et al.* (2016).

Table 3: Genotypic (Above diagonal) and Phenotypic (Below diagonal) correlation matrix for various yield and yield-related traits of rice genotypes.

	DFF	PTH	TLN	PN	FL	PL	PW	GN	TW	YPP
DFF	1	-0.1855	-0.1544	-0.2123	0.3949**	-0.4226**	-0.5089**	-0.1655	-0.4506**	-0.3285**
PTH	-0.1380	1	0.4022**	0.3773**	0.3398**	0.5137**	0.0226	0.3937**	0.2345*	0.7181**
TLN	-0.1522	0.2666*	1	0.8790**	0.2806*	0.2439*	0.111	0.0925	0.2314	0.7238**
PN	-0.2095	0.1909	0.8449**	1	0.1875	0.1051	0.1919	0.2332*	0.2131	0.7366**
FL	0.3739**	0.2229	0.0516	0.0905	1	0.0905	-0.2812*	0.4681**	-0.3465**	0.2461*
PL	-0.3125**	0.2885*	0.0125	-0.0116	0.0698	1	0.2283	0.1929	0.5054**	0.3268**
PW	-0.4744**	0.0152	0.0623	0.1206	-0.2471*	0.1879	1	0.2421*	0.5214**	0.3724**
GN	-0.0955	0.2082	0.0389	0.2320*	0.3268**	0.1245	0.1656	1	-0.2542*	0.3925**
TW	-0.3409**	0.1999	0.0847	0.0912	-0.2693**	0.3493**	0.4480**	-0.2335*	1	0.4499**
YPP	-0.2788*	0.4434**	0.4560**	0.4577**	0.1984	0.2589*	0.3249**	0.2505*	0.3865**	1

*, ** significant at 5% and 1% levels respectively.

Note: Abbreviations are the same as mentioned in Table 1

The negative significant association of grain number per panicle with thousand seed weight (-0.2335) indicates that as the grain number per panicle increases, the grain size decreases. This may be attributed to competition between grains for assimilates. These findings are in line with Agahi *et al.* (2007); Wattoo *et al*. (2010).

Genotypic correlation. Except days to fifty percent flowering, all the other traits *viz.*, plant height (0.7181), tiller number (0.7238), panicle number (0.7366), flag leaf length (0.2461), panicle length (0.3268), panicle weight (0.3724), grain number per panicle (0.3925) and test weight (0.4499) showed positive significant correlation with grain yield per plant indicating the importance of these traits as selection criteria in yield enhancement programs. The genotypic correlation might be attributable to pleiotropic gene activity, linkage, or, most likely, both (Sarangi, 2008). The negative significant association of days to fifty percent flowering with grain yield per plant (-0.3285), panicle length (-0.4226), panicle weight (-0.5089) and test weight (-0.4506) could be the result of pleiotropy exhibited by genes. For example, the gene *Ghd7* enhances the grain number per panicle while delaying the days to flowering. The *GW2* improves the number of panicles per plant and grain size while extending the heading date and decreasing the grain number per panicle (Huo *et al.*, 2017). Similarly, DENSE AND ERECT PANICLE1 (*DEP1*) is pleiotropically responsible for high grain number per panicle, dense and erect panicle, and a consequent increase in grain yield (Xu *et al*., 2016).

Non-significant correlation of tiller number with panicle length and flag leaf length at phenotypic level but significant correlation at genotypic level indicates the effect of environmental factors which might have caused bias in the gene expression. Similar results were also reported by Saha *et al*. (2019) for correlation of tiller number with days to fifty percent flowering and panicle numbers. However, the positive significant genotypic correlation of flag leaf length with grain yield per (0.2461) plant may be attributed to the pleiotropic effect of some QTLs like *qFLL6.2* that showed consistent effects on Flag leaf length and yield traits (Shen *et al.*, 2012).

Significance at the genotypic level indicates that the positive association observed between various traits has a genetic basis and is not due to any favourable environmental effects. Thus selection for a genotype with a higher magnitude of the number of effective tillers per hill, length and panicle weight, number of grains per panicle, and thousand seed weight will ensure higher grain yield per plant. Similar results were also reported by Agahi *et al.* (2007); Yadav *et al.* (2010); Adhikari *et al*. (2018); Kishore *et al.* (2018); Tejaswini *et al.* (2018); Oladosu *et al.* (2018); Saha *et al.* (2019).

CONCLUSION

The Analysis of Variance (ANOVA) indicated the presence of significant differences among the 24 genotypes for all the studied traits. The genetic variability analyses also revealed that the material used in this study possessed significant variability in terms of yield and yield-related attributes, providing a suitable platform to carryout selection by the breeder. Correlation study between the yield and its component characters found that the genotypic correlation coefficients were greater than the phenotypic correlation coefficients in most situations, indicating that the relationship is mostly attributable to genetic factors. In several situations, the phenotypic correlation coefficients were greater than the genotypic correlation coefficients, indicating the significant role of environment in governing the expression of these traits. The strong positive genotypic correlation of grain yield per plant with other yield-related traits like the number of effective tillers per plant, length of panicles, panicle weight, number of grains per panicle and thousand seed weight indicated that simultaneous selection for these characters would result in improvement of high yielding varieties. Although the tillers per plant, length of flag leaf *etc.* did not exhibit positive significant correlation with other grain yield-related traits at the genotypic level, their relevance in contributing to grain yield cannot be overstated, since these component characters demonstrated a positive significant correlation with other key yield attributes. As a result, these characteristics may be believed to indirectly contribute to grain yield control *via* other component yield traits.

FUTURE SCOPE

In the future, this collection of experimental material may be used for diversity analysis and combining ability studies to carry out hybridization followed by selection, which assists in breeding high-yielding rice genotypes.

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Conflicts of Interest. None.

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