row, ear length, ear girth and 100 kernel weight with addition of resistance to turcicum leaf blight. Therefore for developing a high yielding turcicum leaf blight resistant variety, the breeder should take care of all these yield components. The strong positive association of these above yield parameters with grain yield is attributed to gene action of linkage and pleiotropy.

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GENETIC VARIABILITY AND CAUSAL RELATIONSHIPS IN RICE

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ABSTRACT

Variability, correlation and path coefficient analyses were made for 11 characters in a collection of 99 rice genotypes (*Oryza sativa* L.). Bacterial blight severity, plant height, spikelets/panicle and grains/panicle showed high heritability with high genetic advance. Yield/plant was positively associated with days to 50 per cent flowering, spikelets/panicle and milling per cent. Path coefficient analysis revealed grains/panicle, spikelets/panicle and bacterial blight severity are the most important characters contributing to yield.

KEY WORDS :   Rice, Variability, Heritability, Correlation

The improvement of crops is dependent on magnitude to genetic variability and the extent to which the desirable characters are heritable. A critical survey of genetic variability is, therefore, a pre-requisite for planning an effective breeding programme. Yield being a complex character, direct selection would not be reliable approach without giving due importance to its genetic background. Though correlations give information about the components of yield, yet they do not provide a true picture of relative importance of direct and indirect influence of component traits towards yield. Path coefficient analysis helps in examining the relative contribution of both direct and indirect effects of component traits on yield. So, the present investigation was carried out to elucidates the extent of genetic variation and nature of causal relationships in yield attributes in few rice genotypes to determine the important yield

Table 1. Analysis of variance for yield and its components in rice

Sources of variation	df	Mean squares										
		Days to 50% flowering	Plant height (cm)	Panicles / plant	Panicle length (cm)	Grains / panicle	Spikelets / panicle	1000 grain weight (g)	Hulling per cent	Milling per cent	Bacterial blight serverity	Yield / plant (g)
Variety	98	274.27**	1028.55**	13.31**	14.57**	1864.65**	2293.32**	17.33**	10.21**	14.49**	1088.69**	36.69**
Replication	2	0.99	432.25	12.09	2.09	252.65	549.34	1.89	2.96	3.89	1.59	16.40
Error	196	0.26	3.72	1.65	1.10	130.43	147.63	0.89	0.12	0.83	10.41	3.96

*P = 0.05, **P = 0.01

attributing traits for an effective rice improvements programme.

MATERIAL AND METHODS

Ninety nine genotypes of rice, comprising advanced breeding lines, other indigenous and exotic collections were studied on a randomised block design with three replications at the Rice Research Station, Haryana Agricultural University, Kaul, during *kharif* season of 1989 and 1990. Single seedling of each genotype was transplanted at a distance of 15 cm in plots of 3 rows of 3m length with a spacing of 30 cm between rows. The materials were inoculated with bacterial blight *Xanthomonas campestris* pv. *oryzae*) inoculum after 45 days of transplanting. The severity of bacterial blight disease was recorded after 14 days of inoculation. The percentage of leaf area affected with the disease was recorded and the data on percent bacterial blight severity were subjected to angular transformation before analysis as suggested by Fisher and Yates (1957). The data on 50 per cent flowering, plant height (cm), panicles/plant, panicle

length (cm), grains/panicle, spikelets/panicle, 1000 grain weight (g), hulling per cent, milling per cent and grain yield/plant. were recorded from ten randomly selected plants of each plot. Various variability parameters were calculated as per procedures given by Burton (1952), Burton and Devane (1953), Hanson *et al.* (1956) and Allard (1960). Genotypic and phenotypic correlation coefficient were calculated following Johnson *et al* (1955) and the path coefficient analysis was carried out according to Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance revealed that the genotypes differed significantly for all the characters, indicating considerable variation among the genotype for all the characters (Table 1.) The estimates of variability parameters are given in Table 2. The bacterial blight severity and the highest genotypic coefficient of variation (GCV), followed by panicle/plant, grains/panicle and spikelets/panicle, indicating high amount of variability for improvement. High genotypic

Table 2. Estimates of various variability parameters in rice

Characters	Range	Mean	Genotypic co-efficient of variation	Phenotypic co-efficient of variation	Heritability (%)	Genetic advance (as percentage of mean)
Days to 50% flowering	86.00-135.00	106.51	8.97	8.98	99.71	18.46
Plant height (cm)	72.67-160.33	104.95	17.71	17.71	98.92	36.08
Panicles / plant	3.67-17.00	9.39	19.86	24.12	67.83	33.70
Panicle length (cm)	17.53-30.37	24.53	8.63	9.64	80.25	15.93
Grains / panicle	51.00-217.67	129.89	18.50	20.49	81.59	34.44
Spikelets / panicle	72.67-268.00	145.48	18.38	20.19	82.89	34.48
1000-Grain weight (g)	19.04-29.97	24.90	9.40	10.14	85.99	17.96
Hulling per cent	70.17-79.21	75.38	2.43	2.48	96.63	4.93
Milling per cent	56.56-66.87	62.61	3.41	3.71	84.59	6.46
Bacterial blight everity	3.91-68.85	34.56	54.85	55.64	97.18	111.39
Yield / plant (g)	12.12-29.07	22.09	14.94	17.45	73.36	26.37

Table 3. Genotypic and phenotypic correlations for different combinations of characters involving yield and its attributes.

Characters		Plant height (cm)	Panicles / plant	Panicle length (cm)	Grains / panicle	Spikelets / panicle	1000-grain weight (g)	Hulling per cent	Milling per cent	Bacterial blight severity	Yield / plant (g)
Days to 50%	G	0.196*	-0.073	0.299**	0.216*	0.232*	0.071	0.328**	0.264*	-0.372**	0.235**
flowering	P	0.194	-0.622**	0.270**	0.198*	0.213*	0.063	0.323**	0.242*	-0.367**	0.196*
Plant	G		0.018	0.434**	0.218*	0.172	-0.035	-0.116	-0.217*	-0.040	0.089
height (cm)	P		0.018	0.384*	0.193	0.153	-0.031	-0.123	-0.198*	-0.039	0.075
Panicles/	G			0.223*	-0.246*	-0.169	-0.579**	0.056	0.159	-0.191	0.336**
plant	P			0.158	-0.200*	0.126	-0.445**	0.038	0.080	-0.161	0.302**
Panicle	G				0.353**	0.345**	-0.167	0.008	0.031	-0.305**	0.536**
length (cm)	P				0.381**	0.372**	-0.149	0.008	0.034	-0.284*	0.409**
Grains /	G					0.959**	-0.189	0.020	0.160	-0.176	0.569**
panicle	P					0.938**	-0.158	0.031	0.154	-0.158	0.459**
Spikelets/	G						-0.222*	0.071	0.179	-0.212*	0.608**
panicle	P						-0.191*	0.073	0.159	-0.196*	0.498**
1000-grain	G							-0.142	-0.153	0.087	-0.272**
weight (g)	P							-0.128	-0.128	0.083	-0.206*
Hulling	G								0.659**	-0.091	0.155
per cent	P								0.631**	-0.085	0.112
Milling	G									-0.094	0.229*
per cent	P									-0.075	0.157
Bacterial	G										-0.356**
blight severity	P										-0.293**

G = Genotypic correlation   P = Phenotypic correlation
* Significant at 5% lefel of probability   ** Significant at 1% level of probability

coefficient of variation for grains/panicle, tiller number was observed by Bhattacharya (1978) and Das and Borthakur (1974) also. Yield/plant and days to 50 per cent flowering and 1000 grain weight showed moderate estimates of GCV. The low estimates of GCV in hulling per cent and milling per cent indicated limited scope for improvement of this traits for low magnitude of variability. The close correspondence between the estimates genotypic and phenotypic coefficient of variations (PCV) for most of the traits as also reflected by their high heritability values indicated lesser environmental influence on expression of these traits. Most of the characters showed high heritability estimates ranging from 80 to 99 per cent reflecting ample scope for their improvement

Table 4. Direct (diagonal) and indirect effect of component characters on yield/plan in rice.

Characters	Days to 50% flowering	Plant height (cm)	Panicles / plant	Panicle length (cm)	Grains / panicle	Spikelets / panicle	1000-grain weight (g)	Hulling per cent	Milling per cent	Bacterial blight severity	Genotypic correlation with yield / plant
Days to 50% flowering	0.013	-0.036	-0.045	0.075	0.117	0.044	0.019	0.061	-0.033	0.018	0.235**
Plant height (cm)	0.003	-0.182	0.011	0.108	0.118	0.033	-0.009	-0.022	0.027	0.002	0.089
Panicles/ plant	-0.001	-0.003	0.609	0.056	-0.134	-0.032	-0.158	0.010	-0.020	0.001	0.336**
Panicle length (cm)	0.004	-0.079	0.136	0.249	0.192	0.066	-0.046	0.001	-0.003	0.014	0.536**
Grains / panicle	0.003	-0.039	-0.149	0.088	0.544	0.184	-0.052	0.037	-0.020	0.008	0.569**
Spikelets/ panicle	0.003	-0.031	-0.103	0.862	0.522	0.192	-0.060	0.013	-0.022	0.010	0.608**
1000-grain weight (g)	0.001	0.006	-0.353	-0.042	-0.103	-0.043	0.272	-0.026	0.019	-0.004	-0.272*
Hulling per cent	0.004	0.021	0.034	0.002	0.011	0.014	-0.039	0.186	-0.083	0.004	0.155
Milling per cent	0.003	0.039	0.097	0.007	0.087	0.034	-0.042	0.123	-0.126	0.004	0.229*
Bacterial blight severity	-0.005	0.007	-0.116	-0.076	-0.095	-0.041	0.024	-0.017	0.012	-0.047	-0.356**

Residual effect = ± 0.305

through appropriate breeding procedure. In panicles/plant and yield/plant wider difference between corresponding GCV and PCV estimates coupled with low estimates of heritability indicated that, this two traits may not be amenable to direct selection. A relative comparison of heritability values and expected genetic advance expressed as percentage of mean gives an idea about the nature of gene action governing a particular character. Bacterial blight severity, plant height, spikelets/panicle and grains/panicle showed high heritability estimates coupled with high genetic advance. Thus apparently substantial contribution of additive genetic variance in expression of these traits is indicated (Panse, 1957). High heritability estimates coupled with low genetic advance in hulling per cent, days to 50 per cent flowering, milling per cent, 1000 grain weight and panicle length indicated the contribution of non-additive genetic effect and improvement of these traits warrant heterosis breeding. The importance of both additive and non-additive gene action in control of these traits also reported by various workers in rice (Single et al ., 1980; Sukanya Subramanian and Rathinam, 1984; Pawar et al., 1983; Ananda kumar and Sree Rangasamy, 1984).

Genotypic correlation were, in general, higher than the corresponding phenotypic ones (Table 3.) Grain yield/plant showed significantly positive association with days to 50 per cent flowering, spikelets/panicle, grains/panicle, panicle length, panicles/plant and milling per cent. Similar results were also reported by Lal et al.(1983) and Bhattacharya (1981). Negative association of yield/plant was observed with 1000 grain weight and bacterial blight severity. Bacterial blight severity showed negative correlation with days to 50 per cent flowering, panicle length and spikelets/panicle. Grains/panicle showed significantly positive association with days to 50 per cent flowering plant, height, panicle length and spikelets/panicle, but negatively associated with panicles/plant. Spikelets/panicle also showed significantly positive association with days to 50 per cent flowering, panicle length and negative association with 1000 grain weight.

The path coefficient analysis on genotypic correlations in respect of yield/plant are given in Table 4. Panicles/plant had the highest positive direct effect on yield/plant followed by grains/panicle and 1000 grain weight. Similar result was observed by Rao et al., (1980). The high positive direct effect of 1000 grain weight was nullified by indirect effects via most of the component characters, which might have resulted in a negative association with yield/plant. In addition to having positive direct effect, spike lets/panicle contributed substantially to yield/plant via panicle length and grains/panicle. Thus spike lets/panicle becomes an important yield contri buting factor. The negative association of bacterial blight severity with yield/plant might be resul ted from its negative direct effect and negative in direct effects via most of the other characters. The estimate of residual factor indicated that 70% of total variation was explained by the characters studied.

Based on the studies on variability, correlation and causal relationships of various characters spikelets/panicle and bacterial blight severity were the most important characters contributing to grain yield. It is, thus, suggested that these traits may be given due consideration during selection programme to evolve high yielding rice variety.

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CHARACTER ASSOCIATION AND COMPONENT ANALYSIS IN UPLAND COTTON

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ABSTRACT

Genotypic and phenotypic correlation co-efficients and path co- efficients were worked out in 51 diverse, genotypes of upland cotton. Number of bolls per plant and plant height had positive correlation with seed cotton yield both at genotypic and phenotypic levels. And these two characters showed significantly positive correlation between themselves also. Path co-efficient analysis indicated that plant height, bolls per plant, ginning out turn, lint index and seed index contributed directly to yield.

KEY WORDS :   Upland Cotton, Component Analysis, Character Association

Yield is a complex character and is dependent on several component characters. The knowledge of the associations between yield and its components and among components themselves is of immense practical value in making selections. Path co-efficient analysis by (Wright, 1921) provides an effective means of finding direct and indirect causes of association. In the present study, association of certain characters, their direct contribution to yield and indirect effects through other characters on yield in upland cotton (*Gossypium hirsutum L.*) were assessed.

MATERIALS AND METHODS

Fifty one genotypes of upland cotton of diverse origin were taken as the material for the present study. These genotypes were grown in a randomised block design with three replications during March 1991 at the Agricultural College and Research Institute, Madurai. Each genotype was raised in a single row of 6m length with a spacing of 75 x 30 cm.

Data on ten randomly selected plants in each genotypes were collected for days to 50 per cent flowering, plant height, sympodial branches per plant, bolls per plant, boll weight, seed cotton yield per plant, ginning per cent, lint index, seed index and mean halo length. The genotypic and phenotypic correlation co- efficients were computed using genotypic and phenotypic variances and covariances (Al.Jibouri *et al.*, 1958). The path co- efficient analysis was done according to the method by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The genotypic and phenotypic correlation co-efficients between yield and yield attributes are given in Table 1. The present study indicated that seed cotton yield per plant was highly and positively influenced by plant height and bolls per plant, both at phenotypic and genotypic levels. This was in accordance with the result obtained by Sardul Singh Gill and Singh (1981) and Sangwan and Yadava (1987). Increase in bolls per plant may be due to increase in plant height which inturn