

GENETIC VARIABILITY AND ASSOCIATION ANALYSIS IN WILD RICE  
(*ORYZA NIVARA* AND *ORYZA RUFIPOGON*)

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ABSTRACT

Study was conducted at Agricultural Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during Kharif 2011 to evaluate the thirty five rice accessions to assess their genetic variability, character association and path analysis for grain yield and yield attributing traits. The analysis of variance revealed highly significant difference among the accessions for all the traits studied indicating a good amount of variability in a set of material. The magnitude of phenotypic coefficient of variation was higher to corresponding genotypic coefficient of variation. High heritability coupled with high genetic advance as per cent of mean was found in the trait fertile spikelet per panicle, total number of grains per panicle and grain yield per plant. The genotypic correlation coefficient was found to be higher than phenotypic correlation coefficient. Leaf width, plant height, panicle length, fertile spikelet per panicle, total grains per panicle, spikelet fertility, test weight, kernel length and kernel breadth showed positive and significant association with grain yield per plant at genotypic and phenotypic levels. The path analysis with grain yield as dependent variable indicated that the highest positive direct effects were observed by effective tillers per plant followed by panicle length, fertile spikelet per panicle and test weight.

**Key words:** Correlation, path analysis, variability and wild rice

INTRODUCTION

The genus *Oryza* consists 22 wild species and two cultivated species *Oryza sativa* and *Oryza glaberrima*, belonging to the family Poaceae. The wild species are widely distributed in the pantropics and subtropic. The wild rice constitutes an excellent reservoir of variability for several traits resistance to biotic and abiotic stresses quality and productivity traits. In Indian subcontinent four valid wild species are *O. nivara* Sharma et Shastry, *O. rufipogon* Griff., *O. officinalis* Wall. Ex Watt and *O. granulate* Nees et Arn. Ex Watt. The *O. nivara* and *O. rufipogon* are widely distributed over eastern India and used as donors for major diseases, pests, environmental stress and many yield attributing traits. (Hore, 2005). The Indo-Gangetic region is one of the most intensively farmed zones of the world is endowed with a great diversity of wild rice growing in its natural habitats (Thakur and Pandey, 2009). However, there is need to diversify the genetic base of rice varieties and the first step towards this is to evaluate variability of reproductive traits in wild rice accessions, so that these accessions can be used in further breeding program. The knowledge about genetic variability of yield contributing traits, interrelationship among them and their relation with yield are necessary for a successful breeding program. Moreover, knowledge of heritability is essential for selection based improvement, as it indicates the extent of

transmissibility of a trait into future generations (Sabesan *et al.* 2009). Before placing strong emphasis on breeding for yield improvement trait, the knowledge on the association between yield and yield attributes will immense help the breeder in the improvement of yield. The correlation coefficient may also help to identify characters that have little or no importance in the selection programme. The existence of correlation may be attributed to the presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in combination of all (Oad *et al.* 2002). Path coefficient is being widely used in many crop species by plant breeders to understand the nature of complex interrelationships among traits and to identify the sources of variation in yield. The correlation coefficient of causal variable on the dependent variable may include in it the direct and indirect influences of component traits. Therefore, splitting the total correlation into direct and indirect effects of various causes would be more meaningful interpretation to the cause of association between the dependent variable yield and independent variables like yield contributing traits. Keeping in view the above facts, the present investigation was undertaken to assess the genetic variability, correlations among the traits and their path coefficient analysis for grain yield and yield attributing traits.

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## MATERIALS AND METHODS

**Plant material and experimental design:** The seeds of thirty five wild rice germplasm accessions were collected from natural habitat of Eastern Indo-Gangetic region of India during *kharif 2009* and their seeds were multiplied during *kharif 2010*. These accessions were evaluated in randomized block design at Agricultural Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India during *Kharif 2011*. Twenty five days old single seedlings were transplanted in small separate plot at spacing 20 cm x 15 cm apart. Standard agronomic practices were followed in maintaining the crop.

**Data collection:** The observations were recorded on ten randomly selected plants from each replication on fourteen quantitative traits viz. days to 50% flowering, days to maturity, leaf length, leaf width, plant height, panicle length, effective tillers per plant, fertile spikelet per panicle, total number of grains per panicle, fertility percentage, test weight, kernel length, kernel breadth and grain yield per plant.

**Statistical analysis:** The data was analysed for variability as per procedure given by Panse and Sukhatme (1985), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) by Burton and De Vane (1953) and heritability and genetic advance by Johnson *et al.* (1955). Correlation coefficient was worked as per Al-Jibour *et al.* (1958) and path analysis given by Dewey and Lu (1959).

## RESULTS AND DISCUSSION

The analysis of variance revealed highly significant difference among the germplasm accessions for all the traits indicating a large amount of variability was present in the set of material for effective selection of the accessions. Result showed that the magnitude of PCV was higher for yield and yield traits but the difference is very less (Table 1) indicating the presence of environmental influence to some degree in the phenotypic expression of the traits. Similar results were reported by Subudhi *et al.* (2011) and Bhadru *et al.* (2012). The highest estimate of PCV and GCV were observed for fertile spikelet per panicle (56.21 and 55.39) followed by total grains per panicle (42.07 and 40.86) and grain yield per plant (28.51 and 27.60) indicating their importance in selection for improving the yield. Moderate value of PCV and GCV were observed in total number of tillers per plant (24.35 and 22.19), spikelet fertility (20.69 and 20.31), test weight (16.63 and 16.41) and kernel breadth (16.28 and 16.07), and lowest in days to maturity (4.52 and 4.41) followed by days to 50%

flowering (5.41 and 5.26). These findings are similar to those Gangashetty *et al.* (2013).

The estimate of heritability was high for kernel breadth (97.46%), test weight (97.40%) and fertile spikelet per panicle (97.10%). It indicated that variation observed in these traits is primarily due to genetic causes and not only by environmental effects. High heritability does not always indicate high genetic gain. The heritability coupled with high genetic advance as per cent of mean under the control of additive gene action would be effective for selecting superior germplasm. High heritability coupled with high genetic advance as per cent of mean were observed for fertile spikelet per panicle (97.10% and 112.46), total number of grains per panicle (94.30% and 81.74) and grain yield per plant (93.70% and 55.03) which indicates the preponderance of additive gene action and such characters could be improved through selection. Similar findings were earlier reported by Immanuel *et al.* (2011). Whereas high heritability coupled with low genetic advance as per cent mean were observed in days to maturity (95.50% and 8.89), days to 50% flowering (94.60% and 10.55) and kernel length (93.20% and 12.31) which indicates non additive type of gene action and that genotype x environment interaction plays a significant role in the expression of the traits. These results are in conformity with the findings of Rahaman *et al.* (2012).

The estimates of genotypic and phenotypic correlation coefficient are presented in Table 2. The yield attributing traits were investigated for their relationship with yield as well as themselves. The genotypic correlation coefficient was found to be higher than phenotypic correlation coefficient indicating a strong inherent association for grain yield per plant and other traits. Similar observation in rice has been reported by Akter *et al.* (2010). Leaf width, plant height, panicle length, fertile spikelet per panicle, total grains per panicle, spikelet fertility, test weight, kernel length and kernel breadth showed strong positive and significant association with grain yield per plant both at genotypic and phenotypic levels. The association studied indicated that the grain yield of rice can be improved by selecting germplasms having higher performances for these traits. These results are in conformity with Singh *et al.* (2013) for panicle length, total number of tillers per plant and test weight. The grain yield per plant had negative non significant association with days to 50 per cent flowering, days to maturity and leaf length both at genotypic and phenotypic levels.

Table 1: Analysis of variance and genetic variance for twelve traits in thirty five wild rice accession

Source of variation	d.f.	Mean sum of squares													
		DF	DM	LL	LW	PH	PL	ET	FSP	TGP	SF%	TW	KL	KB	GYP
Replcation	2	0.15	1.55	15.40	0.006	6.47	1.13	1.39	108.52	185.70	10.08	0.16	0.0002	0.00002	1.22
Treatment	34	109.02**	130.15**	121.14**	0.126**	943.11**	17.87**	77.56**	4511.04**	5885.81**	505.96**	45.20**	0.432**	0.325**	124.09**
Error	68	2.03	2.00	13.78	0.005	25.67	3.66	4.93	44.032	116.10	6.17	0.39	0.010	0.0028	2.72
Genetic variance															
Range	Min.	91.00	128.66	52.61	1.04	128.72	17.72	3.50	19.12	54.61	23.44	14.10	5.01	1.12	7.89
	Max.	120.66	157.00	78.90	1.80	210.82	28.50	10.15	231.90	267.29	86.77	33.50	7.01	2.62	36.98
SEm (±)		0.82	0.81	2.14	0.04	2.92	1.10	1.28	3.83	6.22	1.43	0.36	0.06	0.04	0.95
Variability (%)	PCV	5.41	4.52	11.11	15.55	11.72	12.54	24.35	56.21	42.07	20.69	16.63	6.42	16.28	28.51
	GCV	5.26	4.41	9.44	14.62	11.26	9.42	22.19	55.39	40.86	20.31	16.41	6.19	16.07	27.60
Heritability (%)		94.60	95.50	72.20	88.40	92.30	56.40	83.10	97.10	94.30	96.40	97.40	93.20	97.46	93.70
Genetic advance as % of mean		10.55	8.89	16.52	28.31	22.28	14.57	41.67	112.46	81.74	41.10	33.38	12.31	32.68	55.03

\*\* and \* Significant at 1 and 5 per cent level, respectively.

DF= Days to 50 % flowering, DM= Days to maturity, LL= Leaf length, LW= Leaf width, PH= Plant height, PL= Panicle length, ET= Effective number of tillers per plant, FSP= Fertile spikelet per panicle, TGP= Total number of grains per panicle, SF%= Spikelet fertility, TW= Test weight, KL= Kernel length, KB= Kernel breadth and GYP= Grain yield per plant

Table 2: Phenotypic ( $r^{ph}$ ) and genotypic ( $r^g$ ) correlation coefficients among twelve traits in thirty eight rice germplasm accessions

Traits	DM	LL	LW	PH	PL	ET	FSP	TGP	SF%	TW	KL	KB	GYP	
DF	$r^{ph}$	0.757**	0.298**	-0.160	-0.213*	-0.001	0.106	-0.109	-0.153	0.044	-0.294**	-0.124	-0.117	-0.195
	$r^g$	0.763**	0.330**	-0.188	-0.239*	0.003	0.107	-0.110	-0.158	0.046	-0.305**	-0.149	-0.133	-0.204
DM	$r^{ph}$		-0.033	0.019	0.066	0.124	0.004	0.144	0.159	0.018	-0.158	-0.029	-0.085	-0.034
	$r^g$		-0.069	0.022	0.077	0.180	-0.006	0.153	0.172	0.025	-0.163	-0.030	-0.090	-0.069
LL	$r^{ph}$			-0.174	-0.232*	-0.011	0.039	-0.131	-0.228*	0.172	-0.037	-0.077	-0.173	-0.144
	$r^g$			-0.271*	-0.341**	-0.182	0.109	-0.159	-0.290*	0.197	-0.048	-0.106	-0.214*	0.180
LW	$r^{ph}$				0.689**	0.578**	-0.621**	0.518**	0.650**	-0.057	0.433**	0.217*	0.397**	0.271*
	$r^g$				0.758**	0.729**	-0.744**	0.550**	0.705**	-0.062	0.472**	0.224*	0.411**	0.372**
PH	$r^{ph}$					0.431**	-0.538**	0.596**	0.729**	-0.046	0.257*	0.220*	0.161	0.277*
	$r^g$					0.636**	-0.618**	0.634**	0.781**	-0.047	0.274*	0.249*	0.183	0.341**
PL	$r^{ph}$						-0.481**	0.523**	0.592**	0.135	0.372**	0.241*	0.206*	0.442**
	$r^g$						-0.689**	0.675**	0.753**	0.172	0.508**	0.333**	0.294**	0.482**
ET	$r^{ph}$							-0.507**	-0.534**	-0.080	0.418**	-0.155	-0.233*	0.206
	$r^g$							-0.559**	-0.604**	-0.083	-0.466**	-0.166	-0.239*	0.209
FSP	$r^{ph}$								0.931**	0.558**	0.583**	0.445**	0.217*	0.738**
	$r^g$								0.933**	0.582**	0.604**	0.475**	0.227*	0.759**
TGP	$r^{ph}$									0.257**	0.454**	0.338**	0.181	0.632**
	$r^g$									0.280**	0.482**	0.376**	0.199	0.290**
SF%	$r^{ph}$										0.502**	0.382**	0.146	0.623**
	$r^g$										0.519**	0.397**	0.148	0.697**
TW	$r^{ph}$											0.636**	0.606**	0.797**
	$r^g$											0.666**	0.621**	0.837**
KL	$r^{ph}$												0.495**	0.576**
	$r^g$												0.507**	0.606**
KB	$r^{ph}$													0.409**
	$r^g$													0.414**

\*\* and \*: Significant at 1 and 5 per cent level, respectively

The results of path analysis between yield and yield related traits showed that the traits via effective tillers per plant, panicle length, fertile spikelet per panicle and test weight exhibited direct positive effect on grain yield (Table 3). The strong positive association of fertile spikelet per panicle and test weight with grain yield was mainly observed through its direct effect whereas panicle length through its indirect effects viz. fertile spikelet per

panicle and test weight. Kumar and Saravanan (2012) reported similar results for days to maturity, number of productive tillers per plant, panicle length, fertile spikelet per panicle and spikelet fertility. The negative association of days to 50 per cent flowering and effective tillers per plant was observed through its indirect effects viz. panicle length, fertile spikelet per panicle and test weight. Similar observation was also made by Minnie *et al.* (2013).

Table 3: Phenotypic (P) and genotypic (G) matrix of direct and indirect effect on grain yield per plant

Traits	Matrix	DF	ET	PL	FSP	TW	Correlation with grain yield plant <sup>-1</sup>
DF	P	0.001	0.038	-0.001	-0.054	-0.180	-0.196
	G	-0.017	0.050	0.001	-0.052	-0.188	-0.206
ET	P	0.001	0.365	-0.062	-0.254	-0.256	-0.206
	G	-0.002	0.489	-0.171	-0.283	-0.288	-0.255
PL	P	0.001	-0.175	0.128	0.262	0.228	0.444**
	G	0.001	-0.337	0.248	0.342	0.314	0.568**
FSP	P	-0.001	-0.185	0.067	0.499	0.356	0.736**
	G	0.002	-0.274	0.167	0.506	0.373	0.774**
TW	P	-0.002	-0.152	0.047	0.291	0.611	0.795**
	G	0.005	-0.228	0.126	0.306	0.617	0.826**

Residual effect = 0.28 (Value in diagonal indicate direct effect)

The results of the present study suggested that there is adequate genetic variability present in the material studied. In the present set of wild rice accession, the traits panicle length, fertile spikelet per panicle, spikelet fertility and test weight influenced

grain yield. Therefore, selections of these accessions with desirable traits are to be effective in accumulation of favourable genes for bringing together into the common genetic background of cultivated *indica* rice *Oryza sativa* L.

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