



ESTIMATION OF GENETIC PARAMETERS OF VARIABILITY FOR YIELD AND ITS ATTRIBUTING TRAITS IN PARENTAL LINES OF HYBRID RICE

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Abstract

Genetic variability is prerequisite for any crop improvement program as it helps breeders in the selection. This study was conducted with the aim of evaluating genetic parameters in 125 parental lines of hybrid rice. High genotypic and phenotypic coefficient of variation exhibited by unfilled spikelets panicle⁻¹, filled spikelets panicle⁻¹, seed yield plant⁻¹, panicle weight plant⁻¹, total spikelets panicle⁻¹, effective tillers plant⁻¹, tillers plant⁻¹, biological yield plant⁻¹, spikelet fertility, spikelet density, harvest index, flag leaf width and culm length. High heritability accompanied with high genetic advance showed by tillers plant⁻¹, plant height, culm length, flag leaf length, flag leaf width, biological yield plant⁻¹, panicle weight plant⁻¹, seed yield plant⁻¹, harvest index, panicle index, spikelet density, total spikelets panicle⁻¹, filled spikelets panicle⁻¹, unfilled spikelets panicle⁻¹ and spikelet fertility. This indicates that these characters governed by additive gene action and selection for these traits would be effective.

Key words : Parental lines, heritability, PCV, GCV.

Introduction

Rice occupies a pivotal place in Indian agriculture, as it is the staple food for two thirds of the population, providing 43% of calorific requirement and 20-25% of agricultural income. But, there is still a large gap between production and demand. To meet this challenge, there is need to develop rice varieties with higher yield potential and greater stability (Khush, 2006). Expansion of hybrid rice cultivation area may be an effective and economic way to meet the future rice demands of growing population. Hybrid rice technology is considered as one of the promising, practical, sustainable and eco-friendly options to break the yield ceiling in rice (Sheeba *et al.*, 2009). Hybrid rice has clearly shown a yield advantage of 1-1.5 tones ha⁻¹ (20 to 30%) over conventionally bred modern varieties (Virmani *et al.*, 2003). Production of rice hybrids using a CMS system is based on cytoplasmic male sterility and fertility restoration systems; hence it involves three lines of male sterile (A), maintainer (B) and restorer (R). Recent breakthrough in tropical hybrid rice technology provides an economically viable option for raising the grain yield and heterosis for economically important traits that enhance abiotic and biotic stress

resistance and sustainable growth in production and productivity.

Genetic variability is of great interest to plant breeders as they play a vital role in forming a successful breeding programme. Knowledge of the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its component is essential for effecting genetic improvement. A critical analysis of genetic variability is a pre-requisite for initiating any crop improvement programme and for adopting the appropriate selection techniques. The essential feature is the partitioning of total variation into phenotypic, genotypic and environmental components and determines the magnitude of these components for various traits which is a measure of the type of gene action, and thus helps in deciding a breeding procedure for the genetic improvement of a trait (Singh and Narayanan, 1993). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimate alone. This help to the breeders in determining traits having better correspondence between phenotypes and genotypes and are expected to give better response to selection.

The present study was carried out to assess the extent

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of variability, heritability, genetic advance among one hundred and twenty five parental lines, so that efforts can be utilized to develop high yielding rice varieties.

Materials and Methods

One hundred twenty five parental lines (85 restorer lines, 30 maintainer lines and 15 A lines) comprise the basic material for study. These parental lines were evaluated in randomized complete block design with 4 m length of 20 rows each with 20 × 15 cm spacing during kharif 2012 and 2013 with three replications at Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV, Jabalpur. Observations were recorded on five plants at random in each replication for the characters tillers plant⁻¹ (TPP), effective tillers plant⁻¹ (ETPP), plant height (PH), culm length (CL), panicle

length (PL), flag leaf length (FLL), flag leaf width (FLW), biological yield panicle⁻¹ (BYPP), panicle weight plant⁻¹ (PWPP), seed yield plant⁻¹ (SYPP), harvest index (HI), panicle index (PI), spikelet density (SD), total spikelets panicle⁻¹ (TSPP), filled spikelets panicle⁻¹ (FSPP), unfilled spikelets panicle⁻¹ (UFSPP), spikelet fertility (SF), 1000 seed weight (1000 SW), seed length (SL), seed width (SW), length breadth ratio (LBR), hulling percent (HP), milling percent (MP), head rice recovery (HRR), decorticated seed length (DSL), decorticated seed width (DSW) and length breadth ratio of decorticated seed (DLBR). However for phenological data *viz.*, days to heading (DH), days to fifty percent flowering (DFF) and days to maturity (DM) were recorded on whole plot basis. Data obtained from the two years were subjected to pooled analysis of variance, heritability (broad sense) and

Table 1 : Genetic parameters for yield attributing traits in parental lines of hybrid rice.

Characters	Mean	Range		Coefficient of variation		Heritability	Genetic advance	Genetic advance as % of Mean
		Max.	Min.	GCV	PCV			
DH	100.68	118.50	79.17	7.93	9.02	77.40	14.48	14.38
DFF	104.84	122.50	83.83	7.59	8.63	77.50	14.45	13.78
DM	147.43	164.00	126.17	5.41	6.13	77.70	14.48	9.82
TPP	8.22	15.07	4.55	29.58	35.34	70.10	4.20	51.02
ETPP	7.57	14.38	4.28	30.39	36.40	69.70	3.96	52.26
PH	111.76	147.08	68.19	17.96	19.33	86.40	38.43	34.38
CL	85.09	118.03	44.86	21.75	23.52	85.50	35.23	41.43
PL	26.65	32.42	22.00	7.83	10.59	54.60	3.17	11.91
FLL	38.55	56.56	26.50	16.57	19.64	71.20	11.10	28.80
FLW	1.86	2.83	1.16	23.34	25.35	84.80	0.82	44.28
BY	69.68	114.10	23.21	29.28	33.57	76.10	36.67	52.62
PWPP	33.71	57.05	6.83	34.48	38.58	79.80	21.39	63.46
SYPP	26.86	50.63	2.08	41.13	46.77	77.30	20.02	74.52
HI	35.98	45.17	8.44	25.74	27.34	88.60	17.96	49.92
PI	74.77	88.73	29.59	18.16	19.82	83.90	25.62	34.27
SD	968.74	1577.96	452.80	28.68	33.42	73.60	491.12	50.70
TSPP	259.85	429.39	106.22	32.26	35.76	81.40	155.79	59.96
FSPP	195.24	331.33	13.19	43.36	47.21	84.30	160.14	82.02
UFSPP	64.46	166.44	11.65	53.08	61.38	74.80	60.94	94.54
SF	72.32	94.95	8.84	29.52	31.20	89.50	41.61	57.53
SL	9.65	11.54	8.20	7.63	10.45	53.30	1.11	11.48
SW	2.74	3.11	2.13	7.80	11.09	49.50	0.31	11.31
LBR	3.58	4.74	2.79	12.72	18.28	48.40	0.65	18.22
1000SW	25.25	33.40	15.02	14.45	17.38	69.10	6.25	24.75
HP	64.19	75.72	47.68	7.79	11.69	44.40	6.86	10.68
MP	58.75	70.88	44.59	8.11	12.53	41.90	6.35	10.81
HRR	42.22	61.12	30.75	11.86	19.50	37.00	6.27	14.85
DSL	6.69	7.92	5.30	7.07	10.80	42.90	0.64	9.53
DSW	2.09	2.61	1.64	8.91	12.26	52.90	0.28	13.36
DLBR	3.25	4.51	2.27	12.34	17.68	48.80	0.57	17.75

Table 2 : Analysis of variance for yield attributing traits in parental line of hybrid rice.

Source of variation	d.f	Mean Sum of Square															
		DH	DFF	DM	TPP	ETPP	PH	CL	PL	FLL	FLW	BY	PWPP	SYPP	HI	PI	SD
Replication	2	18.60711	0.9453	0.5493	0.6695	0.8124	1.1863	0.6053	0.4152	0.7863	0.0022	35.4374	10.1378	7.0649	0.5502	5.9396	825.6773
Genotypes	124	401.4870**	399.2012**	399.6405**	38.0524**	34.0746**	2481.1383**	2114.0907**	29.7246**	261.3476**	1.1598**	2629.1004**	844.4839**	768.3749**	525.6657**	1141.3716**	490789.5398**
Error	620	18.6071	18.3788	18.2114	2.5275	2.3025	63.5387	58.1558	3.6184	16.5065	0.0337	130.8584	34.1106	35.7650	11.0002	35.3339	27639.9298

Source of variation	d.f	Mean Sum of Square											DLBR	
		TSPP	FSPP	UFSP	SF	SL	SW	LBR	1000SW	HP	MP	HRR		DSL
Replication	2	1.6992	3.5895	13.2078	1.9382	0.0076	0.0012	0.0043	2.5278	5.6806	0.4927	0.0152	0.0014	0.0008
Genotypes	124	43769.4328**	44328.0960**	7419.4500**	2788.0043**	3.7302**	0.3207**	1.4647**	181.2923**	167.6449**	193.1230**	1.6408**	0.2399**	1.1356**
Error	620	1606.3679	1331.4403	395.1952	53.3164	0.4751	0.0466	0.2212	31.3511	31.5098	42.7300	0.2984	0.0310	0.1693

** Significant at 1% level of significance

*Significant at 5% level of significance

genetic advance.

Results and Discussion

In the present investigation, analysis of variance showed highly significant differences between parental lines for the characters studied indicated the presence of considerable genetic variation in the experimental material. This was in conformity with the findings of Ganesan *et al.* (1995) for seed length, seed yield plant⁻¹, panicle length, total spikelets panicle⁻¹ and seed width, Singh *et al.* (1999) for plant height, Chetia *et al.* (2000) for spikelet fertility and panicle length and Sahidullah *et al.* (2009) for all the characters.

The means, phenotypic and genotypic coefficients of variation and heritability estimates are presented in table 2. A wide range of variability was observed for all the traits. Phenotypic coefficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all the traits studied, indicating that they all interacted with the environment with the same degree. The difference between PCV and GCV estimates were relatively low for all the traits except for decorticated seed width, milling percent, panicle length, seed width, hulling percent, seed length and decorticated seed length indicating less environmental influence on these traits.

The highest magnitude of genotypic and phenotypic variance was registered for unfilled spikelets panicle⁻¹, filled spikelets panicle⁻¹, seed yield plant⁻¹, panicle weight plant⁻¹, total spikelets panicle⁻¹, effective tillers plant⁻¹, tillers plant⁻¹, biological yield plant⁻¹, spikelet fertility, spikelet density, harvest index, flag leaf width and culm length, therefore, simple selection can be practised for further improvement of these characters. This was in confirmatory with the findings of Sabu *et al.* (2009) and Laxuman *et al.* (2010) for unfilled spikelets panicle⁻¹, Sabu *et al.* (2009) and Kiani (2013) for filled spikelets panicle⁻¹ and seed yield plant⁻¹, Sabu *et al.* (2009) and Kiani (2012) for panicle weight plant⁻¹, total spikelets panicle⁻¹, effective tillers plant⁻¹, biological yield plant⁻¹ and harvest index. Contrary to this, days to heading, days to fifty percent flowering and days to maturity expressed low GCV and PCV and decorticated seed width, milling percent, panicle length, seed width, hulling percent, seed length and decorticated seed length exhibited low GCV. This was in agreement with the findings of Padmaja *et al.* (2008), Laxuman *et al.* (2010) for days to fifty per cent flowering, Bekele *et al.* (2013) for days to maturity, Kiani (2013) for seed length, Padmaja *et al.* (2008), Sabu *et al.* (2009), Kiani (2013) for panicle length. However, other characters showed moderate PCV and GCV estimates.

High heritability accompanied with high genetic advance showed by tillers plant⁻¹, plant height, culm length, flag leaf length, flag leaf width, biological yield plant⁻¹, panicle weight plant⁻¹, seed yield plant⁻¹, harvest index, panicle index, spikelet density, total spikelets panicle⁻¹, filled spikelets panicle⁻¹, unfilled spikelets panicle⁻¹ and spikelet fertility. This was in consonance with the findings of Chandra *et al.* (2009) and Bekele *et al.* (2013) for plant height, Bekele *et al.* (2013) for biological yield plant⁻¹ and panicle weight plant⁻¹, Subbaiah *et al.* (2011) and Bekele *et al.* (2013) for seed yield plant⁻¹, Bekele *et al.* (2013) and Kiani (2013) for harvest index, Subbaiah *et al.* (2011), Bekele *et al.* (2013) and Kiani (2013) for total spikelets panicle⁻¹, Ravindra Babu *et al.* (2012), Bekele *et al.* (2013) and Kiani (2013) for filled spikelets panicle⁻¹, Ravindra Babu *et al.* (2012) for unfilled spikelets panicle⁻¹. High heritability coupled with high genetic advance indicating that most likely the heritability is due to additive gene effects and selection may be effective for these characters based on phenotypic values in order to obtain maximum genetic gain for yield improvement in rice by simple selection process.

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