

Studies on Variability, Heritability and Genetic Advance for Fruit Yield and its Component Traits in Early Segregating Generation in Bhendi [(*Abelmoschus esculentus* (L.) Moench)]

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An experiment was undertaken to study phenotypic and genotypic coefficients of variation, heritability and genetic advance in three double crosses and four single crosses F_2 population of okra. The analysis of variance revealed highly significant differences for the populations under study for the characters. The estimate of phenotypic and genotypic coefficients of variation were moderate to high for all the characters except days to first flowering, stem diameter (in double cross), fruit length and 100 seed weight. Heritability and genetic advance were also high for all the characters indicating the involvement of additive type of gene action in controlling these characters, hence, selection could be effective.

Key Words: *Bhendi*, Coefficient of Variation, Genotypes, Heritability

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] or *Bhendi* is an important vegetable crop cultivated throughout the world and is a native of tropical Africa. It is grown in tropical and sub-tropical parts of the world. India is the largest producer of okra covering an area of 3.91 lakh ha with an annual production of 39.7 lakh tonnes (Anon, 2004). Tender fruits are used as vegetable, eaten boiled or in culinary preparation as sliced and fried pieces. It has good nutritional value, particularly vitamin C (30 mg/100 g), calcium (90 g/100 g) and iron (1.5 mg/100 g) in the edible fruit.

Okra belongs to family Malvaceae with $2n=8x=72$ or 144 and amphidiploid in nature. It is a self pollinated crop, however occurrence of out crossing to an extent of 4 to 19 per cent by insect has been reported which renders considerable genetic diversity.

Bhendi is one vegetable crop where heterosis has been exploited successfully. Yield plateau seems to have been reached in heterotic hybrids. In order to break this barrier there is a need to develop truly potential inbred line which in combination can produce really novel hybrids with desirable maximum heterosis. Among the various approaches for developing inbred lines, selection in potential segregating population is an important one. But then, the key to success lies in developing the really promising potential segregating populations. In this regard the segregating populations developed from double cross combinations involving parents with desired diversity may prove to be better than segregating

population derived from single cross combination. As it is known the double cross combination generated employing two single cross combination which are diverse may produce the desired double cross combination. Such segregating population may serve as good source populations for identifying promising pure line varieties.

Improvement of any character depends on the magnitude of variability present in the population. The desirable variability provides valuable information regarding selection of diverse parents to be used in hybridization programme. Estimates of heritability can serve to identify the factors which can be used as indicators for high yield during selection. Keeping these things in view, the study was planned to assess genetic variability with heritability and genetic advance so as to select superior genotypes in early segregating populations.

Materials Aand Methods

The experimental material for present investigation consisting of 13 potential F_1 hybrids viz., BH 1, BH 2...BH 13 along with popular check Arka Anamika were evaluates in randomized block design (RBD) with three replications during *Kharif* 2005. The plot size was four rows each of 5 m length with a spacing of 60 cm × 30 cm. All recommended cultivation practices were followed to raise good healthy crop. Observations were recorded on five competitive plants for fifteen quantitative characters viz., days to first flowering, plant height (cm), number of branches per plant, internodal length (cm), stem diameter (cm), number of nodes at first flowering,

fruit length (cm), fruit diameter (cm), fruit weight (g), number of seeds per fruit, number of fruit per plant, pedicel length (cm), number of ridges per fruit, 100 seed weight (g) and fruit yield per plot (kg). The data was subjected to Mahalanobis (1936) D^2 statistics to assess the genetic diversity between hybrids. The hybrids were grouped in to different clusters following the Touchers' method (Rao, 1952).

Three double crosses (BH 2×BH 10, BH 2×BH 12 and BH 2×BH 13) were developed which represent maximum single cross hybrid diversity to be chosen as parents for developing double cross hybrids. These double cross hybrids were selfed to obtain F_2 populations during summer 2006. Simultaneously, the single cross hybrids involved in the generation of double cross hybrids were also selfed to derive F_2 populations. Then F_2 population of three double crosses and four single crosses, F_1 parental hybrids of three double crosses and four single crosses along with checks were evaluated in RBD with three replications during *Kharif* 2006. The plot size was two rows each for single and double cross hybrids, sixteen rows each for single and double cross F_2 population and two rows each of commercial and local checks. Row length was 6m length with a spacing of 60×30 cm. Observation were recorded on five competitive plants in each population for above mentioned characters. The data was subjected for analysis of genotypic and phenotypic coefficients of variation using the formulae suggested by Burton and Devane (1953). Broad sense heritability was calculated as per Hanson *et al.* (1956). Genetic advance was estimated by the method suggested by Johnson *et al.* (1955).

Results and Discussion

The analysis of variance for fifteen quantitative characters (Table 1) indicated the existence of highly significant differences among populations for all the characters studied. The data on mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent over mean were characterwise presented in Table 2. In single crosses F_2 population, the fruit yield per plant varied from 135.52 to 652.18 with an average mean of 340.03 g. This trait exhibited high mean PVC (31.40), GCV (26.61) heritability (72.26) and GAM (46.59). In double crosses F_2 population the yield per plant ranged from 123.93 to 759.0 with an average of 341.16 g. The double crosses also exhibited high PVC (32.38), GCV (27.44), heritability (81.71) and GAM (50.46)

Table 1. Analysis of variance (ANOVA) in respect of 16 characters in 3 double cross hybrids

S. No.	Characters	Mean sum of squares Genotypes
Degrees of freedom		8
1	Days to first flowering	2.78**
2	Days to 50 per cent flowering	2.74**
3	plant height (cm)	48.05**
4	Number of branches per plant	0.58**
5	Inter nodal length (cm)	1.53**
6	Stem diameter (cm)	0.01**
7	Number of nodes at first flowering	0.22**
8	Pedicel length (cm)	0.24**
9	Fruit length (cm)	0.57**
10	Fruit diameter (cm)	0.07**
11	Number of ridges per fruit	0.57**
12	Seeds per fruit	71.00**
13	100 seed weight (g)	0.16**
14	Average fruit wt (g)	2.88*
15	Fruits per plant	6.83**
16	Yield per plant (g)	2397.35*

* Significant 5% level, ** Significant at 1% level

For days to first flowering, the mean value in low (43.83) in double cross F_2 compared to single cross F_2 (44.05). It showed low PCV (7.41 and 7.84) and GCV (7.26 and 7.29) and GAM (14.69 and 13.99), respectively, in both single and double crosses.

The plant height ranged from 55.0 to 153.5 cm with mean value of 103.25 cm in single crosses and it was 64.33 to 168.0 with mean value of 113.35 cm in double crosses. High PCV (16.92 and 17.26), GCV (16.66 and 16.94), heritability (96.27 and 96.34) and GAM (33.78 and 34.27) were noticed in both crosses. The mean value was high in double crosses compare to single crosses.

The number of branches per plant ranged from 0 to 4.3 with mean value of 1.43 and 1.44, respectively, in single and double crosses. Very high PCV (61.56 and 62.30), GCV (51.18 and 50.93), heritability (69.71 and 66.91) and GAM (87.87 and 85.79), respectively, observed in both single and double crosses.

The internodal length, the important fruit yielding character ranged from 6.25 to 15.25 with an average mean of 10.48 cm in single crosses. The mean value of double crosses ranged from 6.93 to 14.67 with average of 11.09 cm. Moderate PCV and GCV and high heritability and GAM were observed for this character.

Not many differences were seen for stem diameter in both single and double crosses. In single crosses this trait exhibited range from 0.60 to 2.27 cm with mean of 1.11 cm. This trait exhibited high PCV (25.20), GCV

Table 2. Estimates of genetic variability for quantitative characters in single and double cross F₂ populations of bhendi

S.No	Character	Genotype	Mean	Range	PCV%	GCV%	h ² %	GAM%		
1	Days to first flowering	SC F2								
		BH-2	43.52	39 to 52.00	7.03	6.80	93.56	13.55		
		BH-10	43.94	40 to 56.00	7.53	7.30	93.92	14.57		
		BH-12	43.93	40 to 56.00	7.42	7.38	98.96	15.13		
		BH-13	44.81	41 to 56.00	7.64	7.56	98.02	15.43		
		Mean	44.05	40 to 55.00	7.41	7.26	96.12	14.67		
		DC F2								
		BH-2 X BH-10	43.52	38 to 53.00	7.51	6.78	81.53	12.62		
		BH-2 X BH-12	43.08	39 to 50.00	6.26	5.73	83.68	10.80		
		BH-2 X BH-13	44.89	40 to 57.00	9.74	9.36	92.41	18.54		
		Mean	43.83	39 to 53.33	7.84	7.29	85.87	13.99		
		2	Plant height (cm)	SC F2						
				BH-2	106.92	55.00 to 152	15.29	15.18	98.49	31.03
				BH-10	103.73	65.00 to 146	16.25	15.77	94.13	31.51
BH-12	98.51			40.00 to 158	20.09	19.75	96.66	39.99		
BH-13	103.83			60.00 to 158	16.05	15.94	98.59	32.60		
Mean	103.25			55.00 to 153.5	16.92	16.66	96.27	33.78		
DC F2										
BH-2 X BH-10	111.47			61.00 to 162	17.12	16.64	94.54	33.34		
BH-2 X BH-12	116.97			75.00 to 175	15.97	15.68	96.45	31.72		
BH-2 X BH-13	111.62			57.00 to 167	18.69	18.50	98.03	37.74		
Mean	113.35			64.33 to 168	17.26	16.94	96.34	34.27		
3	Number of branches			SC F2						
				BH-2	1.43	0.00 to 4	56.01	50.86	82.46	95.15
				BH-10	1.50	0.00 to 5	68.13	54.09	63.04	88.48
		BH-12	1.34	0.00 to 4	67.29	55.20	67.28	93.26		
		BH-13	1.43	0.00 to 3	54.82	44.56	66.06	74.60		
		Mean	1.43	0.00 to 4	61.56	51.18	69.71	87.87		
		DC F2								
		BH-2 X BH-10	1.60	0.00 to 5	59.76	49.78	69.38	85.41		
		BH-2 X BH-12	1.40	0.00 to 4	63.08	51.99	67.94	88.28		
		BH-2 X BH-13	1.31	0.00 to 4	64.06	51.01	63.40	83.67		
		Mean	1.44	0.00 to 4.333	62.30	50.93	66.91	85.79		
		4	Internodal length (cm)	SC F2						
				BH-2	11.09	6.50 to 15.2	17.60	17.30	96.64	35.04
				BH-10	10.12	5.20 to 14.5	19.30	17.77	84.75	33.69
BH-12	10.66			6.90 to 15.0	16.76	14.19	71.67	24.74		
BH-13	10.05			6.40 to 16.3	16.62	14.63	77.51	26.53		
Mean	10.48			6.25 to 15.25	17.57	15.97	82.64	30.00		
DC F2										
BH-2 X BH-10	11.64			7.60 to 15.2	17.11	16.22	89.81	31.66		
BH-2 X BH-12	10.84			6.60 to 14.5	15.39	14.49	88.65	28.10		
BH-2 X BH-13	10.79			6.60 to 14.3	18.09	16.71	85.32	31.79		
Mean	11.09			6.93 to 14.67	16.86	15.80	87.93	30.52		
5	Stem diameter (cm)			SC F2						
				BH-2	1.20	0.43 to 2.4	35.28	33.02	87.60	63.67
				BH-10	1.13	0.70 to 2.1	22.97	17.28	56.58	26.77
		BH-12	1.06	0.60 to 2.4	22.52	18.42	66.87	31.02		
		BH-13	1.06	0.67 to 2.2	20.01	11.39	32.41	13.36		
		Mean	1.11	0.60 to 2.275	25.20	20.03	60.86	33.71		
		DC F2								
		BH-2 X BH-10	1.13	0.67 to 2.3	18.98	11.15	34.48	13.48		
		BH-2 X BH-12	1.08	0.64 to 1.622	17.36	9.63	30.76	11.00		
		BH-2 X BH-13	1.15	0.73 to 1.8	16.36	8.99	30.16	10.17		
		Mean	1.12	0.68 to 1.907	17.57	9.92	31.80	11.55		

Contd.

Table 2. Contd.

S.No	Character	Genotype	Mean	Range	PCV%	GCV%	h ² %	GAM%
6	Number of nodes at first flowering	SC F2						
		BH-2	2.59	1.00 to 5	33.37	25.41	57.97	39.85
		BH-10	2.52	1.00 to 4	26.76	22.15	68.50	37.76
		BH-12	2.58	1.00 to 5	30.90	23.95	60.10	38.25
		BH-13	2.55	1.00 to 6	33.67	21.32	40.11	27.82
		Mean	2.56	1.00 to 5	31.17	23.21	56.67	35.92
		DC F2						
		BH-2 X BH-10	2.35	1.00 to 7	36.86	27.24	54.59	41.45
		BH-2 X BH-12	2.29	1.00 to 5	34.41	26.15	57.77	40.95
		BH-2 X BH-13	2.51	1.00 to 6	35.81	28.41	62.97	46.44
Mean	2.38	1.00 to 6	35.69	27.27	58.44	42.95		
7	Fruit length (cm)	SC F2						
		BH-2	13.46	9.70 to 21.30	13.41	12.65	88.92	24.57
		BH-10	13.96	9.88 to 18.75	13.86	12.78	84.96	24.26
		BH-12	14.15	9.75 to 20.68	16.06	15.48	92.90	30.73
		BH-13	13.20	9.98 to 17.38	10.96	8.86	65.39	14.76
		Mean	13.69	9.83 to 19.53	13.57	12.44	83.04	23.58
		DC F2						
		BH-2 X BH-10	13.64	9.62 to 18.68	12.71	11.91	87.80	22.99
		BH-2 X BH-12	14.36	9.78 to 19.92	15.61	14.87	90.82	29.20
		BH-2 X BH-13	13.34	10.15 to 18.60	11.65	10.37	79.32	19.03
Mean	13.78	10.00 to 18.24	12.16	10.67	76.55	19.35		
8	Fruit diameter (cm)	SC F2						
		BH-2	1.69	1.02 to 2.68	16.75	15.56	86.27	29.76
		BH-10	1.73	0.90 to 2.62	19.06	17.60	85.31	33.49
		BH-12	1.64	1.10 to 2.46	15.31	11.97	61.13	19.28
		BH-13	1.62	0.10 to 2.42	19.18	17.96	87.69	34.65
		Mean	1.67	0.78 to 2.545	17.58	15.77	80.10	29.30
		DC F2						
		BH-2 X BH-10	1.58	0.80 to 2.84	23.47	21.84	86.57	41.85
		BH-2 X BH-12	1.72	1.02 to 3.4	31.37	24.94	63.20	40.84
		BH-2 X BH-13	1.65	0.98 to 2.98	20.65	20.64	99.95	42.56
Mean	1.65	0.93 to 3.073	25.16	22.48	83.28	41.75		
9	Fruit weight (g)	SC F2						
		BH-2	17.74	10.30 to 31.75	21.28	18.73	77.46	33.96
		BH-10	17.70	9.80 to 35.00	25.16	23.52	87.37	45.29
		BH-12	16.24	9.20 to 28.26	21.09	19.41	84.74	36.81
		BH-13	16.45	9.50 to 29.30	22.08	18.39	69.37	31.55
		Mean	17.03	9.70 to 31.08	22.40	20.01	79.74	36.90
		DC F2						
		BH-2 X BH-10	17.21	10.00 to 24.40	21.30	20.00	87.64	34.72
		BH-2 X BH-12	18.75	8.30 to 32.00	22.83	20.38	77.84	33.40
		BH-2 X BH-13	16.57	8.30 to 30.00	25.09	22.21	78.36	40.51
Mean	17.51	8.87 to 28.80	23.07	20.86	81.28	36.21		
10	Number of seeds per fruit	SC F2						
		BH-2	57.80	30.00 to 102	17.63	15.80	80.40	29.19
		BH-10	54.10	40.30 to 80	13.45	12.00	79.70	22.08
		BH-12	56.28	20.00 to 110	17.89	15.95	79.42	29.28
		BH-13	55.87	23.00 to 87	15.91	13.78	75.03	24.60
		Mean	56.02	28.33 to 94.75	16.22	14.38	78.64	26.29
		DC F2						
		BH-2 X BH-10	54.69	40.26 to 88	16.27	15.09	85.99	28.83
		BH-2 X BH-12	54.69	39.26 to 110	18.21	17.22	89.42	33.54
		BH-2 X BH-13	55.89	40.20 to 120	15.57	14.55	87.32	28.01
Mean	55.09	39.91 to 106	16.68	15.62	87.58	30.12		

Contd.

Table 2. Contd.

S.No	Character	Genotype	Mean	Range	PCV%	GCV%	h ² %	GAM%		
11	Number of fruits per plant	SC F2								
		BH-2	19.42	10.00 to 32	22.13	19.18	75.11	34.24		
		BH-10	20.39	10.00 to 39	22.37	19.43	75.42	34.76		
		BH-12	20.36	10.00 to 37	21.62	20.19	87.17	38.83		
		BH-13	19.87	6.00 to 30	21.62	18.26	71.28	31.75		
		Mean	20.01	9.00 to 34.5	21.94	19.26	77.24	34.90		
		DC F2								
		BH-2 X BH-10	22.69	8.00 to 32	21.13	20.00	89.64	39.02		
		BH-2 X BH-12	19.09	8.00 to 32	22.49	20.05	79.43	36.80		
		BH-2 X BH-13	19.25	7.00 to 34	24.44	22.35	83.67	42.12		
		Mean	20.34	7.67 to 32.67	22.69	20.80	84.25	39.31		
		12	Pedicel length(cm)	SC F2						
				BH-2	3.05	1.20 to 4.5	24.23	21.26	87.73	43.79
				BH-10	3.24	2.00 to 4.5	18.30	9.97	54.48	20.53
BH-12	3.52			2.15 to 4.52	16.06	5.66	35.24	11.66		
BH-13	3.72			2.24 to 6.68	21.31	16.77	78.66	34.54		
Mean	3.38			1.90 to 5.05	19.97	13.41	64.03	27.63		
DC F2										
BH-2 X BH-10	3.58			1.60 to 5.2	19.75	13.66	69.16	28.14		
BH-2 X BH-12	3.31			1.86 to 5.12	22.25	14.45	64.93	29.77		
BH-2 X BH-13	3.53			2.13 to 6.24	21.95	17.11	77.91	35.24		
Mean	3.47			1.86 to 5.52	21.32	15.07	70.67	31.05		
13	Number of ridges per fruit			SC F2						
				BH-2	5.46	5.00 to 7.9	11.13	11.05	98.57	22.61
				BH-10	5.49	5.00 to 8	13.81	13.27	92.41	26.28
		BH-12	5.40	5.00 to 8.6	14.26	13.94	95.55	28.07		
		BH-13	5.41	5.00 to 8.6	14.71	14.27	94.16	28.53		
		Mean	5.44	5.00 to 8.275	13.48	13.13	95.17	26.37		
		DC F2								
		BH-2 X BH-10	5.48	5.00 to 8.6	14.66	13.92	90.15	27.22		
		BH-2 X BH-12	5.55	5.00 to 8.2	15.35	15.29	99.17	31.36		
		BH-2 X BH-13	5.46	5.00 to 8.6	14.26	13.50	89.67	26.33		
		Mean	5.50	5.00 to 8.467	14.76	14.24	93.00	28.31		
		14	100 Seed weight (g)	SC F2						
				BH-2	6.94	6.56 to 7.26	2.02	1.61	63.87	2.65
				BH-10	7.20	6.69 to 8.6	4.90	4.07	69.20	6.98
BH-12	6.98			6.50 to 8.5	4.02	3.13	60.64	5.03		
BH-13	6.90			6.05 to 7.52	3.53	2.91	67.58	4.92		
Mean	7.00			6.45 to 7.97	3.62	2.93	65.33	4.89		
DC F2										
BH-2 X BH-10	7.19			6.67 to 7.8	4.20	4.11	96.01	8.30		
BH-2 X BH-12	7.08			6.56 to 7.8	3.52	3.34	89.72	6.51		
BH-2 X BH-13	6.99			6.56 to 7.6	2.39	1.82	58.03	2.86		
Mean	7.09			6.60 to 7.733	3.37	3.09	81.25	5.89		
15	Yield per plant (g)			SC F2						
				BH-2	344.60	136.20 to 674.3	31.93	27.26	72.87	47.94
				BH-10	355.57	161.84 to 700	32.59	27.52	66.10	41.30
		BH-12	330.85	160.00 to 638	29.76	27.41	84.85	52.01		
		BH-13	329.11	83.22 to 596.4	32.59	27.52	65.23	45.13		
		Mean	340.03	135.32 to 652.18	31.40	26.61	72.26	46.59		
		DC F2								
		BH-2 X BH-10	356.33	112.16 to 840	32.74	28.64	92.49	54.75		
		BH-2 X BH-12	355.12	142.88 to 747	32.65	25.60	74.56	45.54		
		BH-2 X BH-13	312.04	116.76 to 690	31.77	28.07	78.06	51.08		
		Mean	341.16	123.93 to 759	32.38	27.44	81.70	50.46		

SC – Single cross, DC – Double cross

(20.03), heritability (60.86) and GAM (63.07). In double crosses the range was 0.68 to 1.90 cm with mean of 1.12 cm but it exhibited low PCV, GCV, heritability and GAM (17.57, 9.92, 31.80 and 11.55, respectively).

The number of nodes at first flowering varied from 1 to 5 with a mean value of 2.56 in single crosses and it varied from 1 to 6 with mean of 2.38 in double crosses. High PCV (31.17 and 35.69), GCV (23.21 and 27.27), GAM (35.92 and 42.95) were observed for single and double crosses, respectively.

The mean fruit length was almost same in both single and double crosses (13.69 and 13.78, respectively). PCV, GCV, high heritability and GAM (13.57 and 12.16, 12.44 and 10.67, 83.04 and 76.55 and 23.58 and 19.35) observed for single and double crosses population, respectively.

Fruit diameter was almost same in single and double crosses F_2 population. In single crosses it varied from 0.78 to 2.54 with an average mean of 1.67 and its PCV (17.58), GCV (15.77), heritability (80.00) and GAM (29.30) were high. The double crosses F_2 populations showed the range from 0.93 to 3.07 with mean of 1.65. Its PCV, GCV, heritability and GAM (25.16, 22.48, 83.48 and 41.75, respectively) were high.

Similarly, the fruit weight was almost same in both crosses. In single crosses it varied from 9.70 to 31.08 with the mean of 17.03 and in double crosses it showed 8.87 to 28.80 with mean of 17.51. This character showed high PCV, GCV, heritability and GAM (22.40 and 23.07, 20.01 and 20.86, 79.74 and 81.28 and 36.90 and 36.21) in single and double crosses, respectively.

Number of seeds per fruit observed moderate PCV (16.22 and 16.68), GCV (14.38 and 15.62) and heritability (78.64 and 87.58) and high GAM (26.29 and 30.12) in both single and double crosses, respectively.

The most important yield attributing character the number of fruits per plant ranged from 9.0 to 34.5 with mean of 20.01 and exhibited high PCV (21.94), GCV (19.26), heritability (77.24) and GAM (34.90) in single crosses. In double crosses it varied from 7.67 to 32.67 with mean of 20.34. High PCV (22.69), GCV (20.80), heritability (84.25) and GAM (39.31) were observed.

Pedicle length ranged from 1.90 to 5.05 with mean of 3.38 in single crosses and it varied from 1.86 to 5.52 with mean of 3.47 in double crosses. It recorded moderate PCV (19.97 and 21.32), GCV (13.41 and 15.07)

and heritability (64.03 and 70.67) and high GAM (27.63 and 31.05) in single and double crosses, respectively. Similarly, the number of ridges per fruit recorded moderate PCV (13.48 and 14.76) and GCV (13.13 and 14.24), high heritability (95.17 and 93.00) and GAM (26.37 and 28.31) in both the crosses. The mean 100 seed weight recorded 7.00 g and 7.09 g, respectively, in single and double crosses. It showed very low PCV (3.62 and 3.37), GCV (2.93 and 3.09) and GAM (4.89 and 5.89) in both the crosses.

In the present investigation it was observed that the double crosses populations exhibited higher mean than the single crosses for most of the characters studied. Hence, selection can be more effective in double cross F_2 population. Similar results were reported by Jaiprakashnarayan (2003) in 66 genotypes of Okra. Higher variability were recorded for fruit yield per plant and its components traits except days to first flowering, stem diameter, fruit length and 100 seed weight in both populations. Similar results were also reported by Sahoo *et al.* (1990) and Hazra and Basu (2000) in 45 F_2 populations in single cross chilli. The presence of high variability indicates presence of more variation in the population to select superior segregants.

The heritability estimates helps in effective selection for a particular character. The study show that all the characters exhibited high heritability and GAM. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Based on variability, heritability along with genetic advance, it could be concluded that improvement by direct selection in bhendi is possible for traits like plant height, number of branches, intermodal length, fruit length, fruit diameter, number of fruit per plant and fruit yield per plant.

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