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Genetic variability and components of variance in biparental mating populations of okra (*Abelmoschus esculentus* (L.) Moench)

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Abstract

Studies on genetic variability and components of variance in four biparental mating populations of okra revealed high PCV, GCV for the traits like number of branches per plant, number of fruits per plant and fruit yield per plant, indicating greater scope for selection. Population P_1 exhibited high PCV, GCV, heritability, genetic advance for most of the yield attributing traits, followed by P_4 population. Other two populations P_2 and P_3 did not exhibit much variation for yield and related traits. Populations P_1 and P_4 exhibited highest between and within family variance for yield related traits, indicating potentiality of these cross combinations to release variability and provide ample scope for selection. Similarly P_1 and P_4 populations showed low narrow sense heritability indicating the predominance of non additive variance for number of fruits per plant and fruit yield per plant.

Keywords: Biparental mating population, variability, components of variance, heritability, genetic advance.

Introduction

Okra (*Abelmoschus esculentus* [L.]) belongs to family Malvaceae, native of tropical Africa is commonly known as bhendi or lady's finger in India. It is grown extensively in tropical and subtropical parts of the world. Its tender, green fruits are used as a vegetable and are generally marketed in fresh state, but sometimes in canned or dehydrated form. India is the largest producer of okra covering an area of 4.98 lakh ha with an annual production of 57.84 lakh tons (NHB, 2011).

Inter-mating between the selected plants of F_2 generation derived from diverse hybrids and evaluation of such crosses for genetic variability parameters is informative for forwarding such crosses through suitable breeding approaches. This kind of inter-mating helps in breaking the larges linkage blocks in a crop like okra having unstable genome. As there are no such reports available on the comparison of different biparental mating populations in okra, an attempt has been made in this study to compare the different biparental mating populations for genetic variability generated and components of variance for different quantitative traits.

Materials and Methods

The present investigation was carried out during *rabi* season of 2008 and summer season of 2009 at College of Agriculture, Dharwad. The experimental material comprised of F_2 population derived from 4 hybrids, *viz.,* BH-1, BH-2, BH-3 and BH-4. Inter-mating was done by taking 25 plants in each F_2 population and biparental matting populations (BIP) were developed as fallows.

i. P_1 cross progenies – Obtained by crossing selected F_2 plants of BH-1 as female with selected F_2 male plants of BH-2.

ii. P_2 cross progenies – Obtained by crossing selected F_2 plants of BH-2 as female with selected F_2 plants of BH-1 as male parent.

iii. P_3 cross progenies – Obtained by crossing selected F_2 plants of BH-3 as female with selected F_2 plants of BH-4 as male parent.

iv. P_4 cross progenies – Obtained by crossing selected F_2 plants of BH-4 as female with selected F_2 male plants of BH-3.

The crossed seeds of each population were sown separately in the field with a spacing of 60 cm between the row and 30 cm between the plants along with the commercial checks in two replications. Recommended package of practice were followed to raise the good crop. Observations were recorded on different quantitative characters like days to first flowering, days to 50% flowering, plant height, number of branches per

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plant, internodal length, fruit length, fruit diameter, fruit weight, number of seeds per fruit, 100 seed weight, number of fruits per plant and fruit yield per plant. The genotypic and phenotypic coefficient of variation was computed according to Burton and Devane (1953). Heritability in broadsense was estimated and expressed in percentage Hanson *et al.* (1956). GA at five per cent selection intensity was calculated by the formula given by Robinson *et al.* (1949). GA as per cent mean was calculated as suggested by Johnson *et al.* (1955). Between family variance was calculated for different characters by taking the variance of mean values of all the families and within family variance is calculated for different characters by taking variance of individual plant observations in each family and average of the variances of all the families, expressed as within family variance. Additive variance was computed according to Kearsay and Jinks (1968) and narrow sense heritability was estimated and expressed according to Hanson *et al.* (1956).

Results and Discussion

As far as mean and range are concerned, the population P_1 exhibited the highest values of mean and range among all the populations for the characters such as plant height, number of branches per plant, internodal length, fruit diameter, number of fruits per plant and fruit yield per plant. This population also expressed lower mean and range values for the traits like days to first flowering and days to 50% flowering. This indicates that there is a greater scope for selection in this population and increasing the mean in desired direction. Especially number of fruits per plant and fruit yield per plant was more in the population P_1 followed by the population P_4 as compared to populations P_2 and P_3 (Table 1).

Comparison of genetic variability parameters for different quantitative characters showed that, the characters like number of branches per plant, number of fruits per plant and fruit yield per plant showed high GCV and PCV values. But characters like plant height, fruit weight and fruit length expressed moderate GCV and PCV values. Where as days to first flowering, days to 50% flowering, fruit diameter, number of seeds per fruit and 100 seed weight exhibited low GCV and PCV values. The high GCV and PCV values for fruit yield per plant and number of branches per plant may be attributed to the predominance of repulsion phase linkage for these traits. This higher genetic variability observed might be attributed to their highly diverse nature and increased opportunity for favorable recombination of genes in F_2 population. This indicates that there is ample scope for the selection for increasing yield level of okra. Traits like plant height, internodal length, number of fruits per plant and fruit yield per plant showed moderate to high genetic advance accompanied by moderate to high heritability in broad sense was observed.

The population P_1 showed highest value of GCV, PCV, heritability, GA and GA as per cent mean among all the populations for some of the fruit yield traits like fruit

Table 1: Estimates of variability parameters for different quantitative characters in four biparental F_1 populations of okra

S. No.	Characters	BIP	Mean	Range	GCV (%)	PCV (%)	h^2bs (%)	GA	GAM (%)
1	Days to first flowering	P1	41.50	38-45	3.68	4.35	71	2.71	6.40
		P2	41.71	38-45	4.07	4.61	78	3.11	7.40
		P3	41.92	38-45	3.47	4.30	65	2.44	5.78
		P4	41.95	35-45	3.54	5.00	50	2.18	5.15
2	Days to 50% flowering	P1	47.04	43-50	2.93	3.50	70	2.41	5.07
		P2	47.36	43-52	2.91	3.24	81	2.56	5.40
		P3	47.34	43-51	2.51	3.15	64	1.97	4.13
		P4	47.64	43-52	2.72	3.70	54	1.96	4.11
3	Plant height (cm)	P1	92.03	79.50-155.50	11.98	14.07	73	19.94	21.02
		P2	86.21	75.50-148.00	14.25	17.59	66	21.10	23.76
		P3	87.49	75.50-154.00	8.77	10.30	73	13.65	15.39
		P4	90.03	65.50-130.00	13.94	16.46	72	22.39	24.31
4	Number of Branches/plant	P1	2.99	1-8	32.97	39.90	68	2.22	56.11
		P2	2.64	1-7	37.87	44.63	72	1.28	66.19
		P3	2.70	1-8	38.45	46.30	69	1.82	65.79
		P4	2.88	1-8	21.59	29.89	52	2.11	32.13
5	Internodal length (cm)	P1	8.10	5.80-13.00	22.92	27.38	70	25.27	39.52
		P2	7.08	5.40-12.50	8.92	10.86	68	1.07	15.11
		P3	7.58	5.50-12.50	16.20	20.27	64	14.61	26.68
		P4	7.86	6.00-14.50	14.37	21.14	46	1.58	20.14
6	Fruit weight (gm)	P1	16.71	12.11 - 23.51	8.66	10.12	73	2.55	15.26
		P2	16.66	11.50 - 21.40	10.97	12.65	75	3.27	19.61
		P3	16.01	11.50 - 20.50	8.20	10.36	63	2.14	13.38
		P4	17.25	10.57 - 24.00	10.07	12.42	66	2.90	16.82

Table 1:Contd…

S. No.	Characters	BIP	Mean	Range	GCV (%)	PCV (%)	h^2bs (%)	GA	GAM (%)
7	Fruit length (cm)	P1	14.18	7.90-17.07	10.55	13.70	59	2.37	16.74
		P2	14.59	10.10-21.20	8.04	11.25	51	1.73	11.85
		P3	13.94	10.10-21.22	8.54	13.11	42	1.60	11.47
		P4	16.53	11.25-21.22	9.63	13.00	55	2.14	14.70
8	Fruit Diameter (cm)	P1	1.85	0.91-1.82	9.48	13.32	51	0.21	13.89
		P2	1.53	1.21-1.85	5.67	7.84	52	0.13	8.43
		P3	1.46	0.95-1.82	6.21	7.53	68	0.15	10.56
		P4	1.76	1.10-1.90	5.03	7.97	40	0.10	6.54
10	100 seed weight (gm)	P1	6.71	5.50-7.20	4.13	5.09	66	0.46	6.90
		P2	6.80	6.00-7.50	2.91	4.17	49	0.28	4.19
		P3	6.66	5.50-7.10	3.04	4.47	46	0.28	4.27
		P4	7.01	5.50-7.10	5.22	8.48	38	0.45	6.62
11	Number of fruits/ plant	P1	21.18	9-37	34.38	37.04	86	13.92	65.72
		P2	19.50	10-33	21.76	25.62	72	7.42	38.07
		P3	18.97	10-35	17.95	23.14	60	5.44	28.68
		P4	19.83	9-34	23.60	24.70	91	9.21	46.46
12	Fruit yield / plant (gm)	P1	346.48	101.25-708.00	37.66	40.38	87	250.69	72.35
		P2	328.74	154.00-594.00	25.55	29.15	77	151.69	46.14
		P3	305.90	181.40-697.20	24.96	30.55	67	128.49	42.00
		P4	331.03	148.50-704.48	29.29	30.58	92	191.36	57.81

length (10.55, 13.70, 59, 2.37 and 16.74), fruit diameter (9.48, 13.32, 51, 0.28 and 13.89), number of fruits per plant (34.38, 37.07, 86, 13.92 and 65.72) and fruit yield per plant (37.66, 40.38, 87, 250.69 and 72.35) followed by P_4 population. This indicates that there is greater scope for selection in P_1 and P_4 as far as these traits are concerned. It also signify the importance of parental populations involved in these crosses and the potentiality of the cross combinations to generate more variability. The other two populations *i.e.,* P_2, P_3 did not differ much between themselves for PCV, GCV for most of the traits.

Between and within family variance for different quantitative characters in four biparental mating populations is given in Table 2. Population P_1 exhibited the highest within and between family variances for traits like plant height, number of fruits per plant and fruit yield per plant followed by P_4 population. This indicates that the commercial hybrids BH-1 and BH-2 of population P_1 and BH-4 and BH-3 of population P_4 could release more variability when forwarded to F_2 and the crosses made among these F_2 plants also released more variability.

Table 2: Estimates of within family and between families variance for different quantitative characters in four biparental F_1 populations of okra

Sl. No.	Character	Variance	BIP			
			P1	P2	P3	P4
1	Days to first flowering	Within family	6.43	5.64	5.94	12.54
		Between families	0.87	0.73	0.75	1.41
2	Days to 50% flowering	Within family	3.97	3.93	4.12	10.54
		Between families	0.60	0.42	0.50	1.14
3	Plant height (cm)	Within family	1741.87	229.01	188.29	253.80
		Between families	55.58	9.34	9.35	8.79
4	Number of branches /plant	Within family	3.78	2.83	2.98	4.91
		Between families	0.21	0.28	0.23	0.30
5	Internodal length (cm)	Within family	2.14	1.31	2.64	7.26
		Between families	0.36	0.20	0.30	0.68
6	Fruit weight (g)	Within family	12.47	7.95	9.47	14.82
		Between families	0.96	0.61	0.86	1.08
7	Fruit length (cm)	Within family	12.96	6.83	8.79	15.68
		Between families	1.02	0.56	0.71	1.16
8	Fruit diameter (cm)	Within family	0.04	0.18	0.04	0.14
		Between families	0.00	0.02	0.01	0.01
10	100 seed weight (g)	Within family	0.19	0.18	0.11	16.63
		Between families	0.03	0.02	0.02	1.63
11	Number of fruits/ plant	Within family	405.50	126.47	316.75	323.08
		Between families	9.82	5.54	13.86	8.08
12	Fruit yield / plant (g)	Within family	41552.73	19105.73	22197.18	37247.21
		Between families	950.56	929.52	860.72	1053.93

Table 3: Estimates of additive, total phenotypic variances and narrow sense heritability (h^2_{ns}) for different quantitative characters in four biparental F_1 populations of okra

S. No.	Character	Components of variance	BIP			
			P1	P2	P3	P4
1	Days to first flowering	Additive variance (VA)	3.47	2.91	2.98	5.65
		Phenotypic variance (VP)	7.30	6.37	6.68	13.95
		Heritability (h^2_{ns}) %	48	46	45	41
2	Days to 50% flowering	Additive variance (VA)	2.39	1.67	2.01	4.55
		Phenotypic variance (VP)	4.57	4.35	4.62	11.68
		Heritability (h^2_{ns}) %	52	38	44	39
3	Plant height (cm)	Additive variance (VA)	222.33	37.36	37.42	35.17
		Phenotypic variance (VP)	1797.46	238.35	197.64	262.59
		Heritability (h^2_{ns}) %	12	16	19	13
4	Number of branches/ plant	Additive variance (VA)	0.83	1.12	0.90	1.22
		Phenotypic variance (VP)	3.99	3.11	3.21	5.21
		Heritability (h^2_{ns}) %	21	36	28	23
5	Internodal length (cm)	Additive variance (VA)	1.44	0.80	1.19	2.73
		Phenotypic variance (VP)	2.50	1.51	2.94	7.95
		Heritability (h^2_{ns}) %	58	53	41	34
6	Fruit weight (g)	Additive variance (VA)	3.84	2.43	3.45	4.32
		Phenotypic variance (VP)	15.76	8.56	10.33	15.90
		Heritability (h^2_{ns}) %	29	28	33	27
7	Fruit length (cm)	Additive variance (VA)	4.08	2.23	2.83	4.64
		Phenotypic variance (VP)	13.97	7.38	9.50	16.84
		Heritability (h^2_{ns}) %	29	30	30	28
8	Fruit diameter (cm)	Additive variance (VA)	0.01	0.06	0.02	0.06
		Phenotypic variance (VP)	0.04	0.20	0.05	0.15
		Heritability (h^2_{ns}) %	31	31	45	37
10	100 seed weight (g)	Additive variance (VA)	0.11	0.08	0.08	6.50
		Phenotypic variance (VP)	0.21	0.19	0.13	18.26
		Heritability (h^2_{ns}) %	53	40	62	36
11	Number of fruits/ plant	Additive variance (VA)	39.28	22.15	55.44	32.32
		Phenotypic variance (VP)	415.32	132.01	330.61	331.16
		Heritability (h^2_{ns}) %	09	17	17	10
12	Fruit yield / plant (g)	Additive variance (VA)	3802.24	3718.08	3442.88	4215.71
		Phenotypic variance (VP)	42503.29	20035.25	23057.90	38301.13
		Heritability (h^2_{ns}) %	09	19	15	11

The contribution of additive variance to the total phenotypic variance is higher for the characters like days to first flowering, days to 50 per cent flowering, internodal length and 100 seed weight accompanied with high narrow sense heritability (Table 3).

While for traits like number of fruits per plant and fruit yield per plant, contribution of additive variance to the total phenotypic variance is very less accompanied with low narrow sense heritability. Suggesting predominant role of non-additive gene action for the characters mentioned above. Suggesting that for characters like number of fruits per plant and fruit yield per plant selection is ineffective and hybrid breeding procedures need to be followed for the exploitation of heterosis.

The cross combinations P_1 and P_4 released more variability which represents the ability of the parents involved in these cross combinations to release more of variability and also these cross combinations showed predominance of non additive variance which can be exploited through hybridization followed selection by procedures.

सारांश

भिण्डी की 4 द्विपौत्रिक प्रजनन समूह को प्रयुक्त कर अनुवांशिक विविधता तथा घटक प्रसरण के विश्लेषण से स्पष्ट हुआ कि लक्षण प्ररूप विविधता गुणांक तथा जीन प्रारूप विविधता गुणांका, शाखाओं की संख्या प्रति पौध, फलियों की संख्या तथा फल उपज/पौध जैसे गुणों के लिए उच्चतम पाया गया। जिससे चयन के उच्च संकेत मिलते है। समूह पी–1 ने उच्च लक्ष्ण प्ररूप विविधता, जीन प्ररूप विविधता, वंशागातित्व तथा अनुवांशिक उन्नयन लगभग सभी उपज घटकों में देखा गया तथा इसके उपरान्त समूह पी–4 का स्थान पाया गया। दो अन्य समूह पी–2 एवं पी–3 उपज तथा सम्बन्धित घटको के अधिक विविधता प्रदर्शित नहीं किये। समूह पी–-1 तथा पी–4 ने कुल के बीच तथा अन्दर प्रसरण उपज सम्बन्धित घटकों के बीच उच्चतम पाया गया जो संकेत देता है कि ये सभी संकरण से विविधता प्राप्त होती है। जो चयन के लिए प्रचुर सम्भावना देता है। इसी प्रकार पी–1 तथा पी–4 समूह ने निम्नतम संकीर्ण वंशागतित्व स्पष्ट किया जो संकेत देता है कि पत्तो की संख्या/पौध तथा उपज प्रति पौध में अयोज्य प्रसरण की प्रबलता है।

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