

GENETIC VARIABILITY, CHARACTER ASSOCIATION AND DIVERSITY ANALYSES FOR ECONOMIC TRAITS IN RICE (*Oryza sativa* L.)

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ABSTRACT

One hundred high yielding rice genotypes were evaluated to determine character association, variability and diversity for grain yield, yield components and quality characters. High estimates of heritability, genetic advance, genotypic and phenotypic coefficients of variation were recorded for panicle hill⁻¹, flag leaf area and grain yield hill⁻¹. Majority of the traits showed significant and positive associations between yield and yield components like biological yield hill⁻¹ followed by harvest-index as most important traits which need due consideration at the time of devising selection strategy. Thus, presence of several contrasting types of inter-relationships simultaneously would bring improvement in others due to correlated responses. Path analysis might have resulted into cancellation of contrasting associations by each other which ultimately lead to lowering of the net impact. This suggested that selection would be quite efficient in improving yield and yield components in context of germplasm evaluated. The crossing between superior genotypes of above diverse cluster pairs may provide desirable transgressive segregants for developing high yielding varieties of aromatic and non-aromatic rice. Thus, hybridization of Swarna of cluster XI with promising genotypes of cluster VI (Narendra 118, Vandana, Narendra 1, Akashi and Narendra 97) is recommended.

Key words: Correlation coefficient, diversity, genetic parameters, path analysis and rice

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INTRODUCTION

More than 90 per cent of the world's rice is grown and consumed in Asia, known as rice bowl of the world, where 60 percent of the earth's people and two thirds of world's poor live (Khush and Virk 2000). The world population is expected to reach eight billion by 2030 and rice production must increase by 50 per cent in order to meet the growing demand (Khush and Brar, 2002). Rice, being one of the important cereal crops of India, ranking first among all the cereal crops, is cultivated as pure culture mainly in wet season; cultivated in large area but characterized by poor productivity due to lack of high yielding stable varieties adaptable for different seasons and agroclimatic conditions at different parts of the country. The basic objective of this crop improvement programs is to realize a marked improvement in crop yield through various breeding methods. In order to step up the production potential, it is necessary to launch a dynamic breeding program to develop improved rice varieties suitable for different agro-climatic regions. For planning and execution of a successful breeding program, the most essential pre-requisite is the availability of substantial desirable genetic variability for important characters in the germplasm collections of the plant species. The available variability in a population can be partitioned into genetic parameters such as coefficients of variation, heritability and genetic advance to serve as basis for selection of desirable genotypes than existing ones. However, yield is a complex character which is controlled by association of number of components most of which are under polygenic control. Thus the identification of important components and information about their association with yield and other traits are very useful for developing efficient breeding strategy for evolving high yielding varieties. Genetic diversity is an important tool for a crop improvement programme, as it helps in the development of superior recombinants (Manonmani and Fazlullah Khan 2003). Genetic divergence among the genotypes play an important role in selection of parents having wider variability for different traits (Nayak *et al.*, 2004). The ultimate goal of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic yield. This requires genetic amelioration through maximum utilization of allelic resources to develop ideal genotype.

MATERIALS AND METHODS

The material for the present study comprised 100 rice germplasm accessions along with four checks (Sarjoo 52, Pusa Basmati 1, CSR 30 and Narendra 97), evaluated in an Augmented Design at Research Farm of Department of Genetics and Plant Breeding, N. D. University of Agriculture & Technology, Kumarganj, Faizabad, India, during wet season, 2009 and 2010. Twenty one days old seedlings were transplanted in 5 m² plots with 20 cm x 15 cm spacing, using single seedling hill⁻¹. All the recommended cultural practices and packages were followed to raise a good and healthy crop. In each entry, ten competitive plants were selected randomly, data recorded on eleven quantitative and three qualitative traits viz, plant height (PH),

flag leaf area (FLA), panicle hill⁻¹(P/H), panicle length (PL), spikelets panicle⁻¹ (S/P), spikelet fertility (SF), 1000-grain weight (TW), biological yield hill⁻¹(BY/H), grain yield hill⁻¹ (GY/H), harvest-index (HI), kernel length (KL), kernel breadth (KB) and L:B ratio (L/B), and days to 50% flowering (DF) was recorded on plot basis. The data was subjected to statistical analyses following Gomez and Gomez (1984) using Crop-Stat 7.2 (2009) statistical programme. The genetic parameters, correlation coefficients and path coefficient at genotypic and phenotypic levels were computed following Singh and Chaudhury (1985); Beale (1969) and Spark (1973) and to estimate genetic divergence and grouping of 104 genotypes into different clusters was done using Tocher's method.

RESULTS AND DISCUSSION

Analysis of variance for augmented design revealed highly significant and exploitable variability among tested genotypes for all fourteen characters and non-significant for the blocks. Greater variability in the initial breeding materials ensures better chances of producing desired recombinants for improvement of the crop.

Genetic Parameters

The high genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) recorded for P/H followed by FLA and GY/H indicate the existence of wide spectrum of variability for these traits and offer greater opportunities for desired traits through phenotypic selection (Table 1). Moderate PCV and GCV values recorded for BY/H, S/P, L/B, PH, PL, HI, TW, and DF while, rest of the characters recorded low PCV and GCV. The estimates of PCV were higher than GCV for all the traits. However, Manikya and Reddy (2011) reported, small difference between GCV and PCV for all the characters under study, which indicated less influence of environment over expression of the traits. High heritability coupled with high genetic advance was observed for all the traits except SF, KL and KW. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance hence, amenable of simple selection. The above mentioned three characters had high heritability with moderate genetic advance, indicating that the characters were also governed by both additive and non-additive gene actions. These results are accordance with Jayasudha and Sharma (2010).

Correlation coefficient

Out of 29 significant estimates among the total 91 correlations obtained between different character pairs, 25 correlation coefficients were positive in nature while only 4 estimates were negative (Table 2). This represents highly favourable situation for obtaining high response to selection in improving yield and yield components in rice germplasm evaluated. The measure of degree of symmetrical association between two variables or characters revealed that GY/H had highly significant and positive correlation with BY/H, HI, TW and P/H besides having

significant and positive association with PL. Therefore, these characters emerged as most important associates of grain yield in rice. The TW exhibited strong positive association with HI, BY/H, P/H and FLA besides having strong positive association with GY/H. The above characters except FLA also had strong positive association with GY/H, which augurs well for providing correlated response during selection for improving these characters. The above observations of strong positive associations between yield and yield components are in agreement with the available literature in rice (Chaudhary and Motiramani, 2003), Zahid *et al.*, 2006 and Yadav *et al.*, 2011. Results indicated that the taller genotypes possessed greater FLA and PL besides having late flowering, which appears logical. Janardanam *et al.*, (2002) have also reported positive associations between these characters. Among the grain characteristics, KL had positive association with PH while KB was positively associated with DF and FLA. The negative association of L/B with KB and BY/P indicates that the genotypes with longer grains have lesser breadth as well as biomass production potential.

Path coefficient analysis

Path analysis provides clear picture of character associations for formulating efficient selection strategy. The high positive direct effects on GY/H were exerted by BY/H and HI thus these characters emerged as most important direct yield components on which emphasis should be given during simultaneous selection aimed at improving grain yield of rice (Table 3). These characters have also been identified as major direct contributors towards grain yield by Mishra and Verma (2002) Jayasudha and Sharma (2010) and Yadav *et al.*, (2011).

Biological yield hill^{-1} exerted considerable positive indirect effects on GY/H via, DF, P/H, PL, S/P, SF, TW and KB while, negative indirect effect via L/B ratio. Harvest-index had positive indirect effect on GY/H via TW. Janardanam *et al.*, (2002), Mahto *et al.*, (2003), Patil and Sarawgi (2006) have also identified BY/H and HI as most important yield contributing traits which merit due consideration at the time of devising selection strategy aimed at developing high yielding varieties in rice.

Genetic divergence

The 104 genotype were grouped into eleven distinct clusters (Table 4). Among the eleven clusters, cluster IV was the largest with 21 genotypes, followed by cluster IX with 19 entries and cluster I with 15 entries. Clustering pattern of genotypes showed lack of any relationship between geographic origin and genetic diversity reported by Chandra *et al.*, (2007) and Bhanumathi *et al.*, (2010). Cluster XI exhibited very high inter cluster distances from cluster VI, II, III and I, while VI showed very high inter-cluster distance from cluster X (Table 5). The crossing between superior genotypes of above diverse cluster pairs may provide desirable transgressive segregants for developing high yielding varieties of aromatic and non-aromatic rice. Considering the mean performance of genotypes, diversity of clusters they belonged and cluster means for different characters, hybridization of Swarna of

cluster XI with promising genotypes of cluster VI (Narendra 118, Vandana, Narendra 1, Akashi and Narendra 97), cluster II (CSR-RIL-06-165), cluster III (NDRK 50006, IR 68051-23-NDR-1-2-1-1, CSR-2K-255, Susk Samrat, Saket 4 and IR 77674-3B-8-2-2-14-2-AJY-3) and cluster I (Jal Priya, Taraori Basmati, Basmati 370, Kasturi and Pusa Sugandha 3) may be recommended for isolating transgressive segregants. Similarly, crossing of promising genotypes of cluster VI (Narendra 118, Vandana, Narendra 1, Akashi and Narendra 97) and cluster X (T 3, Kalmuhi, Kalanamak, T 100, Hazardana, Chakia 59 and Madhukar) is likely to be fruitful for obtaining desirable recombinants for developing high yielding rice varieties.

The characters identified as important direct and indirect yield contributing traits, should be given due consideration while devising selection strategy for developing high yield ideotypes. In the light of above findings it is apprehended that the improvements in characters like biological yield and harvest index will help improving the grain yield in this population. These characters also showed high heritability and genetic advance. Intercrossing of divergent genotypes with desirable traits would lead to greater opportunity for maximum amount of heterosis and utilize them for multiple crossing programmes to accumulate favorable genes in single genotypes.

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Table 1: Grand mean, estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability (h^2_b) and genetic advance in per cent of mean for 14 characters in rice

Characters	Grand Mean	Coefficient of variation		Heritability in broad sense (%)	Genetic advance in per cent of mean
		PCV	GCV		
DF	95.94 ± 2.79	10.72	10.68	99.30	21.93
PH	108.68 ± 2.98	12.22	12.19	99.50	25.05
FLA	27.27 ± 2.29	27.93	27.81	99.10	57.04
P/H	10.49 ± 2.29	30.89	30.62	98.20	62.50
PL	26.96 ± 1.97	11.99	11.78	96.50	23.83
S/P	136.56 ± 17.38	15.63	15.13	93.70	30.17
SF	84.94 ± 5.24	5.89	5.58	89.60	10.88
TW	23.43 ± 2.05	10.80	10.46	93.70	20.86
BY/H	46.37 ± 2.97	16.56	16.44	98.60	33.62
GY/H	19.04 ± 1.99	20.38	20.13	97.50	40.94
HI	41.18 ± 5.33	11.21	10.48	87.30	20.18
KL	6.11 ± 0.43	9.17	8.92	94.40	17.86
KB	2.30 ± 0.10	8.96	8.85	97.60	18.01
L/B	2.69 ± 0.26	13.04	12.68	94.60	25.41

Table 2: Estimates of simple correlation coefficients between 14 characters in rice

Characters	PH	FLA	P/H	PL	S/P	SF	TW	BY/H	HI	KL	KB	L/B	GY/H
DF	0.352**	0.280**	0.110	0.259**	0.152	-0.029	0.079	0.152	-0.065	0.002	0.189*	-0.109	0.107
PH		0.200*	-0.304**	0.449**	0.247**	-0.041	-0.049	-0.055	-0.075	0.238**	0.034	0.157	-0.078
FLA			-0.050	0.342**	0.268**	0.028	0.282**	0.047	0.015	-0.077	0.250**	-0.223**	0.079
P/H				-0.042	-0.112	-0.046	0.212*	0.228**	0.162	-0.090	-0.049	-0.048	0.290**
PL					0.355**	0.002	0.013	0.171*	0.041	0.184*	0.133	0.053	0.177*
S/P						-0.003	0.022	0.124	0.043	0.065	0.041	0.021	0.143
SF							-0.018	0.145	0.055	0.101	0.102	-0.011	0.141
TW								0.239**	0.283**	-0.110	0.014	-0.099	0.368**
BY/H									-0.026	-0.110	0.194*	-0.217**	0.802**
HI										0.153	-0.004	0.089	0.564**
KL											-0.064	0.728**	0.018
KB												-0.723**	0.152
L/B													-0.110

** , * Significant at 1 and 5 per cent probability levels, respectively.

Table 3: Direct and indirect effects of 13 characters on grain yields per hill in rice

Character	DF	PH	FLA	P/H	PL	S/P	SF	TW	BY/H	HI	KL	KB	L/B
DF	0.013	0.005	0.004	0.001	0.003	0.002	0.000	0.001	0.002	-0.001	0.000	0.002	-0.001
PH	-0.001	-0.004	-0.001	0.001	-0.002	-0.001	0.000	0.000	0.000	0.000	-0.001	0.000	-0.001
FLA	0.010	0.007	0.035	-0.002	0.012	0.009	0.001	0.010	0.002	0.001	-0.003	0.009	-0.008
P/H	0.001	-0.004	-0.001	0.012	-0.001	-0.001	-0.001	0.003	0.003	0.002	-0.001	-0.001	-0.001
PL	-0.001	-0.002	-0.002	0.000	-0.006	-0.002	0.000	0.000	-0.001	0.000	-0.001	-0.001	0.000
S/P	0.001	0.002	0.002	-0.001	0.003	0.008	0.000	0.000	0.001	0.000	0.001	0.000	0.000
SF	0.000	0.000	0.000	0.001	0.000	0.000	-0.011	0.000	-0.002	-0.001	-0.001	-0.001	0.000
TW	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.002	0.000	-0.001	0.000	0.000	0.000
BY/H	0.124	-0.045	0.038	0.186	0.140	0.101	0.118	0.195	0.817	-0.021	-0.090	0.158	-0.177
HI	-0.038	-0.044	0.009	0.094	0.024	0.025	0.032	0.164	-0.015	0.581	0.089	-0.003	0.052
KL	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.001
KB	0.002	0.000	0.003	-0.001	0.002	0.000	0.001	0.000	0.002	0.000	-0.001	0.011	-0.008
L/B	-0.004	0.005	-0.007	-0.002	0.002	0.001	0.000	-0.003	-0.007	0.003	0.024	-0.024	0.033
GY/H	0.107	-0.080	0.080	0.289**	0.177*	0.142	0.140	0.368**	0.802**	0.563**	0.018	0.150	-0.110

RESIDUAL EFFECT = **0.1151**, Bold Figure represent Direct effect

Table 4: Clustering pattern of 104 rice genotypes based on Non-hierarchical Euclidean cluster analysis for 14 characters.

Cluster number	No. of genotypes	Name of genotypes
I	15	NDRK 50018, Jal Priya, NDRK 5014, Sonalika, Basmati 370, Pusa Basmati 1, Kasturi, Pakistani Basmati, Pusa Sugandha 4, JKRH 2000(Hybrid), CSR 27, Indrasan, Pusa Sugandha 3, NDRK 50019 and Taraori Basmati.
II	2	CSR-RIL-06 -165 and Chaini.
III	10	NDRK 50006, NDCP 608, IR 68051-23-NDR-1-2-1-1, CSR-2K-255, NDRK 50011, CSR 36, Susk Samrat, Narendra 80, Saket 4 and IR 77674-3B-8-2-2-14-2-AJY-3.
IV	21	Panvel 1, Pant Dhan 12, NDRK 5097, CSR 11, NDRK 50008, NDR 2026 (Richa), AURC 02-05-1, NDR 2022, NDR 2064, CR 2472-4-28-2, Y 134, Annada, TKM 9, IR 64, CSR -2K-242, IR 75395-2B-B-19-2-1-2, NDRK 5087, Pant Dhan 10, NDRK 5033, NDRK 50015 and Ratna.
V	5	FL 478, IR 59418-7B-21-3, NVSR 6029, NVSR 6030 and CSR 10.
VI	7	Narendra 118, CSR 30, Nagina 22, Vandana, Narendra 1, Akashi and Narendra 97.
VII	8	CR 661-236-1-3, CSR 13, Pankaj, Sambha Masuri, Narendra Lalmati, CR 2472-1-6-2-1, Jal Lahari and NDR 423.
VIII	8	NDRK 50012, PNR 381, NDR 2031, Pant Dhan 4, TR 2005-041, NDR 8030, IR 24 and NDRK 50013.
IX	19	Pant Dhan 102, NDRK 5088, Raghuvansi 4, NDRRK 5026, IR 72593-B-13-3-3-1, Lalpari No. 3, Sarjoo52, NDR 3026, Sundri, Narendra 359, Jaya, NDRK 50005, NDRK 50007, Narendra Usar 2, NDRK 50016, MRI 18, CSR-RIL-06 -94, NDRK 50002 and Narendra Usar 3.
X	8	T-3, Kalmuhi, Kalanamak, T-100, Hazardana, Chakia 59, Madhukar and T-1.
XI	1	Swarna.

Table 6: Clusters means for 14 characters in rice

Clusters	DF	PH	FLA	P/H	PL	S/P	SF	TW	BY/H	GY/H	HI	KL	KB	L/B
Cluster I	97.13	126.18	27.37	8.89	29.66	138.19	85.04	21.96	44.39	17.17	38.96	6.41	2.20	2.96
Cluster II	86.97	138.30	23.89	8.84	27.81	156.95	82.46	24.93	42.05	20.33	47.61	6.26	2.18	2.87
Cluster III	84.68	112.90	25.07	11.13	27.11	134.60	85.06	22.69	43.01	17.60	41.71	6.35	2.34	2.73
Cluster IV	89.10	96.76	25.50	10.00	25.77	131.45	85.39	23.51	46.71	19.24	41.62	6.09	2.23	2.75
Cluster V	95.73	79.43	25.18	15.51	22.67	120.15	84.84	21.96	44.32	18.33	41.49	6.00	2.29	2.63
Cluster VI	65.67	92.53	22.54	7.38	23.22	118.43	88.59	22.13	41.54	17.53	41.71	5.58	2.28	2.47
Cluster VII	109.53	109.34	32.64	9.39	26.71	145.31	83.92	23.42	49.25	20.01	40.89	5.79	2.41	2.44
Cluster VIII	103.79	114.17	25.68	12.42	27.16	143.34	82.18	24.90	44.08	18.70	42.46	6.13	2.21	2.78
Cluster IX	98.94	103.83	27.02	12.04	27.62	137.56	84.21	24.50	51.14	21.32	41.44	6.16	2.33	2.67
Cluster X	115.11	129.82	35.98	6.73	29.11	143.07	87.13	23.10	44.88	17.77	39.85	6.07	2.45	2.52
Cluster XI	128.70	83.11	25.75	26.06	24.06	105.35	91.23	24.06	57.86	27.81	48.07	5.46	2.49	2.19