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Studies on Variability and Frequency Distribution of Yield and Yield Related Traits in F_2 Population of Rice (*Oryza sativa* L.)

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A B S T R A C T

An investigation was carried out at ZARHS, Shivamogga during summer 2015 to study frequency distribution properties and variability formed in rice F_2 population of Jyothi × Kiruwana' for grain yield and its component characters. The F_2 populations showed high PCV and GCV coupled with high heritability and high genetic advance as per cent of mean for number of tillers per plant and productive tillers per plant Positive skewness and platykurtic distribution recorded for days to flowering, number of tillers per plant, productive tillers per plant, days to maturity, panicle length, grain yield per plant and L: B ratio indicated that dominance based complementary gene interaction involving large number of genes having decreasing effect in the inheritance of these traits. However, dominance based duplicate interaction was noticed for plant height, test weight, grain length and grain breadth.

Introduction

Rice (*Oryza sativa* L.) was the first sequenced crop genome with estimated genome size of 430 Mb (Jackson, 2016). It is the one of the world's most stable food crop for over half of the world's population (Khush, 2005) and serves as a pillar for food security in many developing countries. More than 90 per cent of rice is grown and consumed in Asia where about 60 per cent of the world's population lives, reflecting the value of rice in daily human life. The year, 2004 was declared as International Year of Rice by the United Nations Food and Agriculture Organization by considering its importance.

Rice is cultivated globally in an area of about 161.40 million hectares with production of about 506.30 million tonnes and productivity of 3.14 tonnes per hectare. India is an important centre of rice cultivation and it was cultivated over an area of 44.11 million hectare with an annual production of 105.48 million tonnes and an average productivity of 2.39 tonnes per hectare. In India, rice is grown in almost all the states. Whereas in Karnataka, occupied over an area 13.26 lakh hectares with annual production of 3.54 million tons and it's average productivity was 2.67 tonnes per hectare (Anon, 2016). Based on the trend of consumption in our country, it is estimated that requirement of rice will be 137.30 million tonnes by 2050 (Anon, 2013).

The green revolution in the 1960's increased world rice production. On contrary the production potential of modern cultivars of rice is currently declining, because narrow genetic base in modern cultivars of rice (Wouw *et al.,* 2010). To boost the production of rice in India, knowledge on inheritance pattern of yield and its components is very much essential. Knowledge of genetic variability parameters provides immense value in the selection of superior segregants for yield and related traits. The distribution properties of skewness and kurtosis represent the insight about the nature of gene action and number of genes controlling for each trait, respectively. Hence, the present investigations was undertaken to assess variability and frequency distribution pattern for grain yield and its attributing traits in the F_2 population.

Materials and Methods

The study was conducted at Zonal Agricultural and Horticultural Research Station (ZAHRS), Shivamogga. The experimental material consisted of 226 F_2 individuals resulted from the cross 'Jyothi × Kiruwana' were evaluated for morphogenetic traits during Summer-2016. Seedlings were transplanted (21 days old) to the main field with a spacing of 30 x 10 cm. Observations on 11 of quantitative traits *viz.*, days to flowering, plant height, total number of tillers, productive tillers, days to maturity, panicle length, grain yield, test weight, grain length, grain width and L: B ratio were recorded on individual plant of F_2 and randomly selected five plants of both the parents. The mean values of F_2 generation were used for estimation of coefficients of skewness and kurtosis using 'SPSS (16.0)' software program. Kurtosis indicates the relative number of genes controlling the traits (Robson, 1956). Whereas, Skewness indicates nature of gene action involved in inheritance of yield and yield contributing traits. Variability parameters such as GCV, PCV, h^2 (BS) and GAM were estimated using MS Excel program.

Results and Discussion

The mean, range, skewness and kurtosis for all characters in F_2 generation were tabulated in Table 1. The characters investigated in the present study exhibited both positive and negitive skewness values. The kurtosis value less than three was recorded for all the studied traits and they are platykurtic.

The platykurtic and positively skewed distribution recorded for days to flowering, number of tillers per plant, productive tillers per plant, days to maturity, panicle length, grain yield per plant and L: B ratio indicated that, these traits are governed by large number of segregating genes and majority of them having decreasing effects displaying dominant and dominant based complementary epistasis in inheritance. Hence, intense selection is required for immense genetic gain in these traits. The similar findings were also observed by Rani *et al.,* (2016) for days to flowering and L: B ratio; Kiran *et al.,* (2012) and Rani *et al.,* (2016) for number of tillers per plant, productive tillers per plant, panicle length and also for grain yield per plant.

Whereas, platykurtic and negatively skewed distribution recorded for plant height, test weight, grain length and grain breadth and these traits are governed by large number of genes and majority of them have increasing effects displaying dominant and dominant based duplicate epistasis in inheritance.

Table.1 Descriptive statistics for yield and related traits in F_2 segregating population of cross Jyothi × Kiruwana

Sl No.	Characters	Mean± SE	Range		Skewness	Kurtosis	Kurtosis type
			Min.	Max.			
1	Days to flowering	109.69 ± 0.81	86.00	136.00	0.43	-0.89	Platykurtic
2	Plant height (cm)	102.09 ± 1.21	60.00	148.00	-0.26	-0.33	Platykurtic
3	Number of tillers per plant	16.17 ± 0.57	04.00	36.00	0.86	-0.13	Platykurtic
4	Productive tillers per plant	15.61 ± 0.54	04.00	35.00	0.82	-0.17	Platykurtic
5	Days to maturity	143.88 ± 0.78	120.00	167.00	0.23	-0.97	Platykurtic
6	Panicle length (cm)	21.39 ± 0.18	15.06	28.52	0.11	-0.37	Platykurtic
7	Grain yield per plant (g)	27.65 ± 0.94	03.00	63.00	0.52	-0.46	Platykurtic
8	Test weight (g)	23.01 ± 0.30	12.64	32.97	-0.07	-0.92	Platykurtic
9	Grain length (mm)	07.96 ± 0.04	06.76	09.23	-0.02	-1.14	Platykurtic
10	Grain breadth (mm)	02.38 ±0.05	01.20	03.42	-0.02	-1.58	Platykurtic
11	L:B ratio	03.61 ±0.06	02.27	05.96	0.46	-0.90	Platykurtic

Table.2 Variability parameters for yield and related traits in F_2 segregating population of cross Jyothi × Kiruwana

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h^2 (%)	GAM
			Min.	Max.				
1	Days to flowering	109.69	86.00	136.00	10.99	11.05	98.87	33.42
2	Plant height (cm)	102.09	60.00	148.00	17.21	17.87	92.69	122.22
3	Number of tillers	16.17	04.00	36.00	53.18	54.01	96.94	82.57
4	Number of productive tillers	15.61	04.00	35.00	53.04	53.98	96.56	75.45
5	Days to maturity	143.88	120.00	167.00	08.02	08.13	97.33	22.87
6	Panicle length (cm)	21.39	15.06	28.52	10.97	12.52	76.86	01.85
7	Grain yield per plant (g)	27.65	03.00	63.00	38.47	51.16	56.54	210.81
8	Test weight (g)	23.01	12.64	32.97	20.99	21.49	95.36	09.93
9	Grain length (mm)	07.96	06.76	09.23	07.38	08.04	84.32	00.07
10	Grain breadth (mm)	02.38	01.20	03.42	28.67	28.97	97.94	00.28
11	L:B ratio	03.61	02.27	05.96	25.37	26.24	93.46	00.48

Hence, mild selection is expected to result in rapid genetic gain for these traits. These results agree with the findings of Rani *et al.,* (2016) for test weight, grain length and grain breadth and by Vijaya and Shailaja (2016) for plant height.

The variability parameters viz., PCV and GCV, heritability and genetic advance as per cent of mean for grain yield and its attributing characters are presented in Table 2. The characters investigated in the present study exhibited low, moderate and high PCV and GCV values. In the present study, the estimates of PCV were slightly higher than the corresponding GCV estimates for most of the studied characters indicating that the portion of PCV was more contributed by the genotypic component and less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. These kinds of results also noticed for the studied traits by Savitha and Ushakumari (2015), El-Badri *et al.,* (2016), Hefena *et al.,* (2016), Rani *et al.,* (2016) and Manunatha *et al.,* (2018)

The traits like number of tillers per plant, number of productive tillers per plant, grain yield per plant, test weight, grain breadth and L: B ratio showed high GCV and PCV indicating prominent variation or substantial amount of genetic variability present in the population for the concerned trait and hence, there is scope for selection. Thus, these traits might be controlled by additive gene action, which could be improved through simple selection methods. Similar results also noticed by El-Badri *et al.,* (2016), Hefena *et al., (*2016), Rani *et al.,* (2016) and Kiran *et al.,* (2012) for number of tillers per plant, number of productive tillers per plant and grain yield per plant.

Estimated heritability value alone is less reliable because as these values are prone to alter with change in the environment and experimental material (Swarup and Changale, 1962). Hence, heritability values coupled with genetic advance would be more reliable than heritability alone. In the present investigation, high heritability coupled with high GAM observed for days to flowering, plant height, number of tillers per plant, number of productive tillers per plant and days to maturity. Thus, these traits are most probably controlled by additive gene action and hence these traits can be fixed by selection. These results are in accordance with the findings of Hefena *et al.,* (2016) for days to flowering, plant height, number of tillers per plant and number of productive tillers per plant.

Some traits like panicle length, test weight, grain length, grain breadth and L: B ratio recorded the high heritability coupled with low GAM. The high heritability was exhibited due to the influence of favorable environment rather than genotype. So, selection for such trait might not be rewarding. Hence, these traits may not be useful as a criterion for selection for increased grain yield. These findings are in accordance with earlier reports of and Manunatha *et al.,* (2018) for plant height; Rani *et al.,* (2016) and Savitha and Ushakumari (2015) for panicle length; Sadimantara *et al.,* (2014) for test weight; and Rani *et al.,* (2016) for grain length.

Moderate GCV and PCV, high heritability and high GAM recorded for plant height indicates that although the variation is not so perceptible still there is an opportunity to improve this trait through selection. These results coincide with the findings of Sadimantara *et al.,* (2014), Bhuvaneswari *et al.,* (2015), Kahani and Hittalamani (2015) and Rani *et al.,* (2016).

In the present investigation, the studied quantitative traits governed by both additive and non-additive gene actions and were controlled by multiple genes showing gene interaction these were according to the values of descriptive statistics of F_2 populations. The results of the study also indicate that grain yield cannot be improved by direct selection but can be improved indirectly by selecting F_2 plants with high total tillers per plant and productive tillers per plant, because as these traits showed high heritability coupled with high genetic advance as per cent of mean.

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