Journal of Pharmacognosy and Phytochemistry 2019; 8(1): 1630-1634

Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2019; 8(1): 1630-1634
Received: 16-11-2018
Accepted: 18-12-2018

Mamata Khandappagol
Ph.D Scholar, Dept of Genetics and Plant Breeding, College of Agriculture, UAS Bengaluru, Karnataka, India

MP Rajanna
Scientist, AICRP on Rice Zonal Agriculture Research Station, V. C. Farm, Mandya, Karnataka, India

SK Savita
Senior research fellow, Dept of Genetics and Plant Breeding, Central Research Institute for Dryland Agriculture, Hyderabad, Telangana, India

Correspondence
Mamata Khandappagol
Ph.D Scholar, Dept of Genetics and Plant Breeding, College of Agriculture, UAS Bengaluru, Karnataka, India

Variability and frequency distribution studies in F_2 population of two crosses involving traditional varieties of rice (*Oryza sativa* L.)

Mamata Khandappagol, MP Rajanna and SK Savita

Abstract

An investigation was carried out to study the frequency distribution and variability produced in two F_2 populations of rice *viz.,* ‘Rajamudi × BR-2655’ and ‘Rathnachoodi × BR-2655’ for grain yield and its seven component characters. The F_2 populations of both the crosses showed high PCV and GCV values for grain yield per plant and low PCV and GCV was observed for thousand grain weight and panicle length. The traits Plant height and grain yield per plant had high heritability along with high genetic advance indicate that these characters attributable to additive gene effects. Skewness and kurtosis indicated dominance based complementary gene interaction involving large number of genes. Duplicate type of epistasis was observed in the inheritance of filled grains per panicle in both the crosses. Moderate number of genes among which equal frequency of genes had increasing and decreasing effect with duplicate type of epistasis was observed in the expression of days to fifty per cent flowering and grain yield per plant in both the crosses.

Keywords: Rice, F_2 populations, Genotypic co-efficient of variation, Phenotypic co-efficient of variation, Heritability, Genetic advance as a per cent of mean

Introduction

Rice (*Oryza sativa* L.) is the most widely consumed staple food for a large part of the world's human population, especially in Asia. Rice contributes 43 per cent to the total food grains and 53 per cent to the cereal production. There will be more demand in future for rice and there is need to produce 350 million more tonnes of rice by 2020 in the world. Traditional rice varieties or landraces have a high level of genetic heterogeneity compared to modern cultivars. Landraces comprise of the unique source for gene of high adaptability but are poor yielders. Therefore, it is an indispensable demand for varietal improvement in such situation. To formulate a sustainable breeding program precise knowledge about genetic divergence for yield components is a crucial one as varietal improvement depends mainly on the selection of parents with high genetic divergence in hybridization. Crop improvement for specific trait has been achieved through effective use of F_2 segregating population and fixing desirable combinations. Therefore, the present study has been undertaken to determine the estimates of variability, heritability and genetic advance as per cent of mean for grain yield and its component and frequency distribution pattern based on skewness and kurtosis in F_2 segregating generation for selected two crosses.

Materials and Methods

The present investigation was carried out during rabi/summer 2015 at Zonal Agricultral Research Station, Mandya Karnataka. Experimental material consisted of F_2 population developed involving traditional varieties Rajamudi and Rantnachoodi are high yielders with superior nutritional grain quality but they are photo sensitive and susceptible to lodging because of their tall growing nature and other parent BR-2655 improved semi-dwarf high yielding variety. F_2 population of two crosses of rice *viz.,* ‘Rajamudi × BR-2655’ and ‘Rathnachoodi × BR-2655’ along with their three parents were planted in plots of 4m length in ten rows each maintaining a row to row distance of 20 cm and plant to plant distance of 10 cm in wet lands at ‘C’ block of ZARS, V. C. Farm, Mandya and recommended cultural practices and plant protection measures were taken up as per the packages of practices recommended by University of Agricultural Sciences Bangalore. Data was recorded on 10 randomly chosen plants of parents (Rajamudi, Rathnachoodi and BR-2655) and on 3696 and 1591 competitive plants in the F_2 population of ‘Rajamudi × BR-2655’ and ‘Rathnachoodi × BR-2655’ crosses, respectively. Observations were recorded on grain yield and yield attributing traits *viz* days to 50% flowering, plant height (cm), productive tillers per plant, panicle length (cm), filled grains per panicle, 1000-grain weight (g) and grain yield per plant (g).

Statistical analysis

Statistics such as mean and phenotypic and genotypic co-efficient of variation (PCV and GCV) were computed based on the method suggested by Panse and Sukhatme (1961) [12]. Heritability in the broad sense was computed with the formula suggested by Lush (1940) [48]. The genetic advance was estimated adopting the method suggested by Johnson *et al.*, (1955) [5]. Skewness, the third degree statistics and Kurtosis, the fourth degree statistics were estimated as per Snedecor and Cochran (1974) [17] to understand the nature of distribution of 8 quantitative traits in F_2 population of each. All the above characters were calculated using Microsoft Excel.

Results and Discussion

The potentiality of a cross is measured not only by mean performance but also on the extent of variability. Knowledge on nature and magnitude of genotypic and phenotypic variability present in any crop species plays an important role in formulating successful breeding programmes (Allard, 1960) [2]. Siva Subramanian and Mathavamenon (1973) [16] also highlighted the importance of variability in early segregating generations and suggested that magnitude of genotypic co-efficient of variability and phenotypic co-efficient of variability should be given importance. Jennings *et al.*, (1979) [4] suggested that crosses which will realise early homozygosity are ideally suited for further breeding work. The mean, range, variability estimates i.e., Genetic co-efficient of variation (%), phenotypic co-efficient of variation (%), heritability (%) (Broad sense), genetic advance as *per cent* of mean are furnished in Table 1. The range of variability was high for all the characters studied except panicle weight, panicle length, harvest index and 1000-grain weight, which exhibited low to moderate variability in both the crosses.

The Platykurtic (-1.24 and -1.24 in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655') and positively skewed (0.28 and 0.29 in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655') distribution indicated dominance based complementary gene interaction involving presence of large number of genes having decreasing effect on the trait days to 50 % flowering in both the populations (Fig. 1). The trait plant height appeared to controlled by few segregating genes with majority of them exhibiting decreasing effect and dominance based complementary gene interaction as indicated by the leptokurtic (-0.04 and 1.72) and negatively skewed (-0.34 and -0.66) distribution in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' population respectively (Fig. 2).

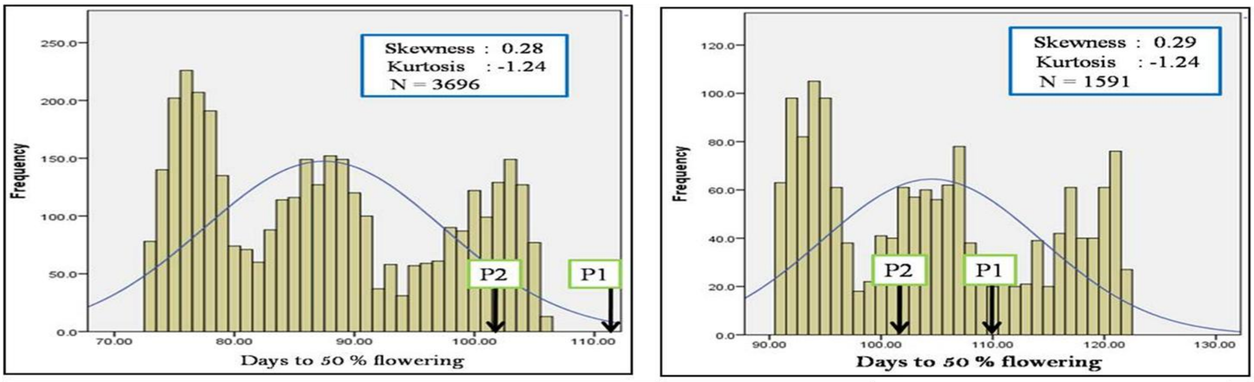
The platykurtic (0.86 and 2.27) and positively skewed (0.70 and 1.17) distribution in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' populations, respectively indicated dominance based complementary gene interaction involving large number of genes having decreasing effect in the inheritance of productive tillers per plant in both the populations (Fig. 3). Panicle length appeared to be controlled by large number of dominant genes with increasing effect and duplicate interaction in the inheritance as indicated by platykurtic (11.68 and 24.13) and positively skewed (1.31 and 2.90) distribution in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' population, respectively (Fig. 4).

The platykurtic (0.16 and 0.10) and negatively skewed (-0.36 and -0.39) distribution in both 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' populations, respectively indicated dominance based complementary gene interaction involving presence of large number of genes having decreasing effect in the inheritance of grains per panicle (Fig. 5). Platykurtic (-0.32) and positive (0.20) distribution in 'Rajamudi × BR-2655'indicated large number of dominant genes having complete ambi-directional epistasis in the expression of 1000-grain weight, while the same trait appeared to be controlled by larger number of genes having decreasing effect and involvement of dominance based complementary interaction as evidenced by platykurtic (0.17) and negatively skewed (-0.06) distribution in 'Rathnachoodi × BR-2655' population (Fig. 6). Platykurtic (0.44 and 0.20) and positively skewed (0.61 and 0.59) distribution in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' populations, respectively suggested the dominance based complementary gene interaction involving presence of large number of genes having decreasing effect in the inheritance of grain yield in both the populations (Fig. 7).

As expected, estimates of PCV values were relatively higher than GCV values in F_2 generation of both the crosses coupled with narrow differences which indicate less environmental influence on the expression of all the traits except productive tillers per plant, panicle weight and grain yield in both the F_2 populations.

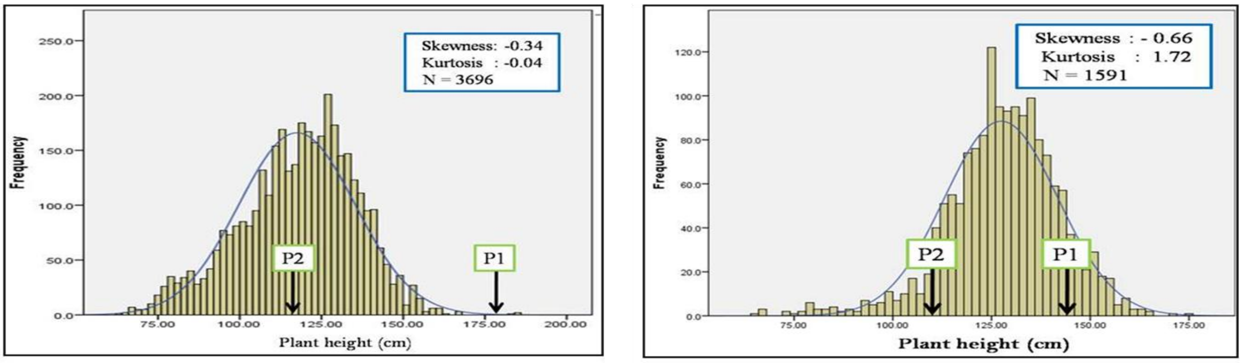
Very low variability was noticed for days to 50 % flowering as evidenced by lower values of PCV (11.4% and 9.41 %) and GCV (10.65% and 8.20%) in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' populations, respectively. Contrary to this, high heritability (97.44%) with moderate genetic advance as per cent of mean (30.33 %) in 'Rajamudi × BR-2655' population indicated major role of non-additive gene action while, high heritability (87.12 %) and moderate genetic advance as per cent of mean (16.88 %) in 'Rathnachoodi × BR-2655' population indicated role of additive gene action in respect of this trait. Kannan Bapu and Soundarapandian (1993) [6] also reported similar result in respect of this trait.

PCV and GCV values (15.11 % and 14.72 %, respectively) in 'Rajamudi × BR-2655' population indicated moderate variability for plant height. Results of present study are at par with the earlier reports of Kannan Bapu and Soundarapandian (1993) [6] and Singh and Choudhary (1996) [15]. Contrary to this, high variability was noticed for this trait as evidenced by moderate values of PCV and GCV (11.25 % and 10.59 %, respectively) in 'Rathnachoodi × BR-2655' population. These results are in agreement with earlier reports of Mohanthy and Singh (1969) [9] and Chauhan *et al.*, (1990) [3]. This trait exhibited high heritability coupled with low to moderate genetic advance expressed as per cent of mean in both the crosses indicating role of non-additive gene action in its genetic control. Results of present study are at par with the earlier reports of Suresh and Reddy (2002) and Kumar *et al.*, (2005) [7].



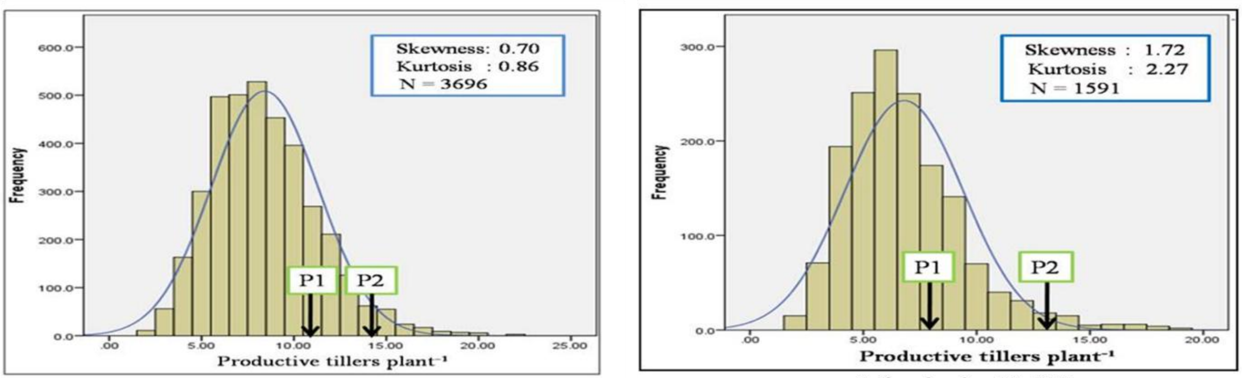
Rajamudi × BR-2655 **Rathnachoodi × BR-2655**

Fig. 1: Frequency distribution of F_2 population of 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' crosses for days to 50% flowering.



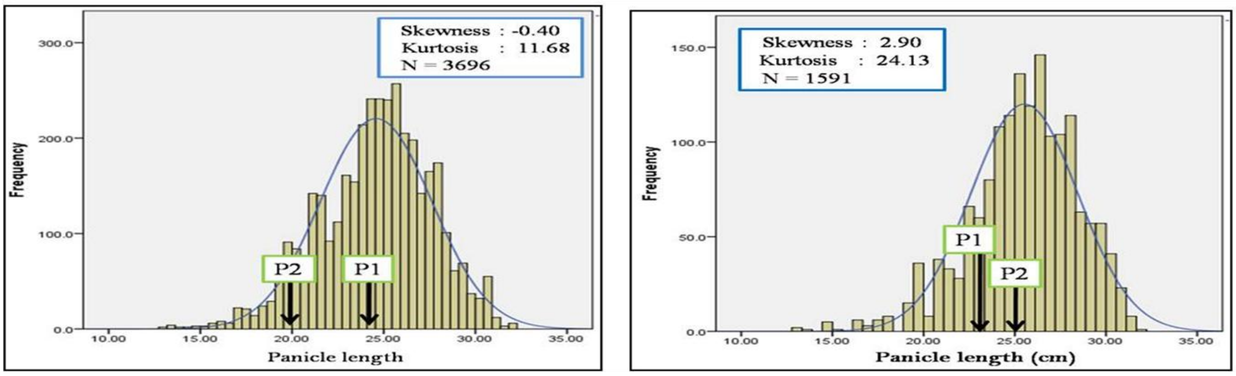
Rajamudi × BR-2655 **Rathnachoodi × BR-2655**

Fig. 2: Frequency distribution of F_2 population of 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' crosses for plant height.



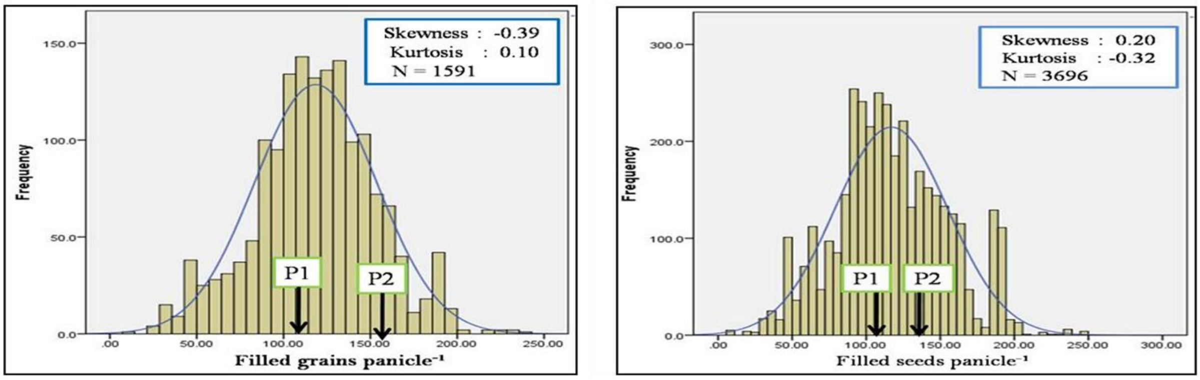
Rajamudi × BR-2655 **Rathnachoodi × BR-2655**

Fig. 3: Frequency distribution of F_2 population of 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' crosses for productive tillers per plant.



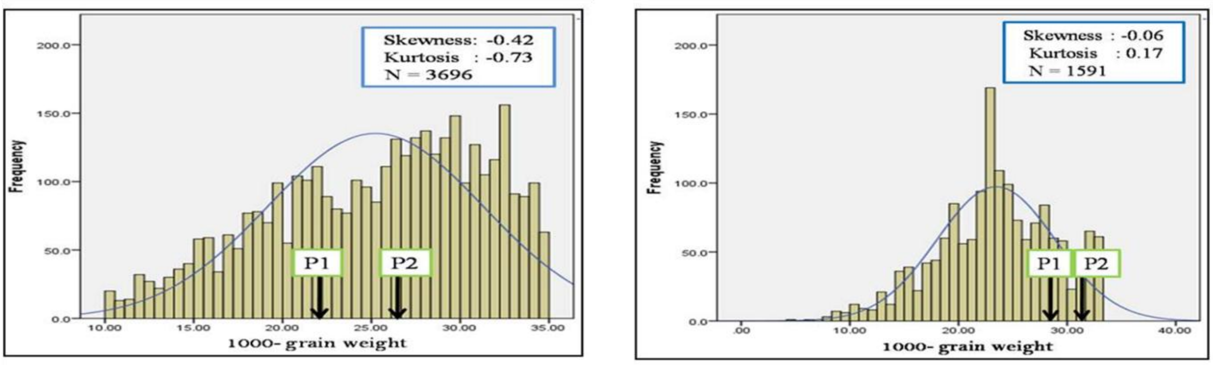
Rajamudi × BR-2655 **Rathnachoodi × BR-2655**

Fig. 4: Frequency distribution of F_2 population of 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' crosses for panicle length.



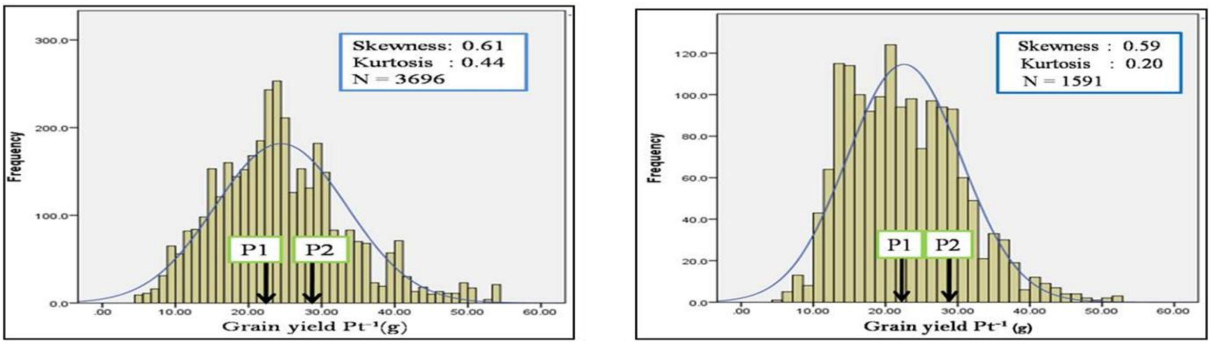
Rajamudi × BR-2655 **Rathnachoodi × BR-2655**

Fig. 5: Frequency distribution of F_2 population of 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' crosses for filled grains per panicle.



Rajamudi × BR-2655 **Rathnachoodi × BR-2655**

Fig. 6: Frequency distribution of F_2 population of 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' crosses for 1000-grain weight.



Rajamudi × BR-2655 **Rathnachoodi × BR-2655**

Fig. 7: Frequency distribution of F_2 population of 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' crosses for grain yield per plant.

Productive tillers exhibited wide variability and high influence of environment as evidenced by wide difference between GCV and PCV as well as higher values of PCV (34.44 % and 38.43 %) and GCV (18.94% and 30.26 %) in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' population, respectively. High broad sense heritability (54.99 % and 78.74 %) coupled with high genetic advance (39.01% and 62.34 %) as per cent of mean in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' population, respectively revealed major role of additive gene action in the genetic control of this trait. Similar results were reported by Nayak (2008) [11] and Nandeshwar *et al*., (2010) [10].

Panicle length in both the crosses registered moderate values of PCV (12.36% and 11.50 %) and low value of GCV (8.05% and 7.94 %), respectively. This is in accordance with the earlier observations made by Mohanthy and Singh (1969) [9] and Paramasivan (1986) [13]. However, high broad sense heritability (65.13% and 69.03 %) but moderate genetic advance expressed as per cent of mean (16.58% and 16.36 %) in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' population, respectively indicated predominant role of non-additive gene action in respect of this trait in both crosses. Agrawal (2003) [1] reported similar results with respect to heritability and genetic advance for this trait.

Filled seeds per panicle exhibited high values of GCV (28.14% and 29.71%) and PCV (15.33% and 24.47%) in 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' population, respectively. In general considerable difference exists between both GCV and PCV, which indicates influence of environment. Result obtained in present study supported with earlier reports of Savitha and Ushakumari (2015) [14]. In both the crosses high (54.49% and 82.35%) broad sense heritability coupled with high (31.59% and 50.40%) amount of genetic advance expressed as per cent of mean was observed. This is in conformity with the reports of Savitha and Ushakumari (2015) [14]. High broad sense heritability with coupled with high genetic advance expressed as per cent of mean of this trait can be utilized as an index for its improvement.

Table 1: Variability parameters for seven quantitative characters in F_2 populations of Cross 1 (Rajamudi × BR-2655) and Cross 2 (Rathnachoodi × BR-2655)

Characters	Crosses	Mean	Range		PCV (%)	GCV (%)	H (%)	GAM
			Minimum	Maximum				
Days to 50 % flowering	Cross-1	87.45	73	106	11.44	10.65	84.37	19.88
	Cross-2	104.54	91	122	9.41	8.2	87.12	16.88
Plant height (cm)	Cross-1	117.51	63	185	15.11	14.72	97.44	30.33
	Cross-2	127.44	65	174	11.25	10.59	94.19	21.83
Productive tillers per plant	Cross-1	8.41	2	22	34.44	18.94	54.99	39.01
	Cross-2	6.8	2	19	38.43	30.26	78.74	62.34
Panicle length (cm)	Cross-1	24.58	13	31.97	12.36	8.05	65.13	16.58
	Cross-2	25.52	13.17	31.83	11.5	7.94	69.03	16.36
Filled grains per panicle	Cross-1	134.15	36	250	28.14	15.33	54.49	31.59
	Cross-2	118.5	12	240	29.71	24.47	82.35	50.4
1000- grain weight(g)	Cross-1	25.23	15.01	34.97	9.85	8.41	68.31	12.97
	Cross-2	23.46	14.22	33.14	9.12	7.02	61.56	11.34
Grain yield per plant(g)	Cross-1	24.44	5	54.4	36.88	22.26	60.37	45.86
	Cross-2	22.57	5.1	51.4	35.02	22.49	64.23	46.34

The PCV (9.85 % and 9.12 %) and GCV (8.41 % and 7.02%) values were low coupled with high (68.13 % and 61.56 %) broad sense heritability and moderate genetic advance expressed as per cent of mean (12.97 % and 11.34%) in ‘Rajamudi × BR-2655’ and ‘Rathnachoodi × BR-2655’ populations, respectively indicated moderate variability and major role of additive gene action in the control of 1000-grain weight in both the populations. Similar results were reported by Kannan Bapu and Soundarapandian (1993) [6] and Chauhan and Chauhan (1994).

Wide variability was noticed for grain yield per plant as evidenced by relatively higher values of PCV (36.88 % and 35.02 %) and GCV (22.26 % and 22.49%) in ‘Rajamudi × BR-2655’ and ‘Rathnachoodi × BR-2655’ populations, respectively. Estimates of broad sense heritability (60.37% and 64.23%) and genetic advance expressed as per cent of mean (45.86 % and 46.34 %) were relatively high in ‘Rajamudi × BR-2655’ and ‘Rathnachoodi × BR-2655’ populations, respectively indicating major role of additive gene action in the genetic control this trait in both the populations. Results of the present study are in conformity with the reports of Kumar *et al*., (2005) [7] and Nayak (2008) [11].

The results of the present study clearly indicate that, grain yield cannot be improved by direct selection as the trait is subjected to greater environmental effect. However, yield can be improved indirectly by selecting F_2 plants with high total tillers per plant, productive tillers per plant, grains per panicle and 1000-grain weight as these traits showed high heritability coupled with high genetic advance as per cent of mean.

References

1. Agarwal KB. Variability studies in segregating populations of rice. Ann. Agric. Res. New series. 2003; 24:707-709.
2. Allard RW. Principles of Plant Breeding. John Wiley and Sons. Inc. U.S.A. 1960, 485.
3. Chauhan JS, Chauhan VS. Genetic analysis of grain dimensions and weight and their association with grain yield in rainfed rice (*Oryza sativa*). Indian J Agric. Sci. 1990; 64:613-618.
4. Jennings PR, Coffman WF, Kauffman HE. Rice improvement. Int. Rice. Res. Inst Los Banos, Manila, Phillipines, 1979.
5. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in Soybean and their application in selection. Agron. J. 1955; 47:477-483.
6. Kannan Babu JR, Soundrapandian G. Genetic variability and association studies in F_3generation of rice. Madras Agric. J. 1993; 80: 711-712.
7. Kumar Sanjeev Singh HB, Sharma JK. Genetic variability for morpho-physiological and some quality traits in rice (*Oryza sativa* L.). Himachal J Agric. Res. 2005; 31: 163-165.
8. Lush JL. Intra - sire correlation and regression of offspring on dams as a method of estimating heritability of characters. Proc. American Soc. Anim. Prod. 1940; 33:293-301.
9. Mohanthy HK, Singh SC. Biometrical studies in rice with special reference to nitrogen response. Oryza. 1969; 6:23-25.
10. Nandeshwar BC, Pal S, Senapati BK, De DK. Genetic variability and character association among biometrical traits in F_2 generation of some rice crosses. Electronic J Pl. Breed. 2010; 1:758-763.
11. Nayak AR. Genetic variability and correlation study in segregating generation of two crosses in scented rice. Agric. Sci. Digest. 2008; 28:280-282.
12. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 2nd Ed., Indian Council. Agric. Res. New Delhi, 1961, 22.
13. Paramasivan KS. Study of genotypic, phenotypic variability in hybrids of dwarf and tall indica rice. Madras Agric. J. 1986; 73:527-529.
14. Savitha P, Usha Kumari R. Genetic variability studies in $F_2$and F_3 segregating generations for yield and its components in rice (*Oryza sativa* L.). Indian. J Sci. Tech. 2015; 8(17):74-84.
15. Singh S, Chaudhary BS. Variability, heritability and genetic advance in cultivars of rice (*Oryza sativa* L.). Crop Res. 1996; 12: 165-167.
16. Sivasubramanian P, Menon PM. Genotypic and phenotypic variability in rice. Madras Agric. J. 1973; 60:1093-1096.
17. Snedecor GW, Cochran WG. Statistical Methods. 6th ed., Oxford and IBH Pub. Co., New Delhi, India, 1974.