

## GENETIC VARIABILITY AND ASSOCIATION AMONG OIL, PROTEIN AND OTHER ECONOMIC TRAITS OF *GOSSYPIUM HIRSUTUM* L. IN F<sub>2</sub> GENERATION

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### ABSTRACT

A study was conducted in the Department of Plant Breeding and Genetics, University College of Agriculture, Bahauddin Zakariya University, Multan, Pakistan during 2004-07. Eight cotton genotypes/lines comprising diverse origin were crossed and segregating generation was studied for different traits with a particular emphasis on seed oil and protein. The data indicated the presence of significant variation in segregating material which could be exploited to improve the lines of interest. Oil and protein contents illustrated positive and significant phenotypic and genotypic relationship with yield, yield components and fibre quality traits. The results indicated that these characters are more related genetically. Therefore, oil and protein contents in cotton seed may be improved without sacrificing the other economic traits in future breeding programme.

**KEYWORDS:** *Gossypium hirsutum*; genotypes; crossbreeding; lipid content; protein content; Pakistan.

### INTRODUCTION

Cotton (*Gossypium hirsutum* L.), the leading natural textile fibre significantly contributes to edible oil production in Pakistan. At present, it accounts for 8.2 percent value added in agriculture and about 2 percent to GDP, and an increase of one million bales in cotton production results in half a percent increase in GDP (3). Pakistan is earning a huge amount of foreign exchange through textile export. Cotton seed is a rich source of oil and protein and contributes the largest share to local oilseed production. However, Pakistan is deficit in edible oil and to meet the local demand, a huge amount of cooking oil is imported annually.

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According to a report (3) 1695.8 thousand tons edible oil was imported during 2006-07, costing about 44212.1 million rupees.

High quality protein has a major impact on dietary requirements of rapidly growing population particularly by in developing countries. It has been reported that in Pakistan per capita per day protein consumption is 62 g, and in contrast to advanced countries like USA, France, and even in United Arab Emirates, it is 114, 118 and 101 g, respectively (4). So a substantial increase in protein quality and quantity in daily diet of common masses through food habit not only improves general health but also keeps away from protein deficiency.

Despite the importance of oil and protein in the country, both these components have not been studied as thoroughly as other characteristics of cotton plant. Thus information on the genetic control of variation in oil and protein contents is not extensively available in literature except a few reports. Earlier scientists (5, 9, 10, 14) observed significant variation in both characters. Rehman *et al.* (19) and Khan *et al.* (13) reported that inheritance of both oil and protein contents in *Gossypium hirsutum* L. was under additive and non-additive gene effect. In other studies (8, 7, 14, 16) cotton seed oil content was reported to be additively controlled while in some other reports (10,11,23) this character was controlled by non-additive genes. Almost similar gene controlling mechanism for protein content in cotton seed was reported by Murtaza *et al.* (16) and Azhar and Khan (7).

Present study was conducted to assess the genotypic and phenotypic association among oil, protein and other economic traits of cotton in segregating generation.

## MATERIALS AND METHODS

Eight genotypes/varieties were selected from the gene pool maintained in the Department of Plant Breeding and Genetics, University College of Agriculture, Bahauddin Zakariya University, Multan, Pakistan during 2004. Among these, four entries (FH-87, NIAB-78, MNH-93 and CIM-70) were high yielding local varieties with good fibre quality having high oil and protein contents while the other four lines (LRA-5166, L-229-29-71, Lumain-1 and H-499-3) were selected possessing low oil and protein contents belonging to exotic origin of *Gossypium hirsutum* L. These eight parents were crossed in 8 × 8 diallel fashion during 2005, and F<sub>2</sub> was produced from F<sub>1</sub> during 2006. The parents F<sub>1</sub> and F<sub>2</sub> populations were planted in the field arranged in RCBD with three replications during 2007. The soil was clay having pH 8.5 and thus farm yard

manure was used to make it appropriate for cotton crop. Seeds of all entries were sown in three meter long three rows. Before sowing seeds were treated with Confidor pesticide to save from the attack of diseases and insects at seedling stage. The growing plants were looked after during the season, and all appropriate protection measures were taken till the harvest of seed cotton. Only one pick was taken at maturity, when at least 75 percent bolls were opened. These were picked and ginned to obtain the seeds for studies on oil and protein contents.

At maturity of the crop, data from ten plants belonging to parents  $F_1$  and 50 plants of  $F_2$  on the traits like number of bolls per plant, boll weight, yield of seed cotton, lint percentage, seed index, lint index, staple length, fibre fineness (micronaire value), oil content and protein content were taken on individual plant basis to study the variability and genetic correlation. Oil content was determined by nuclear magnetic resonance analysis (NMR) and protein contents were determined by using Kjeldhal apparatus in the Post Graduate Laboratory of Department of Plant Breeding and Genetics, University College of Agriculture. To estimate the extent of variation among these genotypes, data collected were subjected to analysis of variance (21). The estimates of phenotypic and genotypic correlation coefficient among various characters were calculated using formula given by Kwon and Torrie (15).

## **RESULTS AND DISCUSSION**

The  $F_2$  population differed significantly in their genetic constitution (Table 1). This indicated highly significant differences in whole genetic material for all characters under study. The presence of genetic variability paves the way for the analysis of genotypic and phenotypic correlation. Genotypic and phenotypic correlation provide the measure of intensity of association among the traits (20), which helps to identify the more important and less important traits to be considered in breeding programme and success of plant breeder depends upon the combination of desired traits in single genotype (17). In this study the genotypic correlation coefficients were higher than phenotypic correlation coefficients (Table 2). It indicated the less involvement of environmental effects and genetic causes were more pronounced in expression of associations among traits studied (22).

The data further revealed that agronomic traits i.e. number of bolls per plant, boll weight and seed cotton yield were significantly associated with lint index and

**Table 1. Mean squares of various plant characters measured in segregating population of *Gossypium hirsutum* L.**

Source of variance	D.F.	Seed cotton yield	No. of bolls	Boll weight	Seed index	Lint index	GOT	Staple length	Fineness	Oil (%)	Protein (%)
Rep.	2	130.7	1.69	0.04	0.01	0.02	0.55	0.50	0.003	0.33	0.07
Entries	63	540.1**	27.35**	0.39**	2.27**	1.25**	7.63**	34.13**	0.139**	8.54**	2.05**
Error	126	109.9	12.06	0.04	0.15	0.03	0.28	0.12	0.032	0.10	0.14

\* Significant (P = 0.05), \*\* Highly Significant (P = 0.01), D.F= Degree of freedom.

**Table 2. Genotypic and phenotypic correlation among yield, yield components, fibre traits and oil protein contents.**

Variables		Boll weight	Seed cotton yield	G.O.T	Seed index	Lint index	Staple length	Fineness	Oil (%)	Protein (%)
No. of bolls	Rg	0.3889**	0.9507**	0.5464**	0.3540**	0.4668**	0.6516**	0.1689	0.4923**	0.3639**
	Rp	0.2545**	0.8808**	0.3953**	0.2396**	0.3348**	0.4618**	0.1461	0.3500**	0.2562**
Boll weight	Rg		0.5916**	0.5850**	0.6776**	0.7130**	0.5543**	0.1324	0.8482**	0.8175**
	Rp		0.43968**	0.4832**	0.3550**	0.5909**	0.4432**	0.0807	0.6844**	0.6652**
Seed cotton yield	Rg			0.5791**	0.5119**	0.5878**	0.7100**	0.1724**	0.6338**	0.5199**
	Rp			0.4578**	0.3804**	0.4538**	0.5398**	0.1306	0.4922**	0.3996**
G.O.T	Rg				0.6231**	0.8525**	0.4190**	0.5780**	0.6649**	0.6296**
	Rp				0.5926**	0.8362**	0.4022**	0.3940**	0.6383**	0.5959**
Seed index	Rg					0.9438**	0.2757**	0.2187**	0.7384**	0.5218**
	Rp					0.9284**	0.2547**	0.2838**	0.7369**	0.6546**
Lint index	Rg						0.3630**	0.2473**	0.7822**	0.7020**
	Rp						0.3461**	0.1976**	0.5338**	0.6604**
Staple length	rg							-0.0385	0.5539**	0.8114**
	rp							-0.0168	0.5084**	0.7780**
Fine-ness	rg								0.1166**	0.1190**
	rp								0.0824**	0.0996**
Oil (%)	rg									0.8165**
	rp									0.7780**

\* Significant (P ≤ 0.01), \*\* Highly significant (P ≤ 0.05), rg = Genotypic variance and rp = Phenotypic variance.

staple length both at genotypic and phenotypic level. It indicated that with increase in number of bolls per plant and boll weight the lint index and staple length also increased. However, at the same time non-significant genotypic and phenotypic correlation of number of bolls per plant and boll weight with fibre fineness was observed. It showed less contribution of genetic effect among these traits. These finding were in contrast to earlier findings (12, 18). This contradiction may be due to use of different genetic material and environmental conditions (2). The data also depicted that bolls per plant, boll weight and seed cotton yield had positive and highly significant association with both oil and protein percentages in cotton seed. It indicated that selection based on number of bolls per plant, boll weight and seed cotton yield could be useful for the cotton breeders to develop elite cotton genotypes with high amount of oil and protein percentages. This positive association also showed the presence of some common genes, controlling these traits.

Quality traits i.e. lint index, staple length and fibre fineness showed positive and highly significant association with both oil and protein percentages at genotypic and phenotypic levels as was observed earlier (5, 10). It indicated that increase in quality traits will cause positive effect on oil and protein percentages in cotton seed. A negative non-significant genotypic and phenotypic association between staple length and fibre fineness (Table 2) showed the presence of some negatively linked genes revealing movement of both traits in opposite direction (6).

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