



An analysis of polygenic variation in the M_4 families of coriander (*Coriander sativum* L.)

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Mutation breeding programme has been undertaken with selective mutagen doses (Sodium azide, 1mM; Hydroxylamine 1% and Gamma rays 10, -25kR doses) in coriander (*Coriander sativum* L.), an important spice crop of the country (1). The objective was to develop improved varieties, which is rather lacking in this crop due to narrow range of genetic variability and susceptibility to biotic and abiotic stresses (2 and 4). This investigation reports on the polygenic variation noted in M_4 progenies of three coriander varieties for yield and yield attributes. The M_4 progenies of the three varieties were developed through inter mating 6-10 plants both in M_2 and M_3 generations by covering them with muslin cloth bag during flowering. The intermating was done to avoid poor seed setting that might result from inbreeding depression where single plant is selfed. Each M_2 progeny, however, was corresponded to single M_1 plant which was selfed and only those M_2 progenies which had significantly higher yield than their respective controls (Parents) were advanced to M_4 generation without evaluating their M_3 generation. There were 63 M_4 progenies of coriander variety RCr-41, 64 of RCr-436 and 23 of RCr-20 included in the present investigation. For progenies of each variety, we expected a variation attributable to the difference between the means of the M_4 progenies, difference between different individuals of progenies, new recombinants resulting from their intermating and expression of the mutated genes. The variance analysis (5) revealed that *between progeny* component of variance was significant for all the characters studied in the M_4 progenies of the three varieties, thus substantiating our expectation. The *within progeny* component of variance was, however, non significant for all the characters studied in respect of three varieties. Non significant *within progeny* variance for yield and its attributes in coriander have been reported (5, 6). Since coriander is a cross-pollinated crop the induction of forward mutations at heterozygous loci may partly be responsible for decreasing the variation within the progenies (3). For yield/plant none of the 23 progenies

of RCr-20 were superior to their parent. However, 1 progeny of RCr-41 and 8 progenies of RCr-436 were superior to others, as it possessed significantly higher values of five out of seven other traits studied. As regards the procedure of handling the progenies in M_2 generation and later, they are well described for self-pollinated crops. However, a similar information in respect of cross-pollinated crops is scanty. The results of present study may be of some use in this regard. It has earlier been shown that selection is most effective in M_2 generation (7). Therefore, only selected progenies were advanced to later generations. Since the M_4 generation may be considered relatively uniform, therefore, the M_4 progenies performing well may also perform well in the subsequent generations. Results of the present study indicated to the existence of influence of genetic constitution of the parents on the fate of their progenies in advanced generation. Most progenies of RCr 20 and RCr 41 seemed to have undergone inbreeding depression whereas those of RCr 436 have frequently out yielded the control. It is remarkable that in case of RCr 436, the parent and M_4 progenies have shown a high magnitude of c.v. for yield per plant and umbels/plant as well (Table 1). Conclusively it may be inferred that (i) selection for yield made in M_2 generation should be accompanied by identification of inbreeding resistant lines in advance generations and (ii) more genotypes should be included to initiate a mutation breeding program for polygenic trait improvement in the cross-pollinated crops.

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Table 1. Magnitude of different yield attributes in high yielding M_4 progenies of the coriander variety RCr-436 and Rcr-41

Varieties	Yield/plant		Plant height		Primary branches/ plant		Umbels/ plant		Umbellets/ umbe		100 seed weight		Seed setting/ umbe (%)		Seeds/umbe	
	Mean (g)	C.V. (%)	Mean (g)	C.V. (%)	Mean (g)	C.V. (%)	Mean (g)	C.V. (%)	Mean (g)	C.V. (%)	Mean (g)	C.V. (%)	Mean (g)	C.V. (%)	Mean (g)	C.V. (%)
RCr-436																
41	4.77**	64.8	35.6*	19.9	5.0	14.1	16.8	37.7	5.0	14.1	1.5*	9.9	60.9**	17.5	30.2	30.2
46	4.92**	103.1	32.0	12.5	4.8	27.2	12.2	66.4	4.2	10.6	1.5	16.8	46.2	23.7	13.6**	33.5
46	8.43**	40.1	39.2**	9.4	4.4	12.4	21.2*	3.1	6.8*	12.3	1.45	4.4	57.4*	29.1	31.8	38.1
136	4.13**	51.6	26.0	25.0	4.8	27.2	18.8**	38.8	4.0	0.0	1.4	9.3	46.7	11.8	21.4	10.2
137	4.18**	15.1	25.1	9.8	4.0	17.7	21.4**	15.7	4.6	11.9	1.4	5.0	50.9	13.1	25.4	18.4
156	6.34**	37.1	32.0	5.9	6.2**	7.2	28.0**	11.3	4.4	20.3	1.5	6.6	61.7	21.8*	31.8*	23.1
209	8.98**	126.9	37.7**	17.3	5.0	24.5	22.6*	101.1	5.0	20.0	1.7**	23.8	58.5**	40.0	32.6*	45.2
N-18	5.09**	59.1	31.8	15.0	6.0**	0.0	18.4**	34.9	5.2*	16.1	1.5	7.9	52.9	11.2	29.8	16.7
Control	2.11	54.9	29.1	14.5	4.7	24.8	11.4	40.0	4.3	17.5	1.4	13.6	46.0	19.5	25.0	25.0
Range	0.74-8.98		21.14-58.6		3.40-6.20		8.6-28.0		3.2-6.8		0.93-1.66		27.0-66.48		9.0-34.2	
RCr-41																
59	5.13	30.6	71.4	30.4	5.6	17.8	3.4*	16.1	18.2**	17.1	1.2	12.3	60.5	24.4	41.8	38.2
Control	2.65	40.3	62.2	25.6	4.7	31.3	9.9	58.5	4.3	18.5	1.2	18.9	52.9	28.6	37.3	43.9
Range	1.99-5.18		39.8-78.8		3.0-6.6		8.0-18.2		3.2-5.8		1.02-1.88		12.99-62.62		16.2-81.6	

*,**Indicate that the progeny means significantly deviated from the control mean at $p>0.05$ and $p>0.01$, respectively. (The difference of the means from the parental mean for each character was tested separately for each progeny using 't' test.

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