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Assessment of genetic variability, correlation and path coefficient analysis for morphological and quality traits in rice *(Oryza sativa* L.)

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ABSTRACT

Nine rice genotypes were evaluated for this present study. Genetic variability parameters, correlation and path coefficient analysis were estimated for eleven agronomic and quality traits. Among all the genotypes, ASD 16 recorded highest significant grain yield per plant. In this present study, the PCV was higher than GCV for all the characters studied. The grain yield per plant recorded highest GCV, high heritability coupled with high genetic advance which indicates that the trait were governed by epistasis and dominant gene action. Number of productive tillers per plant and thousand grain weight showed positive significant correlation and direct effects on grain yield per plant. The purpose of this study is to estimate the amount of variability present in this material, which in turn helps to select these material for further breeding programme to develop high yield hybrids combine with blast and leaf folder resistance.

Key words: Heritability, Genotype, Genetic advance, Mean, Phenotype

INTRODUCTION

Rice as a chief grain, provides predominant dietary energy sources for Asia and African countries. Pest and disease are the major constraints on rice production. Among the rice pest and diseases, rice blast and rice leaf folder cause significant yield losses Ramasamy *et al*. (1996). Plant Breeding approaches combined with biotechnology techniques are implemented to improve grain quality and resistance to pests and diseases (Datta, 2004). Plant breeding begins with the exploration of genetic material to meet the crop improvement goals. Genetic variability in the materials helps the plant breeders to explore in possible ways to develop new cultivars with desirable characters Govindaraj *et al.* (2015). To identify superior parents, several biometrical methods can be adapted to gain information on hybrid vigour, combining ability and nature of gene action from the study of first generation itself. Exploitation of heterosis or hybrid vigour is the most important development in plant breeding in past recent years Malik *et al*. (1986). Keeping in view of the importance of developing superior segregants for high yield and resistance to blast and leaf folder disease, the parents has been assessed for genetic variability, association analysis for morphological and quality traits.

MATERIALS AND METHODS

Plant materials: A set of nine rice genotypes *viz.*, ADT 45, CO 18, BL 4, BL 5, BL 6, BL 10, LFR 293 TKM 9 and ASD 16 were selected for genetic variability studies. Nine genotypes were selected based on high yielding (ADT 45, TKM 9 and ASD 16), resistance against rice blast disease (BL 4, BL 5, BL 6, BL 10 and CO 18) and leaf folder pest (LFR 293). The parental seeds were obtained from Department of Rice, Tamil Nadu Agricultural University (TNAU), Coimbatore, India. The parental genotypes were raised during the year of 2012 kharif season (Elevation of 426.72 m, between 11°00 N latitude and 77° 00 E longitude) at Department of Rice, TNAU, Coimbatore, India.

Agronomic characteristics: The following morphological observations were recorded for the characters, days to 50 per cent flowering (DF, days), plant height (PH, cm), number of productive tillers per plant (NPRT, nos), panicle length (PL, cm), number of filled grains per panicle (NFGP, nos), thousand grain weight (TGW, g), harvest index (HI, %) and grain quality traits like kernel length (KL, mm), kernel breadth (KB, mm) and kernel length /breadth ratio (SES-IRRI, 1996).

Statistical analysis: The collected agronomic data are subjected to INDOSTAT services, Hyderabad. Diversity analysis was done by using DarWin 6.1 software. Genetic parameters like phenotypic variance (σ^2_p), genotypic variance (s^2_g), error variance (σ^2_e), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2) and genetic advance (GA) were calculated by adopting the following formula.

Correlation coefficients analysis: The correlation coefficient was worked out to find out the relationship

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Genetic parameters	Formulas	References
σ^2_p	$(\sigma^2_p) = \sigma^2_g + \sigma^2_e$	Johnson *et al.* (1955)
σ^2_g	$(\sigma^2_g) = M_g - M_e/r$	
σ^2_e	$(\sigma^2_e) = M_e$	
GCV	$GCV = \sqrt{\frac{Genotypicvariance}{Grandmean}} \times 100$	(Burton, 1952)
PCV	$PCV = \sqrt{\frac{Phenotypicvariance}{Grandmean}} \times 100$	
h^2	h^2 (B.S.)= $(\sigma^2_g)/(\sigma^2_p) \times 100$	(Lush, 1940)
GA	$GA = \sigma^2_g / \sigma_p \times K$	Johnson *et al.*(1955)
GA as mean	GA as percent of mean = GA/Mean ×100	

Co efficient of variation (%) (Sivasubramanian and Madhava Menon, 1973)		Heritability (%)(Robinson *et al.*,1979)		GA% as mean(Johnson *et al.*, 1955)	
variation	Category	Heritability	Category	GA % as mean	Category
0 – 10	Low	0 – 30	Low	< 10 %	Low
11 – 20	Moderate	31 – 60	Medium	10 - 20 %	Moderate
>20	High	> 61	High	> 20 %	High

between yield and its components in the parents and their hybrids. The variance and covariance values were used to calculate the correlation coefficients by applying the formula.

$$\text{Genotypic 'r'} = \frac{\sigma\, g_{1,2}}{\sqrt{(\sigma^2 g_1)(\sigma^2 g_2)}}$$

Where,

$\sigma^2 g_1$ = genotypic variance of first trait
$\sigma^2 g_2$ = genotypic variance of second trait
$\sigma g_{1,2}$ = genotypic covariance between the two traits

Path coefficient analysis: Path coefficient analysis was followed as suggested by (Wright, 1921) and (Dewey and Lu 1959). The direct and indirect effects were classified into different scales (Lenka and Mishra, 1973).

Value of Direct or Indirect effects	Rate or scale
More than 1.00	Very high
0.30 to 0.99	High
0.20 to 0.29	Moderate
0.10 to 0.19	Low
0.00 to 0.09	Negligible

RESULTS AND DISCUSSION

Mean performance of parents: The mean performances of parents for yield, yield contributing, and quality traits are furnished in the (Table 1). The parent, ASD 16 (23.50 and 29.21) recorded significantly higher mean value than grand mean for the trait grain yield per plant and thousand grain weight. For days to 50 per cent flowering, it ranged from 76.5 (BL 4) to 97.00 (CO 18). Mean range for the trait plant height ranged from 74.00 (BL 10) to 111.50 (CO 18). None of the parents showed significant difference for the trait panicle length. Among the parents, LFR 293 recorded maximum number of productive tillers per plant (17.50) and number of filled grains per plant (195.0). For the trait harvest index, BL 5 (0.59) showed significant difference and higher mean value than grand mean. For quality traits, 6.30 and 2.45 (BL 6) showed significant difference for kernel length and breadth respectively. Among the parents, the kernel length and breadth ratio recorded maximum by the parent LFR293 (3.23) and highest mean value than grand mean. Mean performance of parental genotypes for yield and yield attributing traits and quality traits in rice also studied by Balakrishnan *et al.* (2016) and Ponnaiah Govintharaj *et al.* (2017).

Variability genetic components: The genetic component of genotypic and phenotypic co-efficient of variation, heritability (broad sense) and genetic advance as per cent of mean (GAM) of eleven characters are calculated and presented in the (Table 2). In general, for all the traits studied, the phenotypic co-efficient of variation were higher than genotypic co-efficient of variation, it is signifying the environment effect for the look of these traits. Similar results were also reported by Balakrishnan *et al.* (2016) in rice crop. The values for genotypic co-efficient of variation obtained for various yield, yield attributing characters and quality characters ranged from to 3.26 per cent to 25.05 per cent. The highest GCV was observed for single plant yield (25.05 %) and number of productive tillers per plant (23.23%). The high GCV indicates that amount of variability for this trait and therefore simple selection can be practiced for further improvement of these characters. The same also reported by Abebe *et al.* (2017). The values of phenotypic co-efficient of variation ranged from 5.57 per cent to 27.73 per cent. The highest magnitude of phenotypic co-efficient of variation was observed for the following characters single plant yield

Table 1: Mean performance of the parents used in this study

PARENTS	DF	PH	NPRT	PL	NFGP	TGW	GYP	HI	KL	KB	K L/B
ADT45	85.50**	93.50**	13.50	22.50	180.00	18.00	19.30	0.38	5.40	2.05**	2.60
ASD16	86.50**	86.75**	14.00	22.75	157.50	23.50**	29.21*	0.51	5.45	2.30**	2.35
BL4	76.50**	76.50**	15.00	21.75	189.00	21.96	21.52	0.41	5.05	2.05**	2.45
LFR293	80.00**	86.50**	17.50**	23.25	195.00**	18.65	21.85	0.31	5.30	1.95**	3.23**
BL6	81.00**	76.25**	16.00	20.25	137.50	16.50	18.68	0.45	6.30**	2.45**	2.57
BL10	78.00**	74.00**	14.50	22.50	116.50	23.50	21.67	0.49	5.35	1.95**	2.74
TKM9	81.00**	84.00**	12.50	21.50	160.00	23.25	21.33	0.43	5.80	2.55**	2.27
BL5	79.50**	77.40**	12.00	24.50	129.00	21.20	20.48	0.59**	5.65	2.45**	2.30
CO18	97.00	111.50	12.50	23.75	121.50	22.00	26.07	0.39	5.75	2.45**	2.34
Mean	82.77	85.15	14.16	22.52	154	20.95	22.23	0.44	5.56	2.24	2.53
SE	0.99	2.61	1.14	1.10	12.50	0.89	2.48	0.02	0.13	0.11	0.14
$C.D_{0.05}$	2.83	7.45	3.25	3.88	35.64	2.54	6.90	0.07	0.39	0.32	0.41
$C.D_{0.01}$	3.79	9.95	4.35	5.91	47.61	3.39	9.46	0.10	0.52	0.43	0.55

*Significant at 5 per cent level **Significant at 1 per cent level

Table 2: Variability parameters for different yield and yield contributing traits

Traits	Mean	Range		GCV (%)	PCV (%)	h^2 (broad sense)	GA as per cent of mean
		Maximum	Minimum				
DFF	82.77	97.00	76.50	6.68	6.92	93.0	13.30
PH	85.15	111.50	74.00	15.02	15.62	92.0	29.77
NPRT	14.16	17.50	12.00	23.23	25.48	83.0	43.61
PL	22.52	24.50	20.25	3.26	7.36	19.0	2.97
NFGP	154	195.00	116.50	16.17	20.86	60.0	25.81
TGW	20.95	23.50	16.50	8.13	9.77	69.0	13.93
GYP	22.23	29.21	18.68	25.05	27.73	81.0	46.60
HI	0.44	0.59	0.31	18.31	20.10	82.0	34.35
KL	5.56	6.30	5.05	4.46	5.57	63.0	7.34
KB	2.24	2.55	1.95	4.93	8.84	31.0	5.66
KL/B	2.53	3.23	2.74	6.02	9.72	38.0	7.66

(27.73%), number of productive tillers per plant (25.48%), number of filled grains per panicle (20.86%) and harvest index (20.10%). Heritability explains the inheritance of traits and genetic advance helps in conveying suitable selection procedure. The genotypes under present study showed that high heritability values for the characters *viz.*, days to 50 % flowering (93%), plant height (92%), number of productive tillers per panicle (83%), harvest index (82%), single plant yield (81%), thousand grain weight (69%) and kernel length (63%). The high heritability recorded in the studied characters indicates that genotypes play a major role in expression of phenotype. Similar results also showed by Govintharaj *et al.* (2016). Genetic advance as per cent of mean ranged from 2.97 to 46.60 per cent. The highest genetic advance was observed for the characters single plant yield (46.60%), harvest index (34.45%) and number of filled grains per panicle (25.81 %). High heritability coupled with high genetic advance as per cent of mean indicate the additive gene effects can be improved by simple selection in the present breeding material. Similar kind of observation was reported by Devi *et al.* (2017) and Govintharaj *et al*. (2016).

Correlation and path analysis: Association of yield and other component traits information helps plant breeder to focus on yield improvement in the desired direction. Among eleven characters studied, the characters *viz.*, plant height (0.49), panicle length (0.56), number of productive tillers (0.92), number of filled grains per panicle (0.29), thousand grain weight (0.58) and harvest index (0.33) showed significantly positive correlation with single plant grain yield (Table 3). For days to 50% flowering (-0.41) and kernel L/B ratio (-0.66) showed significantly negative correlation with single plant yield. In terms of inter correlation among components studied, days to 50% flowering, panicle length (-0.32) and harvest index (-0.32) showed significant and negative inter correlation. Plant height had significant and positive inter correlation with number of productive tillers (0.34) and harvest index (0.51). Number of productive tillers had significant and positive inter correlation with number of filled grains per panicle (0.36) and harvest index (0.32). Panicle length had significant and positive inter correlation with thousand grain weight (0.83). Number of filled grains showed non-significant correlation coefficient. Thousand grain weight showed non-significant correlation coefficient. Harvest index had significant and positive inter correlation with single plant yield (0.80). Kernel length had significant and positive inter correlation with kernel breadth (0.30). Grain yield per plant was positively and highly significantly correlated with plant height, panicle length, number of productive tillers, number of filled grains per panicle, thousand grain weight and harvest index.

Table 3: Genotypic correlation coefficients for different traits

Characters	DF	PH	PL	NPRT	NFGP	TGW	HI	KL	KB	K L/B	GYP
DF	1.000	-0.255	-0.321*	-0.259	0.007	-0.256	-0.320*	-0.160	0.034	-0.149	-0.409**
PH		1.000	0.104	0.336*	0.224	0.158	0.507**	-0.082	0.065	-0.078	0.496**
PL			1.000	0.113	-0.263	0.831**	-0.211	0.173	0.027	0.044	0.569**
NPRT				1.000	0.366*	0.192	0.322*	0.006	-0.007	0.034	0.925**
NFGP					1.000	-0.213	-0.221	-0.103	-0.085	0.016	0.295*
TGW						1.000	0.058	-0.253	-0.201	0.006	0.587**
HI							1.000	-0.268	0.309*	-0.441**	0.334*
KL								1.000	0.162	0.628**	0.126
KB									1.000	-0.659**	-0.006
KL/B										1.000	-0.659**
GYP											1.000

*Significant at 5 per cent level **Significant at 1 per cent level

Table 4: Direct and indirect effects of different traits on single plant yield

Characters	DF	PH	PL	NPRT	NFGP	TGW	HI	K L	K B	K L/B	GYP
DF	**-0.049**	0.011	0.011	0.013	0.0004	0.010	0.015	0.005	-0.001	0.004	-0.338
PH	-0.045	**0.192**	0.015	0.062	0.026	0.020	0.087	-0.006	0.010	-0.007	0.422
PL	0.008	-0.002	**-0.033**	-0.005	0.002	-0.010	-0.001	-0.001	0.004	-0.005	0.190
PRT	-0.155	0.186	0.087	**0.5749**	0.169	0.080	0.183	0.028	0.003	0.025	0.703
FGP	-0.0001	0.001	-0.001	0.003	**0.011**	-0.001	-0.001	-0.0004	0.0004	-0.0005	0.164
TGW	-0.084	0.043	0.121	0.056	-0.036	**0.404**	0.010	-0.069	-0.034	-0.006	0.479
HI	-0.004	0.006	0.0003	0.004	-0.002	0.0003	**0.013**	-0.002	0.002	-0.003	0.287
K L	-0.044	-0.013	0.009	0.019	-0.016	-0.069	-0.084	**0.402**	0.032	0.202	0.053
K B	-0.007	-0.023	0.062	-0.003	-0.015	0.036	-0.068	-0.035	**-0.428**	0.348	0.002
K L/B	0.044	0.020	-0.083	-0.023	0.023	0.008	0.133	-0.267	0.430	**-0.529**	0.0028

Residual effect= 0.554

Diagonal value denote direct effect

Path analysis was undertaken to study the direct and indirect effects of the different traits on yield. The response variable grain yield and other predictor variables results are presented in the (Table 4) and (Figure 1). The traits plant height, number of productive tillers per plant, number of filled grains per panicle, thousand grain weight, harvest index and kernel breadth showed direct effect on grain yield per plant. Among these traits, number of productive tillers per plant showed positive (0.575) and high effect. Other characters such as days to 50% flowering, kernel breadth and kernel length and breadth showed negative indirect effects on grain yield per plant.

In this study, the correlation and path analysis studied revealed that number of filled grains and thousand grain weight had association with grain yield. This result was in similar in with the findings of Hossain *et al.* (2015) and (Devi, 2017) for number of filled grains per panicle. Hence, direct selection for number of filled grains and thousand grain weight could be practiced reducing the undesirable effect of other component traits studied. Also, residual effect coefficient is 0.554, which indicated that 45% of variability relating to the dependent variable grain yield. Similarly, residual coefficient (0.64) report by Priya *et al.* (2017) in their study.

Estimation of diversity among parental genotypes: The nine parents were grouped into four clusters based on morphological and quality traits. The parents TKM 9, ASD 16 and BL 5 falls in cluster 1, BL 4, ADT 45 and BL 10 in cluster II, LFR 293 and BL 6 falls on cluster III and only one genotype CO 18 in cluster IV (Figure 2). The genotypes fall in the cluster I and II were high yielding and blast resistance genotypes and cluster III and IV genotypes were blast resistant and leaf folder and high yielding genotypes

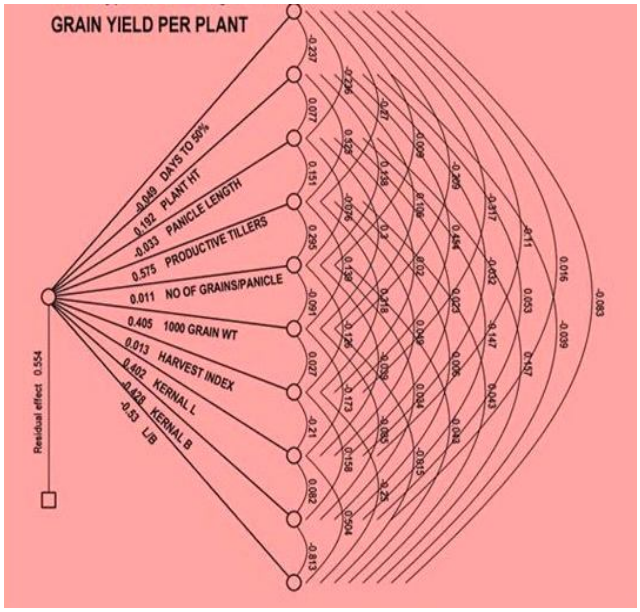

Fig-1: Path diagram for Direct and Indirect effects of rice grain yield.

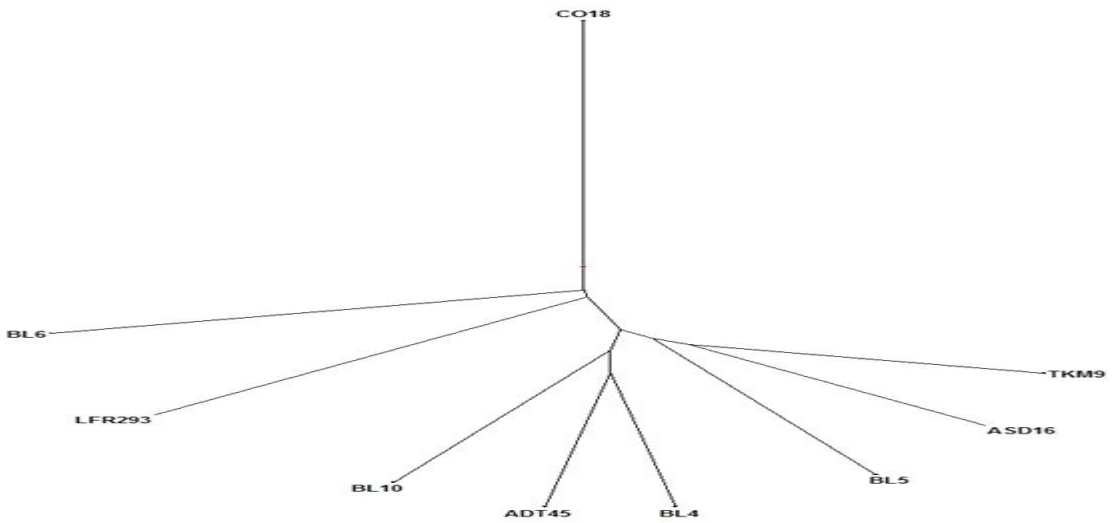

Fig-2: Cluster analysis for morphological and quality traits among parental genotypes.

respectively. The inter cross among these genotypes helps one to identify superior performing hybrids for high yielding and blast resistance lines. Similarly, cluster analysis was also studied for morpho- agronomic traits in rice by Balakrishnan *et al.* (2016).

CONCULSION

The determination of this study is to extent the outcome of this research in the ways such as 1.To evaluates parents and F_1's for their general and specific combining ability respectively 2. To study the nature of gene action involved in the inheritance of important quantitative and qualitative traits. 3. To study the extent of heterosis manifested for yield and its component traits. 4. To observe the nature and extent of relationship existing among yield and its component traits. 5. To identify superior performing hybrids for grain yield, blast and leaf folder resistance lines.

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