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Heritability and Genetic Advance Estimation From Parental Lines of Hybrid Rice

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KEYWORDS : Heritability, Genetic Advance, parental lines

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ABSTRACT

Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. The estimates of heritability, coefficients of variability and genetic advance computed for 31 yield contributing traits. High GCV and PCV reported for the traits Unfilled spikelets panicle-1, filled spikelets panicle-1, seed yield plant-1, pollen viability, total spikelets panicle-1, effective tillers plant-1, panicle weight plant-1, tillers plant-1, spikelet density, spikelet fertility, biological yield plant-1, harvest index, flag leaf length and culm length. The traits viz., unfilled spikelets panicle-1, filled spikelets panicle-1, seed yield plant-1, panicle weight plant-1, total spikelets panicle-1, effective tillers plant-1, pollen viability, spikelet density, tillers plant-1, spikelet fertility, harvest index, biological yield plant-1, flag leaf width, panicle index, length breadth ratio, head rice recovery, 1000 seed weight, length breadth ratio of decorticated seed, culm length, plant height, flag leaf length, panicle length, decorticated seed width, milling percent, hulling percent, decorticated seed length, seed width and seed length had high heritability accompanied with high genetic advance indicating lesser environmental influence and were under the control of additive gene effect.

Introduction

Rice (*Oryza sativa L.*), a member of poaceae family, is one of the world's most important food crops, feeding more than half of the world's population. It is the most diversified crop due to its adaptation to wide range of geographical and climatic regimes. According to estimates from the Directorate of Economics and Statistics, 2013 the average Indian rice productivity was 1907 kg ha^{-1} with a production of 128.20 million tones from 67.22 million hectares. The population, particularly in the rice consuming countries is increasing at a faster rate. By the year 2025, about 756 million tonnes of paddy, which is 70 per cent, more than the current production, will be needed to meet the growing demand (Tuong & Bowman, 2002). The dire need of increasing rice productivity and production encourage rice scientist to develop and disseminate hybrid rice technology in the tropics. To meet this challenge, hybrid rice technology considered as one of the promising, practical, sustainable and eco friendly option to break the yield ceiling in rice (Sheeba et al., 2009). Hybrid rice has clearly shown yield advantage of 1-1.5 tonnes ha-1 (20 to 30%) over conventionally bred modern varieties (Virmani et al., 2003). The success of plant breeding programme depends to a greater extent on the knowledge of the genetic architecture of the population and selection of appropriate breeding method for the improvement of traits of interest. It is essential to estimate the various types of gene action for the selection of appropriate breeding procedure to improve the quantitative and qualitative characters (Banumathy et al., 2003). Keeping in view the genetic studies in parental lines of hybrid rice were undertaken to estimate the genetic component of variance for yield and its components and to compute the heritability and genetic advance for 31 characters.

Materials and methods

The study was conducted in the Seed Breeding Farm of the Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India during 2013. One hundred and twenty five parental lines (85 restorer lines, 25 maintainer lines and 15 A lines) were raised in a Randomized Complete Block Design (RCBD) with three replications. Twenty four days old seedlings of each genotype were transplanted in three rows of 2.0 m length by adopting a spacing of 22.5 cm between rows and 10 cm between plants with in rows at the rate of 20 plants per row. The crop was grown with the application of fertilizer N, P and K at the rate of 120, 60 and 60 kg ha^{-1} respectively. Standard agronomic practices were followed to raise a good crop. Ten plants were selected at random and tagged. Observations were recorded for yield and its component traits viz., days to heading (DH), days to fifty percent flowering (DFF), days to maturity (DM), 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), length breadth ratio of decorticated seed (DLBR) and pollen viability (PV). The analysis of variance of RBD and their significance for all the characters were worked out as suggested by Panse & Sukhatme (1964). Phenotypic and genotypic coefficient of variability (PCV and GCV) were worked out as described by Burton (1952). Heritability (h2) in the broad sense was calculated according to Hanson et al. (1956) and Allard et al. (1960). Genetic advance was derived according to the method of Johnson et al. (1955).

Results and discussion

Analysis of variance showed significant differences among the parental lines for all the traits studied (Table 1). Data in the Table 2 depicted that genetic variability existed in most of the 31 characters and was estimated on the basis of phenotypic and genotypic coefficient of variations. Highest phenotypic co-efficient of variation was observed in Unfilled spikelets $panicle^{-1,}$ filled spikelets $panicle^{-1}$, seed yield $plant^{-1}$, pollen viability, total spikelets $panicle^{-1}$, effective tillers $plant^{-1}$, panicle weight $plant^{-1,}$ tillers $plant^{-1}$, spikelet density, spikelet fertility, biological yield $plant^{-1}$, harvest index, flag leaf length and culm length. Similar findings were reported by Bekele et al. (2013) for seed yield $plant^{-1}$, tillers $plant^{-1}$, effective tillers $plant^{-1}$, Kiani et al. (2013) for filled spikelets $panicle^{-1}$, total spikelets $panicle^{-1}$, and seed yield $plant^{-1}$, Pnawar et al. (2005) for unfilled spikelets $panicle^{-1}$, Subbaiah et al. (2011) for harvest index and effective tillers $plant^{-1}$. Minimum level of phenotypic co-efficient of variation

was recorded in Days to maturity, days to fifty percent flowering and days to maturity. These findings were in consonance with the reports made earlier in rice by Laxuman et al. (2010) for days to fifty percent flowering and Bekele et al. (2013) for days to maturity. Almost similar pattern was observed in genotypic co-efficient of variation. The PCV value was found to be higher in all the 31 characters studied than the GCV. The differences between PCV and GCV for the 31 characters were very less indicating less environmental influence on those characters.

High estimates of broad sense heritability were observed in all traits (Table 2). High heritability accompanied with high genetic advance was recorded in 28 traits viz., unfilled spikelets panicle-1, filled spikelets panicle-1, seed yield plant-1, panicle weight plant-1, total spikelets panicle-1, effective tillers plant-1, pollen viability, spikelet density, tillers plant-1, spikelet fertility, harvest index, biological yield plant-1, flag leaf width, panicle index, length breadth ratio, head rice recovery, 1000 seed weight, length breadth ratio of decorticated seed, culm length, plant height, flag leaf length, panicle length, decorticated seed width, milling percent, hulling percent, decorticated seed length, seed width and seed length had indicating lesser environmental influence and the heritability is due to additive gene effects and selection may be effective. This was in conformity with the earlier findings of Bekele et al. (2013) and Kiani et al. (2013). High heritability along with low genetic advance was observed in days to heading, days to 50 per cent flowering and days to maturity. Similar results were reported by Padmaja et al. (2008) for days to fifty percent flowering. High heritability accompanied with low genetic advance indicates of non additive gene action. The high heritability is being exhibited due to the favorable influence of environment rather than genotypes and selection of such traits may not be rewarding.

Table 4.2.2 Analysis of variance for yield attributing traits for second year

Source of variation	d.f	Mean Sum of Square														
		DH	DFF	DM	TPP	ETPP	PH	CL	PL	FLL	FLW	BYPP	PWPP	SYPP	HI	PI	SD
Replication	2	0.4187	0.1787	0.4027	0.9351	1.4480	1.3939	0.7397	0.5191	0.1340	0.0036	40.6771	7.2637	5.3908	0.3255	3.9911	792.9922
Genotypes	124	198.6300**	198.4625**	195.3769**	20.5720**	19.0850**	1519.4312**	1327.5863**	23.4906**	164.5544**	0.7352**	1101.4889**	366.4693**	345.7679**	258.3519**	544.0835**	326522.9684**
Error	248	0.3380	0.4260	0.3328	0.4741	0.5050	4.3693	4.2792	0.4616	2.2201	0.0018	18.4055	4.5118	4.4542	1.4870	5.3311	867.8189

Contd……

Source of variation	d.f	Mean Sum of Square														
		TSPP	FSPP	UFSPP	SF	SL	SW	LBR	1000SW	HP	MP	HRR	DSL	DSW	DLBR	PV
Replication	2	6.3193	11.8117	1.2692	2.0861	0.0085	0.0004	0.0042	0.2037	1.2428	4.9854	0.5835	0.0155	0.0019	0.0019	8.6513
Genotypes	124	25884.5269**	26277.3228**	4031.6148**	1504.5658**	2.9630**	0.2648**	1.2604**	61.2724**	149.0097**	150.5534**	184.4731**	1.6287**	0.1895**	1.0086**	2033.2229**
Error	248	7.7448	12.3182	7.2913	1.5641	0.0012	0.0034	0.0053	0.3016	0.4332	2.5786	0.7279	0.0043	0.0010	0.0040	9.1039

Table 4.3.2 Table showing genetic parameters of yield attributing traits second year

S. No.	Characters	Mean	Range		Coefficient of variation		Heritability (%)	Genetic Advance	Genetic Advance as % of Mean
			Max.	Min.	GCV	PCV			
1	DH	102.19	122.33	83.33	7.95	7.98	99.50	16.70	16.35
2	DFF	106.23	126.33	87.33	7.65	7.67	99.40	16.68	15.70
3	DM	148.88	169.33	130.33	5.42	5.43	99.50	16.57	11.13
4	TPP	7.60	16.67	3.83	34.04	35.23	93.40	5.15	67.78
5	ETPP	7.13	15.78	3.67	34.92	36.32	92.50	4.93	69.17
6	PH	113.75	156.17	67.28	19.75	19.84	99.10	46.09	40.52
7	CL	87.04	126.72	43.72	24.13	24.25	99.00	43.06	49.47
8	PL	26.72	33.77	20.99	10.37	10.67	94.30	5.54	20.74
9	FLL	41.87	57.45	26.89	17.57	17.92	96.10	14.85	35.47
10	FLW	2.02	3.00	1.23	24.46	24.55	99.20	1.02	50.19
11	BYPP	65.41	111.64	20.53	29.05	29.78	95.10	38.18	58.37
12	PWPP	31.50	55.75	5.86	34.87	35.53	96.40	22.22	70.53
13	SYPP	24.64	50.03	1.35	43.29	44.13	96.20	21.55	87.48
14	HI	35.44	44.80	5.97	26.11	26.33	98.30	18.90	53.32
15	PI	74.00	89.71	20.51	18.11	18.37	97.10	27.20	36.76

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16	SD	967.17	1742.91	406.80	34.07	34.20	99.20	676.01	69.89
17	TSPP	259.71	465.67	105.00	35.76	35.77	99.90	191.23	73.63
18	FSPP	193.89	372.00	11.89	48.26	48.29	99.90	192.61	99.34
19	UFSPP	65.96	188.00	14.33	55.53	55.68	99.50	75.24	114.08
20	SF	71.35	93.72	7.21	31.37	31.42	99.70	46.04	64.53
21	SL	9.62	12.02	7.29	10.32	10.33	99.90	2.05	21.25
22	SW	2.71	3.22	2.00	10.90	11.11	96.30	0.60	22.03
23	LBR	3.61	5.97	2.73	17.91	18.03	98.70	1.32	36.67
24	1000 SW	26.12	34.62	16.90	17.26	17.39	98.50	9.22	35.30
25	HP	64.80	84.37	50.63	10.86	10.91	99.10	14.43	22.28
26	MP	59.22	79.04	43.90	11.86	12.16	95.00	14.10	23.82
27	HRR	42.75	68.07	29.78	18.31	18.42	98.80	16.03	37.49
28	DSL	6.67	8.67	4.55	11.03	11.07	99.20	1.51	22.62
29	DSW	2.08	2.70	1.62	12.05	12.15	98.40	0.51	24.63
30	DLBR	3.26	4.72	2.02	17.74	17.84	98.80	1.18	36.32
31	PV	67.82	90.00	0.00	38.30	38.59	98.70	53.15	78.37

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