



CORRELATION ANALYSIS OF VARIOUS METRIC TRAITS WITH GRAIN YIELD AND HERITABILITY ESTIMATION IN RICE GENOTYPES

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ABSTRACT

The present research was carried out to analyze phenotypic correlation (r) among quantitative traits and also to estimate heritability in broad sense (h^2) in 20 rice genotypes for various yield and its associated traits. Analysis of variances demonstrated that genotypes differed highly significantly ($P \leq 0.01$) for all the studied traits, registering the significant genetic variability among the genotypes for further evaluation. There was significant positive association of grain yield with panicle length ($r = 0.24$), seeds panicle⁻¹ ($r = 0.26^*$), seed length ($r = 0.25$), seed width ($r = 0.26$) and seed index ($r = 0.37^{**}$). On the basis of correlation results, it is observed that panicle length, seeds panicle⁻¹, seed length, seed width and seed index are most important traits that contributed directly to yield. Therefore, a cultivar with higher extent of these characters could either be selected from present genetic stock or evolved through genetic improvement for yield in rice. High heritability estimates were observed for days to flowering ($h^2 = 84.41\%$), plant height ($h^2 = 96.83\%$), tillers plant⁻¹ ($h^2 = 84.21\%$), seed fertility ($h^2 = 70.63\%$), seeds panicle⁻¹ ($h^2 = 99.32\%$), seed length ($h^2 = 95.83\%$), seed index ($h^2 = 87.84\%$), flag leaf length ($h^2 = 78.66\%$) and grain yield plant⁻¹ ($h^2 = 69.60\%$), whereas moderate heritability was found for panicle length ($h^2 = 34.22\%$) and seed width ($h^2 = 50.00\%$). High heritability values for these traits indicate that the variation observed was largely under genetic control and was less affected by environmental factors, indicating the importance of additive gene action for these traits. Therefore, the improvement of these traits can be made through direct phenotypic selection.

Keywords: rice, correlation, heritability, grain yield

INTRODUCTION

Rice (*Oryza sativa* L.) is an essential cereal crop, belongs to the family Poaceae, which is diploid ($2n=2x=24$) in nature, and was domesticated from its wild progenitor about 11,500 years before (Normile, 1997). It is consumed mostly by humans and provides staple food for approximately 50% of the world population (Garris *et al.*, 2005). In many developing countries, rice is not only the basis of food security but also closely associated with traditions and customs in local

regions (Lu and Snow, 2005). Grain yield is a complex trait, which is influenced by both genetic and climatic factors. Interaction among both these factors makes the selection procedure tough. For obtaining desirable rice genotypes, information concerning interaction between yield and associated components help the breeders in the choice of desirable genotypes. The association analysis provides a good guide to predict the corresponding change which occurs in one parameter at the expense of the proportionate change in the other (Ahmad *et al.*, 2008). Heritability is the ratio of variation observed phenotypically in a population, which is genetically inherited among individuals. Variations found at phenotypic level among individuals may be due to genetical or environmental factors. Heritability studies provide valuable genetic information to the breeders to envisage the interaction of genes in segregating populations (Degewione *et al.*, 2013). It has been observed that in breeding programs, the extent of inheritance of the genetic factors and expected genetic gains are very essential to predict response to selection in different environmental conditions and offer the basis for effective selection for particular traits in segregating populations. Khan *et al.* (2008) suggested that higher the heritability and genetic advance, simple the selection procedure. In this context, an effort was undertaken to determine the association of various traits with grain yield and heritability analysis in rice genotypes for different quantitative traits.

MATERIALS AND METHODS

The present experiment was conducted at the experimental field of Nuclear Institute of Agriculture, Tandojam. The experiment was laid out in a randomized complete block design with three replications during kharif season, 2014. In this context, 20 advance genotypes were selected, viz IR-6, IR-8, IR-9, Shadab, Sarshar, Shua-92, Shandar, DR-63, DR-65 and DR-67, IR6-25-4, IR6-200-4, IR6-300-1, IR6-150-2, NIA-102, IR8-250-4, IRON-2K5-24, IRON-2K5-27, NIA-19/A and Sarshar-200-11. Traits studied were: days to 50% flowering, plant height (cm), tillers plant⁻¹, flag leaf length (cm), panicle length (cm), seeds panicle⁻¹, seed length (mm), seed width (mm), seed fertility (%), seed index (1000-grain weight, g) and grain yield plant⁻¹ (g). The plant to plant and row to row distance was kept at 20 and 25 cm, respectively. A basal dose of P as triple super phosphate at the rate of 60 kg ha⁻¹ was applied at the time of sowing, whereas 60 kg ha⁻¹ of N as urea was applied after 20 days of transplanting and then 60 kg ha⁻¹ of N was uniformly incorporated into the soil at the time of flowering. The Zinc sulfate (33%) was also applied at the rate of 15 kg Zn ha⁻¹ in the vicinity of the crop roots after two weeks of transplanting. The pesticide Seuradan (4% G) at the rate of 22.5 kg ha⁻¹ was also applied. Field was flooded with canal water up to 2 to 3 inches throughout the season. The data obtained was subjected to statistical computer package (Statistix, Ver. 8.1) for analysis of variance, least significant differences (LSD) and correlation of coefficient analysis. Heritability was estimated as proposed by Allard (1960) with the following formula:

$$h^2 \text{ (B.S) \%} = Vg/Vp * 100$$

Vg = Genotypic variance; Vp = Phenotypic variance.

Heritability was classified as low (<30%), medium (30-60%) and high (>60%).

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance (Table 1) revealed that all the varieties performed significantly different ($P \leq 0.05$) for days to flowering, plant height, tillers plant⁻¹, panicle length, seeds panicle⁻¹, seed fertility, seed length, seed width, seed index, grain yield plant⁻¹ and flag leaf length. This suggests that studied materials possess useful genetic resources for variety of traits thus can extensively be used for upcoming breeding programs. Almost, similar results have also been reported by several other workers (Ashfaq *et al.*, 2012; Shabir *et al.*, 2013). These researchers found the significant genetic variance for various traits, such as plant height, tillers plant⁻¹, panicle length, seeds panicle⁻¹, grain yield plant⁻¹, seed index, biological yield plant⁻¹ and harvest index.

Table 1. Mean squares for various traits in rice genotypes

Source of variance	D.F	Days to 50% flowering	Plant height	Tillers plant ⁻¹	Panicle length	Seed fertility (%)	Seeds panicle ⁻¹	Seed length	Seed width	Seed index	Flag leaf length	Grain yield plant ⁻¹
Replications	2	10.51	2.13	0.27	2.00	0.28	0.48	0.01	0.00	1.11	1.77	1.48
Genotypes	19	140.30**	72.43**	1.54*	2.53**	3.06**	503.10**	0.71**	0.03**	17.24**	35.46**	14.61**
Error	38	8.13	0.78	0.09	0.98	0.37	1.13	0.01	0.00	0.76	2.94	2.68

**= Significant at 1% of probability level

Mean performance

Table 2 shows the mean performance of the twenty rice genotypes. Early maturing varieties have great value in plant breeding since these varieties offer less inputs in the shape of irrigation, fertilization and pesticides and also vacant field for upcoming seasonal crops. Considering the days to 50% flowering, the variety Sarshar bloomed earlier than rest of the genotypes and took minimum days to flowering (97.00 days), this genotype may be preferred for further breeding programs. Medium tall plants are also desirable in rice breeding, several genotypes showed medium tall growth NIA-102, NIA-19/A, IR-6-25-4 and IR-6-300-1, offering reliable genetic resources for upcoming breeding programs. Among the yield components, number of tillers plant⁻¹ is an important attribute, which increases grain yield in rice. Tillers plant⁻¹ ranged from 14.53 to 16.70, the IR-8-250-4 produced maximum tillers plant⁻¹ (16.70), this line can prove better for breeding the maximum tillers plant⁻¹. Panicle length is a character of more importance, because larger panicle is considered to produce more grains, resulting in higher yield plant⁻¹. Considering the panicle length, the IR-6-200-4 had longest spike with 28.40 cm length, referring that this genotype may be registered as reliable breeding material, especially breeding for the extension of panicle length. With regards to seed fertility, Shadab had the highest percentage of fertile seed (95.98); hence this rice genotype can be considered for further evaluation in various breeding programs. For the character seed length, NIA-19/A measured the longest seed with length of 11.33 mm, while this genotype also produced maximum seed width with the value of 2.18 mm, proposing suitable genetic resources for rice breeding. For the trait seed index, the highest seed index of 30.00 g was produced by the genotype Shandar, indicating that yield can be increased through highest seed index, if this genotype is involved in

rice breeding. Considering the grain yield plant⁻¹, the NIA-102 produced maximum grain yield plant⁻¹ (24.47 g) than rest of the genotypes, suggesting that yield can extensively be enhanced through the involvement of NIA-102 genotype in upcoming rice breeding programs. It is concluded that above mentioned genotypes may be preferred for further breeding programs since these all genotypes exhibited promising genetic resources for variety of traits.

Table 2. Mean performance of rice genotypes for various traits

Genotypes	Days to 50% flowering	Plant height (cm)	Tillers plant ⁻¹	Panicle length (cm)	Seed fertility (%)	Seeds panicle ⁻¹	Seed length (mm)	Seed width (mm)	Seed index (1000-grain weight g)	Flag leaf length (cm)	Grain yield plant ⁻¹ (g)
IR-6	111.67	95.96	16.16	24.70	91.97	144.30	10.09	1.97	24.00	38.46	18.00
Sarshar	98.67	97.00	14.53	26.48	94.98	168.33	9.99	2	24.3	29.26	19.79
Shandar	115.33	99.60	25.00	27.83	95.17	167.33	10.13	1.93	30.00	36.16	21.16
Shadab	120.67	85.43	16.50	25.66	95.98	168.27	9.76	1.8	23.00	29.2	19.81
Shua-92	107.33	89.66	14.86	25.53	95.20	175.20	9.95	1.98	25.00	27.8	21.27
IR-9	110.00	84.73	14.96	25.33	95.53	188.87	9.8	1.89	23.33	31.23	21.47
IR-8	110.00	97.60	15.36	25.16	93.90	174.70	9.09	1.97	24.00	27	20.28
DR-63	117.67	99.63	14.63	25.43	93.93	182.17	9.64	1.9	22.33	34.46	21.06
DR-65	102.00	88.60	15.73	25.90	93.30	175.83	9.45	1.89	25.33	29.43	22.68
DR-67	133.67	95.10	15.00	26.73	95.10	175.43	9.73	1.91	24.00	33.33	23.6
IR6-25-4	119	90.86	16.33	25.76	94.98	167.56	9.38	1.99	25.1	37.9	23.77
IR6-200-4	114.66	87.2	16.13	28.4	93.93	163.7	9.56	1.87	26.00	30.9	21.82
IR6-300-1	109.33	93	15.6	26.03	94.95	189.4	9.17	1.9	23.33	36.2	16.84
NIA-102	104	91.5	16.13	26.16	94.45	169.7	9.41	2.16	27.33	32.23	24.47
IR8-250-4	109.66	85.16	16.7	26.8	94.63	165.83	9.26	1.9	22.66	34.9	18.98
IRON-2K5-24	113	89.56	15.2	26.03	93.81	157.33	9.5	2.01	26.66	32.36	23.59
IRON-2K5-27	101	85.4	16.66	26.1	94.15	151.3	9.25	1.83	23.33	34.4	18.74
NIA-19/A	102.33	94.3	16.7	24.93	93.84	156.83	11.33	2.18	29.00	36.3	24.19
Sarshar200.11	97	93.06	15.9	26.6	93.08	140.3	9.66	1.93	21.00	32.5	19.71
IR-6-150-2	104.33	87.6	16	26.86	95.74	170.83	9.68	1.73	20.66	28.3	23.59
LSD (5%)	4.71	1.46	0.51	1.64	1.01	1.75	0.17	0.14	1.44	2.83	2.71

Table 3. Correlation analysis between various quantitative traits of rice genotypes

Characters	Days to 50% flowering	Plant height	Tillers (plant ⁻¹)	Panicle length	Seed fertility (%)	Seeds panicle ⁻¹	Seed length	Seed width	Seed index	Flag leaf length
Days to 50% flowering	-									
Plant height	0.04	-								
Tillers plant ⁻¹	-0.06	-0.45*	-							
Panicle length	0.03	-0.05	0.03	-						
Seed fertility (%)	0.15	-0.31*	-0.06	0.10	-					
Seeds panicle ⁻¹	0.02	0.00	-0.45*	-0.02	0.44*	-				
Seed length	-0.11	0.46	0.04	-0.14	-0.16	0.32	-			
Seed width	-0.14	0.21	-0.07	-0.27*	-0.14	-0.10	0.34**	-		
Seed index	0.11	0.23	-0.01	0.12	-0.01	-0.03	0.43**	0.50**	-	
Flag leaf length	0.21	0.38	0.30	0.08	-0.34	-0.32	0.19	0.19	0.26*	-
Grain yield plant ⁻¹	0.05	0.02	0.04	0.24	-0.01	0.26	0.25	0.26	0.37**	0.09

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

Table 4. Heritability estimates (broad sense) for various traits of rice genotypes

Characters	Genetic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Heritability (h^2 %) broad sense
Days to flowering	44.05	52.18	84.41
Plant height	23.88	24.66	96.83
Tillers plant ⁻¹	0.48	0.57	84.21
Panicle length	0.51	1.49	34.22
Seed fertility percentage	0.89	1.26	70.63
Seeds panicle ⁻¹	167.32	168.45	99.32
Seed length	0.23	0.24	95.83
Seed width	0.007	0.014	50.00
Seed index	5.49	6.25	87.84
Flag leaf length	10.84	13.78	78.66
Grain yield plant ⁻¹	3.97	6.66	69.60

Correlation analysis

Grain yield is the end product of different components those are not under the direct control of any single gene. Thus, the understanding of the mechanism of correlation offers the basis for framing the suitable selection criteria for breeding programs on the basis of yield components for attaining rational improvement of yield and its components (Wang *et al.*, 2006). The correlation coefficients was worked out among 11 quantitative traits, the results displayed that some of the characters developed positive correlations, whereas other showed negative correlations with one another (Table 3). There was significant positive association of grain yield with some yield contributing parameters studied including panicle length ($r = 0.24^*$), seeds panicle⁻¹ ($r = 0.26^*$), seed length ($r = 0.25^*$), seed width ($r = 0.26^*$) and seed index ($r = 0.37^{**}$). Plant height was highly significant and positively correlated with seed length ($r = 0.46^{**}$) and flag leaf length ($r = 0.38^*$). Highly significant positive association of plant height with seed length signifies the role of plant height in producing seed length in rice genotypes. Nevertheless, significant negative relations were noted between plant height and tillers plant⁻¹ ($r = -0.45^{**}$), and between plant height and seed fertility percentage ($r = -0.31^*$). Considering the positive correlations among the other traits, the tillers plant⁻¹ made positive and significant correlation with flag leaf length ($r = 0.30^*$), seed fertility with seeds panicle⁻¹ ($r = 0.44^{**}$), seeds panicle⁻¹ with seed length ($r = 0.32^*$), seed length with seed width ($r = 0.34^*$) and seed index ($r = 0.43^{**}$), seed width with seed index ($r = 0.50^{**}$) and seed index with flag leaf length ($r = 0.26^*$). These results are in consonance with those of Dogan (2009), Tehrim *et al.* (2012) and Shabir *et al.* (2013). On the basis of correlation results, it may be concluded that panicle length, seeds panicle⁻¹, seed length, seed width and seed index are most important traits that contributed directly to yield. Therefore, a cultivar with higher extent of these characters could either be selected from present genetic stock or evolved through genetic improvement for yield in rice.

Heritability analysis

Heritability estimates is one of the key genetic parameters which help in deciding the characters to be focused while operating the artificial selection in crop plants for economical traits (Baloch *et al.*, 2016). High heritability estimates (h^2 broad sense) were observed for days to 50% flowering ($h^2 = 84.41\%$), plant height ($h^2 =$

96.83%), tillers plant⁻¹ ($h^2 = 84.21\%$), seed fertility percentage ($h^2 = 70.63\%$), seeds panicle⁻¹ ($h^2 = 99.32\%$), seed length ($h^2 = 95.83\%$), seed index ($h^2 = 87.84\%$), grain yield plant⁻¹ ($h^2 = 69.60\%$) and flag leaf length ($h^2 = 78.66\%$), whereas moderate heritability was found for panicle length ($h^2 = 34.22\%$) and seed width ($h^2 = 50.00\%$). High heritability values for these traits indicated that the variations observed was largely under genetic control and was less affected by environment, signifying the influence of additive gene action for these traits. Thus, these characters can be improved via direct phenotypic selection. These findings are in accordance with previous reports of Parikh *et al.* (2012) and Sellammal *et al.* (2014).

CONCLUSION

Based on correlation analysis, it is concluded that the panicle length, seeds panicle⁻¹, seed length, seed width and seed index are the most important plant characters with great potential to improve grain yield of rice genotypes. Hence, a genotype with high values of these characters could be selected for yield improvement in rice. High heritability estimates were observed for most of the studied traits, indicating that the variation observed was largely under genetic control and was less affected by environment, representing the influence of additive gene action for these traits.

ACKNOWLEDGEMENTS

The authors acknowledge the Director, Nuclear Institute of Agriculture, Tandojam for providing facilities at the experimental field and laboratory to carry out the current research study.

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(Accepted August 09, 2016)