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Studies on Genetic Characteristic of Upland Rice (*Oryza sativa* L.)

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Abstract

The considerable amount of genetic variability was exhibited among the accessions of local collection obtained from natural habitat of Eastern U. P. (India) under the UPCAR project. High genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean was recorded for total number of grains per panicle, filled grains per panicle, number of effective tillers, leaf width and grain yield per plant. Positive and significant association was recorded by days to 50% flowering, days to maturity, leaf length, leaf width, filled grains per panicle and total number of grains per panicle among themselves and also with grain yield per plant at genotypic and phenotypic levels. Days to maturity, plant height, number of filled grains per panicle and test weight exhibited positive direct effect both at genotypic and phenotypic levels.

Highlights

- The traits days to maturity, number of filled grains per panicle and test weight influenced grain yield.

- The accessions have higher performance for these traits would be utilized as donor parent.

Keywords: Correlation, path analysis, upland rice and variability

Rice (*Oryza sativa* L.) is the world's second most important cereal crop belonging to the family Poaceae grown under diverse eco-geographical conditions in various tropical and subtropical countries. India is a primary centre of origin of rice and has many local landraces. The most of them are not in cultivation while many are lost but few are still cultivated by resource-poor traditional farmers in areas practicing subsistence farming. The upland rice harbours a great genetic potential for rice improvement as subjected to subtle selection over a long period of time. This aids in the adaptation of upland to wide agro-ecological niches and rich variability of complex quantitative traits. The exact genetic potential, differences from commercial varieties, and the magnitude of heterogeneity still present in local landraces are not well catalogued.

Grain yield is dependent on many yield contributing traits as well as on the environmental influence. 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 analysis proposed by Wright (1921) help the portion the total correlation into direct and indirect effects of various causes. Thus the breeder can select the genotypes critically. The present investigation was undertaken to assess the genetic variability, association among the traits and their path coefficient analysis for grain yield other traits.

Materials and Methods

Plant material and experimental design

Panicles of forty eight upland rice germplasm accessions were collected from natural habitat of Eastern of India during *kharif 2007 to 2009* and their seeds were multiplied during *kharif 2010 to 2011*. The details of the source of landraces are presented in Table-1. These accessions were evaluated in randomized block design with three replications during *kharif 2012*. Twenty five days old single seedlings were transplanted in small separate plot 20 cm apart between row and 15 cm within row. The recommended packages of practices were followed to raise a healthy crop.

Data collections

The observations were recorded fourteen quantitative traits viz. days to 50% flowering, days to maturity, leaf length, leaf width, plant height, panicle length, effective tillers per plant, filled grain per panicle, total number of grains per panicle, fertility percentage, test weight, kernel length, kernel breadth and grain yield per plant. Ten randomly selected plant in each accession in each replication were tagged for recording observation on fourteen quantitative traits, and mean value were used for statistical analysis.

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

Variation and genetic parameters among accessions

The analysis of variance revealed highly significant difference among the accessions for all the traits indicating a large amount of variability was present in the studied material for effective selection (Table 2). The magnitude of phenotypic coefficient of variation was higher for yield and yield attributing traits but the difference is very less indicates the presence of environmental influence to some degree in the phenotypic expression of the traits (Table 3). Similar results were reported by Bhadru *et al.,* (2012) and Singh *et al.,* (2013). The highest estimate of PCV and GCV were observed for filled grains per panicle, total grains per panicle, number of effective tillers per plant and grain yield per plant while lowest in spikelet fertility percentage followed by days to maturity. These finding are similar to those Gangashetty *et al.,* (2013). The estimate of heritability were high for days to maturity (97.20%), plant height (97.10%), days to 50% flowering (96.80%) and kernel breadth (96.00%) due to genetic causes rather 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 varieties. High heritability coupled with high genetic advance as per cent of mean were recorded for total number of grains per panicle, filled grains per panicle, number of effective tillers, leaf width and grain yield per plant, while high heritability coupled with low genetic advance as per cent mean were observed in days to maturity, days to 50 per cent flowering and panicle length. These results are conformity with the earlier reports of Devi *et al.,* (2012) and Rahaman *et al.,* (2012).

Character association and path analysis

The estimates of phenotypic and genotypic correlation coefficient are presented in Table 4. The yield attributing traits was 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 and other traits. Similar observation in rice has been reported earlier by Singh *et al.,* (2012). Days to 50% flowering, days to maturity, leaf length, leaf width, filled grains per panicle and total number of grains per panicle showed 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

Table 1: List of forty eight upland rice germplasm accessions and their collection site

S.N.	Accession Number	Collection site			
		Village	Block	District	Country
1.	PKSLGR-1	Hingutarghar	Dhanapur	Chandauli	India
2.	PKSLGR-2	Nakenampur	Dhanapur	Chandauli	India
3.	PKSLGR-3	Bhaluadai	Shahabganj	Chandauli	India
4.	PKSLGR-4	Bishunpura	Chakiya	Chandauli	India
5	PKSLGR-5	Mamarakpur	Shahabganj	Chandauli	India
6	PKSLGR-6	Ramghar	Chakiya	Chandauli	India
7	PKSLGR-7	Muzafferpur	Chakiya	Chandauli	India
8	PKSLGR-8	Diberiya	Chakiya	Chandauli	India
9	PKSLGR-9	Nawajganj	Chakiya	Chandauli	India
10	PKSLGR-10	Ghorawal	Newarpura	Sonbhadra	India
11	PKSLGR-11	Dumahar	Babhani	Sonbhadra	India
12	PKSLGR-12	Dadvahani	Babhani	Sonbhadra	India
13	PKSLGR-13	Satvahani	Babhani	Sonbhadra	India
14	PKSLGR-14	Chhiyari	Babhani	Sonbhadra	India
15	PKSLGR-15	Mahuariya	Babhani	Sonbhadra	India
16	PKSLGR-16	Nibi	Vijaypur	Mirzapur	India
17	PKSLGR-17	Tilai	Vijaypur	Mirzapur	India
18	PKSLGR-18	Joya	Vijaypur	Mirzapur	India
19	PKSLGR-19	Tamua	Madiyan	Mirzapur	India
20	PKSLGR-20	Katariya	Madiyan	Mirzapur	India
21	PKSLGR-21	Barakachha	Madiyan	Mirzapur	India
22	PKSLGR-22	Gulalpur	Madiyan	Mirzapur	India
23	PKSLGR-23	Dhanawal	Madiyan	Mirzapur	India
24	PKSLGR-24	Ninwar	Lalganj	Mirzapur	India
25	PKSLGR-25	Sikhar	Sikhar	Mirzapur	India
26	PKSLGR-26	Baburi	Vijaypur	Mirzapur	India
27	PKSLGR-27	Shisotar	Nawanagar	Ballia	India
28	PKSLGR-28	Maturi	FatehpurManda	Ballia	India
29	PKSLGR-29	Deorara	Bansdih	Ballia	India
30	PKSLGR-30	Mehnagar	Meghnaghar	Ajamghar	India
31	PKSLGR-31	Naretha	Jahanaganj	Azamgarh	India
32	PKSLGR-32	Shahpur	Jahanaganj	Azamgarh	India
33	PKSLGR-33	Kotila	Rani kiSarai	Azamgarh	India
34	PKSLGR-34	Mehnagar	Meghnaghar	Ajamghar	India
35	PKSLGR-35	Naretha	Jahanaganj	Azamgarh	India
36	PKSLGR-36	Shahpur	Jahanaganj	Azamgarh	India
37	PKSLGR-37	Kotila	Rani kiSarai	Azamgarh	India
38	PKSLGR-38	Ganjari Dheeh	Gangapur	Varanasi	India
39	PKSLGR-39	Raghunathpur	Sewapuri	Varanasi	India
40	PKSLGR-40	Bhainsa	Sewapuri	Varanasi	India
41	PKSLGR-41	Newada	Sewapuri	Varanasi	India
42	PKSLGR-42	Mhuar	Brahmpur	Buxar	India
43	PKSLGR-43	Balua	Buxar	Buxar	India
44	PKSLGR-44	Jalilpur	Chausha	Buxar	India
45	PKSLGR-45	Mathila	Dumraon	Buxar	India
46	PKSLGR-46	Nibi	Bhagwanpur	Kaimur	India
47	PKSLGR-47	Baspurwa	Mohania	Kaimur	India
48	PKSLGR-48	Imlia	Ramghar	Kaimur	India

Table 2: Analysis of variance of fourteen quantitative traits in forty eight upland rice germplasm accessions

Source of variation	d.f.	Mean sum of squares													
		DF	DM	LL	LW	PH	PL	ET	FG	TGP	SF%	TW	KL	KB	GYP
Replication	2	1.090	4.881	5.726	0.014	32.646	13.653	1.118	0.295	0.811	2.405	1.203	0.180	0.004	7.560
Treatment	47	183.559**	252.538**	194.043**	0.184**	1363.680**	19.886**	9.953**	4682.705**	5649.727**	128.297**	31.198**	1.403**	0.131**	64.019**
Error	94	1.998	2.420	2.870	0.007	13.653	1.121	0.646	110.218	107.157	8.413	0.718	0.023	0.001	6.371

** 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, FG= Filled grains 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 3: Genetic variance of fourteen quantitative traits in forty eight upland rice germplasm accessions

Parameters	Traits	DF	DM	LL	LW	PH	PL	ET	FG	TGP	SF%	TW	KL	KB	GYP
Range	Min.	74	106.33	25.88	0.72	82.47	15.53	3.89	48.47	52.60	63.71	12.07	4.67	1.71	9.31
	Max.	107	132.33	56.38	1.57	158.95	30.24	12.33	205.00	213.20	99.30	27.29	7.89	2.52	27.60
Mean		88.18	118.65	41.52	1.08	114.68	24.77	7.03	119.06	131.60	90.76	20.23	6.19	2.19	18.42
SEm (±)		0.82	0.90	0.98	0.05	2.13	0.61	0.46	6.06	5.98	1.67	0.49	0.09	0.02	1.46
Variability (%)	PCV	8.97	7.81	19.65	23.98	18.78	10.96	27.54	33.96	33.59	7.66	16.30	11.22	9.65	27.46
	GCV	8.82	7.70	19.22	22.58	18.50	10.10	25.05	32.79	32.66	6.97	15.76	10.95	9.46	23.80
Heritability (%)		96.80	97.20	95.70	88.70	97.10	84.80	82.80	93.30	94.50	82.60	93.40	95.30	96.20	75.10
Genetic advance as % of mean		17.88	15.63	38.74	43.79	37.54	19.15	46.95	65.23	65.41	13.04	31.37	22.03	19.12	42.48

Table 4: Phenotypic (r^{ph}) and genotypic (r^g) correlation coefficients among fourteen traits in forty eight upland rice germplasm accessions

Traits		DM	LL	LW	PH	PL	ET	FG	TGP	SF%	TW	KL	KB	GYP
DF	r^{ph}	0.579**	0.215**	0.219**	-0.106	0.145	-0.390**	0.429**	0.519**	-0.331**	-0.011	0.196*	-0.179*	0.411**
	r^g	0.599**	0.223**	0.227**	-0.111	0.167*	-0.442**	0.455**	0.549**	-0.374**	-0.012	0.214*	-0.185*	0.475**
DM	r^{ph}		0.134	0.169*	-0.187*	0.271**	-0.383**	0.096	0.186*	-0.326**	-0.032	0.234**	-0.153	0.182*
	r^g		0.138	0.191*	-0.189*	0.305**	-0.424**	0.098	0.194*	-0.376**	-0.029	0.246**	-0.161	0.206**
LL	r^{ph}			0.608**	0.688**	0.281**	-0.262**	0.574**	0.501**	0.269**	-0.191*	-0.243**	0.131	0.296**
	r^g			0.662**	0.721**	0.306**	-0.281**	0.599**	0.520**	0.293**	-0.201*	-0.255**	0.137	0.343**
LW	r^{ph}				0.438**	0.294**	-0.325**	0.561**	0.535**	0.080	0.168*	-0.028	0.231**	0.264**
	r^g				0.463**	0.348**	-0.382**	0.623**	0.589**	0.099	0.174*	-0.041	0.259**	0.291**
PH	r^{ph}					0.431**	-0.096	0.321**	0.228**	0.339**	0.073	-0.175*	0.261**	0.146
	r^g					0.453**	-0.119	0.347**	0.249**	0.376**	0.078	-0.183*	0.274**	0.177*
PL	r^{ph}						-0.146	0.149	0.173*	-0.096	0.249**	0.422**	-0.197*	0.006
	r^g						-0.180*	0.183*	0.206*	-0.105	0.278**	0.470**	-0.229**	0.005
ET	r^{ph}							-0.269**	-0.312**	0.092	0.027	-0.077	-0.066	-0.012
	r^g							-0.318**	-0.360**	0.103	0.024	-0.089	-0.075	-0.170*
FG	r^{ph}								0.967**	0.119**	-0.213	-0.093	-0.111	0.599**
	r^g								0.969**	0.090	-0.218**	-0.101	-0.123	0.682**
TGP	r^{ph}									-0.132	-0.177*	0.023	-0.192*	0.577**
	r^g									-0.157	-0.180*	0.018	-0.205**	0.662**
SF%	r^{ph}										-0.148	-0.445**	0.322**	0.082
	r^g										-0.160	-0.487**	0.353**	0.039
TW	r^{ph}											0.573**	0.281**	-0.073
	r^g											0.610**	0.295**	-0.102
KL	r^{ph}												-0.461**	-0.006
	r^g												-0.497**	-0.021
KB	r^{ph}													-0.127
	r^g													-0.153

* and ** :Significant at 1% and 5% level of significance, respectively.

can be improved by selecting germplasms having higher performances for these traits. These results are in conformity with Singh *et al.,* (2013). The grain yield per plant had a positive significant association with plant height at genotypic level only, while positive non-significant with panicle length and spikelet fertility percentage. The result of path coefficient analysis between yield and yield related traits showed that, the traits via total number of grains per panicle, spikelet fertility percentage, days to maturity, days to 50% flowering, number of effective tillers per plant, plant height, test weight and number of filled grains per panicle (Table 5) revealed that the major yield component of grain yield in rice. Kumar and Saravanan (2012) reported similar results for days to maturity, number of productive tillers per plant, panicle length, filled grains per panicle and spikelet fertility. The filled grains per panicle and total number of grains per panicle exhibited highest positive and significant association with grain yield per plant, due to high direct and indirect effect of total number of grains per panicle on grain yield per plant. Some other traits like leaf length, leaf width and panicle length showed negative direct effect on grain yield per plant, but overall showed positive indirect effect through other traits resulting the positive significant association with grain yield per plant. Similar observation was also made by Minnie *et al.,* (2013).

Conclusion

The results of the present study suggested that there is adequate genetic variability present in the material studied. The separation and selection of varieties based on high heritability of traits make it easy for breeders to exploit their knowledge and skill in transgressive segregation breeding programme, while many researchers are agreed with high heritability alone does not effective but high heritability along with high genetic advance would be effective for selecting superior varieties. In the present set of upland rice germplasm accessions, the traits days to maturity, plant height, number of filled grains per panicle and test weight exhibited the positive direct effect at phenotypic and genotypic levels and influenced grain yield. The genetic gains in the grain yield can be made by stressing on the aforesaid characters during selection.

Acknowledgement

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