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RESEARCH **P**APER

Genetic variability analysis for yield and its component traits in rice (*Oryza sativa* L.)

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A wide range of phenotypic, genotypic and environmental co-efficient of variation was observed for most of the characters. Maximum phenotypic and genotypic co-efficient of variation was recorded for panicle bearing tillers per plant followed by grain yield, test weight, number of total tillers per plant, spikelets fertility percentage, plant height, total spikelets per panicle and days to 50 per cent flowering. The range of broad sense heritability (h²b) was obtained from (72.82%) panicle length to (99.64%) spikelets fertility percentage. The genetic advance in absolute terms hanged from 2.87 for panicle length to 34.25 for spikelets fertility percentage followed by panicle length.

Key words : Heritability, Genetic advance, Co-efficient of variation, Rice

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INTRODUCTION

Rice is the most important food crop of the world's. It is warm season crop grown broadly south eastern Asia, Korea, account for 90 per cent of world rice production. In India the main state Andhra Pradesh, Karnataka, Tamil Nadu, Maharashtra, Assam, Oddisa, Bengal, Bihar, Uttar Pradesh, Madhya Pradesh and Haryana where the rice cultivated in large scale. The rice belongs to family Gramineae (Poaceae) having chromosome (2n=2 x = 24).

Identification of hybrid rice breeding as thrust area for continued and enhance support by the ICAR an several state government reflected how strong a conviction of the various sources have on the potential of the hybrid rice technology. New heterotic hybrid in the pipeline combing consumer preferred quality and resistance to pest and diseases, progress being made towards development of high yielding India/Japonica hybrids availability of parental line for extending the technology to rain-fed low -lands. Genetic variability is pre requisite for selection of superior genotype over parental population in any crop. Heritability provide the knowledge for making the appropriate strategy for breeding programme and also helps for selection.

RESEARCH METHODOLOGY

Twenty four crosses, their parents three female, eight male line and one standard variety were used as a experimental material for study of present investigation in the Farm of Genetics and Plant Breeding N.D.U.A. and T. Kumarganj, Faizabad during *Kharif* 1997: to analysis genetic variability. The experimental material comprised of population of 24F1^s, their parents mainly eight male lines NDRK 5026, NDRK5023, NDRK 5031, NDRK 5032, Swarna, MT 20-1-1, NDR 507, NDRK 5027 and three CMS lines *viz.*, IR 58025A PMS 8 A and PMS 1DA and one standard variety Sarjoo 52 were sown in 20th June 1997 in nursery bed treating with 0.2 per cent Bavistin solution for about a minute and then washed in water. After 25 days single seedling per hill were transplanted with 20 cm row to row and 15 cm plant to plant spacing having 4 rows of 2.5 meter long for each test entry in Randomized Block Design with three replications. The crop was maintained properly at 120:60:60 kg/ha NPK level and zinc sulphate at the rate 25 kg/ha as usual half of the nitrogen and entire quantities of phosphorus potash and zinc sulphate was applied as basal dose and two split application remaining 60kg/ha nitrogen was at tillering and panicle initiation stage. The experiment was grown under irrigated condition and all intercultural and plant protection measures were applied for raising good crop. Analysis of variability carried out by mean value from the different characters viz., seedling growth (cm), days to 50 per cent flowering, plant height (cm), total number of tillers/plant, panicle bearing tillers, panicle length (cm), spikelets per panicle, spikelets fertility percentage test weight (g) and grain yield (g) for which five plant were randomly selected from each replication.

Research Findings and Analysis

The analysis of variance for 36 entries (twenty four hybrids + eleven parental lines + one standard variety) was done for quantitative characters viz., seedling growth, days to 50 per cent flowering plant height, number of total tillers per plant, panicle bearing tillers per plant, panicle length, total spikelets per panicle, spikelets fertility percentage test weight and grain yield per plant. The mean square value for treatments, parents, males, females, females vs males hybrids and parents vs hybrid are presented in Table 1. Finding reveals that variances due to treatment parents, male hybrids parents vs hybrid were statistically significant among them-selves while variances due to females were significant different for all the characters except number of tillers per plant, spikelets fertility percentage, test weight and grain yield per plant due to using. CMS lines as female parents and variances due to females vs males for panicle length. More-ever significant interaction effects due to parents vs hybrids and males vs females for all the characters indicating presence of over-all significant heterotic effects. Replication difference between genotypes were non-significant for all the characters except seedling growth and grain yield per plant. The proportion of genetic variance to total variance in terms of heritability and genetic advance were calculated in absolute terms as well as per cent mean for ten characters. The results on

Table 1: Analysis of variance for parents and their hybrids in rice												
Source of variation	d.f	Seedling growth	Days to 50% flowering	Plant height (cm)	Number of total tillers/ plant	Panicle bearing tillers/ plant	Panicle length (cm)	Total spikelet/ panicle	Spikelet fertility %	Test weight in (g)	Grain yield/ Plant (g)	
Replications	2	7.89**	0.12	1.00	2.48	0.45	0.37	0.77	4.49	0.57	7.12**	
Treatments	35	2.84**	66.65	80.24**	33.75**	68.28**	9.04**	3.87**	652.56**	149.21**	288.55**	
Parents	10	26.03**	142.6**	435.11**	18.68**	34.99**	12.40**	5241.81**	5303.46**	365.04**	316.65**	
Hybrids	23	58.94**	96.74**	315.14**	32.24**	31.48**	12.79**	3984.60**	166.61**	9.08**	555.89**	
Error	70	124.00	1.64	4.11	0.99	0.55	1.37	15.97	2.82	0.94	1.67	

** indicate significance of value at P=0.01

Table 2 : Mean co-efficient of variation, heritability, broad sense, genetic advance for 10 characters										
Sr No	Characters	General mean	Co-efficient of variation			Heritability	Genetic	Genetic advance		
51. 10.	Characters	General mean	GEV	PCV	ECV	broad sense	advance	in per cent mean		
1.	Seedling growth (cm)	28.12 ± 0.78	10.75	11.32	3.55	90.14	5.89	20.95		
2.	Days to 50% flowering	102.67 ± 0.91	4.55	4.65	0.97	95.62	9.37	9.13		
3.	Plant height (cm)	84.46 ± 1.05	6.08	6.19	1.18	96.35	10.36	12.27		
4.	No. of total tillers/plant	11.94 ± 0.73	27.66	28.90	8.39	91.60	6.48	54.33		
5.	Panicle bearing tillers plant	11.28 ± 0.64	41.97	42.90	8.86	95.73	9.53	84.51		
6.	Panicle length (cm)	27.77 ± 0.67	6.60	7.74	4.03	72.82	2.87	11.61		
7.	Total spikelets/panicle	184.47 ± 1.47	5.49	5.51	0.54	99.06	20.76	11.25		
8.	spikelets fertility %	75.81 ± 0.96	22.00	22.04	1.31	99.64	34.25	45.17		
9.	Test weight (g)	21.02 ± 0.73	35.62	35.93	4.75	98.24	15.26	72.59		
10.	Grain yield (g)	26.10 ± 0.084	37.51	37.70	3.83	98.96	19.97	75.51		



all these parameters are given in Table 2. PCV of variation were higher than GCV and ECV for all the characters were studied. It was highest for panicle bearing tillers followed by grain yield, test weight number of total tillers per plant, spikets fertility per cent seedling growth, panicle length, plant height, total spikelets per pinicle and days to 50 per cent flowering. Higher phenotypic co-efficient of variation was abserved for panicle bearing tillers per plant followed by grain yield, test weight, number of total tiller per plant, spikelet fertility per cent, seedling growth, panicle length, plant height, total spikelets per panicle and days to 50 per cent flowering. These results are also in confinity with the finding of Chandra et al. (2009); Singh (2011); Bhadru et al. (2012) and Dhanwani et al. (2013) for grain yield per plant and number of grain per panicle. The extent of heritability of the various attributes studied was calculated in broad sense. The value obtained have been presented in Table 2. The range of broad sense heritability obtained from panicle length (72.82%) to total spikelets fertility per cent (99.64%). The higher value of heritability were observed for total spikelets fertility per cent, total spikelets per panicle, grain yield, test weight, plant height, panicle bearing tillers per plant, days to 50 per cent flowering, total number of tillers per plant, seedling growth and panicle length.

The genetic advance in absolute terms ranged from (2.87) for panicle length to (34.25) for spikelets fertility percentage. High genetic advance was observed for spikelets fertility percentage followed by panicle length, grain yield, test weight, plant height, panicle bearing tillers per plant, days to 50 per cent flowering, total number of tillers per plant, seedling growth and panicle length. The expected genetic advance expressed as per cent of mean ranged from 9.13 to 84.51 per cent moderate value of genetic advance was observed for panicle bearing tillers per plant followed by grain yield, test weight, total number of tillers per plant, spikelets fertility percentage seedling growth, days to 50 per cent flowering showed low expected genetic advance. High magnitude of variability in population provide the opportunity of selection to evolve a variety having desirable characters. Phenotypic coefficients of variation were higher than genotypic and environmental co-efficients of variations for all characters. Genotypic co-efficients of variation were slightly lower than corresponding phenotypic co-efficients of variation for all characters. Environmental co-efficient of variation was highest for panicle bearing tillers followed by total tillers per plant. It was lower for total spikelets per panicle. High co-efficient of variation indicate that the traits under study can be improved through selection. Low value indicate the need to create variability either by hybridization or mutation followed by selection. Knowledge of heritability of a character is important to breeder since it indicated the possibility and extent to which improvement is possible to selection.

High heritability alone is not enough to make efficient selection in advance generation, unless accomplished by substantial amount of genetic advance. Heritability in combination with intensity of selection and amount of variability present in population influence the gain to be obtained from selection (Robinson *et al.*, 1949).

The genetic advance is yet another important selection parameter which is although not independent and represent expected genetic advance (Burtons, 1952). Without genetic advance the estimates of heritability would not be practical importance in selection based on phenotypic appearance (Johnson *et al.*, 1955).

Research Methodology

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