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Cause and Effect Relations of Panicle Traits in Rice (*Oryza sativa* L.)

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Abstract: Analysis of variance indicated highly significant differences among the genotypes for all the traits studied except for number of branches per panicle. Covariance studies reflected significant to highly significant as well as negative differences among majority of character combinations. Broad sense heritability estimates for number of spikelets per plant, number of nodes per panicle and number of grains per panicle ranged from 41.20 to 48.20. Panicle length, spikelet number and number of nodes per panicle revealed significant genotypic correlation to number of grains per panicle. Among the characters studied, number of nodes per panicle depicted the highest direct and indirect contribution of 1.071 and 0.873 respectively towards number of grain per panicle. Path coefficient analysis demonstrated that for greater number of grains per panicle, number of nodes per panicle should be increased.

Key words: Path analysis, heritability, genotypic and phenotypic correlation, panicle traits, rice

Introduction

The production of rice is the basic component of agriculture sector in most Asian countries. Rice is placed on second position in cereal cultivation around the globe (FAO, 2000) and occupies an important position in the economy of Pakistan as an export item as well as a staple food. Pakistan is fortunate to have "Kallar tract" which is considered to be the best region in the world for producing best quality rice, especially aromatic rice. However, in Pakistan the yield of rice on per unit area basis is low than other countries. Improvements in yield and quality directly as well as indirectly through the improvement of its components traits to evolve a biologically superior and physiologically efficient genotype, are of eager need to feed our increasing population and to compete in the international market.

The inheritance of grain yield is a complex phenomenon and is being influence through a number of morphogenetic characters which in turn are made up of their component traits. Gravois and Hilms (1992) reported that direct effect of filled grains per panicle on rice yield was positive and moderate. Ise (1992) observed that phenotypically panicle length had negative association with number of panicles per plant. The study of panicle traits and its components through genetic correlation provide the information that how strongly these panicle traits are genetically associated with one another and ultimately associated with the grain yield; where as path analysis (Dewey and Lu, 1959) assesses the contribution of each component to the resultant variable directly as well as indirectly. This would provide sufficient confidence to breed high yielding varieties.

The present studies had been undertaken to estimate the direct and indirect contributions of components of panicle traits with reference to grain yield to sort out selection criteria to evolve high yielding rice genotypes. Path analysis for number of grains per panicle would serve another opportunity to determine the way to improve grains per panicle and consequently grain yield per plant.

Materials and Methods

Fourteen different fine quality rice genotypes along with a standard variety (Basmati-385) were used as an experimental material (Table 2). The breeding nursery was obtained from Rice Research Institute, Kala Shah Kaku. Two seedling of each genotype were transplanted in earthen pots (30x30 cm²) filled with normal soil. The experiment was conducted in a Complete Randomized Design with three repeats. Each replication consisted of six plants in three pots for each genotype. Required irrigations, fertilizations and plant protections were carried out for all the genotypes, during the growth period. At the time of maturity data per plant basis was recorded in the field as well as in the laboratory for the following morphological traits, panicle length (cm), number of spikelets per panicle, number of nodes per panicle, number of branches per panicle and number of grains per panicle. The length of five panicles per plant was measured from, bottom to the tip of the panicle with the help of meter rod at the time when panicles turned brown. Sterile as well as fertile spikelets were counted for each panicle. Spikelets of five panicles were counted and then there average is computed. Total no of nodes present on each panicle were counted and then their average was

computed for each repeat for each genotype. Branches arising from, the nodes were counted for each panicle. Branches of five panicles were counted then average is computed for each genotype for each repeat. Number of filled grains per panicle was counted separately from each genotype in each repeat. The data then were averaged for number of grains per panicle.

Statistical analysis: The data collected for the panicle traits was subjected to statistical analysis of variance and co-variance following the methodology given by Steel and Torrie (1980) to ascertain the differences among various genotypes for variability and co-variability. Comparisons of genotypic means were accomplished using "Duncan's New Multiple Range Test". Heritability coefficients (Broad sense) as an index of transmissibility associated with various plant performance traits were estimated following the methodology given by Burton and DeVane (1953). Genotypic and phenotypic correlations were computed to determine the extent of association of characters on both genotypic as well as phenotypic levels following Kwon and Torrie (1964). Genotypic correlations were tested for their statistical significance using formulae given by Lothrop *et al.* (1985). The methodology proposed by Reeve (1955) and Robertson (1959) for the computation of standard error for heritability was applied on the data. A genetic correlation was considered significant statistically if its absolute value exceeded the twice of the respective standard error. Path analysis according to Dewey and Lu (1959) was performed in grain quality index and its components keeping grain quality index as resultant variable and its components as causal variable.

Results and Discussion

Analysis of variance and heritability: The results from the 15 rice genotypes relating to mean squares, genotypic and phenotypic coefficients of variability (G.C.V. and P.C.V.) and heritability estimates associated with number of grains per panicle and its components are presented in Table 1. The results revealed that genotypes had highly significant difference for panicle length, spikelets per panicle, nodes per panicle and number of grains per panicle, except for number of branches per panicle.

Panicle length, number of spikelets per plant, number of nodes per plant and number of grains per panicle showed moderate heritability of 41.101, 41.20, 44.40 and 48.20 %, respectively. The data on mean performance of genotypes (Table 2) indicated that the mean values for panicle length, number of spikelets per plant, number of nodes per plant and number of grains per panicle ranged from 23.12 to 29.42 cm, 85.75 to 136.9, 7.0 to 9.33 and 42.11 to 93.64, respectively. The data revealed a tremendous scope for improvement in panicle traits.

Genotype 41028 showed the maximum panicle length closely followed by genotype 41013 while genotype 41016 exhibited the minimum value. Little difference was recorded in genotypic and phenotypic coefficients of variability, which indicate that the said trait is less influenced by the environment. Genotypes showed most consistent performance due to the low value of genotypic coefficient of variability (5.21). Highest number of spikelets per panicle were recorded in genotype 40097 followed by genotype 41026 while genotype 41025 had minimum one, relatively high

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Table 1: Mean squares, heritability (broad sense) and coefficients of variability estimates for number of grains per panicle and its components in rice (*Oryza sativa* L.)

Traits	Mean squares		Coefficient of variability		Heritability + Standard error $h^2 \pm SE$
	Treatment	Error	Genotypic G.V.C	Phenotypic P.C.V	
Panicle length	8.419 **	2.719	5.211	8.125	0.411 \pm 0.097
Number of spikelets per panicle	801.037 **	258.193	12.120	18.880	0.412 \pm 0.010
Number of nodes per panicle	1.520 **	0.448	7.375	11.072	0.444 \pm 0.233
Number of branches per panicle	2.063 NS	1.541	-	-	-
Number of grains per panicle	511.502 **	134.977	15.274	22.004	0.482 \pm 0.013

Treatment degree of freedom = 14 **Highly significant NS = Non significant Error degree of freedom = 30

Table 2: Mean performance of various genotypes and their statistical significance for number of grains per panicle and its components in rice (*Oryza sativa* L.)

Genotype No.	Panicle length	Number of spikelets per panicle	Number of nodes per panicle	Number of grains per panicle
40083	27.55a-c	99.26b-e	8.220a-d	60.48de
40084	27.33a-c	127.80ab	8.333a-c	68.53b-d
40086	26.67a-c	120.70a-d	9.333a	85.68a-c
40097	25.42b-d	136.90a	8.000b-d	74.18a-d
41004	27.17a-c	123.80a-c	9.333a	83.07a-d
41011	26.28a-d	121.70a-c	7.443c-d	73.75a-d
41012	24.33cd	106.30a-e	9.000ab	80.86a-d
41013	29.11a	113.90a-e	8.440a-c	78.71a-d
41016	23.12d	106.30a-e	8.333a-c	93.64a
41024	25.83b-d	89.98de	7.667cd	63.11cd
41025	25.83b-d	85.75e	7.000d	42.11e
41026	27.72ab	136.50a	7.633cd	90.57ab
41028	29.42a	101.50b-e	7.667cd	69.61b-d
41030	25.67b-d	101.10b-e	7.250cd	69.39b-d
Basmati 385	25.34b-d	93.47c-e	7.917b-d	66.51cd

Means followed by a common letter are not significantly different from each other at 5 % level by DMRT

Table 3: Mean products for analysis of covariance for number of grains per panicle and its components in all possible combinations in rice (*Oryza sativa* L.)

Traits	Source of variations	Degree of freedom	Panicle length	Numbers of spikelets/panicle	Number of nodes/panicle
Number of spikelets per panicle	Treatment	14	16.705 **		
	Error	30	5.553		
Number of nodes per panicle	Treatment	14	-0.029NS	12.214 **	
	Error	30	-0.131	-1.269	
Number of grains per panicle	Treatment	14	-6.825NS	195.645 *	15.966 **
	Error	30	7.265	87.450	-1.9224

NS = Non significant. * Significant. ** Highly significant.

Table 4: Genotypic and phenotypic correlation coefficients among number of grains per panicle and its components in rice (*Oryza sativa* L.)

Traits	Correlation (r)	Panicle length	No. of spike lets per panicle	No. of nodes per panicle
No. of spikelets per panicle	Genotypic	0.201 \pm 0.051		
	Phenotypic	0.206		
No. of nodes per panicle	Genotypic	0.041 \pm 0.249	0.559 \pm 0.055	
	Phenotypic	-0.051	0.171	
No. of grains per panicle	Genotypic	-0.304 \pm 0.051	0.240 \pm 0.017	0.890 \pm 0.017
	Phenotypic	0.074	0.365	0.279

Table 5: Direct and indirect effects of various plant traits to number of grains per panicle in rice (*Oryza sativa* L.)

Traits	Panicle length	Number of spikelets per panicle	Number of nodes per panicle	Genotypic correlation with number of grain per panicle
Panicle length	(-0.288)	-0.061	0.044	-0.304
No. of spikelets per panicle	-0.058	(-0.301)	0.598	0.240
No. of nodes per panicle	-0.012	-0.168	(1.071)	0.890

values of genotypic and phenotypic coefficients of variability were recorded. Maximum number of nodes per panicle was observed in the genotypes 40086 and 41004 and both the genotypes were significantly different from Basmati-385. Co-efficient of variability at both genotypic and phenotypic levels was also relatively low. Genotypes 41016 had maximum number of filled grains per panicle followed by genotype 41026 and both of these genotypes are significantly different from the standard variety.

Analysis of covariance: Covariance of number of grains per panicle with number of nodes per panicle and with number of spikelets per panicle were highly significant, while covariance of number of grains per panicle with panicle length was non-significant similarly covariance of number of nodes per panicle in combination with number of spikelets per panicle was highly significant while with panicle length was non-significant (Table 3). Covariance of panicle length with number of spikelets per panicle was not significant. It was noted that all the significant covariance are positive.

Correlations: The association of panicle traits with other characters was estimated by genotypic and phenotypic correlation coefficient (Table 4). Panicle length had a significant positive genetic association while non-significant positive phenotypic association with number of spikelets per panicle. It had non significant correlation both at genotypic and phenotypic levels with number of nodes per panicle. Correlation of panicle length with number of grains per panicle at genotypic level was negative and significant while at phenotypic levels was positive and non-significant.

The corresponding decrease in panicle length with the increase in number of grains per panicle and vice versa is reflected from the study of present results. Ganesan and Subramanian (1990), Dawande *et al.* (1991) and Khan *et al.* (1991) reported significant positive correlation between panicle length and number of grains per panicle. Number of spikelets per panicle had significant positive genetic correlation while non-significant positive phenotypic correlation with number of nodes per panicle and number of grains per panicle, so it is clear that increase in number of spikelets per panicle might bring increase in number of nodes per panicle and number of grains per panicle. Earlier research workers like Yao *et al.* (1990), Bashar *et al.* (1991), Khan *et al.* (1991), Sharama and Reddy (1991) and Deshmukh and Chau (1992) reported positive significant correlation between number of grains per panicle and grain yield per plant. Number of nodes per panicle had positive and significant genetic association while positive and non-significant phenotypic association with number of grains per panicle. This revealed that increase in number of nodes per panicle might bring increase in number of grains per panicle.

Path analysis: Path coefficient analysis as an effort to assess the magnitude of contribution of various agro morphological characters to yield in the form of cause and effect is discussed, Table 5 revealed the results of direct and indirect effects of various panicle traits. Panicle length has negative direct effect (-0.288) to number of grains per panicle. Indirect effect through number of spikelets per panicle was also negative. A positive indirect effect was presents through number of nodes per panicle, due to negative direct and indirect contribution of panicle length to number of grains a negative correlation (-0.304) between the two said characters developed. The increase in length to panicle there would a decrease in the number of grains per panicle.

A positive genotypic correlation coefficient (0.240) was observed between the numbers of spikelets per panicle and number of grains per panicle, While the direct effect of spikelet number-to-number of grains was negative (-0.301). The indirect effect through panicle length was also negative but the

positive and greater indirect effect (0.598) through number of nodes per panicle was observed which might be the cause of positive association between the number of spikelets and number of grains per panicle. So for greater number of grains per panicle number of spikelets per panicle should be improved.

Greater positive direct effect (1.071) of number of nodes per panicle to number of grains per panicle is observed. Indirect effects through panicle length and number of spikelets per panicle were negative. But the positive direct effect was so greater that a highly significant and positive genotypic correlation (0.890) was observed between number of nodes and number of grains per panicle. So during indirect selection for greater number of grains per panicle, number of nodes per panicle must emphasized, because with the increase in number of nodes per panicle number of grains per panicle would increase directly.

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