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Short Communication

Inheritance of leaf margin in fenugreek (*Trigonella foenum-graecum* L.)

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Fenugreek (*Trigonella foenum-graecum* L.) is an important multipurpose legume crop grown during winter season. It is gaining importance for its medicinal value, higher market price and rich source of protein and minerals and diosgenic content. It also enhances the soil fertility by fixing atmospheric nitrogen. Smooth and serrated leaf margin, being qualitative trait could be used as marker trait during selection, varietal identification and gene mapping programmes in fenugreek. Presently, information on inheritance of this character in fenugreek is non-existent. Therefore, the present study was carried out to get information on inheritance of serrated and smooth leaf margin in fenugreek.

The experimental material comprised three genetically diverse genotypes of fenugreek viz., HM 350 (having smooth margin), NLM and HM 65 (having serrated leaf margin). The genotype HM 350 was reciprocally crossed to both NLM and HM 65 and two crosses, HM 350 × HM 65 and NLM × HM 350 were developed. The F_1, F_2 and backcross generations of these two crosses were generated to study the inheritance pattern of leaf margin. The genetic material comprising six generations of both the crosses was planted in randomized block design with three replications at research farm of CCS Haryana Agricultural University, Hisar during winter, 2000-01. A row to row spacing of 30 cm was kept in the layout. The non-segregating generations (P_1, P_2 and F_1) were planted in single rows, whereas F_2's and backcrosses had four and two rows each, respectively. Observations on the trait were recorded on individual plants in each generation. Chi-square test was applied for testing goodness of fit for the observed segregation ratios.

Table 1. Mode of segregation for leaf margin in cross HM 350 × HM 65 in fenugreek

Parent/ generation	Number of plants in each class		Expected ratio	χ^2 value	P value
	Smooth margin	Serrated margin			
HM 350	54	-	-	-	-
HM 65	-	66	-	-	-
F_1	-	52	-	-	-
F_2	37	105	1 : 3	0.084	0.80-0.70
B_1	48	54	1 : 1	0.353	0.70-0.50
B_2	-	92	-	-	-

Table 2. Mode of segregation for leaf margin in cross NLM × HM 350 in fenugreek

Parent/ generation	Number of plants in each class		Expected ratio	χ^2 value	P value
	Smooth margin	Serrated margin			
NLM	-	52	-	-	-
HM 350	58	-	-	-	-
F_1	-	48	-	-	-
F_2	52	150	1 : 3	0.059	0.90-0.80
B_1	-	97	-	-	-
B_2	41	43	1 : 1	0.023	0.90-0.80

All the 100 F_1 plants in the crosses, NLM × HM 350 and HM 350 × HM 65 had serrated leaf margin (Table 1 and 2) indicating that serrated leaf margin was dominant over smooth margin. Occurrence of F_1 plants with serrated margin in the reciprocal crosses between HM 350 and HM 65 over ruled the presence of cytoplasmic inheritance. In F_2 generations of the crosses, HM 350 × HM 65 and NLM × HM 350 segregation of 37 : 105 and 52 : 150 plants, respectively showed a good fit to 1 : 3 monohybrid ratio, thus, indicating that serrated leaf margin was governed by a single dominant gene and its recessive counterpart was responsible for smooth leaf margin. Although reports to confirm these finding are not available in fenugreek, however, similar results have been reported in Chinese cabbage [1] and jute [2]. Whereas, Singh [3] ascribed two pairs of genes with inhibitory effects for controlling serrated leaf margin in *guar*. Both the backcrosses involving HM 350 also segregated showing a good fit to 1 smooth : 1 serrated, which further confirmed the above findings.

On the basis of present results, the gene symbol 'S_m' is assigned to serrated margin. The genetic constitution of the parental genotype with serrated margin, would be 'S_m S_m' whereas the plants with smooth margin would be having genotype as 's_m s_m'.

The present study, thus, reveals that gene controlling serrated leaf margin is dominant over that responsible for smooth leaf margin and is under single dominant gene control in fenugreek. The segregation pattern rules out the possibility of cytoplasmic inheritance for leaf margin. This trait, hence can easily be incorporated into desirable genotypes and it can also be used as a marker trait for easy identification of varieties in breeding and seed production programmes.

References

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