

Generation Mean Analysis of Flowering and Maturity in Sesame

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Objectives

This study conducted to get the general information of the inheritance pattern of flowering and maturity of sesame by generation mean analysis method to make new types of sesame

Materials and Methods

- Three crosses : Yek / Namwon, Yek / Ik22, Namwon / Ik22
- Gene effect based on six parameter model were estimated using the non-weighted method and notation described by Gamble(1962).

$$m = F_2, d = +BC_1-BC_2, h = -0.5P_1-0.5P_2+F_1-4F_2+2BC_1+2BC_2$$

$$i = -4F_2+2BC_1+2BC_2, j = -0.5P_1+0.5P_2+BC_1-BC_2,$$

$$l = P_1+P_2+2F_1+4F_2-4BC_1-4BC_2$$

Results and Discussion

- The analysis reiterated that the importance of additive (d) gene effects for days from seeding to flowering as compared to dominance (h) gene effects. However, significant and negative additive effects were noticed for in both of traits in different crosses.
- The three types of gene interactions (additive, dominance and epistasis) were significantly involved for days from seeding to flowering and maturity in cross.
- Among the digenic epistatic interactions, both additive × additive (i) and dominance × dominance (l) contributed more for both of traits, however, it varied among the crosses.
- The type of epistatic gene actions were all duplicate rather than complementary.
- Populations having earliness can be developed as indicated by reducing dominance effects.
- Pedigree selection and heterosis breeding is suggested to exploit the fixable and non-fixable components of variation respectively in *Sesamum indicum*

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Table 1. Means and standard deviation of days from seeding to flowering in P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of three sesame germplasm cross combinations.

Generation	Cross combination		
	Yek/Namwon	Yek/Ik22	Namwon/Ik22
P_1	49.33 ± 1.78	50.67 ± 1.55	59.50 ± 1.67
P_2	59.52 ± 2.20	64.00 ± 1.35	64.47 ± 0.93
F_1	54.50 ± 2.09	56.20 ± 1.51	60.89 ± 1.85
F_2	53.27 ± 2.72	55.73 ± 2.73	58.67 ± 2.94
BC_1	51.88 ± 1.65	53.83 ± 1.66	60.47 ± 1.46
BC_2	56.83 ± 1.55	60.07 ± 2.05	62.17 ± 1.20

Table 2. Genetic components of days from seeding to maturity in P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of three sesame germplasm cross combinations.

Generation	Cross combination		
	Yek/Namwon	Yek/Ik22	Namwon/Ik22
$m^{1)}$	53.27 ± 1.57 ^{a)}	55.73 ± 1.56	58.67 ± 0.99
$d^{2)}$	-4.95** ± 0.10	-6.24** ± 0.22	-7.70** ± 0.15
$h^{3)}$	4.41* ± 2.51	3.74* ± 1.93	6.50** ± 0.58
$i^{4)}$	4.34* ± 2.57	4.88* ± 1.96	0.60** ± 0.90
$j^{5)}$	0.10 ± 0.18	0.43 ± 0.28	0.79 ± 0.37
$l^{6)}$	-3.80 ± 3.64	-5.61* ± 1.13	-10.13** ± 1.47
Type of epistasis	Duplicate	Duplicate	Duplicate

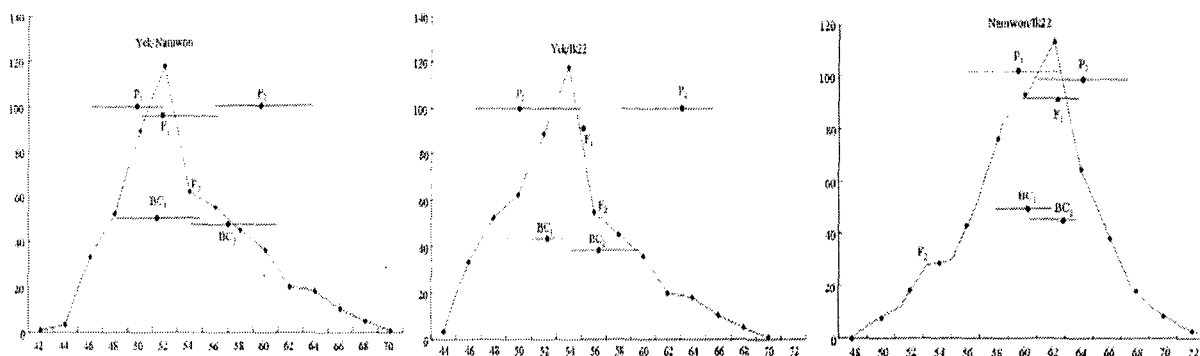


Fig. 1. Frequency distribution of days from seeding to flowering at the P_1 , P_2 , F_1 , F_2 , BC_1 , and BC_2 according to different sesame germplasm crosses.

Table 3. Means and standard deviation of days from seeding to flowering in P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of three sesame germplasm cross combinations.

Generation	Cross combination		
	Yek/Namwon	Yek/Ik22	Namwon/Ik22
P_1	82.00 ± 1.00	82.13 ± 0.90	92.13 ± 1.10
P_2	92.62 ± 0.55	104.57 ± 0.51	104.27 ± 0.87
F_1	85.00 ± 1.00	92.77 ± 2.45	98.50 ± 1.49
F_2	83.60 ± 2.51	89.83 ± 3.20	97.20 ± 1.50
BC_1	83.30 ± 1.50	87.80 ± 2.05	97.00 ± 1.05
BC_2	88.87 ± 1.35	97.80 ± 1.80	102.70 ± 1.10

Table 4. Genetic components of days from seeding to maturity in P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of three sesame germplasm cross combinations.

Generation	Cross combination		
	Yek/Namwon	Yek/Ik22	Namwon/Ik22
$m^{1)}$	83.60 ± 1.45 ^{a)}	82.13 ± 0.52	92.13 ± 0.65
$d^{2)}$	-5.57* ± 0.09	-10.00** ± 0.14	-5.70* ± 0.03
$h^{3)}$	7.62* ± 0.90	10.90** ± 1.96	11.20** ± 0.70
$i^{4)}$	9.94** ± 2.50	11.48** ± 2.96	10.90* ± 0.98
$j^{5)}$	0.25 ± 0.04	1.22 ± 0.03	0.37 ± 0.11
$l^{6)}$	-9.65** ± 2.40	-10.84** ± 2.16	-16.60** ± 1.35
Type of epistasis	Duplicate	Duplicate	Duplicate

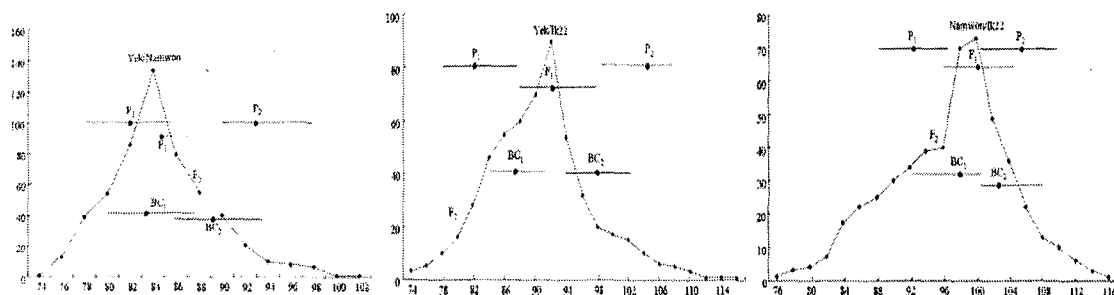


Fig. 2. Frequency distribution of days from seeding to maturity at the P_1 , P_2 , F_1 , F_2 , BC_1 , and BC_2 according to different sesame germplasm crosses.

1) m : mean. 2) d : additive effect. 3) h : dominance effect. 4) i : additive x additive type of genetic interaction. 5) j : additive x dominance type of genetic interaction. 6) l : dominance x dominance type of genetic interaction. a) standard error. *, ** : Significant at the 5%, 1% level respectively