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Studies on genetic parameters, correlation and path analysis in rice (*Oryza sativa* L.)

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Abstract

An experiment was conducted to study the genetic variability in seventy seven rice genotypes for grain yield and its component characters. Analysis of variance revealed the existence of sufficient amount of variability in the material under study. The magnitude of phenotypic coefficient of variation was found to be higher than genotypic coefficient of variation for the characters studied indicated the influence of environment on the manifestation of these characters. The characters such as number of filled grains per panicle and 1000 seed weight exhibited higher estimates of phenotypic and genotypic coefficient of variation indicates that these character could be improved through direct selection. High heritability coupled with high genetic advance was observed for 1000 seed weight, reveals the role of additive gene action controlling this trait. While the trait spikelet fertility (%) is controlled by non-additive gene action and suggesting the improvement of this character through heterosis breeding. The traits such as plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle and spikelet fertility (%) and 1000 seed weight had positive phenotypic and genotypic correlation with grain yield per plant. Path analysis indicated that number of filled grains per panicle and 1000 seed weight exhibited positive direct effects on grain yield at both genotypic and phenotypic level. The characters exhibiting high direct effects for grain yield also exhibited high degree of positive correlation with grain yield. The traits, number of filled grains per panicle and 1000 seed weight could be used as selection criteria for the improvement of grain yield.

Keywords: Genetic parameters, correlation, path analysis

Introduction

Rice is one of the most important cereal crop of the world meeting the dietary requirements of the people living in the tropics and sub tropics. As the yield is a complex character and the multiplicative effect of individual components understanding the relationship between yield and its component traits is essential for making effective selections in plant breeding. The success of breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable (Tiwari *et al.* 2011)^[17]. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement (Dutta *et al.* 2013)^[4]. Character association derived by correlation coefficient, forms the basis for selecting the desirable plant, aiding in evaluation of relative influence of various component characters on grain yield. The existing relationships between traits are, generally determined by the genotypic, phenotypic and environmental correlations. However, the correlation coefficient between two characters does not necessarily imply a cause and effect relationship. Path analysis splits the correlation coefficient into direct and indirect effects so as to measure the relative contribution of each variable towards yield (Mohsin *et al.* 2009)^[8]. Keeping in view of the above, the present study was taken up to understand the association and path analysis of component characters for grain yield in rice accessions.

Material and Methods

The material for the present study consists of seventy seven rice genotypes. These genotypes were evaluated in a randomized block design with three replications during *kharif*, 2014 at Seed Research and Technology Centre, Rajendranagar, Hyderabad. All the genotypes were sown in nursery beds and thirty days old seedlings transplanted into main field. Each entry was transplanted in a row of 4 m length with a spacing of 20 cm between rows and 15 cm between plants. Data was collected from five randomly selected plants from each replication for seven quantitative traits *viz.*, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, spikelet fertility (%), 1000 seed weight (g) and grain

yield per plant (g). The mean data for all the characters were subjected to analysis of variance on the basis of model proposed by Panse and Sukhatme (1961)^[9]. The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton (1952)^[2]. Heritability in broad sense (h^2) was calculated by the formula given by Lush (1940)^[7] as suggested by Johnson *et al.* (1955). From the heritability estimates, the genetic advance (GA) was calculated by the following formula given by Johnson *et al.* (1955)^[6]. The correlations between characters was calculated by using the method suggested by Snedecor and Cochran (1967)^[15] and path analysis as per Dewey and Lu (1959)^[3].

Results and Discussion

Analysis of variance revealed the presence of significant differences among the genotypes for all the characters studied (Table 1) and it indicating the presence of considerable amount of genetic variation in the material studied. The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were presented in Table 2. The range of mean variation observed among yield components revealed that highest range of mean variation was notice for number of filled grains per panicle (219.8) and plant height (44.8) while the range was found to be least for number of productive tillers per plant (5.7) and panicle length (8.3). Similarly, highest magnitude of genotypic variance was registered for number of filled grain per panicle (2754.68), grain yield per plant (59.77) and spikelet fertility percentage (59.42) while least estimates were recorded for number of productive tillers per plant (3.57) and panicle length (5.03). Rukmini Devi *et al.* (2016)^[13] also reported highest range of mean variation and genotypic variance for number of filled grain per panicle. Phenotypic correlations were higher in magnitude than the phenotypic correlations for the characters studied. Similar results were reported by earlier workers Rukmini Devi *et al.* (2016)^[13] and Rajendra Singh *et al.* (2018)^[12].

The magnitude of phenotypic coefficient of variation (PCV) was found to be higher than genotypic coefficient of variation (GCV) for all the characters studied. It indicates the influence of environment on the expression of these traits. The high estimates of phenotypic coefficient of variation were recorded for number of productive tiller per panicle (21.65), number of filled grains per panicle (22.47), 1000 seed weight (22.08) and grain yield per plant (34.80). Sonu Kumar *et al.* (2018)^[16] and Pragnya *et al.* (2018)^[10] noticed high PCV for number of productive tillers per plant and grain yield per plant. The trait plant height (11.04) showed moderate estimate of PCV while panicle length (9.88) and spikelet fertility (9.01) exhibited low estimate of PCV. Gaurav Kumar *et al.* (2018)^[5] also reported moderate and low estimates of PCV for plant height and spikelet fertility (%) respectively in their studies. The high estimates of genotypic coefficient of variation were recorded for number of filled grains per panicle (22.47) and 1000 seed weight (22.08). Low estimates of GCV was found for the traits such as plant height, number of productive tillers per plant, panicle length and spikelet fertility (%) while grain yield per plant (18.41) showed the moderate estimates of GCV. Biswaranjan Behera *et al.* (2018)^[1] and Pratibha *et al.* (2018)^[11] reported low PCV and GCV estimates for panicle length and spikelet fertility (%) respectively. Among the characters studied, higher estimates of phenotypic and genotypic coefficient variation were observed for number of filled grains per panicle (22.47) and 1000 seed weight (22.08). This indicates the existence of wide genetic base among the

genotypes taken for study and possibility of genetic improvement through direct selection for these traits. Lower value of PCV and GCV were noticed for panicle length and spikelet fertility (%). It indicates that there is narrow range of total variability and high influence of environment in the expression of this character. So there is little scope for direct selection for this character.

Heritability in narrow sense was found to be high for 1000 seed weight (90.1%). The traits plant height, panicle length and number of filled grains per panicle exhibited moderate heritability while number of productive tillers per plant, spikelet fertility (%) and grain yield per plant showed lower estimates. Low to moderate heritability estimates were observed for the most of the traits under study except for 1000 seed weight indicating the influence of environment in the expression of these traits. Genetic advance over mean was found to be high for number of filled grains per panicle, 1000 seed weight and grain yield per plant; medium values observed for plant height and number of productive tillers per plant and low values was recorded for panicle length and spikelet fertility (%). High heritability coupled with high genetic advance was observed for 1000 seed weight, indicating that this trait is controlled by additive gene action. It is suggesting that this character could be improved through mass selection and progeny selection. Similar results were observed by Pratibha *et al.* (2018)^[11], Pragnya *et al.* (2018)^[10] and Sonu Kumar *et al.* (2018)^[16]. Low values of heritability and genetic advance was recorded for spikelet fertility (%). It indicates the role of non-additive genes in inheritance of this character hence improvement of this trait through heterosis breeding rather than selection could be adopted. Heritability estimates along with genetic advance are more helpful in predicting gain under selection than heritability estimate alone (Johnson *et al.* 1955)^[6].

The traits such as plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle and spikelet fertility (%) and 1000 seed weight had positive phenotypic and genotypic correlation with grain yield per plant (Table-3). Ruth Elizabeth *et al.* (2011)^[14] also observed positive correlation for plant height, panicle length and number of filled grains per panicle and 1000 seed weight with grain yield. Rajendra Singh *et al.* (2018)^[12] reported positive association of grain yield with number of productive tillers per plant and spikelet fertility (%) in their studies. Among the other yield contributing characters, plant height had significant and positive association with panicle length, spikelet fertility (%) and 1000 seed weight at phenotypic level while it showed positive non-significant correlation at genotypic level. Number of productive tillers per plant exhibited negative relationship with panicle length, spikelet fertility (%) and 1000 seed weight while it showed positive correlation with number of filled grains per panicle. Positive association was also observed between panicle length and 1000 seed weight; spikelet fertility (%) and 1000 seed weight. It was found that number of filled grains per panicle and spikelet fertility (%) has positive association. This indicated that spikelet fertility led to higher seed set which in turn resulted more number of filled grains per panicle. Seed yield had highest positive association with panicle length (0.5287) and 1000 seed weight (0.4931) at genotypic level.

Path analysis indicated that number of filled grains per panicle and 1000 seed weight exhibited positive direct effects on grain yield (Table-4) at both genotypic and phenotypic level. Plant height, number of productive tillers per plant and spikelet sterility (%) showed direct negative effect on grain

yield at genotypic level. Number of filled grains per panicle and 1000 seed weight exhibited highest direct effect on grain yield followed by and panicle length at genotypic. In general, characters exhibiting high direct effects for grain yield also exhibited high degree of positive correlation with grain yield. The indirect effect of productive tillers per plant on grain yield through plant height, panicle length, spikelet fertility (%) and 1000 seed weight at genotypic level were found to be positive while it showed negative effect through all traits except for number of filled grains per panicle at phenotypic level. Panicle length exhibited positive indirect effect on grain yield via plant height, spikelet fertility (%) and 1000 seed weight at genotypic level. Positive indirect effect was

observed on grain yield by number of filled grains per panicle through number of productive tillers per plant and spikelet fertility (%) at both genotypic and phenotypic level. The trait 1000 seed weight exerted indirect positive influence on grain yield through plant height, panicle length and spikelet fertility (%) while it showed negative influence through number of productive tillers per plant and number of filled grains and panicle.

The study reveals that the characters exhibiting high direct effects for grain yield also exhibited high degree of positive correlation with grain yield. The traits, number of filled grains per panicle and 1000 seed weight could be used as selection criteria for the improvement of grain yield.

Table 1: Analysis of various for grain yield and its component characters in rice

Characters	d.f	Plant height (cm)	No. of productive tillers / plant	Panicle length (cm)	No. of filled grains / panicle	Spikelet fertility (%)	1000 seed weight (g)	Grain Yield / plant (g)
Replication	2	530.531**	42.669**	7.626	141.404	197.106*	9.831**	910.99**
Treatments	76	207.134**	4.889**	8.595**	5312.611**	89.25**	47.758**	93.225**
Error	152	57.071	2.913	3.253	1475.707	44.506	1.688	43.043

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 2: Mean, Range and genetic parameters for grain yield and its attributing characters in rice

Traits	Mean	Range		PV	GV	PCV	GCV	Heritability in broad sense (h ²)	Genetic advance over mean (%)
		Min.	Max.						
Plant height (cm)	86.93	67.57	112.33	107.09	50.02	11.04	8.14	46.7	14.68
No. of productive tillers / plant	8.73	5.89	11.54	3.57	0.66	21.65	9.30	18.4	10.54
Panicle length (cm)	22.72	18.89	27.17	5.03	1.78	9.88	5.87	35.4	9.22
No. of filled grains / panicle	159.15	65.88	285.66	2754.68	1278.97	32.98	22.47	46.4	40.42
Spikelet fertility (%)	85.61	65.70	94.18	59.42	14.92	9.01	4.51	25.1	5.97
1000 seed weight (g)	17.75	10.80	25.21	17.05	15.36	23.26	22.08	90.1	55.33
Grain Yield / plant (g)	22.22	11.34	34.91	59.77	16.73	34.80	18.41	28.0	25.71

Table 3: Correlation coefficients for grain yield and its attributing characters in rice

Characters		Plant height (cm)	No. of productive tillers / plant	Panicle length (cm)	No. of filled grains / panicle	Spikelet fertility (%)	1000 seed weight (g)	Grain Yield / plant (g)
Plant height (cm)	G	1.000	-0.5615	0.7806	-0.0411	0.2819	0.4385	0.4092
	P	1.000	-0.1134	0.2351**	-0.0190	0.1491*	0.2970**	0.2221
No. of productive tillers / plant	G		1.000	-0.4304	0.1871	-0.2416	-0.1659	0.2000
	P		1.000	-0.1227	0.0276	-0.1336*	-0.0860	0.3342
Panicle length (cm)	G			1.000	-0.2880	0.3318	0.4717	0.5287
	P			1.000	0.0424	-0.0186	0.3001**	0.0542
No. of filled grains / panicle	G				1.000	0.0652	-0.7121	0.2447
	P				1.000	0.2436**	-0.4353**	0.1555
Spikelet fertility (%)	G					1.000	0.1453	0.3771
	P					1.000	0.1139	0.1661
1000 seed weight (g)	G						1.000	0.4931
	P						1.000	0.2510

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 4: Phenotypic and Genotypic path coefficients for grain yield and its attributing characters in rice

Characters		Plant height (cm)	No. of productive tillers / plant	Panicle length (cm)	No. of filled grains / panicle	Spikelet fertility (%)	1000 seed weight (g)	Grain Yield / plant (g)
Plant height (cm)	G	-1.1347	0.6371	-0.8857	0.0466	-0.3198	-0.4976	0.4092
	P	0.1627	-0.0184	0.0382	-0.0031	0.0243	0.0483	0.2221
No. of productive tillers / plant	G	0.0036	-0.0064	0.0027	-0.0012	0.0015	0.0011	0.2000
	P	-0.0430	0.3796	-0.0466	0.0105	-0.0507	-0.0326	0.3342
Panicle length (cm)	G	0.8750	-0.4824	1.1209	-0.3228	0.3719	0.5287	0.5287
	P	-0.0142	0.0074	-0.0603	-0.0026	0.0011	-0.0181	0.0542
No. of filled grains / panicle	G	-0.0714	0.3252	-0.5006	1.7380	0.1133	-1.2376	0.2447
	P	-0.0056	0.0081	0.0125	0.2940	0.0716	-0.1280	0.1555
Spikelet fertility (%)	G	-0.0106	0.0091	-0.0124	-0.0024	-0.0375	-0.0054	0.3771
	P	0.0115	-0.0103	-0.0014	0.0189	0.0774	0.0088	0.1661
1000 seed weight (g)	G	0.7473	-0.2824	0.8038	-1.2134	0.2477	1.7040	0.4931
	P	0.1107	-0.0320	0.1118	-0.1622	0.0425	0.3727	0.2510

Bold values are direct effects

Genotypic residual effect = 0.3783,

Phenotypic residual effect = 0.8295

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