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Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.)

K Parimala[1*], Ch Surender Raju[2], S Sudheer Kumar[3], S Narender Reddy[4]
[1] Seed Research and Technology Centre, PJTSAU, Rajendranagar, Hyderabad, Telangana, India
[2] Rice Research Centre, PJTSAU, Rajendranagar, Hyderabad, Telangana, India
[3] Administrative Office, PJTSAU, Rajendranagar, Hyderabad, Telangana, India
[4] Agricultural College, PJTSAU, Jagtial, Telangana, India

Abstract

An investigation was carried out to study the genetic variability, character association and path coefficient analysis for grain yield and its components in rice genotypes. Analysis of variance revealed the presence of considerable amount of genetic variation in the material evaluated. The difference between phenotypic and genotypic coefficient of variation was relatively low for the traits studied indicating less influence of environment on the expression of these characters. The traits such as number of filled grains per panicle and grain yield per plant showed higher estimates of PCV and GCV. This shows the existence of wide genetic base among the genotypes and possibility of genetic improvement through direct selection of these characters. High heritability in broad sense coupled with high genetic advance as per cent of mean recorded for plant height, number of effective tillers per plant, number of filled grains per panicle, test weight and grain yield per plant revealed the role of additive gene action. The correlation studies indicated that grain yield per plant had positive association with number of effective tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility (%) and test weight at both phenotypic and genotypic level. Hence, these traits could be considered as criteria for selection of higher yield. Path coefficient analysis revealed that number of filled grains per panicle had positive direct effect on seed yield per plant followed by number of effective tillers per plant, test weight, panicle length and days to 50% flowering. Hence these traits may be taken as principal traits while selecting for grain yield.

Keywords: rice, variability, correlation, path analysis

Introduction

Rice is the most important stable food crop of India with world ranking first in area and second in production. The productivity of rice is stagnated. Genetic variability is the key component of breeding programmes for broadening the gene pool in crops. Understanding the correlation between yield and its components is of the utmost importance for making the best use of the relationships in selection (Sarawgi *et al*., 1997) [10]. Variability in genotypes for yield and its component traits forms the basis for making selection. Knowledge of heritability provides the information on transmissibility of characters into future generations. Johnson *et.al* (1955) [6] suggested that heritability estimates along with genetic advance would be more useful in predicting grain yield under phenotypic selection than heritability estimates alone. Path coefficient analysis partitions the genetic correlation between yield and its component traits into direct and indirect effects and hence has effectively been used in identifying useful traits to improve grain yield. Knowledge about relationship between yield and its contributing characters is needed for an efficient selection strategy for the plant breeders to evolve an economic variety. In view of the above, the present investigation was undertaken to study genetic variability, correlation and path analysis of component characters in rice genotypes.

Material and Methods

The experimental material for the present study consists of thirty four genotypes of rice including ten parents and their twenty four hybrids. The hybrids were generated by crossing four lines with six testers in line x tester design during *Rabi* 2013-14. The crosses along with their parents were evaluated during *kharif*, 2014 in Randomized Block Design with three replications at Seed Research and Technology Centre, Rajendranagar, Hyderabad. Each entry was transplanted in row of 4 m length with a spacing of 20 cm between the rows and 15 cm between the plants. The recommended cultural practices were followed to raise the good crop. Observations were recorded on 10 plants selected randomly from each entry and replication for the traits *viz*., days to 50% flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, 1000 grain weight (g), spikelet fertility (%) and grain yield per plant (g). The mean data were subjected to analysis of variance as per the model proposed by Panse and Sukhatme (1961) [8]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by using the method suggested by Singh and Chaudhary (1985) [11]. Heritability in broad sense was estimated as per the formula given by Hanson *et al* (1956) [5]. Genetic advance was calculated according to the method proposed by Johnson *et al* (1955) [6]. The path analysis was done following the method of Dewey and Lu (1959) [2].

Results and Discussion

Analysis of variance revealed that the genotypes differed significantly for the traits studied (Table-1) and indicating the presence of considerable amount of genetic variation in the material studied. A wide range of mean values for the traits indicated the existence of variation among the genotypes. High genetic variability for different quantitative traits in rice was also reported by Khan *et al.* (2009) [7]. The difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was very less for all the traits studied indicating less influence of environment on the expression of these characters (Table-2). Higher estimates of PCV and GCV were observed for filled grains per panicle (27.17 & 25.74) and grain yield per plant (30.73 & 24.19). This indicates the presence of wide genetic variability among the genotypes and possibility of genetic improvement through direct selection of these characters. Similar findings were observed by Bhadru *et al.* (2012) [1], Dhanwani *et al.* (2013) [3] and Rukmini Devi *et al.* (2017). The trait test weight showed moderate phenotypic (16.99%) and genotypic (16.81 %) coefficient of variation which suggest that there is a scope for improvement of this trait. The lower estimates of PCV and GCV for the traits *viz*., days to 50% flowering (3.47 & 3.14), panicle length (8.07 & 7.25) and spikelet fertility percentage (4.66 & 3.65) reveals the existence of narrow range of variability and little scope for direct selection for these characters. High heritability coupled with high genetic advance as per cent of mean observed for plant height, number of effective tillers per plant, number of filled grains per panicle, test weight and grain yield per plant and it reveals the role of additive gene action in controlling these traits. These results are in accordance with the findings of Dhurai *et al*. (2014) [4] and Rukmini Devi *et al*. (2017) [9]. High heritability (80.80%) with moderate genetic advance as per cent of mean (13.43) was recorded for panicle length suggesting that simple selection would be effective for the improvement of this character. The traits days to 50% flowering and spikelet fertility showed high heritability and low genetic advance. Correlation analysis revealed that the difference between phenotypic and genotypic correlation coefficient was very less for the characters studied and it indicated the negligible influence of environment on these traits (Table-3). The trait grain yield per plant had positive association with number of effective tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility (%) and test weight at both phenotypic and genotypic level. Hence, these traits could be considered as criteria for selection for higher yield as they were mostly inter related positively in addition to a positive association with grain yield. The trait days to 50% flowering showed positive correlation with plant height, number of effective tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility while it showed significant association with test weight at both phenotypic and genotypic level. Increased flowering duration resulted in increased number of tillers per plant, panicle length and filled grains per panicle which in turn helped to realize higher grain yield per plant. Panicle length expressed positive association with number of filled grains per panicle and test weight. Positive association was found between number of filled grains per panicle and spikelet fertility (%).

The results of the path coefficient analysis revealed that number of filled grains per panicle had maximum positive direct effect on seed yield followed by number of effective tillers per plant, test weight, panicle length and days to 50% flowering (Table-4). Therefore, these traits may be considered as principal traits while selecting for grain yield. Plant height showed direct negative effect on grain yield at both phenotypic and genotypic level. In general, characters exhibiting high direct effects for grain yield also exhibited high degree of positive correlation with grain yield. The positive indirect effect of days to 50% flowering through plant height, number of effective tillers per plant, panicle length, number of filled grains per panicle and spikelet fertility (%) on seed yield per plant have been observed. The trait panicle length exhibited higher positive indirect effect on grain yield through days to 50% flowering, number of effective tillers per plant, number of filled grains per panicle and test weight. Number of filled grains per panicle exhibited high indirect effect on grain yield through spikelet fertility, days to 50% flowering and panicle length.

Table 1: Analysis of variance for grain yield and its attributing characters in rice

Source of variation	df	Days to 50% flowering	Plant height	No. of effective tillers / plant	Panicle length	No. of filled grains / panicle	Spikelet fertility (%)	Test weight	Grain yield / plant
Replications	2	5.175	46.461*	1.177	1.598	609.592	16.063	4.019**	55.556
Treatments	35	33.551**	207.328**	13.001**	10.501**	6283.875**	32.725**	40.021**	209.186**
Error	70	2.328	11.965	2.201	0.771	229.349	5.665	0.304	35.478

Table 2: Components of genetic parameters for yield and its components in rice

Parameters	Days to 50% flowering	Plant height	No. of effective tillers / plant	Panicle length	No. of filled grains / panicle	Spikelet fertility (%)	Test weight	Grain yield / plant
Mean	102.852	83.865	10.871	24.829	174.519	82.299	21.650	31.451
Range	94.66-109.00	70.41-99.50	6.28-15.86	20.26-28.13	102.33-269.33	75.73-90.20	15.10-27.27	14.93-46.66
PV	12.736	77.086	5.803	4.015	2247.522	14.685	13.543	93.380
GV	10.408	65.121	3.602	3.243	2018.177	9.020	13.239	57.903
PCV	3.47	10.47	22.16	8.07	27.17	4.66	16.99	30.73
GCV	3.14	9.62	17.46	7.25	25.74	3.65	16.81	24.19
Heritability broad sense h^2 (%)	81.70	84.50	62.10	80.80	89.80	61.40	97.80	62.00
Genetic advance over mean (%)	5.84	18.22	28.33	13.43	50.25	5.89	34.23	39.25

Table 3: Phenotypic and genotypic correlation coefficients among grain yield and its components in rice

Character		Days to 50% flowering	Plant height	No. of effective tillers / plant	Panicle length	No. of filled grains / panicle	Spikelet fertility (%)	Test weight	Grain yield / plant
Days to 50% flowering	r_p	1.0000	0.0452	0.1519	0.1148	0.3064**	0.0749	-0.3659**	0.1462
	r_g	1.0000	0.0145	0.1731	0.1260	0.3494	0.0294	-0.4022	0.2282
Plant height	r_p		1.0000	0.1943*	-0.3301**	-0.2655**	0.1910*	-0.2126*	-0.1896
	r_g		1.0000	0.2280	-0.4000	-0.3079	0.2549	-0.2269	-0.2954
No. of effective tillers / plant	r_p			1.0000	0.3788**	-0.0685	-0.2476**	-0.0093	0.4990
	r_g			1.0000	0.5376	-0.1738	-0.4225	-0.0127	0.4419
Panicle length	r_p				1.0000	0.1548	-0.1826	0.1569	0.5250
	r_g				1.0000	0.1940	-0.1650	0.1800	0.7636
No. of filled grains / panicle	r_p					1.0000	0.4522**	-0.5345**	0.3654
	r_g					1.0000	0.5003	-0.5696	0.3765
Spikelet fertility (%)	r_p						1.0000	-0.1599	0.1997
	r_g						1.0000	-0.2114	0.1793
Test weight	r_p							1.0000	0.1380
	r_g							1.0000	0.1878

* Significant at 0.05% (0.189) level ** Significant at 0.01 % (0.246) level

r_p = phenotypic correlation r_g = genotypic correlation

Table 4: Phenotypic (P) and genotypic (G) path coefficient analysis among yield components in rice

Character		Days to 50% flowering	Plant height	No. of effective tillers / plant	Panicle length	No. of filled grains / panicle	Spikelet fertility (%)	Test weight	Grain yield / plant
Days to 50% flowering	P	0.0432	0.0020	0.0066	0.0050	0.0132	0.0032	-0.0158	0.1462
	G	0.1629	0.0024	0.0282	0.0205	0.0569	0.0048	-0.0655	0.2282
Plant height	P	-0.0041	-0.0902	-0.0175	0.0298	0.0239	-0.0172	0.0192	-0.1896
	G	-0.0043	-0.2961	-0.0675	0.1184	0.0912	-0.0755	0.0672	-0.2954
No. of effective tillers / plant	P	0.0783	0.1001	0.5154	0.1952	-0.0353	-0.1276	-0.0048	0.4990
	G	0.1027	0.1353	0.5934	0.3190	-0.1032	-0.2507	-0.0075	0.4419
Panicle length	P	0.0249	-0.0716	0.0822	0.2169	0.0336	-0.0396	0.0340	0.5250
	G	0.0344	-0.1092	0.1467	0.2729	0.0529	-0.0450	0.0491	0.7636
No. of filled grains / panicle	P	0.6660	-0.5771	-0.1488	0.3365	2.1739	0.9830	-1.1619	0.3654
	G	0.8331	-0.7341	-0.4145	0.4627	2.3844	1.1930	-1.3582	0.3765
Spikelet fertility (%)	P	-0.0039	-0.0098	0.0127	0.0094	-0.0233	-0.0515	0.0082	0.1997
	G	0.0061	0.0526	-0.0871	-0.0340	0.1032	0.2062	-0.0436	0.1793
Test weight	P	-0.1366	-0.0794	-0.0035	0.0586	-0.1996	-0.0597	0.3734	0.1380
	G	-0.1622	-0.0915	-0.0051	0.0726	0.2296	-0.0852	0.4032	0.1878

Phenotypic residual effect = 0.5888 Genotypic residual effect = 0.3851

P- Phenotypic path coefficient G-Genotypic path coefficient

Bold values are direct effects

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