

Original Research Article

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Studies on Variability, Heritability and Genetic Advance in parental lines of Hybrid Rice (*Oryza sativa* L.)

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ABSTRACT

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Genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance for twenty-one characters in twenty-eight parental lines of hybrid rice were studied. The analysis of variance revealed highly significant differences for all the characters among the genotypes. The magnitude of differences between PCV and GCV was relatively low for all the traits, indicating less environmental influence. The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were high for spikelets per panicle, flag leaf area, days to 50 % flowering, days to maturity and grain yield per plant. Heritability and genetic advance were high for all the characters except pollen fertility which had low genetic advance along with high heritability indicating the involvement of additive and non-additive type of gene action respectively in controlling this character.

Introduction

Rice (*Oryza sativa* L.), belongs to the family Graminae, recognized as “millennium crop” expected to contribute towards food security in the world, as it is one of the staple cereal crops of the world and a primary source of food for more than half the world’s population. With an alarming increase in the population throughout the world, the demand for rice will continue to increase in near future. Therefore, rice breeders across the world aim at increasing the grain yield of rice. A better understanding of the relationship

between grain yield and its component traits becomes necessary for making an efficient selection for the development of new varieties with improved economically important traits. The knowledge of heritability and genetic variability is a prerequisite for carrying out selection-based improvement. The information about these help in the breeding programme by broadening the gene pool of rice and gives an indication about the efficiency of transformation of characters into future generations respectively. In any crop species setting the breeding objective to improvement of crop yield is prime importance.

Understanding of nature and magnitude of genetic variation governing the inheritance of relatively quantitative traits like yield and attributing traits are essential. Plant breeder has to analyze certain genetic variability parameters like Genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), Heritability, and Genetic Advance of various economic important quantitative traits to plan future crop improvement programmes. Genetic variability plays an important role in study and identification of promising rice genotypes. Heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of the characters from parents to offspring (Falconer, 1981). Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.*, 1992). Hence the present investigation was undertaken to study the genetic variability, heritability and genetic advance in some parental lines of hybrid rice.

Materials and Methods

A field experiment was conducted with 28 parental lines of hybrid rice, developed by pedigree breeding method, in a Randomized Block Design with two replications during *kharif* 2015 at Zonal Agriculture Research Station (Z.A.R.S), V. C. Farm, Mandya, Karnataka. Twenty five days old seedlings were transplanted with a spacing of 15 cm and 15 cm between rows and plants, respectively. Five representative plants for each genotype in each replication were randomly selected to record observations on days to 50% flowering [DFF], days to maturity [DM], plant height [PH] (cm), tillers per plant [TPP], panicles per plant [PPP], panicle length [PL] (cm), panicle weight [PW] (g.), spikelets per panicle [SPP], pollen fertility [PF] (%), spikelet fertility [SF] (%), test grain weight [TGWT] (g.), grain yield per plant [GYPP] (g.), flag leaf length

[FLL] (cm.), flag leaf width [FLW] (cm.), flag leaf area [FLA] (cm²), grain length [GL] (mm.), grain breadth [GB] (mm.), grain L/B ratio [GL/B], kernel length [KL] (mm.), kernel breadth [KB] (mm.) and kernel L/B ratio [K L/B].

The mean of the 28 genotypes were analyzed statistically by the method outlined by Ostle (1966). The analysis of variance for different characters was carried out in order to assess the genetic variability among genotypes as given by Cochran and Cox (1950). The level of significance was tested at 5% and 1% using F table values given by Fisher and Yates (1963). Both phenotypic and genotypic coefficient of variability for all characters as estimated using the formula of Burton and De Vane (1953). The broad sense heritability (h^2) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance as suggested by Lush (1949) and Hanson (1956). Genetic advance for each character was estimated by using the formula of Johnson *et al.*, (1955). Genetic advance as per cent mean was categorized as suggested by Johnson *et al.*, (1955).

Results and Discussion

The mean sum of squares for 21 characters in 28 genotypes under study were presented in Table 1. Analysis of variance revealed highly significant differences among genotypes for all the characters studies indicating the presence of adequate variability among the genotypes.

The estimates of range and mean were presented in Table 2. A wide range of variation was observed in the parental lines of hybrid rice for all the quantitative characters and yield. However, widest range of variability was recorded for spikelets per panicle (119.78-285.37) followed by plant height (81.64-131.76 cm) and flag leaf area

(19.56-42.37 cm²). The range of variation obtained for kernel breadth (1.75-2.5 mm), grain breadth (2.0-3.0 mm) and panicle weight (2.16-3.88 g) was least when compared to all the other characters.

The estimates of genotypic and phenotypic variance components and coefficients of variability (PCV and GCV) were presented in Table 3 and Fig. 1. Variability is essential for wide adaptability and resistance to biotic and abiotic factors and hence, an insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. The phenotypic and genotypic variances measure the magnitude of variation arising out of differences in phenotypic and genotypic values. The absolute values of phenotypic and genotypic variances cannot be used for comparing the magnitude of variability for different characters, since the mean and units of measurement of the characters may be different. Hence, the coefficients of variation expressed at phenotypic and genotypic levels have been used. The relative values of these two types of coefficients give an idea about the magnitude of variability present in the germplasm (Lokesh *et al.*, 2013).

Spikelets per panicle exhibited high genotypic and phenotypic variances, followed by days to 50 % flowering, days to maturity and grain yield per plant. Similar results were obtained earlier by Sawant *et al.*, (1994) and Deb Choudhary and Das (1998).

In general, the values of PCV were higher than the values of GCV indicating that the apparent variation is not only due to genotypes but also due to influence of environment. The estimates revealed that PCV for all characters are slightly more than that of GCV indicating the less influence of environment. Similar results are found by Shobha Rani *et al.*,

(2001), Subbaiah *et al.*, (2011), and Patel *et al.*, (2014).

The GCV was higher for the characters grain yield per plant (23.843), spikelets per plant (20.98) and flag leaf area (19.288). Hence, these characters are relied upon in stabilized homozygous population and simple selection can be practiced for further improvement. The results are in consonance with Vanisree *et al.*, (2013), Subbaiah *et al.*, (2011), Panwar (2005), Hasib (2005) and in contrast with Yumnam *et al.*, (2011).

The estimates of heritability in broad sense (h^2) and expected genetic advance (GA) and genetic advance as per cent of mean (GAM) presented in Table 4 and Fig. 2. High heritability (broad sense) estimates (>60%) were recorded for all the characters under study indicating characters are least influenced by environment and selection for improvement is rewarding. Highest heritability tillers per panicle (0.99) followed by test grain weight (0.99), kernel breadth (0.99). Similar findings are suggested by Mani *et al.*, (1997), Chand *et al.*, (2005), Panwar (2005), Hasib (2005), Yumnam *et al.*, (2011), Sawarker and Senapati (2014), and Dhanwani *et al.*, (2013); Hasan *et al.*, (2013), found low heritability for spikelet fertility, are in contrast with present findings. Since the estimates of heritability are in broad sense selection based on heritability alone is misleading hence another estimate called genetic advance is used for better prediction of characters under study.

The high genetic advance revealed by characters spikelets per panicle (83.74), followed by plant height (38.07), days to 50 % flowering (13.94) days to maturity (13.43) grain yield per plant (13.14) flag leaf area (12.89) and tillers per plant (11.78) while other yield traits and all grain dimension traits exhibited moderate to very low GA values

(Table 4). The values of genetic advance as per cent of mean (GAM 5%) were high (>20%) for characters tillers per plant (62.52) followed by grain yield per plant (48.25), spikelets per panicle (42.83), flag leaf area (39.33), panicles per plant (38) panicle length (36.38), plant height (34.47). However low GAM (<10%) were revealed by pollen fertility (5.44).

Table.1 ANOVA for yield and yield contributing characters in rice genotypes

Character	Replication (d.f=1)	Treatment (d.f=27)	Error (d.f=27)
DFP	0.662	91.62**	0.62
DM	0.092	94.32**	0.046
PH	0.053	687.72**	1.485
TPP	1.18	65.8**	0.11
PPP	3.37	18.57**	0.19
PL	0.46	29.135**	0.24
PW	0.17	0.4827**	0.041
SPP	83.69	3394.59**	30.04
PF	0.02	16.801**	3.45
SF	0.036	58.737**	2.047
TGWT	0.065	7.895**	0.039
GYPP	0.923	85.948**	1.522
FLL	2.086	30.189**	0.501
FLW	0.002	0.0244**	0.001
FLA	2.01	80.748**	0.811
GL	0.01	1.044**	0.007
GB	0.034	0.104**	0.012
GL/B	0.002	0.339**	0.001
KL	0.016	0.6154**	0.003
KB	0.012	0.053**	0.002
KL/B	0.003	0.224**	0.001

** Significant at 1% level

Table.2 Range, Mean for different traits in parental lines of hybrid rice

Character	Range	Mean	SE(m)
DFP	88-109	102.03	0.312
DM	116-137	130.03	0.416
PH	81.64-131.76	110.46	0.8618
TPP	9.95-29.35	18.84	0.238
PPP	9.64-22.36	16.26	0.308
PL	14.19-26.45	21.33	0.352
PW	2.16-3.88	3.12	0.144
SPP	119.78-285.37	195.49	3.876
PF	73.56-84.19	79.32	1.315
SF	64.53-88.99	79.82	1.0117
TGWT	13.3-22.22	16.5	0.141
GYPP	16-36.83	27.25	0.872
FLL	21.37-36.09	29.49	0.5006
FLW	1.22-1.66	1.46	0.0089
FLA	19.56-42.37	32.77	0.637
GL	7.02-9.5	7.84	7.84
GB	2.0-3.0	2.42	0.026
GL/B	2.68-4.65	3.25	0.026
KL	5.1-7.5	6.05	0.041
KB	1.75-2.5	2.03	0.012
KL/B	2.44-4.05	3.04	0.0227

Table.3 Genotypic and Phenotypic variance components, coefficient of variability for different traits

Character	Phenotypic variance	Genotypic variance	PCV%	GCV%
DFE	45.813	45.769	6.639	6.634
DM	45.741	45.713	5.205	5.205
PH	344.6	343.12	16.805	16.769
TPP	32.95	32.84	30.45	30.4
PPP	9.38	9.19	18.83	18.64
PL	14.69	14.44	17.96	17.81
PW	0.26	0.22	16.407	15.03
SPP	1712.32	1682.27	21.16	20.98
PF	10.13	6.67	4.012	3.256
SF	30.392	28.345	6.906	6.669
TGWT	3.968	3.928	12.065	12.009
GYPP	43.736	42.213	24.268	23.843
FLL	15.346	14.844	13.28	13.06
FLW	0.012	0.012	7.553	7.505
FLA	40.78	39.96	19.483	19.288
GL	0.526	0.518	9.25	9.18
GB	0.052	0.052	9.434	9.434
GL/B	0.17	0.169	12.691	12.641
KL	0.303	0.306	9.182	9.132
KB	0.027	0.027	8.2	8.2
KL/B	0.123	0.122	11.52	11.47

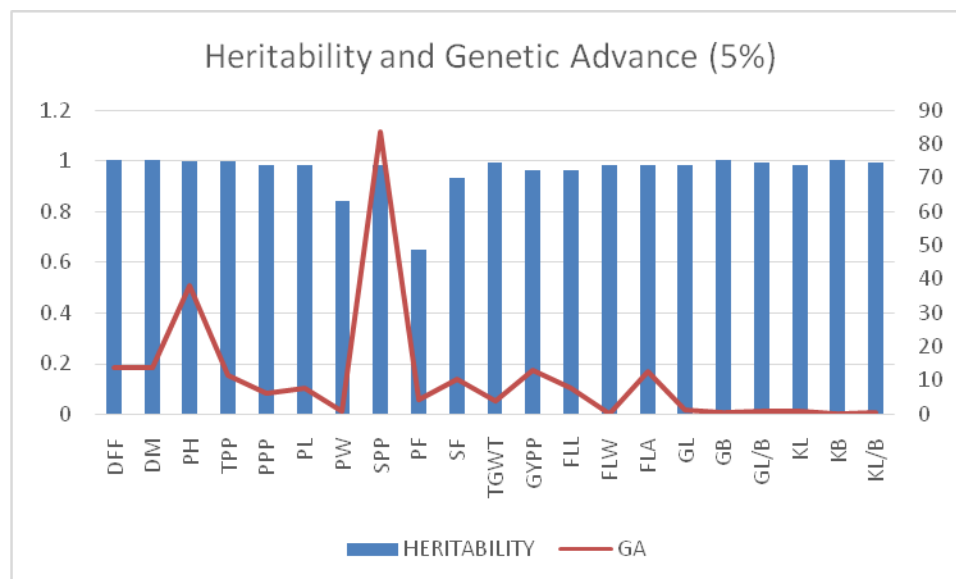
Fig.1 Graphical representation of PCV and GCV



Table.4 Heritability and Genetic Advance for different traits in rice

Character	Heritability	GA	GA	GAM	GAM
		5%	1%	5%	1%
DFF	0.986	13.94	17.86	13.66	17.51
DM	0.984	13.43	17.24	13.16	17.17
PH	0.996	38.07	48.79	34.47	44.17
TPP	0.997	11.78	15.1	62.52	80.13
PPP	0.98	6.18	7.92	38	48.7
PL	0.98	7.76	9.94	36.38	46.62
PW	0.84	0.88	1.13	28.39	36.39
SPP	0.98	83.74	107.32	42.83	54.89
PF	0.65	4.31	5.53	5.44	6.97
SF	0.93	10.59	13.57	13.26	17.04
TGWT	0.99	4.06	5.2	24.6	31.53
GYPP	0.96	13.14	16.85	48.25	61.83
FLL	0.96	7.8	10	26.46	33.91
FLW	0.98	0.22	0.28	15.36	19.68
FLA	0.98	12.89	16.52	39.33	50.41
GL	0.98	1.47	1.88	18.77	24.05
GB	0.99	0.47	0.6	19.43	24.9
GL/B	0.99	0.84	1.08	25.93	33.23
KL	0.98	1.13	1.45	18.71	23.97
KB	0.99	0.33	0.43	16.89	21.64
KL/B	0.99	0.71	0.91	23.53	30.16

Fig.2 Graphical representation of h^2 and Genetic advance (5%)



Heritability should be considered along with genetic advance as per cent of mean, however it is not necessary that character showing high heritability will also exhibit high genetic advance (Johnson *et al.*, 1955). High heritability coupled with high GAM was observed with tillers per plant grain yield per plant, spikelets per panicle, flag leaf area, panicles per plant, panicle length, plant height, panicle weight, flag leaf length, grain L/B ratio, and test grain weight are governed by additive genes and improvement is rewarding. Similar kind of results were obtained by Tirumala rao *et al.*, (2014) Dhanwani *et al.*, (2013), Vanisree *et al.*, (2013), Babu *et al.*, (2012). However, low GAM for days to 50% flowering was reported by Sawarker and Senapati (2014), Tirumala rao *et al.*, 2014, Seyoum *et al.*, (2012) and Kole *et al.*, (2008); low GAM for grain yield per plant was reported by Venkanna *et al.*, (2014) and Kole *et al.*, (2008); low GAM for panicle length was reported by Babu *et al.*, (2012), Seyoum *et al.*, (2012), Subbaiah *et al.*, (2011) and Kole *et al.*, (2008); moderate GAM for days to 50% flowering, plant height and low GAM for panicle length, spikelet fertility, days to maturity, test weight, grain

yield per plant are reported by Hasan *et al.*, (2013).

High heritability coupled with moderate GAM was observed for characters days to 50 % flowering, days to maturity, spikelet fertility, flag leaf width, grain length, grain breadth, kernel length and kernel breadth indicating characters governed by additive genes though influenced by environment. Similar findings are reported by Allam *et al.*, (2015), Patel *et al.*, (2014), Dhanwani *et al.*, (2013), Vanisree *et al.*, (2013), Subbaiah *et al.*, (2011).

However Babu *et al.*, (2012) and Subbaiah *et al.*, (2011) reported low GAM for kernel breadth; Sawarker and Senapati (2014) reported low GAM for days to maturity. High heritability coupled with low GAM is observed for the character pollen fertility (table 4) indicating the character is highly influenced by environmental effects and selection would be ineffective. From the present study, it is evident that genotypes studied may provide good source of material for further breeding programme. Therefore, the information on the genetic parameters

such as coefficient of variation, heritability, genetic advance can help the breeder to evolve high yielding cultivars.

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