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RESEARCH PAPER

Variability, heritability and genetic advance in rice (*Oryza sativa* L.)

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Genetic parameters for yield and its correspondent characters in rice were estimated from a trial with two CMS, twenty testers and forty hybridscross evaluated for ten characters related to yield. The highest GCV was recorded for grain yield plant^{-1}. High heritability and the low genetic advance were recorded for grain yield plant^{-1}, spikelet fertility, plant height, harvest index, seedling height, flag leaf area, panicle bearing tillers plant^{-1}, test weight and panicle length suggesting apredominance of non-additive gene action in the inheritance of these traits.

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

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INTRODUCTION

Rice (*Oryza sativa* L.) is a major food crop in the world. At present, rice is the major source of nutrition for about 40 per cent of world's population. In India, about 65 per cent of the population has rice as a major constituent in the diet. More over rice consumers are increasing every year at the rate of 1.8 per cent and estimates reveal that the production of rice should be doubled by 2025 to meet our Indian requirements. This, in turn, elucidates that we must reorient our research towards yield improvement. Genetic variability helps to choose desirable genotypes. The genetic variation and genetic gain obtained by selection are studied by predicting the heritability and genetic advance. Genetic parameters such as genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

RESEARCH METHODOLOGY

The experimental material for this investigation comprised of 2 CMS lines *viz*., IR 68897 A and IR 58025 A possessing "wild abortive" (WA) cytoplasm as lines (females), 20 diverse rice varieties/genotypes as testers (males) and 40 crosses obtained through crossing in a "line × tester" mating design (Kempthorne, 1957). The resulting set of 40 F_1's along with their 22 parents were evaluated in a Randomized Complete Block Design with three replications during *Kharif*, 2010. The seeds of each entry were sown on 21st June 2010 in separate plots and 30 days (20th July 2010) old seedlings were transplanted single seedling per hill in single row plots of 3 m length with inter- and intra- row spacing of 20 cm and 15 cm, respectively. Observations were recorded for ten characters *viz.*,$^{-1}$, days to 50 per cent flowering, flag leaf area, plant height, panicle bearing tillers plant^{-1}, panicle length, spikelets panicle^{-1}, grain yield plant^{-1}, test weight, biological yield plant^{-1}and harvest index. Genotypic, phenotypic and environmental variance, heritability and genetic advance were estimated for all ten characters.

RESEARCH FINDINGS AND ANALYSIS

Variability, heritability and genetic advance were estimated as described here.

Variability :

Present finding showed the higher phenotypic co-efficient of variation (PCV) than the genotypic co-efficient of variation (GCV) for all the characters. PCV was highest for grain yield plant^{-1} followed by biological yield plant^{-1}, harvest index, panicle bearing tillers plant^{-1}, spikelet panicle^{-1}, flag leaf area, test weight, panicle length, plant height and but it was lowest days to 50 per cent flowering. The highest GCV was recorded for grain yield plant^{-1} (45.66%) and lowest for days to 50 per cent flowering (5.16%), indicating that highest variability of genotypes are found for the trait, grain yield plant^{-1} and thus, selection would be more effective than days to 50 per cent flowering (Table 1). Traits like spikelet panicle^{-1} (18.73%) and spikelet fertility (14.34%) are showing moderate PCV, indicating it is less affected by

Table 1 : Analysis of variance including parent and crosses for 13 characters in rice

Source of variation	Treatments	Parent (P)	P vs C	Crosses (C)	Error
DF	82	22	1	59	164
Days to 50 per cent flowering	63.89470**	74.05534**	74.57029**	59.92505**	9.11906
Flag leaf area (cm^2)	58.21665**	29.46020**	166.66999**	67.10120**	1.38531
Plant height (cm)	332.16561**	296.37668**	360.26262**	345.03441**	2.22651
Panicle bearing tillers per plant	30.91970**	46.28136**	219.45789**	21.99606**	0.92006
Panicle length (cm)	21.22930**	20.87312**	63.13962**	20.65176**	1.10053
Spikelets per panicle	3619.19725**	3080.81021**	79434.13423**	2534.95281**	223.63900
Test weight (g)	26.43394**	23.929.80**	1.30959	27.79352**	0.35839
Biological yield per plant (g)	6208.78878**	1749.81149**	123148.89195**	5889.42263**	32.28695
Harvest-index (%)	286.97919**	263.16995**	68.62616**	299.55812**	8.97803
Grain yield per plant (g)	1020.17782**	358.40551**	11471.26994**	1089.80323**	18.76614

** indicate significance of value at P=0.01

Table 2: Estimates of phenotypic (PCV) and genotypic (GCV) co-efficient of variation, heritability broad (h^2_{bs}) and narrow sense (h^2_{ns}), additive (σ^2_A) and dominance (σ^2_D) genetic components of variance, degree of dominance (DD), predictability ratio, genetic advance (GA), genetic advance as per cent of mean (GM%) for 13 characters in rice

Characters	CV (%)		Heritability (%)		Genetic components of variance		DD	GA	GM (%)
	PCV	GCV	h^2_{bs}	h^2_{ns}	$\pm^2_A$	$\pm^2_D$			
Days to 50 per cent flowering	5.167	4.220	66.69	22.84	5.354	15.051	1.677	7.188	7.10
Flag leaf area (cm^2)	13.534	13.064	93.19	58.70	14.883	10.285	0.831	8.655	25.98
Plant height (cm)	10.640	10.534	98.02	76.69	144.802	43.470	0.548	21.388	21.48
Panicle bearing tillers per plant	24.453	23.397	91.55	53.20	2.494	1.886	0.870	6.233	46.12
Panicle length (cm)	11.053	10.245	85.91	46.81	3.335	3.424	1.013	4.946	19.56
Spikelets per panicle	18.738	17.121	83.48	19.79	172.394	624.227	1.903	63.321	32.23
Test weight (g)	13.343	13.076	96.04	@	-0.721	9.619	3.653	5.952	26.40
Biological yield per plant (g)	36.967	36.680	98.46	37.38	922.160	1534.241	1.290	92.747	74.98
Harvest-index (%)	29.635	28.296	91.17	21.57	23.849	84.025	1.877	18.934	55.66
Grain yield per plant (g)	45.668	44.436	94.68	@	-3.437	288.757	9.166	36.621	89.07

@ Negative estimates

anenvironmental factor, may focus to enhance grain yield. Similar results were observed by Ghara *et al.* (2014) and Chakraborty and Chaturvedi (2014).

Heritability in narrow sense:

Hanson (1963) while reviewing the importance of heritability in plants pointed out that this parameter is influenced by the method of estimation, generation of hybrid, the experimental material used and the environment. Low heritability (<10%) was noted for a number of test weight and grain yield plant^{-1} indicating there by control of non-additive gene action for these traits. Heterosis breeding can improve these traits in F_1. Days to 50 per cent flowering^{-1}, spikelets panicle^{-1}, harvest index showed moderate heritability whereas flag leaf area, plant height, panicle bearing tillers plant^{1}, panicle length and biological yield plant^{-1} shown high heritability indicating that improvement can be done with phenotypic selection. Above findings were also confirmed from the estimates of variance due to an additive genetic component in the present study. These results are in conformity with the finding of Ketan and Sarkar (2014) and Allam *et al.* (2015).

Broad sense heritability and genetic advance:

Heritability of a character is important to the breeder since it indicates the possibility and extent to which improvement is possible through selection (Robinson *et al.*,1949). It also indicates towards selection pressure applied for a trait during selection because it measures the genetic relationship between parent and their progeny hence, widely used in determining the degree to which a character may be parent transmitted from to offspring. However, high heritability alone is not enough to make an efficient selection in advance generation unless accompanied by the substantial amount of genetic advance, the heritability in combination with the intensity of selection and amount of variability present in the population (Table 2).

In the present study, the high heritability (h^2_b) coupled with high genetic advance was recorded for biological yield plant^{-1}, followed by spikelets panicle^{-1}, hence, these traits were predominantly under the control of additive gene action. High heritability and the low genetic advance were recorded for grain yield plant^{-1}, plant height, harvest index, flag leaf area, panicle bearing tillers plant^{-1}, test weight and panicle length suggesting a predominance of non-additive gene action in the inheritance of these traits. Days to 50 per cent flowering and number of leaves seedling^{-1} had low heritability and low genetic advance suggesting character is highly influenced by environmental effects and selection would be ineffective. The findings are supported by Roy *et al.* (2001); Babu *et al.* (2006); Bisne *et al.* (2009); Tuwar *et al.* (2013); Shiva Prasad *et al.* (2013); Rai *et al.* (2014); Rajput *et al.* (2014) Ketan and Sarkar (2014); Allam *et al.* (2015) and Lingaiah (2015).

Genetic components of variance and gene action:

The relative magnitude of variance components revealed that SCA variance was greater than the GCA variance for all the character except flag leaf area, plant height, panicle bearing tillers plant^{-1}. The degree of dominance was higher than unity (>1) except flag leaf area, plant height, panicle bearing tillers plant^{-1} and predictability ratio was low (<1) for all the characters. Dominance variance was greater than additive variance for each character except flag leaf area, plant height, panicle bearing tillers plant^{-1}. These findings showed that dominance gene action had agreater role in the inheritance of these traits and fully supported by Munhat *et al.* (2000), Thirumeni and Subramanian (2000) and Mahmood *et al.* (2002) studied under salinity and also found yield traits was governed by non-additive gene action.

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