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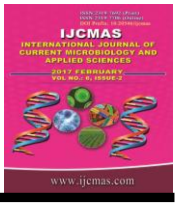

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Genetic Variability for Yield and Yield Components Characters in Bacterial Blight and Blast Resistance Genes Introgressed Backcross Populations in Rice

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ABSTRACT

An experiment was framed to study the variability, nature of gene action and number of genes controlling the characters in bacterial blight and blast resistance genes introgressed three backcross population in rice. Mean variation was high for number of grains and plant height for all the crosses. The characters like plant height, number of productive tillers and number of grains were showed complementary gene interaction for all back cross population. While for thousand grain weight and single plant yield were explained complementary gene interactions in two backcross populations. Selection on these traits would obtain low genetic advance than expected. Panicle length in two crosses and thousand grain weight and single plant yield in one cross was showed duplicate gene interaction suggests that selection would be effective to gain higher genetic advance than expected. Kurtosis for plant height and panicle length was influenced by only few genes for all crosses, whereas number of productive tillers and number of grains were controlled by few genes for at least two crosses. Platykurtic distribution was prevalent in most of the characters in all crosses. Leptokurtic distribution was found in the cross TNAU CMS 2B × (TNAU CMS 2B × Zenith) for number of grains, suggesting that controlled by fewer genes.

Keywords

Rice bacterial blight,
Rice blast,
Skewness,
Kurtosis.

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Introduction

Rice is one of most important cereal stable food crop in the world, nearly 2.7 billion livelihoods depends on it (Tannidi *et al.*, 2016). Variability is an important and basic requirement in any breeding programme. Hybridization between genetically diverse parental lines with selection may result huge variation. The skewness and kurtosis statistical analysis provides the information about nature of gene action (Fisher *et al.*, 1932) and number of genes controlling the trait (Robson, 1956).

Generally, skewed distribution of the characters implies that the control of non-additive type of gene effects and influenced by environmental variables. Positive skewness explained the complementary gene action whereas, negative skewness related to duplicate (additive × additive) gene effects (Kiran, 2012; Malikarjuna, 2013; Vishnu *et al.*, 2014; Vanitha *et al.*, 2016). Moreover, genes controlling characters with skewed distribution leads to be predominantly dominant irrespective of increasing or decreasing genes effect of the characters (Pooni *et al*., 1997). Positive kurtosis of the characters indicated that presence of gene interactions while for negative sign of kurtosis or near to zero leads the absence of gene interactions (Kotch *et al*., 1992). The leptokurtic and platykurtic distribution of the characters are controlled by fewer and large number of genes, respectively. The present study aimed to study the variability, nature of gene action and number of genes controlling the characters in bacterial blight and blast resistance genes introgressed three backcross population in rice.

Materials and Methods

An experimental material comprised of bacterial blight resistance genes governed two backcross population and one blast resistance gene governed backcross population. The backcross populations were grown in Department of Rice, Tamil Nadu Agricultural University, Coimbatore, India. Six agro-morphological characters like plant height, number of productive tillers, panicle length, number of grains, thousand grain weight and single plant yield were recorded on the basis of single plant. Statistical analysis was performed in Microsoft Excel 2007 (Microsoft Corp., Redmond, WA, USA).

Results and Discussion

The statistical parameters *i.e.* maximum, minimum, mean, standard deviation, variance, standard error, skewness and kurtosis for three set of backcrosses were given in table 1, 2 and 3.

CB 87 R × IRBB 60

Greater amount of variability was present in CB 87 R × IRBB 60 for all studied characters. Among all, thousand grain weight showed substantial variation with the mean (74.00-122.00) followed by plant height (76.00-50.00 cm). This finding gets supported with Govintharaj *et al.*, (2016) and Ponnaiah Govintharaj *et al.* (2016). Negative skewness was found all the studied characters except plant height, number of productive tillers and number of grains. This finding concluded that single plant yield showed complementary gene action and other traits were showed duplicate gene action. This finding get supported with (Kiran *et al*., 2013; Vishnu *et al*., 2014) for the characters of number of productive tillers and single plant was positive skewness and, negative skewness for plant height and number of grains. The positive kurtosis was found only in thousand grain weight and single plant yield were controlled by cumulative genes, and negative for all other characters controlled by few genes. This finding suggests that characters were platykurtic nature indicating that low phenotypic variability for the cross (Vishnu *et al*., 2014; Kiran, 2012). Moreover, negative skewness and platykurtic distribution for the traits indicated that these evolved from dominance and dominance based duplicate gene action, which helps to conserve the individual plants from deleterious alleles arising from existing variability (Roy, 2000).

CB 174 R × IRBB60

Mean variation was high for number of grains (90.00-146.00) followed by plant height (89.00-127.00 cm). Skewness was positive sign for all studied characters. This finding was resulted for characters were showed duplicate gene interaction and explaining that low performer than average of the population. Positive kurtosis was noticed only for thousand grain weight influenced by more number of genes and others characters were governed by few genes, suggesting platykurtic distribution, suggesting that low agronomical variability for the cross (Vishnu *et al*., 2014).

Table.1 Descriptive statistics in BC_1F_1 cross CB 87 R × IRBB 60

Variables	Mean	Range		Standard Deviation	Variance	Standard Error	Skewness	Kurtosis
		Max.	Min.					
PH	82.32	90.00	76.50	4.07	16.59	11.88	0.29	-1.22
NPT	10.10	16.00	6.00	2.91	8.48	1.46	0.63	-0.67
PL	19.61	25.50	12.00	3.21	10.28	2.83	-0.41	-0.08
NG	94.56	122.00	74.00	14.16	200.63	13.65	0.52	-0.91
TGW	20.07	25.80	11.20	2.55	6.51	2.90	-0.94	2.44
SPY	19.80	24.78	12.31	2.64	6.97	2.86	-0.50	0.15

Table.2 Descriptive statistics in BC_1F_1 cross CB 174 R × IRBB 60

Variables	Mean	Range		Standad Deviation	Variance	Standard Error	Skewness	Kurtosis
		Max.	Min.					
PH	108.26	129.00	89.00	11.70	137.01	14.73	0.10	-1.20
NPT	10.57	15.00	8.00	2.07	4.29	1.44	0.52	-0.88
PL	22.34	27.50	18.00	2.38	5.65	3.04	0.18	-0.80
NG	113.50	146.00	90.00	15.94	253.95	15.45	0.42	-0.79
TGW	18.26	24.70	14.10	2.25	5.07	2.48	0.78	0.52
SPY	19.93	29.17	14.27	3.86	14.88	2.71	0.59	-0.48

Table.3 Descriptive statistics in BC_1F_1 cross TNAU CMS 2B × Zenith

Variables	Mean	Range		Standard Deviation	Variance	Standard Error	Skewness	Kurtosis
		Max.	Min.					
PH	101.59	128.00	84.00	14.25	203.12	14.66	0.46	-1.26
NPT	7.85	13.00	3.00	2.01	4.04	1.13	0.21	0.48
PL	21.86	27.00	17.00	2.69	7.21	3.16	-0.37	-0.78
NG	100.46	190.00	77.00	18.98	360.34	14.50	2.36	9.53
TGW	19.85	26.60	16.11	2.57	6.58	2.87	0.44	-0.66
SPY	20.64	28.89	16.20	3.03	9.17	2.98	0.78	0.19

TNAU CMS 2B × Zenith

Mean variation was high for thousand grain weight (77.00-190.00) followed by plant height (84.00-128.00). This finding was line up with (Ameenal *et al*., 2016; Ponnaiah Govintharaj *et al*., 2016). Negative skewness was noticed only in panicle length and it explained that duplicate gene interaction plays major role (Lestari *et al*, 2015). Positive kurtosis was observed for number of productive tillers, numbers of grains and single plant yield were controlled by more genes and other examined characters were influenced by few genes, indicating that these were platykurtic distribution (Vishnu *et al*., 2014). Number of grains was distributed leptokurtic nature, which is controlled by few genes.

In conclusion, this study revealed that variability was exists in studied characters of all the crosses. Selection could be effective for panicle length, thousand grain weight and single plant yield would be gain higher genetic advance than expected at early stage of one or two crosses. Selection needs to be done at later generation for plant height, number of productive tillers and number of grains in all back crosses.

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