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Research Notes

Genetic variability for panicle characters in segregating populations of aromatic rice

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The performance of traditional basmati varieties is very poor in high humid condition of eastern India. The local aromatic rice cultivars popularly grown in Gangetic West Bengal are not considered as basmati type for export purposes due to their short kernels. Very little attention has been paid for the improvement of such aromatic rice. The improvement of aromatic rice through hybridization would be easier if the cross-parents having aroma differ in panicle characters. Considering the above mentioned aspects, the present study was undertaken for assessing the variability in F_2 generation through crosses of two induced mutants of local aromatic cultivar Gobindabhog with three basmati varieties.

The experimental materials consisted of F_2 populations of six cross combinations utilizing two γ-ray induced mutants *viz.*, 124- 17-4 and 21-6-1 of local aromatic cultivar Gobindabhog (Ghosh, 1993) and three basmati varieties *viz.*, Basmati 370, Pakisan Basmati and Pusa Basmati 1. The mutants had short grains with an average length of 6mm and an average of 230 spikelets in 124-17-4 and 150 spikelets in 21-6-1 , whereas the basmati varieties had long grain (above 10.5 mm) with an average of 70 spikelets in Basmati 370, and 100 spikelets in Pakistan Basmati and Pusa Basmati 1. Ten rows of F_2 plants and three rows of each parent with a row length of 3m, spaced 20 cm between plants and 30 cm between rows, were planted in each replication following randomized block design during *kharif* season at Agricultural Farm, Visva-Bharati, West Bengal. Observations on nine panicle characters were recorded from fifty F_2 plants and ten plants in each parent per replication in each cross combinations. Phenotypic and genotypic coefficients of variation (Burton, 1952), heritability (Mahmud and Kramer, 1951) and genetic advance (Allard, 1960) were computed following standard methods.

The F_2 is a critical generation in breeding as it determines eventual success or failure in the hybridization programme (Jennings *et al*., 1979). The estimates of mean values, PCV, GCV, heritability and genetic advance studied from F_2 generation are given in Table 1. The cross 124-17-4 x Pakistan Basmati showed highest mean performance for panicle weight, spikelet fertility, grain length, length/breadth ratio and grain yield per panicle and the cross 124-17-4 x Pusa Basmati 1 displayed highest mean values for panicle length, secondary branches per panicle and spikelet number per panicle. The cross with high mean values is relatively effective in identifying the superior recombinants, when mean is considered as an index of selection (Finkner *et al.*, 1973).

The estimate of variability in different panicle characters is the major prerequisite

Table 1. Mean, range, phenotypic and genotypic coefficients of variation, heritability and genetic advance for nine panicle characters of five crosses in aromatic rice

Characters	Cross combination	Mean	Range		Coefficients of variation(%)		Heritability in broad sense (%)	Genetic advance as % of mean
			Min.	Max.	Phenotypic	Genotypic		
Panicle length (cm)	124-17-4 x Basmati 370	25.86	20.8	30.8	9.47	9.00	90.20	17.60
	124-17-4 x Pakistan Basmati	26.22	20.6	31.8	8.91	7.76	75.72	13.90
	124-17-4 x PusaBasmati 1	26.67	19.0	32.2	17.45	16.88	93.60	33.65
	21-6-1 x Basmati 370	22.87	15.8	27.8	10.09	9.00	79.61	16.55
	21-6-1 x Pakistan Basmati	24.58	17.4	30.4	10.78	9.53	78.03	17.33
Panicle weight (gm)	124-17-4 x Basmati 370	1.79	0.88	3.72	27.37	26.32	92.50	52.15
	124-17-4 x Pakistan Basmati	2.31	1.13	3.63	26.44	25.91	96.01	52.29
	124-17-4 x Pusa Basmati 1	2.08	0.85	3.88	35.33	35.13	98.89	71.97
	21-6-1 x Basmati 370	1.40	0.65	2.76	35.57	34.70	95.16	69.73
	21-6-1 x Pakistan Basmati	2.15	0.91	3.93	30.00	29.64	97.55	60.28
Primary branches panicle^{-1}	124-17-4 x Basmati 370	10.73	8.0	14.0	7.99	6.85	73.47	12.09
	124-17-4 x Pakistan Basmati	11.36	8.4	14.4	10.16	7.49	54.27	11.36
	124-17-4 x Pusa Basmati 1	11.59	8.8	15.8	7.56	6.31	69.53	10.83
	21-6-1 xBasmati 370	9.31	6.2	12.6	13.35	9.57	51.33	14.11
	21-6-1 x Pakistan Basmati	12.30	8.0	16.8	14.10	12.04	72.85	21.16
Secondary branches panicle^{-1}	124-17-4 xBasmati 370	26.70	9.2	59.6	35.78	35.31	97.42	71.80
	124-17-4 x Pakistan Basmati	31.51	9.4	68.2	35.41	34.68	95.90	69.96
	124-17-4 x Pusa Basmati 1	35.29	10.0	67.6	41.99	41.77	98.93	85.58
	21-6-1 xBasmati 370	21.82	9.4	60.0	39.68	38.52	94.23	77.02
	21-6-1 x Pakistan Basmati	34.35	12.0	62.4	31.68	30.98	95.64	62.41
Spikelet number panicle^{-1}	124-17-4 xBasmati 370	120.25	62.6	253.6	19.05	18.88	98.28	38.56
	124-17-4 x Pakistan Basmati	140.36	68.4	265.8	29.86	28.76	92.77	57.07
	124-17-4 xPusaBasmati 1	147.84	55.0	345.8	25.14	24.95	98.46	50.99
	21-6-1 xBasmati 370	103.29	56.2	247.6	29.70	27.32	84.63	51.78
	21-6-1 x Pakistan Basmati	136.55	62.2	242.8	25.85	24.50	89.81	47.83

Table 1. Contd..

Characters	Cross combination	Mean	Range		Coefficients of variation(%)		Heritability in broad sense (%)	Genetic advance as % of mean
			Min.	Max.	Phenotypic	Genotypic		
Spikelet fertility (%)	124-17-4 x Basmati 370	84.26	54.36	93.53	4.88	3.98	66.70	6.70
	124-17-4 x Pakistan Basmati	85.45	48.54	94.24	4.18	3.33	63.30	5.45
	124-17-4 x Pusa Basmati 1	83.94	56.75	93.80	2.95	1.61	29.71	1.80
	21-6-1 x Basmati 370	79.82	42.86	92.68	7.43	6.16	68.78	10.53
	21-6-1 x Pakistan Basmati	78.62	49.28	93.72	4.58	2.48	29.33	2.77
Grain length (mm)	124-17-4 x Basmati 370	7.71	5.8	10.8	17.47	17.46	99.83	35.93
	124-17-4 x Pakistan Basmati	7.89	5.5	10.8	17.61	17.56	99.40	36.05
	124-17-4 x Pusa Basmati 1	7.76	5.0	11.0	23.67	23.65	99.82	48.68
	21-6-1 x Basmati 370	7.60	5.5	10.6	17.24	17.18	99.30	35.27
	21-6-1 x Pakistan Basmati	7.74	5.2	10.5	16.85	16.79	99.32	34.47
Grain length/ breadth ratio	124-17-4 x Basmati 370	3.45	2.61	5.00	20.72	20.66	98.87	42.20
	124-17-4 x Pakistan Basmati	3.54	2.39	5.25	19.73	19.48	97.41	39.60
	124-17-4 x Pusa Basmati 1	3.53	2.17	5.30	24.29	24.19	99.18	49.62
	21-6-1 x Basmati 370	3.51	2.29	5.26	20.39	20.11	97.29	40.86
	21-6-1 x Pakistan Basmati	3.45	2.20	5.26	18.12	17.78	96.24	35.93
Grain yield/ panicle (gm)	124-17-4 x Basmati 370	1.42	0.72	2.90	4.22	4.04	92.65	8.06
	124-17-4 x Pakistan Basmati	1.85	0.81	3.01	3.24	2.59	63.25	4.23
	124-17-4 x Pusa Basmati 1	1.69	0.62	2.86	6.75	6.54	93.56	13.00
	21-6-1 x Basmati 370	1.06	0.47	2.78	10.63	10.55	98.89	21.66
	21-6-1 x Pakistan Basmati	1.71	0.59	3.05	12.61	11.61	84.79	22.03

for genetic improvement of rice crop. The potentiality of a cross is assessed from the extent of variability generated in different traits (Allard, 1960) and the estimate of heritability along with genetic advance is very useful in predicting the resultant effects of selection (Johnson *et al.*, 1955). In this investigation, the estimates of PCV, GCV, heritability and genetic advance were high in all the crosses for panicle weight, secondary branches per panicle, spikelet number per panicle and grain length/breadth ratio; and moderate to high for grain length. Similar results of high PCV and GCV had been reported by Reddy and De (1996) for panicle weight, Sharma and Dubey (1997) for secondary branches per panicle and Vivekanandan and Giridharan (1998) for kernel length/breadth ratio. High estimates of heritability and genetic advance were also noticed by Lokaprakash *et al*. (1992) for panicle weight and spikelet number per panicle, Borbora and Hazarika (1998) for secondary branches per panicle, Chauhan (1996) for kernel length and Vivekanandan and Giridharan (1998) for kernel length/breadth ratio. According to Panse (1957) this association of high genetic advance with high heritability would indicate that additive gene effects -are probably more important for expression of these characters. Phenotypic selection would therefore be effective in improving these traits. Grain yield per panicle had low genetic gain with high heritability which indicated the predominant role of nonadditive gene action. Low genetic advance for grain yield was also noticed by Borbora and Hazarika (1998). Therefore, grain yield per panicle can be improved indirectly by selecting the F_2 plants having higher panicle weight, higher number of secondary branches and spikelets per panicle and long slender grains.

The above results on different genetic parameters along with mean performance indicated that it would be possible to identify the high yielding lines of aromatic rice having agroclimatic adaptability of induced mutants of high humid condition of eastern India and superior grain size of basmati varieties through recombination breeding. The crosses of mutant 124-17-4 with Paistan Basmati and Pusa Basmati 1 are most likely to be promising.

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Research Notes

Correlation and regression analysis in scented rice

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The knowledge of genetic variation is important for selection in crop improvement programme. The genetic gain expected from selection depends on the amount of variability available in the quantitative traits in the germplasms of a crop. A successful selection programme depends upon the information on genetic variability and association of yield components with grain yield. Grain yield is interrelated with many of the component characters which are themselves associated with one another. Correlation studies provide better understanding of yield components which helps the plant breeder during selection (Robinson *et al*., 1951). Considering the above mentioned aspects, the present investigation was undertaken to gather information on genetic variability and to determine inter relationships among yield and yield contributing characters in scented rice.

Seeds of twenty true breeding genotypes of scented rice comprising seven mutant lines of each of two local aromatic cultivars-Gobindabhog and Tulaipanja and their parents, two local cultivars-Kanakchur and Dudhsar of South 24 Parganas districts of West Bengal and two basmati varieties-Basmati 370 and Pusa Basmati 1 were sown during *kharif* season at Agricultural Farm, Visva-Bharati (23°39' N, 87°42' E and 58.9 m above msl). Single seedling hill^{-1} was transplanted in a randomized block design with three replications spaced 15cm between plants and 20cm between rows. Each plot consisted of 4 rows with 15 plants in each row. Observations were recorded on five randomly selected plants from each plot in each replication for twelve quantitative characters. Estimates of phenotypic and gcnotypic coefficients of variation (Burton, 1952), heritability in broad sense (Lush, 1940), genetic advance