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Inheritance of Oil and Protein Content in Some Cotton Generations

Mehmet Mert, Yasar Akiscan and [1]Oktay Gencer
Department of Field Crops, Faculty of Agriculture, Mustafa Kemal University, 31034-Hatay, Turkey
[1]Cotton Research and Application Center, Çukurova University, 01330-Adana, Turkey

Abstract: The value of cottonseed is determined largely by oil and protein content. Determining the inheritance of these traits and studying their influence on lint yield and fiber properties might improve breeding program efficiency. The main objective of this study was to determine the inheritance of oil and protein content and the influence of environment on oil and protein content in cotton (*Gossypium hirsutum* L.). For this investigation, Sure Grow 125 (P_1), PAUM 401 (P_2), F_1, F_2 and backcross generations were planted in a randomized complete block design at two locations in Turkey. Environment influenced the level of oil and protein content far more than did the genotypes. Generation mean analysis indicated that dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) effects were the main source of genetic variations for the oil and protein content. Since nonadditive effects were predominant, selection for these traits could be made in advanced generation.

Key words: *Gossypium hirsutum* L., environment, inheritance, oil, protein

INTRODUCTION

Increasing fiber production, producing high quality, early ripening, mechanical harvesting and improvements in resistance to diseases and pests are the most important breeding aims in cotton[1]. Additionally, increasing seed oil content is of interest. In the world market, cottonseed production ranks second among the five major oilseeds, which includes soybean seed, cottonseed, sunflower seed, peanut seed and rapeseed[2]. Competition from other seed sources in the oil and feed industries and the developing prospect of using cottonseed as a food, have increased the awareness of the potential importance of cottonseed to food and feed reserves of the world[3,4].

Although the effects of environment and genotype on oil and protein content are well documented and relationship of yield, seed quality and fiber properties in cotton have been identified[5-7], studying the inheritance of oil and protein content has not been widely undertaken. This is partly attributable to a lack of understanding of the genetics of the traits involved. Objectives of the study were to determine the inheritance of oil and protein content and the influence of environment on oil and protein content in cotton (*Gossypium hirsutum* L.).

MATERIALS AND METHODS

Two cotton cultivars, Sure Grow 125 (P_1) and PAUM 401 (P_2), were utilized to determine the inheritance of the oil and protein content. Sure Grow 125, which is derived from a cross between Des 119 and Deltapine 50, is registered in Turkey since 1999. PAUM 401 is a general-purpose line for both rainfed and irrigated conditions. The seed of this line was supplied by Dr. O. Gençer, Çukurova University, Cotton Research and Application Center (CRAC), Adana, Turkey. Sure Grow 125 was crossed to PAUM 401 at CRAC under field conditions, during the summer of 2000. The F_1 plants backcrossed to both parents at Adana, in the summer of 2001. Seeds of parents, F_1, F_2, BC_1P_1 and BC_1P_2 were planted in a randomized complete block design with three replications both at Adana on 7 May and at Hatay on 11 May 2002, Turkey. The experiments were grown at Adana on alluvial soil with a pH 7.5 and at Hatay on clay soil with a pH 7.3. Sowing was made in 5 m long rows with 71x20 cm row spacing at both locations. Standard cultural practices for the production of cotton were followed with regard to cultivation and chemical control of diseases and insects. Fertilizer was applied at the rate of 120 kg N, 60 kg P and 60 kg K ha^{-1}. Half of the N, all P and K were applied at sowing and the remaining N was applied at square stage. Fertilizer application rates were identical for Hatay and Adana. Crop was kept free from weeds. Experiments at both locations were irrigated five times throughout the growing season.

Plots were harvested by hand on 28 September at Adana and on 1 October at Hatay. Samples containing 20 bolls were hand-harvested from each plot prior to picking. The boll samples were ginned on a laboratory gin.

Corresponding Author: Mehmet Mert, Department of Field Crops, Faculty of Agriculture, Mustafa Kemal University, 31034-Hatay, Turkey, Tel. (+90) 326 2455837, Fax : (+90) 326 2455832 E-mail: mmert@mku.edu.tr

Table 1: Mean squares and values of oil and protein content for parents, F_1, F_2, $BC_1 P_1$ and $BC_1 P_2$ generations at Adana and Hatay

	Hatay (L_1)		Adana (L_2)		Mean	
(G) ‡	Oil (%)	Protein(%)	Oil (%)	Protein (%)	Oil (%)	Protein (%)
P_1	22.9b	26.2	22.7b	24.8	22.8	25.5
P_2	25.2a	24.7	19.1e	22.9	22.2	23.8
F_1	23.5b	25.8	21.6cd	23.1	22.6	24.5
F_2	24.7a	24.9	21.5cd	23.9	23.1	24.4
$BC_1 P_1$	23.2b	26.0	21.8c	25.8	22.5	25.9
$BC_1 P_2$	23.2b	25.7	20.9d	24.7	22.1	25.2
MP	23.9	25.6	20.9	23.9	22.5	24.7
EM	23.8	25.6	21.3	24.4	22.6	24.8
Loc. (L)					55.75**	12.13**
(G)					0.89	2.72
L x G					6.20**	1.90

**, Significant at the 0.01 level of probability
‡ Generations; P_1 = parental line 1, P_2 = parental line 2,
F_1 = first filial of crosses, F_2= second filial, MP = mid-parent mean,
EM= environment mean

Cottonseeds from sample bolls were delinted with H_2SO_4. Samples were then analyzed for oil and protein content using Soxhlet extraction method and Kjeldahl method, respectively.

Means and variances were estimated for every generation from individual plant data and estimates of genetic effects were determined. Information on the nature of the gene effects involved in oil and protein content was obtained by a weighted least square analysis with joint scaling test based on the methods reported by Singh and Chaudhary[8]. Parameters estimated were checked for their fit to the three-parameter model with the chi-square analysis. Since the three-parameter genetic model was not adequate to explain the data, the six-parameter genetic model for epistasis was used[8].

RESULTS

The mean squares and values of oil and protein content are presented by locations in Table 1. Oil content ranged from 19.1 to 25.2% across the two locations, while protein content ranged from 22.9 to 26.2%. In the combined analysis, the differences in traits content among the generations did not exist (Table 1). Both oil and protein content means from F_1 and F_2 populations were intermediate between the parental means. The backcrosses means in respect to oil content were intermediate between F_1 and the recurrent parent.

Although the best approximation of additive and dominance effects can be obtained from the three parameter additive-dominance model because these effects are unbiased due to the absence of epistasis[9], the three-parameter model was found not to be sufficient to explain the genetic control of oil and protein content in Sure Grow 125 x PAUM 401 cross (Table 2). Therefore, the six-parameter model was fitted to determine the type and magnitude of gene effects involved in the inheritance of oil and protein content in this cross. The results of the six-parameter model analysis indicated that dominance (*h*), additivexadditive (*i*) and dominancexdominance (*l*) effects contributed significantly to the inheritance of both traits. The dominance x dominance effects for oil content (4.20±0.15) and additive x additive effects for protein content (4.60±0.59) were the only significant epistatic effects (Table 2).

Table 2: Estimated gene effects with standard errors for oil and protein content for Sure Grow 125 x PAUM 401 cross

Model and effect	Oil content	Protein content
Three-parameter		
m	22.40±0.15	24.55±0.15
d	-0.15±0.15	-0.74±0.44
h	0.63±0.44	0.48±0.15
χ^2	4.58	7.37
P‡	<0.05	< 0.05
Six-parameter		
m	23.10±0.12	24.40±0.12
d	0.40 ±0.85	0.70±0.62
h	3.10±0.59	4.45±0.17
i	-3.20±0.57	4.60±0.59
j	0.10±0.21	-0.15±0.22
l	4.20±0.15	-8.50±0.92

m = Mean of F_2, *d* = Sum of additive effects,
h = Sum of dominance effects,
I = Sum of additive x additive epistatic effects,
j = Sum of additive x dominance epistatic effects and
l = Sum of dominance x dominance epistatic effects.
P‡ = Probability of obtaining a large χ^2 value.

DISCUSSION

The analyses of variance (Table 1) clearly show that environmental influences associated with locations contributed far more than genotypes to the variability in oil and protein content. However the significant locationxgenotype interactions for oil content indicated that genotypes did not respond to the environments similarly, as reported by Turner *et al.*[5] and Sun *et al.*[10]. Location x genotype interactions for protein content was nonsignificant, suggesting that genotypes maintain their rank for protein content across the environments. Non-significant genotype x environment interaction indicates that selection for protein content at one location might be effective for a broad range of environments.

Generation mean analyses showed that dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) gene actions plays a role in the inheritance of oil and protein content (Table 2). Similar results were obtained by Dani and Kohel[11] who determined that dominance (*h*), additivexadditive (*i*) and dominancexdominance (*l*) effects play a significant role in the inheritance of oil content. The negative additivexadditive (*i*) estimates shows the gene pairs responsible for oil content are in dispersive form[12]. The sign of dominance effect (*h*) was positive while the sign of dominance x dominance effect (*l*) was negative (Table 2). This suggests that duplicate types of gene interactions were present confirming the importance of dominance effects[13].

In conclusion, considerably nonadditive genetic effects observed in this study suggests that selection in advanced generations may be more appropriate because effective selection in early generations of segregating material can be achieved only when additive gene effects are substantial and environmental effects are small.

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