GENETIC ANALYSIS IN F_2 GENERATION OF IRRADIATED INTERSPECIFIC HYBRIDS IN OKRA (*ABELMOSCHUS* SPP.)

Okra is one of the most important vegetable crops grown for its green tender fruits. The variability available in a population can be partitioned into heritable and non-heritable components using the genetic parameters, phenotypic and genotypic coefficients of variation, heritability and genetic advance based on which selection can be effectively carried out. A high genetic advance along with high heritability shows the most effective condition of selection. The present study is aimed to estimate the extent of genetic variability present in the F_2 population of irradiated inter-specific hybrids of okra.

The study was undertaken in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Trivandrum. In the present study selfed seeds obtained from two parents A. *esculentus* var. Kiran and the semi-wild parent A. *manihot,* their F_1 (un-irradiated) and F_1M_1(gamma irradiated) seeds were used to raise the F2M2 generation. The experiment was laid out in a compact family block design with seven treatments as main plot (the un-irradiated treatment 0 kR, the four radiation treatments 10 kR, 20 kR, 30 kR, and 40 kR and the two parents), five replications and 10 progeny rows per treatment (subplot). Each progeny row consisted of 10 plants. Observations were recorded on the characters like days to first flowering, leaf axil bearing the first flower, leaf number, leaf area, number of flowers per plant, number of fruits per plant,

Table 1. Genotypic coefficient of variation in F_2M_2 generation

Characters	Level of radiation					P1	P2
	0 kR	10 kR	20 kR	30 kR	40 kR		
1	2.31	2.03	3.20	7.81	ne	ne	2.28
2	3.29	ne	6.92	13.40	ne	5.59	3.60
3	1.01	13.64	114.14	47.64	7.87	3.84	3.27
4	12.96	34.13	32.67	40.00	7.37	2.45	ne
5	47.58	85.47	194.22	143.69	183.90	43.40	0.00
6	1.63	15.09	133.33	55.31	13.64	4.45	4.33
7	4.17	14.27	35.46	37.27	17.96	13.02	16.69
8	0.00	9.80	6.87	13.78	4.76	6.16	4.34
9	ne	ne	137.66	58.24	11.06	4.23	ne
10	2.11	8.09	28.76	15.80	12.14	2.87	ne
11	ne	7.85	51.55	16.52	11.41	7.84	ne
12	ne	72.54	22.18	13.19	7.45	3.40	ne
13	6.90	2.87	13.02	14.24	8.98	1.00	1.67
14	14.54	47.39	131.02	101.33	56.4	5.80	9.60
15	1.92	6.21	10.51	4.99	1.63	0.00	1.27
16	2.04	3.69	7.32	13.21	ne	ne	0.79
17	4.94	31.3	23.27	23.99	10.82	0.00	2.63
18	0.00	0.00	0.00	ne	0.00	7.94	ne
19	2.71	0.00	ne	12.36	0.00	9.44	0.00
20	2.24	3.22	0.30	9.23	ne	0.48	3.02

Characters: 1. Days to first flowering, 2. Leaf axil bearing first flower, 3. Leaf number, 4. Leaf area, 5. Number of branches per plant, 6. Number of flowers per plant. 7. Pollen sterility, .8. First fruiting node, 9. Number of fruits per plant, 10. Average fruit weight, 11. Weight of fruits per plant, 12. Length of fruit, 13. Girth of fruit, 14. Number of seeds per fruit, 15. Number of ridges per fruit, 16. Fruiting phase, 17. Height of plant, 18. Incidence of YVM disease, 19. Fruit and shoot borer, 20. Duration of plant

ne = not estimable

Table 2. Heritability and genetic advance in F_2M_2

Chara- cters	0 kR		10 kR		20 kR		30 kR		40 kR		P1		P2	
	H^2	GA	H^2	GA	H^2	GA	H^2	GA	H^2	GA	H^2	GA	H^2	GA
1	12	1.16	11	1.38	22	3.16	75	13.93	ne	ne	ne	ne	15	9.29
2	8	1.90	ne	ne	39	8.88	68	22.67	ne	ne	21	5.17	18	3.16
3	1	0.30	40	17.68	99	234.40	85	90.39	9	4.83	30	4.34	9	2.06
4	52	19.29	89	66.18	91	64.45	93	79.65	84	32.73	3	0.88	ne	ne
5	18	40.22	69	148.79	97	393.14	88	277.52	87	354.03	11	24.13	1	1.81
6	1	0.32	33	17.88	98	271.67	85	105.31	27	14.67	21	4.25	8	2.59
7	22	4.03	71	24.82	92	69.89	87	71.63	73	31.57	10	8.45	57	25.87
8	0	0.00	65	16.28	50	9.93	88	26.55	13	3.57	25	6.28	19	3.80
9	ne	ne	ne	ne	99	282.27	90	113.78	24	11.22	20	3.82	ne	ne
10	2	0.62	11	5.42	62	46.73	48	22.53	62	19.17	13	2.21	ne	ne
11	ne	ne	6	3.93	73	90.61	24	16.81	26	11.99	30	8.83	ne	ne
12	ne	ne	86	43.12	83	41.64	81	24.51	37	9.37	23	3.40	ne	ne
13	32	97.00	14	2.34	63	21.38	89	27.61	66	14.95	9	1.00	6	0.85
14	40	18.98	78	86.24	97	265.26	94	202.74	80	103.88	16	5.80	30	8.07
15	11	1.37	20	5.68	55	15.97	22	4.90	1	0.22	0	0.00	9	0.70
16	13	1.50	30	4.16	37	9.22	80	24.28	ne	ne	ne	ne	40	3.40
17	24	4.96	81	57.99	86	44.53	85	45.58	50	15.76	0	0.00	12	1.44
18	1	0.26	22	4.06	2	0.61	ne	ne	13	3.24	35	7.94	ne	ne
19	17	2.12	1	0.12	ne	ne	66	20.72	3	0.35	56	9.44	2	0.37
20	30	2.53	45	4.44	1	0.06	83	145.16	ne	ne	7	0.48	51	4.44

Characters: 1. Days to first flowering, 2. Leaf axil bearing first flower, 3. Leaf number, 4. Leaf area, 5. Number of branches per plant, 6. Number of flowers per plant, 7. Pollen sterility, 8. First fruiting node, 9. Number of fruits per plant, 10. Average fruit weight, 11. Weight of fruits per plant, 12. Length of fruit, 13. Girth of fruit, 14. Number of seeds per fruit, 15. Number of ridges per fruit, 16. Fruiting phase, 17. Height of plant, 18. Incidence of YVM disease, 19. Fruit and shoot borer, 20. Duration of plant
ne = not estimable

average fruit weight, weight of fruits per plant, length and girth of fruit, number of ridges of per fruit, number of seeds per fruit, plant height, incidence of YVM disease and fruit and shoot borer, fruiting phase and plant duration. The data were statistically analyzed and genotypic coefficient of variation (Burton, 1952), heritability in broad sense (Jain, 1982) and genetic advance (Allard, 1960) were estimated for each character in each treatment.

The genotypic coefficient of variation, heritability in broad sense and genetic advance for the seven treatments with respect to the different characters under study are presented in Tables 1 and 2. High genotypic coefficient of variation (above 50%) was observed in majority of the irradiated treatments for number of branches per plant and number of seeds per fruit. However, Sheela (1994) observed only moderate level of genotypic coefficient of variation for number of seeds per fruit. High genotypic coefficient of variation was noticed in the treatment 20 kR for number of leaves per plant (114.14%), number of flowers per plant (133.33%) and number of fruits per plant (137.66%). Moderately high genotypic coefficient of variation was noticed for weight of fruits per plant in the treatment 20 kR (51.55%). Very low genotypic coefficient of variation was noticed for yellow vein mosaic disease incidence in all the treatments, which is in agreement with the findings of Mathews (1986). The characters - days to first flowering, leaf axil bearing the first flower, first fruiting node, length and girth of fruits, number of ridges per fruit, fruiting phase, plant duration and incidence of fruit and shoot borer recorded low genotypic coefficient of variation in all the treatments. This indicates the

low amount of genetic variability and limited scope of improvement of these characters through selection.

Broad sense heritability includes additive gene action also and hence can be utilized in seed propagated crops. High heritability with very high genetic advance was observed for number of branches per plant and number of seeds per fruit in all the irradiated treatments. High heritability with moderately high genetic advance was observed in the four irradiated treatments for leaf area. High heritability with very high genetic advance was observed in the treatment 20 kR for leaf number (99 and 234.4%), number of flowers per plant (98 and 271.67%) and number of fruits per plant (99 and 282.27%). High heritability and high genetic advance were observed for fruit yield per plant in 20 kR (73 and 90.61%) and for leaf number (85 and 90.39%), number of flowers per plant (85 and 105.31%), number of fruits

per plant (90 and 113.78%), pollen sterility (87 and 71.63%) and plant duration (83 and 145.16%) in 30 kR respectively. High heritability and high genetic advance were noticed for fruit yield per plant by Sheela (1994). High heritability along with high genetic advance indicates additive gene action and results in the most effective condition for selection of these characters (Jain, 1982). Heritability and genetic advance were low for yellow vein mosaic incidence in all treatments except the cultivated parent, which had moderately high heritability (35%) and low genetic advance. Low heritability and genetic advance suggests the predominant role of environment in the inheritance of YVM disease and it indicates lesser scope for improvement of this trait through selection.

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