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Khonang Longkho
Department of Genetics and
Plant Breeding, Visva-Bharati
University, Santiniketan,
West Bengal, India

Paresh Chandra Kole
Professor, Department of
Genetics and Plant Breeding,
Visva-Bharati University,
Santiniketan,
West Bengal, India

Partha Pratim Behera
Department of genetics & plant
breeding, IAS, B.H.U, Varanasi,
Uttar Pradesh, India

Genetic parameter studies in F₄ segregating generation of rice

Khonang Longkho, Paresh Chandra Kole and Partha Pratim Behera

Abstract

The present investigation was carried out on F₄ families grown from individual F₃ plants, selected from a large number of F₃ families of rice genotypes. The analysis of variance revealed that mean square due to F₄ families were highly significant for all the characters under study indicating considerable genetic variation among the F₄ families derived from the crosses. From the values of coefficient of variation (CV), the variability was highest in grain yield panicle⁻¹, followed by number of productive tillers, grain yield, 100 grains weight, number of secondary branches. Flag leaf area, secondary branches panicle⁻¹, grain yield panicle⁻¹ and grain yield plant⁻¹ showed high estimates of GCV and PCV whereas, moderate estimates of GCV and PCV were observed in plant height, primary branches plant⁻¹, number of spikelet, number of filled grains and 100-grain weight. Low estimates of GCV and PCV were found in panicle length and spikelet fertility. The estimates of GCV and PCV values for number panicle plant⁻¹, 100-grain weight, primary-branches panicle⁻¹ and panicle length showed wide difference which indicated the greater role of environmental factors influencing the expression of these characters. The estimates of heritability was very high for number of spikelet panicle⁻¹, number of filled grains panicle⁻¹, plant height, flag leaf area, secondary branches panicle⁻¹, grain yield plant⁻¹, grain yield panicle⁻¹ and spikelet fertility. Panicle number, primary branches panicle⁻¹ and 100-grain weight have moderate heritability. High heritability coupled with high genetic advance was observed for flag leaf area, grain yield panicle⁻¹, grain yield plant⁻¹ and secondary branches panicle⁻¹ indicating that the expression of these characters is under the control of predominant additive gene actions and hence selection would be effective.

Keywords: PCV, GCV, heritability, genetic advance, variability, segregation

Introduction

Rice is one of the most important staple food and widely consumed cereal crops. It is also considered to sustain the livelihood of the ever growing rapid population of the third world countries particularly India. Although it is grown in large scale, the major constraints in rice production are poor yield. Poor yield in rice is mainly induced by different factors like susceptibility to new diseases, rise in temperature and other factors. So, development of elite genotype to cater the need of the growing population is an important way out. The large spectrum of genetic variability in segregating population depends on the level of genetic diversity among genotypes which offers better scope for selection. In any plant breeding programme, availability of large genetic variability in the crop species is the first step to select better performing types among the divergent group. If vast amount of variability present, attempts can be made to improve the trait of interest by enforcing selection. Variability generally exists in germplasm collection and when this is exploited to a maximum extent by way of selection, additional variability can be created by crossing best available varieties. Heritability and genetic advance are other important selection parameters. The estimation of heritability helps to determine the characters for which selection would be rewarding. The major function of heritability estimates is to provide information on transmission of character from parents to offspring. Genetic advance provides information on expected genetic gain resulting from selection of superior individuals. Relatively high heritability and genetic advance estimates for the desired traits help in advancing the potential segregating generations to develop desirable recombinant inbred lines and commercial cultivars (Pervaiz *et al.* 2010) [25]

Material and Methods

The field experiments were conducted at the Agricultural Farm, Institute of Agriculture, Visva-Bharati, Sriniketan. The present investigation was carried out on F₄ families grown from individual F₃ plants, selected from a large number of F₃ families. (Table 1) Thirty-day old single seedling per hill was transplanted in randomized complete block design (RCBD) with

Corresponding Author
Khonang Longkho
Department of Genetics and
Plant Breeding, Visva-Bharati
University, Santiniketan,
West Bengal, India

three replications. Each plot consisted of 4 rows each with 20 plants with a spacing of 20cm x 15cm spacing. Standard agronomic package and practices were followed to raise a good and healthy crop. Data were recorded on randomly selected 20 plants from each plot in each replication. Out of 30 families only 27 families were selected for analysis of performance as the rest 3 families were greatly infested with disease rendering them quite unfit to be carried forward. Observations were recorded for the twelve different yield contributing quantitative characters.

List of parents involved in crossing

S. No.	Parents		
1	Subhasita	6	Shantibhog
2	Sitabhog	7	IET 14142
3	Kerala Sundari	8	IET 14143
4	Kalonunia	9	Khaskhani Long
5	Dudheswer	10	Chamarmoni

Result and Discussion

The analysis of variance of 27 F₄ families derived from 15 crosses for 12 quantitative characters *viz.* plant height, flag leaf area, panicle length, number of panicles plant⁻¹, number of primary branches and secondary branches panicle⁻¹, number of spikelet and filled grains panicle⁻¹, spikelet fertility, 100-grain weight, grain yield panicle⁻¹ and grain yield plant⁻¹. It revealed that mean square due to F₄ families was highly significant (Table 2) for all the characters under study indicating considerable genetic variation among the F₄ families derived from the crosses. The mean performance of 27 F₄ families derived from 15 crosses for 12 characters is given in (Table 2). From the values of coefficient of variation (CV), the variability was highest in grain yield panicle⁻¹ (15.67) followed by number of productive tillers (13.10), grain yield (12.47), 100 grains weight (10.81), number of secondary branches (10.11), flag leaf area (9.87), number of primary branches (7.71), panicle length (5.67), spikelet fertility (4.36), number of spikelet (3.53), number of filled grain (3.37) and plant height (3.31). Therefore, considerable amount of variability have also been reported earlier for grain yield panicle⁻¹ (Akter *et al.* 2004 and Nandeshwar *et al.* 2010) [22]; for number of productive tiller (Sameera *et al.* 2016) [27]; for grain yield (Gampala *et al.* 2015; Khare *et al.* 2015 and Bagati *et al.* 2016) [2]; for 100 grains weight (Krishna *et al.* 2014; Khare *et al.* 2015 and Sameera *et al.* 2016) [27]. Considering the performance of the families in the populations for yield and other characters involved, the family consisting of cross-combination of IET 14142 × Subhasita recombined characters of seed yield, primary and secondary branches, high amount of filled grains with bold seed dimensions of Subhasita with short stature and number of tiller from IET 14142. Sitabhog × IET 14143 also showed good grain dimensions, high number of spikelet and spikelet fertility with high seed yield of Sitabhog, while short to medium plant stature was contributed by the genotype IET 14143. Sitabhog × IET 14142 is another cross-combination which showed moderate amount of yield having majority of the characters from Sitabhog, combined with short height of the genotype IET 14142. Therefore, performance of the above mentioned families reveals scope for further selection of promising segregates to be carried forward to the next F₅ generation. The knowledge of genetic variability present in a population for the characters under study is of paramount importance for the success of any plant breeding programme. The estimates of genotypic and phenotypic coefficients of

variance (GCV and PCV) ranged from 14.29 and 14.68 in plant height to 27.57 and 30.25 in grain yield (Table 3). The values of GCV and PCV were grouped under three categories *viz.* low (<10%), moderate (10-20%) and high (>20%). On the basis of the above grouping, flag leaf area, secondary branches panicle⁻¹, grain yield panicle⁻¹ and grain yield plant⁻¹ showed high estimates of GCV and PCV whereas, moderate estimates of GCV and PCV were observed in plant height, primary branches plant⁻¹, number of spikelet, number of filled grains and 100-grain weight. Low estimates of GCV and PCV were found in panicle length and spikelet fertility. On the contrary, moderate estimates of GCV and high PCV were observed in panicle number. Similar results were reported for high magnitude of flag leaf area (Kumar *et al.* 2014) [17-17-18]; high GCV and PCV for secondary branches panicle⁻¹ (Ketan and Sarkar 2014) [13] and high GCV and PCV for grain yield plant⁻¹ (Krishna *et al.* 2014; Singh *et al.* 2014; Khare *et al.* 2015; Manohara and Singh 2015 and Gayatonde *et al.* 2017) [6]. Similarly moderate GCV and high PCV for panicle number (Bhatia *et al.* 2015) [3]; moderate GCV and PCV for plant height (Toshimela and Changkija 2013; Manohara and Singh 2015 and Mahesh Babu *et al.* 2017) [19]; moderate GCV and PCV for primary branches panicle⁻¹ (Hasib and Kole 2008) for number of spikelet panicle⁻¹ (Hasib and Kole 2008 and Gampala *et al.* 2015) [5]; moderate GCV and PCV for number of filled grain panicle⁻¹ (Kole *et al.* 2008; Singh *et al.* 2012; Manohara and Singh 2015 and Bagati *et al.* 2016) [2]; moderate GCV and PCV for 100-grain weight (Gampala *et al.* 2015; Khare *et al.* 2015 and Sameera *et al.* 2016) [27]. And similar results reported for low GCV and PCV for panicle length (Kole *et al.* 2008; Gampala *et al.* 2015; Imsong *et al.* 2015; Sameera *et al.* 2016 and Gayatonde *et al.* 2017) [6] and for spikelet fertility panicle⁻¹ (Khare *et al.* 2015 and Bagati *et al.* 2016) [2]. The estimates of GCV and PCV values for number panicle plant⁻¹, 100-grain weight, primary branches panicle⁻¹ and panicle length showed higher difference which indicated the greater role of environmental factors influencing the expression of these characters. However, low difference was observed for plant height, number of filled grain panicle⁻¹, number of spikelet panicle⁻¹ and flag leaf area which indicates less sensitivity of these characters in the fluctuating environment. The heritability estimates in segregating generation helps to know genetic variance of genotype environment interaction and genetic component to be expected from selection in the next generation (Kahani and Hittalmani 2016) [12]. The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. The estimates of heritability in broad sense (Table 3) were very high for number of spikelet panicle⁻¹ (96.3), plant height (95), number of filled grain (93.4), flag leaf area (91.3), secondary branches panicle⁻¹ (86), grain yield (83), grain yield panicle⁻¹ (78.2), spikelet fertility (75.5) which revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values. Similar results have been reported for number of spikelet panicle⁻¹ (Tiware *et al.* 2011; Jha *et al.* 2014; Khare *et al.* 2015; Sameera *et al.* 2016 and Gayatonde *et al.* 2017) [6]; plant height (Biswash *et al.* 2015; Gampala *et al.* 2015; Khare *et al.* 2015; Manohara and Singh 2015; Konate *et al.* 2016; Sameera *et al.* 2016 and Gayatonde *et al.* 2017) [6]; number of filled grain (Khare *et al.* 2015; Gokulakrishnan *et al.* 2014; Sameera *et al.* 2016; Bagati *et al.* 2016 and Konate *et al.* 2016) [16]; flag leaf area (Rahman *et al.* 2015; Yadav *et al.* 2017) [32]; secondary branches (Ketan and Sarkar 2014) [13]; grain yield plant⁻¹

¹(Singh *et al.* 2012; Krishna *et al.* 2014; Singh *et al.* 2014; Khare *et al.* 2015; Manohara and Singh 2015 and Gayatonde *et al.* 2017); spikelet fertility (Khare *et al.* 2015 and Gayatonde *et al.* 2017) ^[6]. However, moderate heritability was observed in panicle number plant⁻¹, primary branches panicle⁻¹, 100-grain weight and were moderately influenced by environment. These results were similar for panicle number plant⁻¹ (Manohara and Singh 2015 and Konate *et al.* 2016) ^[16]; primary branches panicle⁻¹ (Hasib and Kole 2008); 100-grain weight (Gampala *et al.* 2015; Khare *et al.* 2015 and Sameera *et al.* 2016). On the contrary, low heritability was observed in panicle length and is highly influenced by environmental fluctuation (Kole *et al.* 2008; Gampala *et al.* 2015; Imsong *et al.* 2015; Sameera *et al.* 2016 and Gayatonde *et al.* 2017) ^[6]. The genetic advance as per cent of mean is a useful indicator of the progress that could be expected as a result of exercising selection on the pertinent population. It is classified as low (<25%), moderate (25-50%) and high (>50%). Accordingly, genetic advance as a per cent of mean (Table 3) revealed that high GAM was for grain yield panicle⁻¹ (69.23) followed by grain yield plant⁻¹ (66.31) and flag leaf area (63.03). Similar results were reported for grain yield (Pal *et al.* 2011; Gokulakrishnan *et al.* 2014; Manohara and Singh 2015; Sameera *et al.* 2016 and Mamata *et al.* 2018) ^[20] and flag leaf area (Rahman *et al.* 2015) ^[26]. Moderate GAM were observed for plant height (28.68), panicle number tiller⁻¹(31.91), secondary branches panicle⁻¹(47.01), number of spikelet

panicle⁻¹(36.56), number of filled grain panicle⁻¹(32.67) and 100-grain weight (27.18). Similar results were obtained earlier for plant height (Gampala *et al.* 2015; Sameera *et al.* 2016 and Yadav *et al.* 2017) ^[32]; panicle number tiller⁻¹(Manohara and Singh 2015); secondary branches panicle⁻¹; number of spikelet panicle⁻¹ (Singh *et al.* 2011) ^[19]; number of filled grain panicle⁻¹ (Kole *et al.* 2008; Manohara and Singh 2015 and Patroti *et al.* 2015) ^[24]. On the contrary, low genetic advance was found in panicle length (8.82), primary branches panicle⁻¹(19.81) and spikelet fertility (10.63). Similar results were obtained for panicle length (Kumar *et al.* 2014; Gampala *et al.* 2015; Konate *et al.* 2016 and Mahesh Babu *et al.* 2017) ^[19]; primary branches panicle⁻¹(Singh *et al.* 2012; Toshimela and Changkija 2013 and Biswash *et al.* 2015); spikelet fertility (Manohara and Singh 2015 and Khare *et al.* 2015) ^[14] respectively. Heritability estimates along with genetic advance would be more useful in predicting yield under phenotypic selection than heritability estimates alone as suggested by Johnson *et al.* (1955) ^[11]. High heritability coupled with genetic advance was observed for flag leaf area, grain yield panicle⁻¹ and grain yield plant⁻¹, which indicates that the expression of these characters is under the control of predominant additive gene actions. Therefore, improvement in these characters would be possible through direct selection. Similar findings were observed for flag leaf area (Kumar *et al.* 2014) ^[7-17-18]; grain yield plant⁻¹(Pal *et al.* 2011; Duria *et al.* 2013; Biswash *et al.* 2015; Mamata *et al.* 2018) ^[20].

Table 1: Analysis of variance (Mean square) for twelve quantitative characters in F₄ families of rice

Source	d. f.	Plant height (cm)	Flag leaf area (cm ²)	Number of panicle	Panicle length (cm)	Primary branches panicle ⁻¹	Secondary Branches panicle ⁻¹	Number of spikelet	Number of filled grain	Spikelet fertility (%)	100-grain weight (g)	Grain yield/panicle (g)	Grain yield/plant (g)
Replication	2	21.64*	35.13	1.17	4.93	0.82	20.18*	2.25	6.78	1.97	0.64	0.04	3.19
Families	26	1159.47**	274.21**	15.13**	8.60**	6.07**	119.43**	1789.00**	626.42**	49.75**	0.35**	0.50**	46.67**
Error	52	20.40	8.40	2.09	2.01	0.78	6.33	22.52	14.41	4.85	0.04	0.04	2.97

*, **: Significant at P=0.05 and P=0.01, respectively

Table 2: Mean performance of 27 F₄ families for twelve quantitative characters of rice

Character	Plant height (cm)	Flag leaf area (cm ²)	Number panicle	Panicle length (cm)	Primary branches	Secondary Branches	No. of spikelet	No. of filled grain	Spikelet fertility %	100- grain weight (g)	Grain yield/panicle (g)	Grain yield/plant (g)
Sitabhog × IET 14142- 1	151.33	45.68	7.95	25.42	13.01	32.16	157.43	100.41	63.81	2.12	1.62	12.88
Sitabhog × IET 14142- 2	102.33	35.47	8.32	23.52	14.07	25.86	144.37	97.92	67.80	2.26	2.15	17.63
Sitabhog × IET 14142- 3	156.26	45.01	8.91	27.83	11.32	27.11	135.02	94.10	69.69	2.24	1.75	15.47
Sitabhog × IET 14143- 1	144.50	21.66	11.28	27.31	13.64	35.27	181.15	110.03	60.76	1.70	1.83	20.65
Sitabhog × IET 14143- 2	151.54	32.09	12.47	26.20	12.65	34.10	183.29	102.53	55.94	2.03	1.47	18.27
Kerala Sundari × IET 14143 -1	148.51	29.55	10.65	25.86	12.39	30.41	142.77	101.27	70.95	1.81	1.55	15.44
Kerala Sundari × IET 14143- 2	131.22	27.46	11.36	24.64	9.7	21.86	125.22	77.02	61.51	1.72	0.80	10.33
Kerala Sundari × IET 14143-3	144.15	27.78	8.08	24.81	10.98	22.44	117.96	80.23	68.04	2.47	1.75	12.35
Kerala Sundari × IET 14143- 4	144.81	26.75	11.40	23.46	10.80	19.83	118.69	75.35	63.49	1.95	1.18	13.26
Kerala Sundari × IET 14143- 5	126.62	24.85	10.08	25.43	10.42	21.79	127.75	90.92	71.17	2.07	0.94	9.59
Kerala Sundari × Kalonunia -1	153.97	11.86	12.08	25.35	13.82	33.86	165.69	110.34	66.61	2.03	1.20	14.47
Kerala Sundari × Kalonunia -2	135.79	28.28	7.57	23.93	11.91	21.91	136.89	81.61	59.64	2.04	1.74	13.20
Kerala Sundari × IET 14142 -1	138.83	33.65	13.00	25.36	12.15	27.84	152.93	97.13	63.51	1.97	1.14	14.88
Kerala Sundari × IET 14142 -2	141.800	30.81	12.42	23.67	12.41	28.16	146.38	101.39	69.26	2.00	1.48	18.39
IET 14142 × Kalonunia	112.84	23.35	8.05	24.81	10.10	16.00	107.59	73.87	68.62	1.30	0.65	5.00
IET 14142 × Dudheswer	117.17	20.02	11.86	25.09	12.18	24.89	123.77	76.30	61.64	1.94	1.09	12.95
IET 14142 × Subhasita -1	161.25	26.30	11.83	26.31	10.27	26.05	136.30	82.1	60.29	2.10	0.74	8.53
IET 14142 × Subhasita -2	138.95	31.08	13.00	25.62	12.15	31.35	139.41	81.32	58.35	2.01	1.76	22.30
Shantibhog × IET 14142- 1	126.83	25.85	9.33	23.86	11.30	20.66	131.69	86.30	65.54	1.80	1.35	12.20
Shantibhog × IET 14142 -2	114.22	25.24	11.22	23.00	11.18	22.81	126.40	80.66	63.84	2.28	1.23	13.63

Shantibhog × Subhasita	95.08	23.87	15.91	20.46	10.83	15.97	102.50	70.97	69.33	1.61	0.95	14.82
Shantibhog × Kerala Sundari- 1	145.27	48.52	10.50	26.91	12.75	31.35	160.04	103.32	64.54	2.51	1.32	13.84
Shantibhog × Kerala Sundari -2	140.25	32.60	10.30	24.58	11.29	27.08	129.31	90.25	69.77	2.31	1.67	17.31
Shantibhog × Kalonunia	172.11	42.19	10.47	25.67	10.80	23.10	145.36	93.58	64.35	2.50	1.65	17.31
Khaskhani Long × IET 14142	141.800	30.81	12.42	23.67	12.41	28.16	146.38	101.39	69.26	2.00	1.48	18.39
IET 14143 × Kalonunia	122.82	13.04	14.12	22.94	8.15	9.28	74.25	48.85	66.22	1.49	0.64	8.63
IET 14143 × IET 14142	101.39	16.01	16.14	24.26	8.98	16.13	100.52	69.65	68.65	1.45	0.76	8.91
RANGE (Min)	95.08	11.86	7.57	20.46	8.15	9.28	74.25	48.85	55.94	1.30	0.64	5.00
RANGE (Max)	172.11	48.52	16.14	28.70	14.07	35.27	183.29	110.34	71.17	2.77	2.15	22.30
GM	136.33	29.37	11.04	25.00	11.48	24.89	134.17	87.04	65.18	2.02	1.32	13.84
CV	3.31	9.87	13.10	5.67	7.71	10.11	3.53	3.37	4.36	10.811	15.67	12.47
SE	2.60	1.67	0.83	0.81	0.51	1.45	2.74	2.19	1.27	0.13	0.11	0.99
CD At 5%	7.40	4.74	2.37	2.32	1.45	4.12	7.77	6.22	3.60	0.35	0.33	2.82
CD At 1%	9.86	6.32	3.16	3.09	1.93	5.49	10.36	8.28	4.80	0.47	0.45	3.76

Table 3: Phenotype and Genotype coefficients of variability, heritability and genetic advance for twelve quantitative characters in F₄ families of rice

Characters	Grand mean	Range		Coefficient of Variation%		Heritability (%)	Genetic advance	Genetic advance as percent of mean
		Min	Max	GCV	PCV			
Plant height (cm)	136.34	95.08	172.11	14.29	14.68	95	39.10	28.68
Flag leaf area (cm ²)	29.37	11.86	48.52	32.04	33.52	91.3	18.53	63.08
Number of panicle	11.04	7.58	16.14	18.87	22.97	68	3.52	31.91
Panicle length(cm)	25.00	20.46	28.70	5.93	8.20	52.2	2.20	8.82
Primary branches	11.49	8.15	14.07	11.56	13.89	69.2	2.27	19.81
Secondary branches	24.89	9.28	35.27	24.66	26.66	86	11.70	47.01
Number of spikelet	134.17	74.25	183.28	18.08	18.42	96.3	49.05	36.56
Number of filled grain	87.04	48.85	110.34	16.41	16.97	93.4	28.43	32.67
Spikelet fertility%	65.18	55.94	71.17	5.93	6.83	75.5	6.92	10.63
100-grain weight(g)	2.02	1.30	2.77	15.95	19.26	68.5	0.54	27.18
Grain yield/panicle (g)	1.32	0.64	2.15	29.66	33.54	78.2	0.71	69.23
Grain yield/plant (g)	13.84	5.00	22.30	27.57	30.25	83	7.16	66.31

Conclusion

The analysis of variance revealed that mean square due to F₄ families was highly significant for all the characters under study indicating considerable genetic variation among the F₄ families derived from the crosses. The mean performance of F₄ families showed considerable variation for important characters. From the values of coefficient of variation (CV), the variability was highest in grain yield panicle⁻¹ (15.67), followed by number of productive tillers (13.10), grain yield (12.47), 100 grains weight (10.81), number of secondary branches (10.11). Flag leaf area, secondary branches panicle⁻¹, grain yield panicle⁻¹ and grain yield plant⁻¹ showed high estimates of GCV and PCV whereas, moderate estimates of GCV and PCV were observed in plant height, primary branches plant⁻¹, number of spikelet, number of filled grains and 100-grain weight. Low estimates of GCV and PCV were found in panicle length and spikelet fertility. The estimates of GCV and PCV values for number panicle plant⁻¹, 100-grain weight, primary branches panicle⁻¹ and panicle length showed wide difference which indicated the greater role of environmental factors influencing the expression of these characters. However, little difference was observed for plant height, number of filled grain panicle⁻¹ number of spikelet panicle⁻¹ and flag leaf area which indicates less sensitivity of these characters in the fluctuating environments. The estimates of heritability was very high for number of spikelet panicle⁻¹, number of filled grains panicle⁻¹, plant height, flag leaf area, secondary branches panicle⁻¹, grain yield plant⁻¹, grain yield panicle⁻¹ and spikelet fertility revealing that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values. Panicle number, primary branches panicle⁻¹ and 100-grain weight have moderate heritability and are moderately

influenced by environment and panicle length having low heritability is highly influenced by environmental fluctuation. High heritability coupled with high genetic advance was observed for flag leaf area, grain yield panicle⁻¹, grain yield plant⁻¹ and secondary branches panicle⁻¹ indicating that the expression of these characters is under the control of predominant additive gene actions and hence selection would be effective.

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