Electronic Journal of Plant Breeding, 1(5): 1358-1362 (Sep 2010)
ISSN 0975-928X

Research Note

Genetic variability studies in single and double cross advanced generation segregating progenies of Bhendi [A*belmoschus esculentus* (L.)Moench]

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(Received: 29 Jul 2010; Accepted: 10 Aug 2010)

Abstract:
An investigation was carried out to study the genetic variability, in fruit yield per plant and its component traits in four single cross (BH10,BH11,BH12 and BH 13) and three double cross (BH14,BH15 and BH16) F_4 and F_5 progenies of bhendi at ARS, Hanumanamatti during summer and kharif 2008. The results indicate that, high GCV and PCV values for number of branches per plant, number of fruits per plant and fruit yield per plant. Moderate GCV and PCV values were recorded for internodal length, fruit length, fruit diameter and fruit weight in both single and double cross F_4 and F_5 progenies which indicate existence of wide range of genetic variability in the material evaluated. High heritability coupled with high genetic advance was observed for number of branches per plant, number of fruits per plant and fruit yield per plant in both single and double cross F_4 and F_5 progenies indicating additive gene action in the control of expression of these characters. From the experimental results it was found that the amount of variability was more in double cross derived progenies as compared to single cross derived progenies for most of the characters studied.

Key words:
Bhendi, single cross, double cross, genetic variability

Bhendi [*Abelmoschus esculentus* (L.) Moench] has good nutritional value, particularly vitamin C (30 mg/100 g), calcium (90 mg/100 g) and iron (1.5 mg/100 g) in the edible portion.. It is a potential export earner accounting for 13 per cent of export of fresh vegetables. All forms of plant improvement activities through breeding contemplate an eventual boost in genetic potential for yield. Since yield is polygenically controlled and highly influenced by environment, selection based on yield alone is not effective. The breeder while selecting for high yield has to select indirectly through yield associated and highly heritable characters after eliminating environmental components of phenotypic variance. An attempt to improve a character by selection would be futile unless a major portion of variation is heritable which depends entirely on the magnitude of genetic variability in the source population. The variability is a pre-requisite for any breeding programme aimed at improving the yield and other characters. Thus, it is imperative to have information on both genotypic and phenotypic coefficients of variation together with heritability and GAM will be handy for prediction of the possible genetic advance by selection for the character. The genetic parameter such as genotypic coefficient of variation and genetic advance helps to split the total variability into heritable and non-heritable components. Therefore, the present investigation has been undertaken to compare the variability in single and double cross F_4 and F_5 populations of bhendi.

The experimental material in the present study consisted of F_4 and F_5 populations of four single crosses (BH-10, BH-11, BH-13 and BH-14) and three double crosses (BH-15, BH-16 and BH-16) along with popular checks. The experiment was laid out in

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RBD with three replications during summer 2008 (F_4) and *kharif* 2008 (F_5) at Agricultural Research Station, Hanumanamatti, University of Agricultural Sciences, Dharwad. Each progeny line was sown at a spacing of 60 × 30 cm with a row length of 5 m having eight progeny lines in each single cross and 10 progeny lines in each double cross in both the generations. All the recommended agronomic package of practices were followed to raise good healthy crop. The observations were recorded from five competitive plants from each row (totally 40 plants in each single cross and 50 plants in each double cross) on twelve quantitative characters viz., days to first flowering, days to 50 per cent flowering, plant height (cm), number of branches per plant, internodal length (cm), fruit weight (g), fruit length (cm), fruit diameter (cm), number of seeds per fruit, 100-seed weight (g), number of fruits per plant and fruit yield per plant (g). The genotypic and phenotypic coefficients of variability were calculated according to the method suggested by Burton and Devane (1953).

The genotypic and phenotypic coefficient of variability, heritability and genetic advance, character-wise are presented in Table 1and 2.The magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all characters under study. Higher magnitude of GCV and PCV were recorded for number of branches per plant and number of fruits per plant in both single and double cross F_4 and F_5 populations. This reflects greater genetic variability among genotypes for these characters and is desirable for further improvement by selection. However moderate to low GCV and PCV were recorded for days to first flowering, days to 50 per cent flowering, inter nodal length, fruit weight, fruit length, fruit diameter, number of seeds per fruit and 100 seed weight (Table 1). Panda and Singh (1997) obtained similar results in okra hybrids and Singh *et al.* (1998) reported parallel results while evaluating different induced mutants in okra. Most of the characters in double cross F_4 and F_5 populations revealed presence of high magnitude of genetic variability. Low GCV and PCV for most of the characters in single cross revealed that low genetic variability in single cross populations compared to double cross populations. The variability was more in double cross as compared to single cross populations and also the variability observed was more in F_4 populations compare to F_5 populations.The magnitude of heritability ranged from 59 per cent (number of fruits per plant in double cross progeny) to 99 per cent (plant height) in F_4 populations and 67 per cent (fruit diameter) to 92 per cent (number of branches per plant) in F_5 populations. More than 70 per cent heritability was recorded for days to first flowering, days to 50 per cent flowering, plant height, inter nodal length, number of branches per plant, fruit weight, fruit diameter, 100 seed weight, number of seeds per fruit in both single and double cross F_4 and F_5 populations. High heritability suggested the major role of genetic constitution in the expression of the characters and such traits are considered to be dependent on genetic upgradation of bhendi. The estimates of heritability along with genetic advance were more reliable than heritability alone for predicting the effect of selection (Johanson *et al.,*1955*).* The value of GAM ranged from 3.31 per cent (days to first flowering) to 53.58 per cent (number of branches per plant in single cross) and from 3.63 per cent (days to first flowering) to 43.84 per cent (number of branches per plant in double cross) in F_4 populations and 4.4 per cent (days to first flowering) to 52.43 per cent (plant height) in single cross and 7.04 per cent (days to first flowering) to 36.02 per cent (number of fruits per plant) in double cross populations of F_5 generation. High heritability coupled with high genetic advance over mean in number of branches per plant, inter nodal length, fruit weight, number of fruits per plant; and fruit yield per plant in both single and double crosses indicated that these characters had additive gene effects and therefore, they are more reliable for effective selection. High to moderate heritability coupled with moderate to low GAM for days to first flowering, days to 50 per cent flowering, plant height, number of seeds per fruit in both the generations were observed. These findings are in agreement with the earlier reports of Panda and Singh (1997), Singh *et al.* (1998) Dhall *et al* (2001) and Dhankar and Dhankar (2002).

From the present study on the basis of variability, it could be concluded that generally double cross populations exhibited higher magnitude of genetic variability compared to single cross populations.

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Table 1: Comparison of variability between single cross and double cross F_4 populations for twelve quantitative characters

Character	Populations	Mean	Range	GCV (%)	PCV (%)	Heritability (%)	GA	GAM (%)
Days to first flowering	SCF_4	43.59	34.0-49.0	2.56	2.64	73	1.68	3.85
	DCF_4	42.52	30.0-52.0	2.79	3.12	80	2.20	5.17
Days to per cent flowering	SCF_4	48.63	45.0-54.0	1.86	2.10	78	1.61	3.31
	DCF_4	49.00	43.0-59.0	1.96	2.24	76	1.78	3.63
Plant height	SCF_4	87.15	45.0-97.4	11.79	11.81	99	8.58	9.86
	DCF_4	95.85	45.0-135.6	17.39	17.42	99	14.55	15.28
No. branches per plant	SCF_4	2.65	0.0-5.0	25.78	26.27	96	1.42	53.58
	DCF_4	2.60	0.0-7.0	24.24	24.44	98	1.14	43.84
Internodal length	SCF_4	7.68	6.0-12.0	10.04	10.11	99	1.57	20.44
	DCF_4	6.65	6.0-14.0	20.63	20.68	99	2.86	43.00
Fruit weight	SCF_4	16.01	9.0-20.0	11.67	12.45	82	2.37	14.80
	DCF_4	15.75	8.0-23.0	12.13	13.86	76	3.44	21.84
Fruit length	SCF_4	12.55	8.0-16.5	9.63	11.91	65	1.94	15.46
	DCF_4	12.80	7.0-18.0	12.94	14.17	77	2.07	16.17
Fruit diameter	SCF_4	1.99	1.3-2.4	9.76	11.11	77	0.26	13.07
	DCF_4	1.82	1.2-2.6	14.40	16.10	80	0.39	21.43
Number of seeds per fruit	SCF_4	63.85	52.0-69.0	4.63	4.97	86	5.67	8.88
	DCF_4	63.73	51.0-76.0	4.65	5.18	80	5.34	8.38
100-seed weight	SCF_4	6.43	5.0-8.0	9.63	10.52	83	1.18	18.35
	DCF_4	6.35	4.0-8.0	11.61	12.86	81	1.37	21.57
Number of fruits per plant	SCF_4	18.27	8.0-35.0	20.45	22.42	83	6.86	33.66
	DCF_4	18.99	9.0-40.0	24.52	25.69	59	4.73	22.30
Fruit yield per plant	SCF_4	294.76	135.0-520.5	17.45	18.96	85	102.11	34.64
	DCF_4	304.66	123.0-670.5	20.50	23.75	60	78.78	25.86

Table 2: Comparison of variability between single cross and double cross F_5 populations for twelve quantitative characters

Character	Populations	Mean	Range	GCV (%)	PCV (%)	Heritability (%)	GA	GAM (%)
Days to first flowering	SCF_5	43.44	34.0-46.0	3.90	4.29	82	3.06	7.04
	DCF_5	42.14	32.0-49.0	4.38	4.78	74	1.73	4.10
Days to per cent flowering	SCF_5	48.37	46.0-52.0	3.88	4.27	82	3.47	7.17
	DCF_5	49.16	44.0-56.0	4.36	4.61	82	2.08	4.23
Plant height	SCF_5	87.30	45.0-93.0	6.99	7.34	90	11.80	13.52
	DCF_5	96.95	45.0-127.0	8.11	8.42	83	4.98	5.14
No. branches per plant	SCF_5	2.70	0.0-5.0	25.07	28.16	79	1.01	37.41
	DCF_5	2.67	0.0-5.0	31.02	32.37	92	1.4	52.43
Internodal length	SCF_5	7.42	6.0-9.0	16.57	18.15	83	2.25	30.32
	DCF_5	7.05	5.0-11.0	21.22	25.56	89	0.96	13.62
Fruit weight	SCF_5	15.64	9.5-18.2	10.22	12.16	70	2.84	18.16
	DCF_5	16.53	8.0-17.5	11.43	13.24	81	2.11	12.77
Fruit length	SCF_5	12.64	8.0-14.5	12.20	13.87	77	3.14	24.84
	DCF_5	13.44	7.5-14.11	20.33	22.14	83	1.99	14.80
Fruit diameter	SCF_5	2.05	1.5-2.4	11.54	14.06	67	0.27	13.17
	DCF_5	1.90	0.98-2.65	10.06	11.05	83	0.28	14.74
Number of seeds per fruit	SCF_5	62.79	54.0-69.0	8.40	8.92	88	10.35	16.48
	DCF_5	63.62	54.0-73.0	9.66	9.97	85	4.42	6.96
100-seed weight	SCF_5	6.40	5.5-7.0	8.72	8.72	88	1.11	17.34
	DCF_5	6.67	5.0-8.5	8.77	9.07	86	0.48	7.21
Number of fruits per plant	SCF_5	20.38	8.0-32.0	18.20	19.36	88	6.58	36.02
	DCF_5	21.21	8.0-39.0	20.55	23.33	73	4.91	25.86
Fruit yield per plant	SCF_5	306.36	159.0-510.6	17.13	18.42	87	97.02	31.66
	DCF_5	316.11	165.0-629.2	22.49	25.98	75	115.46	36.52