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Genetic component and association studies in segregating generation of rice

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Abstract

Rice (*Oryza sativa* L.) is one of the staple cereal crops which feed more than half of the world population. Therefore, a better insight to the association of yield with its component traits can be helpful in improving the rice yield. The present study comprised of 371 F₂ segregating progenies of the cross (Sahbhagidhan and BPT-5204 Sub-1), which were evaluated to assess the genetic variability, heritability and genetic advance, correlation and direct and indirect effects among yield and yield components. The correlation studies revealed that seed yield per plant was positively and significantly correlated with number of tillers per plant, number of panicles per plant, number of spikelets per plant, number of grains per plant, number of spikelets per panicle, number of grains per panicle, fertility percent and panicle length in F₂ generation. The path analysis indicated that number of panicles per plant, number of spikelets per plant and number of grains per plant exhibited high and positive direct effects and thus, may be considered as useful traits for yield improvement of rice.

Keywords: Rice, genetic variability, heritability, genetic advance, correlation and path coefficient analysis

Introduction

Rice (*Oryza sativa* L., 2n=24) belongs to family Poaceae and subfamily Oryzoidae. It is believed to be originated in South East Asia. Among the food grain crops grown in India, rice has the largest area of about 38 Mha with the production of about 116 million tonnes during 2018-2019 (www.indiastat.com). The population is expected to reach nearly 1.63 billion by the year 2050 (Ashok *et al.*, 2016) [2]. To feed the increasing population it is essential to increase the production and productivity. Hence, rice breeders are interested in developing cultivars which are high yielding along with desirable agronomic characters. Rice is a self-pollinated crop, the efforts of the breeder to evolve better yielding genotypes is mainly aimed at exercising selection in segregating generation. The selection within a segregating generation partly may fulfill the objective in improving polygenic character like yield. Generally direct selection for yield is not effective due to its low heritability; hence it is desirable to adopt indirect selection of component traits for yield improvements. Furthermore, a critical estimate of nature and magnitude of genetic variability is a prerequisite for any crop improvement programme. The estimates of variability, heritability and genetic advance for the yield components and their correlations with yield have been considered to be of great importance. The variation which is observed in any population could be due to the genetic and environmental factors and also due to the interaction (G × E) between these factors. The genetic variability could be determined with the help of genetical parameters such as Genetic Coefficient of Variation (GCV), heritability estimates and genetic advance (GA). GCV indicates the relative degree of genetic variability existing for different characters in a population of genotypes. The heritability expresses the relative amount of heritable portion of the variation. However, the heritability estimates along with genetic gain is more useful in selecting the best population individual. Furthermore, the study of character correlations is important to design appropriate selection strategy for genetic improvement in yield and other characters. The relationship between yield and its main economic components, in segregating populations of rice, has been studied by several researchers (Surek and Beser, 2005;

Kumar *et al.*, 2009; Yogameenakshi and Vivekanandan, 2010)^[26, 14, 30]. The information on relative direct and indirect contribution of each component character toward yield will help breeders to formulate the effective criteria in selecting desirable genotypes in early segregating populations. In view of this, the present study was planned to determine the correlation and path coefficients of yield and yield contributing characters by using F₂ generations of the cross.

Materials and Methods

The experiment was conducted with 371 F₂ segregants of the cross (Sahbhagidhan and BPT-5204 Sub-1) at Rice Research Farm of department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi during *kharif* 2018. Sahbhagidhan has phosphorus uptake and drought tolerance genes. However, BPT-5204 Sub-1 has submergence tolerance gene (Sub-1) and has an excellent grain cooking quality. The crop was raised with the spacing of 20 × 15 cm and all the recommended agronomic practices were followed. Phenotypic observations were recorded for fifteen traits *viz.* seed yield per plant, days to flowering, plant height, spikelets per plant, spikelets per panicle, grains per plant, grains per panicle, fertility percent, tillers per plant, number of panicle per plant, panicle length, grain length, grain width, L/B ratio and 100 seed weight. The phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated using the formula given by Burton and Devane (1953)^[4] and heritability and genetic advance by Johnson *et al.*, (1955)^[12]. The correlation coefficient was calculated as per Goulden (1952) and coefficient of correlation was partitioned into path coefficient using the technique outlined by Dewey and Lu (1959)^[7].

Results and Discussions

Variability, heritability and genetic advance

All the characters displayed low values of genotypic and phenotypic coefficient of variation in F₂ generation indicating

little environmental influence their expression. Days to flowering, plant height, number of spikelets per panicle, number of grains per panicle, grain width and 100 seed weight displayed little differences in GCV and PCV in F₂ generation which indicated little environmental influence on the expression of these characters. Among these characters, comparatively more values of GCV and PCV were observed for the characters *viz.* seed yield per plant, number of panicles per plant, number of grains per plant, number of spikelets per panicle and number of grains per panicle which indicated existence of variability for these traits and thus, better opportunities for the selection of genotype when compared to rest of the traits. This has been depicted in (Table-1) and (Figure-1). Similar results were revealed by Devi (2006)^[6], Raut *et al.* (2009)^[24], Nandeshwar *et al.* (2010)^[19], Gala *et al.* (2016)^[9]. However, phenotypic coefficient of variation of all the characters were higher than genotypic coefficient of variation indicating additive effect of environment on the expression of these trait. Similar findings were reported previously by Praveen *et al.* (2010)^[23], Chakraborty *et al.* (2010)^[5] and Gala *et al.* (2016)^[9]. These segregants possessed high heritability coupled with high genetic advance as percent of mean for the characters; *viz.* plant height, number of spikelets per panicle and number of grains per panicle indicating preponderance of additive gene action and thus selection may be effective for these traits. Similar findings were reported by Dutta *et al.* (2013)^[8], Tuhina *et al.* (2015)^[28] and Lingaiah *et al.* (2015)^[17]. High heritability coupled with moderate genetic advance as percent of mean was reported in F₂ segregants for the characters *viz.* grain width, L/B ratio and 100 seed weight which indicated preponderance of additive and non-additive gene action. Similar findings were reported by Chakraborty *et al.* (2010)^[5]. High genetic advance as percent of mean coupled with moderate heritability was reported in F₂ generation for characters *viz.* number of spikelets per plant and number of grains per plant.

Table 1: Estimates of statistical and genetical parameters of different characters for F₂ generation of rice (*O. sativa* L.)

Parameters	Range	AV	GCV(%)	PCV(%)	h ² (%)	GA	GA%
Seed yield per plant (g) (SYP)	2.8-90.5	38.1	2.5	4.7	28.7	1071.1	28.0
Days to flowering (days) (DTF)	83.0-96.0	91.0	0.2	0.3	46.4	267.8	2.9
Plant height (cm) (PHT)	67.0-145.0	106.1	1.3	1.3	97.0	2934.7	27.6
Number of tillers/plant (TLN)	0.0-30.0	14.0	1.8	3.4	29.9	294.9	21.0
Number of panicles/ plant (PLN)	1.0-28.0	12.0	1.7	4.1	18.1	179.2	15.3
Number of spikelets/plant (SPP)	129.0-4287.0	1813.0	2.8	4.7	36.6	64726.4	35.6
Number of grains/plant (GPP)	22.0-3782.0	1372.0	3.2	5.2	37.3	55428.8	40.4
No. of spikelets/panicle (SPL)	12.0-533.0	157.0	3.1	3.3	92.3	9901.6	63.0
Number of grains/panicle (GPL)	1.0-455.0	118.0	3.6	3.7	93.6	8463.3	72.0
Fertility percent (%) (FER)	8.3-96.8	74.1	0.7	1.6	16.8	436.6	5.8
Panicle length (cm) (PLL)	13.0-35.0	26.2	0.1	0.8	2.9	13.6	0.5
Grain length (mm) (GRL)	7.0-9.5	8.1	0.2	0.5	18.6	16.5	2.0
Grain width (mm) (GRW)	1.9-3.2	2.6	0.6	0.7	65.3	26.1	10.0
L/B ratio (LBR)	2.4-4.2	3.1	0.6	0.8	59.2	34.2	10.8
100 Seed weight (g) (SWT)	1.7-2.4	2.1	0.4	0.5	69.3	16.7	7.8

AV- Average, GCV(%) - Genotypic coefficient of variation, PCV(%) - Phenotypic Coefficient of Variation, h² (%) - heritability, GA - Genetic Advance, GA% - Genetic Advance as percent of mean

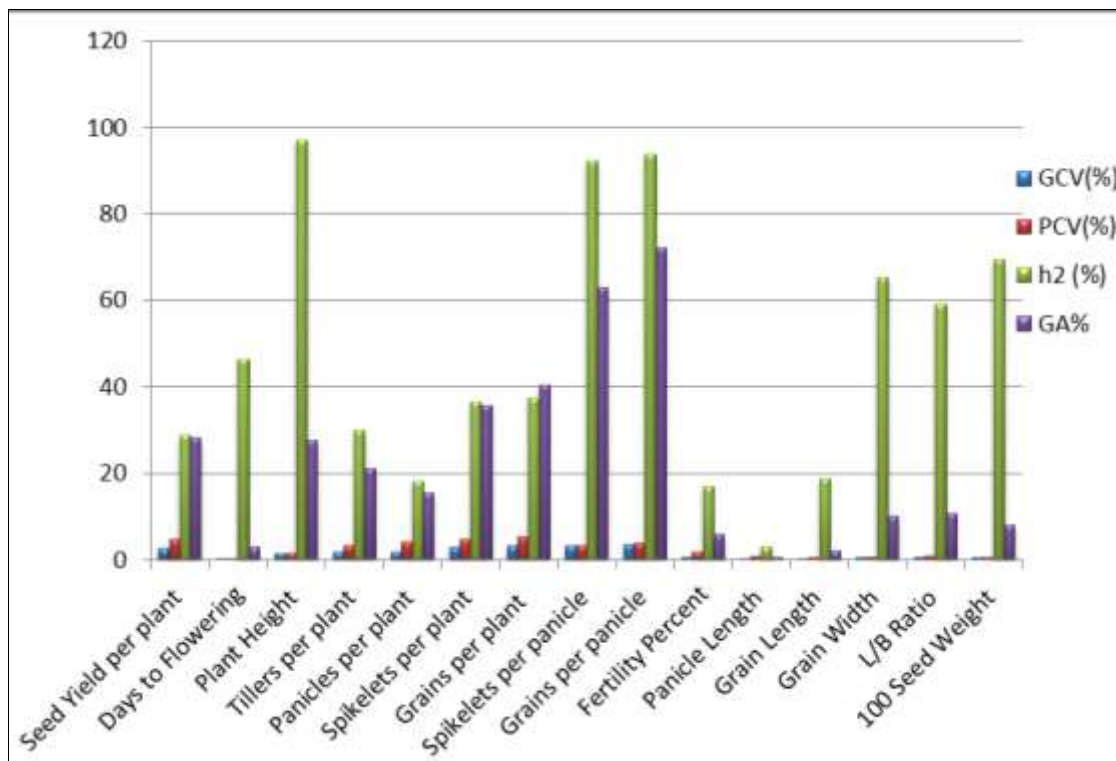


Fig 1: Graphical representation of genetical parameters of different characters for F₂ generation of rice

Correlation analysis

The knowledge about the nature and level of inter-relationship of yield and other components is very valuable because selection based on one trait may directly or indirectly affect the performance of another trait. Assessment of inter-relationships among a number of component characters is, therefore, an important requisite to bring improvement. In the present study, correlation analysis revealed that seed yield per plant had positive and significant correlation with number of tillers per plant (0.496), number of panicles per plant (0.836), number of spikelets per plant (0.989), number of grains per plant (0.949), number of spikelets per panicle (0.357), number of grains per panicle (0.404), fertility percent (0.249) and panicle length (0.207). This has been presented in (Table-2). This is in agreement with Agahi *et al.* (2007)^[11], Lakshmi *et al.* (2014)^[16], Hossain *et al.* (2015)^[10], Konate *et al.* (2016)^[13], Janakbhai *et al.* (2017)^[11], Swapnil *et al.* (2018)^[27], Oladosu *et al.* (2018)^[21], Welalaw *et al.* (2018)^[29] and Kumar *et al.* (2018)^[15]. Days to flowering exhibited positive and significant correlation with number of spikelets per panicle (0.134) and number of grains per panicle (0.132). In the same way, positive and significant association of number of tillers per plant was observed with number of panicles per plant (0.603), number of spikelets per plant (0.494) and number of grains per plant (0.477). Number of panicles per plant displayed positive and significant correlation with number of spikelets per plant (0.829), number of grains per plant (0.789), fertility percent (0.160) and panicle length (0.135). Similarly, positive and significant association of number of spikelets per plant was observed with number of grains per plant (0.958), number of grains per panicle (0.417), number of spikelets per panicle (0.370), fertility percent (0.254) and panicle length (0.206). Number of grains per plant exhibited positive and significant correlation with number of spikelets per panicle (0.352), number of grains per panicle (0.497), fertility percent (0.451) and panicle length (0.179). This is in accordance with Hossain *et al.* (2015)^[10], Janakbhai *et al.* (2017)^[11], Kumar *et al.* (2018)^[15], Oladosu *et al.* (2018)^[21] and Welalaw *et al.*

(2018)^[29]. Spikelets per panicle displayed positive and significant correlation with number of grains per panicle (0.743), fertility percent (0.150) and panicle length (0.169). However, it was found negatively and significantly correlated with 100 seed weight (-0.104) and L/B ratio (-0.117). Similarly, number of grains per panicle was found positively and significantly correlated with fertility percent (0.525) and panicle length (0.152). However, it was negatively and significantly correlated with grain length (-0.116), 100 seed weight (-0.131) and L.B. ratio (-0.112). Fertility percent was found negatively and significantly correlated with grain length (-0.130) and 100 seed weight (-0.120). Positive and significant association of grain length with 100 seed weight (0.673) and L/B ratio (0.515). Grain width was found positively and significantly correlated with 100 seed weight (0.050). Whereas, it was negatively and significantly correlated with L/B ratio (-0.796). Positive and significant correlation of L/B ratio with 100 seed weight (0.361). Selection based on these traits may be rewarding and thus, leads to higher yield.

Path Coefficient Analysis

Determination of association among the traits by correlation analysis may not provide exact idea of the relative importance of direct and indirect effects of each yield contributing characters towards yield. By using path analysis, direct and indirect effects were worked out to find out the clear idea of inter relationship between yield and yield contributing characters. In the present study, the path coefficient analysis was done at the phenotypic level. The results of phenotypic path coefficient analysis revealed that direct effect of number of panicles per plant was positive (0.126) as well as the indirect effect of spikelets per plant via panicles per plant was very high (0.633) and positive except number of tillers per plant, number of spikelets per panicle and number of grains per panicle for which the indirect effects on yield were negative. This has been depicted in (Table-3) and this is in agreement with Bagheri *et al.* (2011)^[3] and Nayak *et al.* (2011)^[20]. Number of spikelets per plant (0.764)

and number of grains per plant (0.111) had high and positive direct effect and indirect effect of all characters via these were positive except number of tillers per plant and number of grains per panicle character for which the indirect effects on yield were negative. High and positive direct effect suggests that these may be considered as the prime traits for enhancing yield. This is in accordance with Agahi *et al.* (2007) [1], Bagheri *et al.* (2011) [3], Nayak *et al.* (2011) [20], Mohanty *et al.* (2012) [18], Sarker *et al.* (2014) [25] and Prasad *et al.* (2017) [22]. Direct effect of number of spikelets per panicle was positive (0.134) as well as indirect effect of all characters via spikelets per panicle was positive

except number of panicles per plant and number of grains per panicle for which the indirect effects were negative. Direct effect of number of grains per panicle (-0.101) was negative and indirect effect of all characters via grains per panicle was positive except number of tillers per plant for which the indirect effects was negative. This is in agreement with Agahi *et al.* (2007) [1], Mohanty *et al.* (2012) [18], Sarker *et al.* (2014) [25], Prasad *et al.* (2017) [22] and Welalaw *et al.* (2018) [29]. The direct effects of other characters were very low and hence, are not given due consideration.

Table 2: Genotypic and Phenotypic correlation between different pairs of characters in F₂ segregants of rice (*O. sativa* L.)

		DTF	PHT	TLN	PLN	SPP	GPP	SPL	GPL	FER	PLL	GRL	GRW	LBR	SWT
SYP	G	0.106	-0.109	0.778	0.675	0.864	0.907	0.530	0.431	-0.002	-0.411	-0.469	-0.197	0.472	-0.140
	P	0.078	-0.038	0.496**	0.836**	0.989**	0.949**	0.357**	0.404**	0.249**	0.207**	0.001	0.019	-0.009	0.046
DTF	G		0.065	0.772	0.120	0.188	0.532	-0.299	0.159	0.143	0.075	0.086	0.175	-0.097	0.175
	P		0.085	-0.06	-0.035	0.085	0.088	0.134**	0.132**	0.072	-0.023	-0.033	-0.064	0.034	-0.005
PHT	G			0.859	0.130	0.086	0.029	0.618	-0.046	0.173	0.087	0.086	0.004	0.042	-0.008
	P			-0.077	-0.027	-0.037	-0.044	-0.014	-0.041	-0.068	0.027	0.007	-0.002	0.012	0.056
TLN	G				0.865	0.697	0.578	-0.041	-0.065	-0.265	-0.291	-0.171	0.036	0.869	0.192
	P				0.603**	0.494**	0.477**	-0.025	0.051	0.163**	0.107*	0.019	-0.026	0.034	0.034
PLN	G					0.476	0.275	-0.207	-0.256	-0.571	-0.545	0.165	-0.005	0.076	0.596
	P					0.829**	0.789**	-0.066	0.018	0.16**	0.135**	-0.011	-0.067	0.059	0.055
SPP	G						0.546	0.381	0.295	-0.044	0.190	0.144	-0.056	0.239	0.416
	P						0.958**	0.37**	0.417**	0.254**	0.206**	-0.073	0.008	-0.043	-0.053
GPP	G							0.337	0.347	0.406	-0.150	-0.068	-0.075	0.375	0.345
	P							0.352**	0.497**	0.461**	0.179**	-0.095*	0.002	-0.048	-0.077
SPL	G								0.433	0.091	0.752	0.330	0.075	-0.379	0.322
	P								0.743**	0.15**	0.169**	-0.072	0.086	-0.117*	-0.104*
GPL	G									0.438	0.393	0.016	-0.133	-0.269	0.275
	P									0.525**	0.152**	-0.119*	0.052	-0.112*	-0.131**
FER	G										-0.025	-0.065	-0.076	0.267	-0.070
	P										-0.042	-0.13**	-0.013	-0.056	-0.120*
PLL	G											0.007	-0.036	0.075	-0.065
	P											0.009	-0.032	0.032	0.032
GRL	G												-0.006	0.275	-0.016
	P												0.089	0.515**	0.673**
GRW	G													0.464	-0.076
	P													-0.796**	0.05
LBR	G														0.476
	P														0.361**

*,** significant at 5% and 1% level of probability, respectively

Table 3: Partitioning of correlation into direct and indirect effects by phenotypic path coefficient analysis in F₂ sergeants of rice (*O. sativa* L.) for seed yield per plant

	Correlation (Seed yield/plant) r (SY)	Number of tillers /plant	Number of panicles /plant	Number of spikelets / plant	Number of grains/ plant	Number of spikelets/ panicle	Number of grains/ panicle	Fertility percent (%)	Panicle length (cm)
Number of tillers /plant	0.496	-0.004	0.075	0.377	0.053	-0.003	-0.005	0.003	0.001
Number of panicles /plant	0.836	-0.002	0.125	0.633	0.087	-0.009	-0.001	0.003	0.001
Number of spikelets / plant	0.989	-0.002	0.104	0.764	0.106	0.055	-0.045	0.004	0.001
Number of grains/plant	0.949	-0.002	0.099	0.732	0.111	0.052	-0.053	0.008	0.001
Number of spikelets/ panicle	0.4	0.000	-0.009	0.317	0.043	0.134	-0.090	0.003	0.001
Number of grains/ panicle	0.43	-0.000	0.002	0.340	0.058	0.119	-0.101	0.010	0.001
Fertility percent (%)	0.249	-0.001	0.020	0.194	0.051	0.022	-0.056	0.018	-0.000
Panicle length (cm)	0.207	-0.001	0.017	0.157	0.019	0.025	-0.016	-0.001	0.005

Note: Bold and diagonal figures indicate the direct effect, Residual effect: 0.1260

Conclusion

Days to flowering, plant height, number of spikelets per panicle, number of grains per panicle, grain width and 100 seed weight displayed little differences in GCV and PCV in F₂ generation which indicated little environmental influence on the expression

of these characters. The segregants exhibited high heritability coupled with high genetic advance as percent of mean for the characters namely; plant height, number of spikelets per panicle and number of grains per panicle indicating preponderance of additive gene action and thus, selection may be effective for

these traits. Seed yield per plant was found positively and significantly correlated with number of tillers per plant, number of panicles per plant, number of spikelets per plant, number of grains per plant, number of spikelets per panicle, number of grains per panicle, fertility percent and panicle length. By improving these traits in desirable direction we can also improve yield of the plant. Path analysis revealed that if the correlation between grain yield per plant and its contributing traits is due to direct effect of traits, it reveals true relationship between them and direct selection for this trait will be rewarding for grain yield improvement.

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