Original Research Article

Genetic Variability Studies in F$_2$ Generation of Rice (*Oryza sativa* L.)

Ruchi Asati* and Rakesh Kumar Yadav

Department of Plant Breeding and Genetics, JNKVV College of Agriculture,
Rewa-486001, M.P., India
Corresponding author

A B S T R A C T

Keywords

Oryza sativa,
Flowering, Plant
height, Panicles
per plant, Panicle
length

In present study, the estimates of heritability, coefficient of variability, genetic advance were computed in F$_2$ segregating population of 9 crosses and its 9 parents for 11 characters including yield and contributing traits during kharif 2019. The analysis of variance was recorded that huge amount of variability is present between crosses and their parents for all the traits. The PCV is greater than GCV revealing the little influence on the environment for most of the traits. The estimates of PCV and GCV were high for biological yield per plant followed by panicles per plant, panicle weight for both progenies and parent indicated the presence of high genetic variability for the traits which may facilitate selection. In the F$_2$ population, observed high heritability with high genetic gain over per cent mean for biological yield per plant and harvest index. High heritability coupled with low genetic gain over per cent mean was observed for grain yield per plant and 100 grain weight. In parental population, obtained high heritability coupled with high genetic gain over per cent mean for grain yield per plant followed by grains per panicle and panicles per plant. Its forces to conclude that these characters are governed by additive action.

Introduction

Rice (*Oryza sativa L.*) is a cereal crop, belongs to genus *Oryza* of family Poaceae. It is cultivated in 114 countries across the globe, but 90 % of world's rice is grown in Asia (FAO, 2016).Rice is a complex trait, depends upon the various yield contributing traits like days to 50 % flowering, plant height, panicles per plant, panicle length, panicle weight, grains per panicle, fertility %, 100 grain weight, biological yield per plant, grain yield per plan, harvest index etc. Existence of genetic variability is the basic necessity in any crop improvement programme. The genotypic coefficient of variation provides a measure to collate genetic variability present in various quantitative traits (Akinwale *et al.,* 2011). The genotypic co-efficient of variation estimates the heritable variability, while phenotypic co-efficient measures the role of environment on the genotype. High PCV and low GCV for a trait designate high influence of environment in its appearance. The knowledge of heritability and genetic advance assist the breeder to decide and select superior plants, where high heritability values indicate the occurrences of additive gene action in their expression, while lower values are indicative are presence of non-additive gene action. High estimates of

heritability and genetic advance shows that plant can perform superior for the traits of interest in subsequent generation. If high heritability is accompanied by a low genetic advance shows the effect of epistasis and dominance therefore, the estimates of expected genetic gain are important to have an idea of the efficiency of selection.

Materials and Methods

In present study, the estimates of heritability, coefficient of variability, genetic advance were computed in F_2 segregating population of 9 crosses and its 9 parents for 11 characters including yield and contributing traits during kharif 2019 at, Instructional Farm, JNKVV., College of Agriculture, Rewa (M.P.). Twenty days old seedlings were transplanted in the main field with three replications. Each replication consisted of 9 F_2 population and 9 parental lines with spacing of 20 cm × 15 cm inter and intra row spacing. Each F_2 was raised with minimum of 500 plant population and individual plant observations were recorded from 20 randomly selected plants. The data was recorded for days to 50 % flowering, plant height (cm), panicles per plant, panicle length (cm), panicle weight (gm), grains per panicle, fertility %, 100 grain weight (gm), biological yield per plant (gm), grain yield per plan (gm), harvest index %. The mean data after computing for each trait was subjected to analysis of variance and genetic parameters of variation. The list of crosses and parents used in the present study are presented here under.

Parents

IR 113016-3-4-7

IR 113016-4-12-13

IR 113013-4-1-18

IET 3614

IET 3636

IET 3641

IET 3643

IET 3648

IET 3653

Crosses

Rewa 1331 (IR 113016-3-4-7 x IET 3643)

Rewa 1332 (IR 113016-3-4-7 x IET 3614)

Rewa 1333 (IR 113016-3-4-7 x IET 3636)

Rewa 1334 (IR 113016-3-4-7 x IET 3653)

Rewa 1335 (IR 113016-3-4-7 x IET 3641)

Rewa 1336 (IR 113016-3-4-7 x IET 3648)

Rewa 1337 (IR 113016-4-12-13 x IET 3648)

Rewa 1338 (IR 113013-4-1-18 x IET 3648)

Rewa 1339 (IR 113013-4-1-18 x IET 3636)

Result and Discussion

Variability

Analysis of variance revealed that variance was found to be highly significant for most of the characters and just significant for remaining characters those are panicle length, panicle weight, fertility %, harvest index, 100 grain weight in parental population, while panicle weight, biological yield per plant and harvest index exhibited highly significant variance in f_2 population (Table 1 and 2). The extent of variability is measured by PCV and

GCV also give information regarding the relative amount of variation in different populations. The phenotypic coefficient (PCV) and genotypic coefficient of variation (GCV) exhibited wide variation for most of the characters in f_2 population.

In f_2 population, high PCV and GCV value was recorded for biological yield per plant followed by harvest index. The finding of Subbaiah *et al.,* (2011), Singh *et al.,* (2011), Patel *et al.,* (2018) found similar (Table 4).

Among the parents, recorded high PCV value for grain yield per plant followed by biological yield per plant and GCV value for grains per panicle followed by grain yield per plant. Similar results were reported by Babu *et al.,* (2012), Kiran *et al.,* (2014), Nandeshwar *et al.,* (2010), Lingaiah *et al.,* (2014), Sala *et al.,* (2016).

Moderate estimates of phenotypic and genotypic coefficient of variation were observed for 100 grain weight and panicle length in crosses and parental population, indicating the possibilities for direct phenotypic selection. Similar results were reported by Abebe *et al.,* (2017), Kahani *et al.,* (2015) (Table 3). The phenotypic expression of a trait is the result of interaction between genotype and environment. Hence, the total variance needs to be partitioned in to heritable and non-heritable components so as to assess the true breeding nature of particular trait.

Heritability

In F_2 population, broad sense heritability estimates were high for biological yield per plant followed by harvest index, grain yield per plant and 100 grain weight for crosses. Similar results revealed by Panwar and Mathur (2007), Sadimantara *et al.,* (2014), for grain yield per plant Hussain *et al.,* (2014), for harvest index Rahman *et al.,*

(2016), Konate *et al.,* (2016), for 100 grain weight Islam *et al.,* (2016). In parental populations plant height, grain yield per plant, biological yield per plant and grains per panicle, days to 50% flowering, panicles per plant and fertility % had high heritability. Selection for biological yield per plant, grain yield per plant and grains per panicle are most suitable for segregating generations on the basis of broad sense heritability. Similar results revealed by Hussain *et al.,* (2015), Singh *et al.,* (2013), Shrivastava *et al.,* (2014) (Table 3 and 4).

Genetic Advance

The genetic advance is commonly predicted as a product of heritability ratio and the selection differential. The result revealed high to moderate genetic gain over the percent mean for biological yield per plant followed by harvest index (high) and panicles per plant (moderate). Remaining characters observed low genetic gain over the percent mean.

Among the parental population grains per panicle followed by grain yield per plant, panicles per plant (high) and biological yield per plant, panicle weight, plant height and harvest index (moderate) recorded high to moderate genetic gain over the percent mean.

Remaining characters observed low genetic gain over the percent mean. Results of the present study closely agree with earlier reports in rice by Patel *et al.,* (2018), Panwar and Mathur (2007), Rahman *et al.,* (2016) (Table 3 and 4)

In the f_2 population, observed high heritability with high genetic gain over the percent mean for biological yield per plant and harvest index. It concludes that these characters are governed by additive action. Similar finding was found by Panwar and Mathur (2007).

Table.1 Analysis of variance for yield and yield component character in parents

Source	Df	Days to 50% flowering	Plant height (cm)	Panicles/ plant	Panicle length (cm)	Panicle weight (gm)	Grains/ panicle	Fertility %	100 grain weight (gm)	Biological yield/ plant (gm)	Grain yield / plant (gm)	Harvest index (%)
Replication	2	4.099	7.040	0.117	2.822	0.161	198.250	2.989	0.0349	6.294	1.521	1.351
Treatment	8	18.838***	226.796***	3.603***	5.386**	1.134**	4400.528***	27.202**	0.0711**	244.168***	64.917***	35.129**
Error	16	2.582	13.341	0.528	1.192	0.268	412.655	4.721	0.0170	21.398	5.681	7.3951

Mean sum of squares
* Significant at 5% level** Significant at 1% level   *** Significant at 0.1% level

Table.2 Analysis of variance for yield and yield component character in f_2 crosses

Source	Df	Days to 50% flowering	Plant height (cm)	Panicles/ plant	Panicle length (cm)	Panicle weight (gm)	Grains/ panicle	Fertility %	100 grain weight (gm)	Biological yield/ plant (gm)	Grain yield / plant (gm)	Harvest index (%)
Replication	2	3.557	12.324	0.810	0.201	0.0393	5.0892	7.553	0.0633*	5.112	2.819	2.0832
Treatment	8	13.201**	36.671**	2.238**	5.875**	0.1986**	431.234**	35.364**	0.070**	365.620***	7.882**	57.314***
Error	16	2.7903	8.722	0.535	1.393	0.0449	79.565	6.970	0.0125	5.825	1.326	4.386

Mean sum of squares
* Significant at 5% level** Significant at 1% level   *** Significant at 0.1% level

Table.3 Estimates of variability, heritability, genetic advance, and genetic gain over per cent mean of parent populations

S. N.	Character	Mean	Range		PCV	GCV	H^2(bs) %	Genetic Advances	GA over percent mean
			Min	Max					
1	Days to 50% flowering	87.14	83.86	90.26	3.24	2.67	67.7	3.94	4.52
2	plant height (m)	93.21	78.26	108.06	9.86	9.04	84.2	15.94	17.10
3	Panicles / plant	8.23	7.00	10.13	15.13	12.29	66.0	1.69	20.56
4	Panicle length (cm)	23.98	22.16	26.83	6.71	4.93	54.0	1.79	7.46
5	Panicle weight (g)	4.20	3.36	5.42	17.76	12.78	51.8	0.79	18.96
6	Grains / panicle	187.07	142.26	244.86	22.31	19.48	76.3	65.61	35.07
7	Fertility %	86.73	82.33	90.98	4.03	3.15	61.3	4.41	5.09
8	100 grain weight (g)	2.45	2.26	2.64	7.61	5.46	51.5	0.19	8.07
9	Biological yield / plant (g)	79.05	62.53	89.60	12.371	10.90	77.6	15.64	19.78
10	Grain yield / plant	32.76	24.00	38.53	15.39	13.56	77.7	8.06	24.62
11	Harvest index %	41.43	36.77	47.18	9.84	7.33	55.6	4.66	11.26

PCV= Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h^2 = Heritability (broad sense), GA= Genetic advance

Table.4 Estimates of variability, heritability, genetic advance, and genetic gain over per cent mean crosses (F$_2$)

S. N.	Character	Mean	Range		PCV	GCV	H^2(bs) %	Genetic Advances	GA over percent mean
			Min	Max					
1	Days to 50% flowering	87.52	84.00	90.66	2.859	2.12	55.4	2.85	3.26
2	Plant height (cm)	96.63	91.86	102.39	4.395	3.15	51.6	4.51	4.67
3	Panicles / plant	7.67	6.53	9.66	13.68	9.81	51.5	1.11	14.50
4	Panicle length (cm)	24.33	22.33	27.33	6.98	5.02	51.7	1.81	7.44
5	Panicle weight (gm)	3.86	3.66	4.48	8.026	5.86	53.3	0.34	8.81
6	Grains / panicle	190.78	180.00	210.86	7.353	5.67	59.6	17.21	9.02
7	Fertility %	85.45	80.00	90.75	4.744	3.60	57.6	4.80	5.62
8	100grain weight (gm)	2.43	2.24	2.64	7.327	5.69	60.4	0.22	9.12
9	Biological yield / plant (gm)	72.33	63.33	94.18	15.504	15.14	95.4	22.03	30.45
10	Grain yield / plant (gm)	26.22	23.00	28.40	7.147	5.63	62.2	2.40	9.16
11	Harvest index %	36.79	30.14	41.78	12.758	11.417	80.1	7.74	21.04

PCV= Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h^2 = Heritability (broad sense), GA= Genetic advance

While in parental population, high heritability coupled with high genetic gain over the percent mean exhibited for grain yield per plant followed by grains per panicle and panicles per plant. Its forces to conclude that these characters are governed by additive action. Similar results observed by Tuwar *et al.,* (2013), Sadimantara *et al.,* (2014), Anis *et al.,* (2016) (Table 3 and 4).

References

Abebe T, Alamerew S and Tulu L. 2017. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L) genotypes at Fogera and Pawe Ethiopia. Adv. Crop Science Technology 5(2):1-8.

Akinwale MG. 2011. Heritability and correlation coefficient analysis for yield and components analysis for yield and components in rice (*Oryza sativa* L.). African Journal of Plant Science 5: 207-212.

Anis G. 2016. Evaluation of promising lines in rice (*Oryza sativa* L.) to agronomic and genetic performance under Egyptian conditions. International journal of Agronomy and Agricultural Research 8(3):52-57.

Babu VR, Shreya K, Dangi KS, Usharani G and Nagesh P. 2012. Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. International Journal Scientific and Research Publication, 2(6):1-5.

Hossain MA and Hassan AK, Islam MA, Raffi SA. 2014. Character association and path coefficient analysis of grain and yield related traits in some promising early to medium duration rice advance lines. International Journal of Experiment Agriculture 5(1): 8-12.

Islam MA, Raffi SA, Hossain MA and Hassan AK. 2015. Character association and path coefficient analysis of grain and yield related traits in some promising early to medium duration rice advance lines. International Journal of Experiment Agriculture 5(1): 8-12.

Islam MZ, Khalequzzaman M, Basher MK, Ivy NA, Haque MM and Mian MAK. 2016. Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. The Scientific World Journal 1-15.

Kahani F and Hittalman S. 2015. Genetic Analysis and Traits Association in F_2Intervarietal Populations in Rice Under Aerobic Condition. Rice Research: Open Access 3:(4)1-5.

Kiran KK, Gururaj Rao MR, Rajanna MP, Rao MA, Mahadevu P and siddegowda DK. 2012. Variability, heritability and genetic advance studies in F_2 population of two process (*Oryza sativa* L.). Mysore Journal Agriculture Science, 46(4): 917-919.

Konate AK. 2016. Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits. African Journal of Agricultural Research. Academic Journal 11(35): 3340-3346.

Lingaiah N, Venkanna V, Cheralu C and Satish Chandra B. 2014. Variability for yield and yield attributing trait in mid early genotype of rice (*Oryza sativa* L.). International Journal Research of Science, Engineering and Technology, 1(4): 179-180.

Mallimar M. 2015. Genetic variability for yield and yields attributing trait in f_3 generation of rice (*Oryza sativa* L.). Research Environment Life Science 9:24-28.

Nandeshwar BC, Pal S, Senapati BK and De DK (2010) Genetic variability and character association among biometrical traits in F_2 generations of some rice crosses. Electronic Journal Plant Breeding 1(4):758-763.

Panwar LL and Mathur SS. 2007. Variability studies in segregating populations of rice *(Oryza sativa* L.*)*. Annual Agricultural Research New Series 28 (1): 53-56.

Patel HR, Patel VP, Patel PV and Patel UV. 2018. Genetic Variability Studies in Segregating Generation for Yield and Component Traits in Rice (*Oryza sativa* L.). International Journal Pure Application Bioscience 6 (5): 863-871.

Rahman A, Shah SMA, Rahman H, Khalil IH, Ismameel M, Raza MA and khan A. 2015. Genetic variability for morphological parameters in f_2 segregating populations of rice. Pakistan Journal botany 47(5): 1759-1764.

Sadimantara GR, Muhidin and Cahyono E. 2014. Genetic analysis on some agro-morphological characters of hybrid progenies from cultivated paddy rice and local upland rice. Advanced studies in Biological 6(1): 7-18.

Sala M and Shanthi P. (2016). Variability, heritability and genetic advance studies in F_2 population of rice (*Oryza sativa* L.). International Journal of Forestry and Crop Improvement 7(1):57-60.

Shrivastava A, Mishra DK and Singh SK. 2014. Characterization of JNPT line in rice. Plant Archibes, 15(1): 397-403.

Singh AK, Nandan R, Singh PK. 2013. Genetic variability and association analysis in rice germplasm under rainfed conditions. Crop Research Hisar. 47(1/3):7-11.

Singh SK, Singh CM and Lal GM. 2011. Assessment of genetic analysis and correlation studies for grain yield in rice *(Oryza sativa* L.*)*. Journal of Plant Biology 1(4):73-76.

Subaiah PV, Sekher RM, Reddy KHP and Reddy NPA.2011. Variability and genetic parameters for grains yield and its components and kernel quality attributes in cms based rice hybrids. International journal of applied biology and Pharmaceutical Technology, 3(2); 603.

Tuwar AK, Singh SK, Sharma A &Bhati PK. 2013. Appraisal of genetic variability for yield and its component characters in rice *(Oryza sativa* L.*)*. Biolife 1(3): 239-246.