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Genetic Variability, Heritability and Genetic Advance in Rice (*Oryza sativa* L.)

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ABSTRACT

A field experiment comprised of 72 genotypes of upland rice (Oryza sativa L.) was to investigate the magnitude of genetic variability, character association and genetic divergence in upland rice. The higher estimates of genotypic and phenotypic coefficient of variation were obtained for number of non-effective tillers per plot, number of unfilled grains per panicle, harvest index, grain yield per plot and number of effective tillers per plot which also had high heritability coupled with high genetic advance indicating better scope for improvement of these traits by an effective selection program. Grain yield per plot showed positive and highly significant association with harvest index, number of effective tillers per plot, milling percentage, number of filled grains per panicle and plant height while highly significant but negative correlation with number of non-effective tillers per plot and days to 50% flowering at genotypic as well as phenotypic levels. Hence, it can be advocated to give priority to these traits in the selection programme to develop high yielding and early varieties with bold grains.

Key words: *Rice, Genetic, variability, Heritability, Genetic advance.*

INTRODUCTION

Rice is an important staple food crop in the world. There is an ample scope for improving the productivity of this crop through varietal improvement and development of hybrids. The primary consideration to bring about genetic improvement of a crop is the study of genetic variability. Assessment of variability for any trait is pre-requisite for a plant breeder to planning effective breeding programmes. Heritability is an index of the transmission of characters from parents to their offspring and it plays an important role in the selection process in plant breeding. Genetic advance provides information on expected gain resulting from selection of superior individuals.

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Heritability and genetic advance are important selection parameters which help in predicting the gain under selection. The present study was undertaken to determine the extent of variability and heritability for yield contributing characters with involvement of mid early group (duration 120-130 days) genotypes.

MATERIAL AND METHODS

The experiment was carried out during *Kharif* 2012 at Cotton Research Sub- Station, Navsari Agricultural University, Achhalia. The material comprised of 72 elite mid early group genotypes of rice (Table-1) having duration of 120- 130 days sown in a Randomized Block Design with two replications with spacing of 30 × 10 cm. Data were recorded on five randomly selected plants in each entry in each replications. The data was subjected to INDOSTAT software to estimate genetic coefficient of variation (%) (GCV), phenotypic coefficient of variation (%) (PCV), heritability (%) (broad sense). The path analysis suggested by Wright[43] and applied in plant selection by Dewey and Lu[13] was followed in order to partition genotypic correlation of different variables with grain yield into direct and indirect effects of these variables on yield.

RESULTS AND DISCUSSION

Presence of genetic variability is unambiguously the most important prerequisite for crop improvement programme. The assessment of extent of variation present in the genetic material, therefore, becomes an essential step to know the magnitude of improvement that can be attained for various characters and to decide the ways to achieve it.

In the present investigation, it was evident from highly significant differences among the genotypes for all the characters studied scope of exploitation of the characters under study. Significant variations in one or more characters studied in the present investigation have also been reported in rice by several workers like Singh *et al.*[30], Amirthadevarathinam[2] , Singh *et al.*[31], Pathak and Patel[24] , Deosarkar *et al.*[12], Singh *et al*[32], Anand *et al.*[42], Borbora and Hazarika[6], Dhananjaya *et al.*[14] , Mokate *et al.*[18], Singh *et al.*[33], Verma *et al.*[42], Pandey and Awasthi[21], Agrawal[1], Shukla *et al.*[29], Suman *et al.*[37], Panwar and Mathur[22], Bastia *et al.*[5], Chandra *et al.*[8] , Chandra *et al.*[9], Saidaiah *et al.*[26], Fatema *et al.*[15], Fukrei *et al.*[16], Subbaiah *et al.*[38], Osman *et al.*[20], Seyoum *et al.*[28], Sohrabi *et al.*[35], Sravan *et al.*[36], Toshimenla and Sapu[40], Veni *et al.*[41], Nilamani *et al.*[19] and Patel *et al.*[23].

A wide range of phenotypic variance were observed for grain yield per plot (853.85) and number of filled grains per panicle (852.16) and followed by plant height, number of effective tillers per plot, number of non-effective tillers per plot which were evident from the perusal of results for range of phenotypic variations (Table 3). This indicated that there is enormous scope for selection of desirable and ideal genotypes from the population for greater chances of success in breeding programmes.

These results corroborated with the findings reported in upland rice for number of filled grains per panicle by Mokate *et al.*[18], for grain yield per plot by Agrawal *et al.*[1] for plant height by Singh *et al.*[30], Singh *et al.*[31], Chookar *et al.*[11], Rathod *et al.*[25], Dhananjay *et al.*[14] and Seyoum *et al.*[28] for number of effective tillers per plot, number of non-effective tillers per plot by Singh *et al.*[30], Amirthadevarathinam[2] , Chookar *et al.*[11] and Rathod *et al.*[25].

The intermediate range of phenotypic variation was possessed by harvest index, milling percentage, head rice recovery and days to 50% flowering. The lower value of genotypic variance were exhibited by amylose content, days to maturity, panicle length and test weight.

These results were in accordance with the findings reported in upland rice for milling percentage, head rice recovery by Tavisha *et al.*[39] and Nilamani *et al.*[19] , for days to 50% flowering by Singh *et al.*[30], Chookar *et al.*[11] , Hedge and Patil[17] and Seyoum *et al.*[28] for amylose content by Tavisha *et al.*[30] , for harvest index by Chauhan *et al.*[10] .

The phenotypic variation is jointly determined by genotypes and environment under which they are grown. The study of phenotypic range of variation alone is not sufficient for judging the amount of genetic variability present in a population. The genetic parameters such as components of variance, coefficient of variation, heritability and genetic advance should be used for judgment of genetic variability more precisely as well as for prediction of extent of improvement possible in various traits.

Perusal of results (Table 3) revealed that high values of genotypic variance observed for number of filled grains per panicle, grain yield per plot, plant height, number of effective tillers per plot and number non-effective tillers per plot indicated the presence of high amount of phenotypic variability for these traits in the genetic material studied. These finding were in agreement with the results of Singh *et al.*[30], Amirthadevarathinam[2], Pathak and Patel[24], Chookar *et al.*[11], Rathod *et al.*[25], Dhananjay *et al.*[14], Anand[4] , Suman *et al.*[37], Seyoum *et al.*[28], Toshimenla and SapuChangkiji[40].

The moderate estimates of genotypic and phenotypic components of variance were found for number of unfilled grains per panicle, harvest index, milling percentage, head rice recovery and days to 50% flowering. These results were in conformity with the findings of Singh *et al.*[31] , Chookar *et al.*[11], Hedge and Patil *et al.*[17], Singh *et al.*[33], Seyoum *et al.*[28], Tavisha *et al.*[39], Veni *et al.*[41] and Nilamani *et al.*[19].

The estimation of genotypic and phenotypic variance were low for amylose content, days to maturity, panicle length and test weight which indicated that the phenotypic variance in these traits were not the true reflection of genotypic variance. Simultaneously, it was also found that these characters had low genotypic variance coupled with low environmental variance, which pointed towards the non-additive gene action. So selection for these traits might be less effective. Similar results were also reported for one or more character by Singh *et al.*[31], Agrawal[1] and Tavisha[39].

In the present investigation, it was found that genotypic component of variance were higher than their environmental counterpart for all the traits studied indicating least influence of environment in deciding the amount of variance present in the material. Moreover, there was close correspondence between genotypic and phenotypic components of variance for majority of the characters specifying that the phenotypic variability was reliable measure of genotypic variability. The findings of Agrawal *et al.*[1] and Suman *et al.*[37] were similar to the results of the present study.

To compare the different characters with respect to genotypic and phenotypic variability, the variance estimates were expressed as per cent of mean by working out genotypic and phenotypic co-efficient of variation. Since, the latter are unit free estimation, they are useful to judge the relative quantum of variation in different characters of a population.

In the present study, it was clear from the results (table 3) that the estimation of GCV (%) and PCV (%) were comparatively high for non-effective tillers per plot followed by number of unfilled grains per panicle, harvest index, grain yield per plot, number of effective tillers per plot and number of filled grains per panicle indicating the presence of high amount of genotypic and phenotypic variability for these traits in the genetic material. The results coincided with findings of Singh *et al.*[30], Singh *et al.*[31], Hedge and Patil[17], Singh *et al.*[33], Bastia *et al.*[5], Vange, Chandra *et al.*[9] and Seyoum *et al.*[28].

The characters *viz.*, days to 50% flowering, test weight, days to maturity and amylose content expressed low degree of genotypic and phenotypic coefficient of variation. These results were supported by findings of Singh *et al.*[31], Deosarkar *et al.*[12].

A comparison of estimates of GCV (%) with their corresponding PCV (%) for different traits (Table 3) revealed that in general, the GCV (%) were close to the estimates of PCV (%) for all characters except number of filled grains per panicle , panicle length and grain yield per plot were least influenced by environment. The traits did not exhibit close estimates of GCV (%) and PCV (%) in the present study pointing out the fact that it was by environment. This was in accordance with the findings of Anand *et al*.[4].

The coefficient of variation measures the amount of variability present in the characters, but it does not determine the amount of variation that is heritable. The estimates of variability unless interpreted in conjunction with heritability and genetic advance have less utility in drawing conclusion regarding identification of useful characters for selection programme and in prediction of possibilities of yield improvement. The joint interpretation of these parameters would provide a better insight of gain expected through phenotypic selection[7].

The estimation of heritability in broad sense for different traits (Table 3) revealed that the high values were observed for number of non-effective tillers followed by head rice recovery, number of unfilled grains, milling percentage, harvest index, number of filled grains per panicle, number of effective tillers per plot, plant height, days to 50% flowering, grain yield per plot, amylose content and panicle length.

Similar findings for high heritability estimates were also obtained by Singh *et al*.[32] for number of non-effective tillers per plot, Sawant and Patil[27] for head rice recovery, Singh *et al*.[30], Singh *et al*.[32] and Toshimenla and Sapu[40] for milling percentage. Amirthadevarathinam[2] and Singh *et al*.[32] for number of effective tillers per plot, Pathak and Patel[24] for plant height, Deosakar *et al*.[12] for days to 50% flowering.

In the present investigation, the estimates of genetic advance expressed as percentage of mean (% of mean) (Table 3) revealed that high estimation of genetic advance (% of mean) for number of non-effective tillers per plot, number of unfilled grains per panicle, harvest index, number of effective tillers per plot, number of filled grains per panicle and grain yield per plot. This indicated that these characters were governed by additive genes and selection would be rewarding for their improvement.

High estimates of genetic advance (% mean) were reported by Singh *et al*.[30] for number of non-effective tillers per plot, Singh *et al*.[30] and Toshimenla and Sapu[40] for number of unfilled grains per panicle, Singh *et al*.[32]. Amirthadevarathinam[2] and Singh *et al*.[32] for harvest index, Singh *et al*[30], Patil *et al*.[23] and Singh *et al*.[32] for number of effective tillers per plot and by Fukrei *et al*.[16] for grain yield per plot.

The High heritability and moderate genetic advance (% mean) was observed for head rice recovery, milling percentage, plant height, days to 50% flowering and panicle length (Table 3) indicating that these characters were governed by both additive and non-additive gene effect thereby suggesting that reciprocal recurrent selection would be beneficial to improve these traits. Moderate estimates of genetic advance were also observed by Tavisha *et al*.[39], Sawant and Patil[27] for head rice recovery, Nilamani *et al*.[19] for milling percentage, whereas.

In the present investigation, considering the estimation of genetic parameters like GCV %, heritability and genetic advance together, it is evident that filled grains per panicle, number of filled tillers per plot, grains yield per plot and harvest index are most important characters. Selection of these traits in the segregating generations could be more effective for genetic improvement in upland rice. The findings of present study are significant in the improvement of rice as it throws light on the spectrum of variability in the crop. The intercrossing of the genotypes showing variability should result in generating sufficient variability to operate selection in segregating populations. It is likely that from these genotypes, which demonstrated great genetic potential, new upland rice varieties can be synthesized to increase the production substantially.

Table 1: List of genotypes used in this study

Sr. No.	Genotypes	Source	Sr. No.	Genotypes	Pedigree / Source	Sr. No.	Genotypes	Pedigree / Source
1	IET 16803	ARS, AAU, Derol	25	IET 22740	RRRS,NAU,Vyara	49	KIRRALA	RRRS,NAU,Vyara
2	IET 17900	ARS, AAU, Derol	26	IET 22742	RRRS,NAU,Vyara	50	DHANHAR	RRRS,NAU,Vyara
3	IET 18651	ARS, AAU, Derol	27	IET 22743	RRRS,NAU,Vyara	51	NICARU	RRRS,NAU,Vyara
4	IET 18816	ARS, AAU, Derol	28	IET 22744	RRRS,NAU,Vyara	52	LALDHANHAR	RRRS,NAU,Vyara
5	IET 18906	ARS, AAU, Derol	29	IET 22745	RRRS,NAU,Vyara	53	VARALU	RRRS,NAU,Vyara
6	IET 19838	ARS, AAU, Derol	30	IET 22747	RRRS,NAU,Vyara	54	BASKA-1	ARS, AAU, Derol
7	IET 19850	ARS, AAU, Derol	31	IET 22803	ARS, AAU, Derol	55	DDR-100	ARS, AAU, Derol
8	IET 20153	ARS, AAU, Derol	32	IET 22808	ARS, AAU, Derol	56	DDR 101	ARS, AAU, Derol
9	IET 20312	ARS, AAU, Derol	33	IET 22820	ARS, AAU, Derol	57	DDR 119	ARS, AAU, Derol
10	IET 20319	ARS, AAU, Derol	34	IET 22824	RRRS,NAU,Vyara	58	DDR 125	ARS, AAU, Derol
11	IET 20853	RRRS,NAU,Vyara	35	IET 22859	ARS, AAU, Derol	59	DDR 130	ARS, AAU, Derol
12	IET 20860	ARS, AAU, Derol	36	IET 23373	RRRS,NAU,Vyara	60	DDR 134	ARS, AAU, Derol
13	IET 22020	ARS, AAU, Derol	37	IET 23375	RRRS,NAU,Vyara	61	DDR 143	ARS, AAU, Derol
14	IET 22021	ARS, AAU, Derol	38	IET 23376	RRRS,NAU,Vyara	62	ANJALI	RRRS,NAU,Vyara
15	IET 22022	ARS, AAU, Derol	39	IET 23379	RRRS,NAU,Vyara	63	NWGR- 2001	MRRS, AAU, Nawagam
16	IET 22024	RRRS,NAU,Vyara	40	IET 23380	ARS, AAU, Derol	64	NWGR-2011	MRRS, AAU, Nawagam
17	IET 22026	RRRS,NAU,Vyara	41	IET 23385	RRRS,NAU,Vyara	65	RR-363-4	RRRS,NAU,Vyara
18	IET 22032	RRRS,NAU,Vyara	42	IET 24061	ARS, AAU, Derol	66	IR 28	RRRS,NAU,Vyara
19	IET 22034	RRRS,NAU,Vyara	43	IET 24065	ARS, AAU, Derol	67	GR-5(C)	RRRS,NAU,Vyara
20	IET 22035	ARS, AAU, Derol	44	IET 24069	ARS, AAU, Derol	68	GR-8 (C)	RRRS,NAU,Vyara
21	IET 22037	RRRS,NAU,Vyara	45	IET 24070	ARS, AAU, Derol	69	GR-9 (C)	RRRS,NAU,Vyara
22	IET 22038	ARS, AAU, Derol	46	IET 24071	ARS, AAU, Derol	70	ASHOKA200(C)	ARS, AAU, Derol
23	IET 22051	RRRS,NAU,Vyara	47	VAKVEL	RRRS,NAU,Vyara	71	AAUDR-1 (C)	ARS, AAU, Derol
24	IET 22739	RRRS,NAU,Vyara	48	MALVE	RRRS,NAU,Vyara	72	PURNA (C)	RRRS,NAU,Vyara

Table 2: Analysis of variance of 14 quality characters

Source of Variation	Replication	Treatment	Error
d. f.	2	71	142
Days to 50% flowering	0.81	201.12**	6.36
Days to maturity	14.37	66.41**	8.1
Panicle length(cm)	3.67	27.69**	2.88
Plant height(cm)	47.62	931.89**	25.56
Test weight(g)	8.12	18.41**	2.13
Number ofeffective tillers per plot	2.46	518.30**	10.65
Number of non-effective tillersper plot	2.09	519.59**	1.11
Number of filled grainsper panicle	8.36	2486.61**	34.93
Number of unfilled grainsper panicle	10.59	423.68**	3.16
Harvestindex (g)	6.59	377.14**	4.69
MillingPercent(%)	1.44	292.84**	3.1
Head ricerecovery (%)	3.58	249.28**	1.5
Amylose content(%)	1.19	3.80**	0.3
Grainyield per plot (g)	266.09	2354.75**	103.4

Table 3: Estimation of population mean, range and genetic parameters for 14 quality traits in rice genotypes

Parameters	Days to 50% flowering	Days to maturity	Panicle length (cm)	Plant height (cm)	Test weight (g)	Number of effective tillers per plot	Number of non-effective tillers per plot	Number of filled grains per panicle	Number of unfilled grains per panicle	Harvest index (g)	Milling percent (%)	Head rice recovery (%)	Amylose content (%)	Grain yield per plot (g)
Mean	64.55	101.01	21.70	111.89	22.67	30.42	13.54	70.82	20.68	21.18	63.61	42.10	22.58	58.10
Range	51.00 to 85.67	90.00 to 115.33	13.67 to 27.33	70.00 to 145.67	16.67 to 28.33	7.33 to 59.67	2.67 to 62.00	21.67 to 153.00	7.20 to 20.07	6.27 to 59.28	31.00 to 78.00	23.67 to 59.37	20.00 to 25.00	7.00 to 153.60
σ^2g	64.92	19.43	8.270	302.10	5.42	169.21	172.82	817.20	140.17	124.15	96.58	82.59	1.16	750.45
σ^2p	71.28	27.54	11.15	327.60	7.56	179.86	173.94	852.16	143.33	128.84	99.68	84.09	1.47	853.85
σ^2e	6.36	8.10	2.88	25.56	2.13	10.65	1.11	34.93	3.15	4.69	3.10	1.50	0.30	103.40
GCV%	12.48	4.36	13.25	15.53	10.27	42.75	97.08	40.36	57.25	52.58	15.44	21.58	4.78	47.14
PCV%	13.07	5.19	15.38	16.17	12.13	44.07	97.39	41.21	57.89	53.57	15.69	21.77	5.37	49.20
Heritability (%)	91.07	70.57	74.16	92.20	71.73	94.08	99.36	95.59	97.80	96.36	96.89	98.21	79.17	87.89
Genetic Advance (%Mean)	24.53	7.55	23.50	30.75	17.92	85.42	199.34	81.42	116.62	106.33	31.32	44.06	8.76	91.04

Where, σ^2g, σ^2p and σ^2e are the genotypic, phenotypic and environmental variance, respectively. GCV% and PCV% are genotypic and phenotypic coefficient of variation, respectively. GA (% of mean) is genetic advanced expressed as per cent of mean.

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