

Genetics of earliness in fenugreek under powdery mildew inoculated and natural environments

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Abstract

Inheritance of days to flower and maturity in fenugreek (*Trigonella foenum-graecum* L.) was studied using six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of a cross between HM 350 (early) and HM65 (late) in two different environments *i.e.* inoculated with conidia of powdery mildew disease (E_1) and normal (E_2). Partial dominance was observed for both the traits under both the environments. The variances of F_2 and backcross generations revealed the predominance of non-additive gene action. Genetic analysis suggested that generally all types of epistatic effects were significant for both the traits studied in one environment or another. Intermating of selects in early generations has been suggested for further improvement in these traits.

Key words: *Erysiphe polygoni*, fenugreek, genetics, genotype environment, interaction, maturity

Breeding early varieties is the major objective of any legume improvement programme. In fenugreek (*Trigonella foenum-graecum* L.), powdery mildew caused by *Erysiphe polygoni* DC is the most devastating disease which causes more than 50 per cent losses in seed yield (Rathi *et al.* 2000). Early flowering and early maturing genotypes usually escape from this disease resulting in minimal yield losses. There are conflicting reports on the relative importance of additive and dominance gene effects in the inheritance of days to flower and days to maturity (Raghuvanshi & Singh 1984; Singh & Raghuvanshi 1986; Singh 1995). Therefore, the present investigation was conducted to gather information on genetics of days to flower and maturity in fenugreek under two different environments.

The experimental material comprised six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of a cross between HM 350 (early in flowering and maturity) and HM 65 (late in flowering and maturity) grown during winter 2000-01 in completely randomized block design with three replications under two different environments *i.e.* inoculated with conidia of powdery mildew (E_1) and normal or uninoculated (E_2). Days taken for flowering and maturity were counted on five plants randomly selected for from each plot from parents and F_1 s, 30 plants from F_2 s and 15 plants from back cross generations. A generation mean analysis was carried out using six parameter model of Mather & Jinks (1971).

Partial dominance was observed for both days to flower and maturity under both the environments. The variance of the F_2 popu-

Table 1. Genetic variances for days to flower and maturity in different generations of a cross between HM 350 and HM 65 under two environments

Generation	df	Variance			
		Days to flower		Days to maturity	
		E ₁	E ₂	E ₁	E ₂
P _E	12	4.81	3.13	0.98	3.63
P _L	12	5.59	3.90	3.97	2.93
F ₁ (P _E × P _L)	12	6.19	4.03	1.78	5.19
F ₂	87	13.60	12.93	25.70	40.21
BC _E	42	9.57	4.50	13.58	27.74
BC _L	42	7.00	5.10	16.00	15.89

lation in both E₁ and E₂ was much greater than the variance of the parents and the F₁ generations in which variation is attributed to environmental effects. Since twice the variance of F₂ (Table 1) was greater than the sum of the variances of the back cross generations ($2VF_2 - VBC_L - VBC_E = 10.77$ for days to flower in E₁, 16.26 in E₂; for days to maturity 21.82 in E₁ and 36.79 in E₂), predominance of non-additive gene action is indicated. Cavalli's (1952) joint scaling test revealed the inadequacy of additive dominance model in the inheritance of both days to flower and maturity in fenugreek. Accordingly, genetic analysis (Mather & Jinks 1971) indicated the occurrence of epistasis for both the traits under both the environments.

The additive (d) and non-additive (h) gene effects were highly significant, the magnitude of latter being larger suggesting its importance (Table 2). These results are in agreement with those reported earlier in fenugreek (Raghuvanshi & Singh 1984; Singh 1995). The negative estimates of non-additive components observed for days to maturity indicated that these gene effects could further reduce the expression of this character. Among epistatic effects, (i) and (l) type were significant for both the traits in E₁, whereas in E₂, (i) and (j) were significant for days to maturity and only (l) was responsible for the expression of days to flower. A minimum of one to maximum three genes have been reported earlier (Singh 1995) to control days to flower and days to maturity. It is now obvious that both these traits are governed by several genes with preponderance of dominance action and epistatic effects. However, influence of additive gene action in sizeable proportion can not be ruled out. Under such a situation, intermating of selects in early segregating generations is suggested for simultaneous exploitation of both fixable and non-fixable gene effects, to break undesirable linkages and to get desirable recombinants with early flowering and maturity combined with better yield levels.

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Table 2. Estimates of gene effects for days to flower and maturity in a cross between HM 350 and HM 65 under two environments

Estimate	Days to flower		Days to maturity	
	E ₁	E ₂	E ₁	E ₂
m	57.77±2.45	59.27±2.20	124.14±3.30	122.14±4.08
(d)	1.52**±0.40	1.64**±0.34	2.45**±0.29	2.64**±0.33
(h)	18.01**±6.02	13.07**±5.16	-18.48**±7.98	-18.69**±7.82
(i)	4.76*±2.38	4.18±2.17	-10.60**±3.29	-6.88*±3.06
(j)	-1.80±1.59	-2.60±1.35	3.77±2.07	-7.15**±2.50
(l)	-6.46*±3.16	-9.74**±3.45	16.17**±4.84	5.65±5.98

*, ** Significantly different from zero at 0.05 and 0.01 levels of probability, respectively

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