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## Genotype Variability in Fatty Acid Composition and Chemical Characteristics of Cotton (*Gossypium hirsutum* L.)

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**Abstract:** Cottonseeds (*Gossypium hirsutum* L.) from lines 84027 and 84033, characterized by enhanced salt tolerance, and their parental line DP62 were studied qualitatively and quantitatively to determine fatty acid composition and proximate analysis. Proportions in fatty acid composition were found to be modified as a result of the salt selection-breeding program. Linoleic acid (18:2) was higher in both salt tolerant lines while palmitic acid (16:0) was lower in line 84027. Significantly different unsaturated/saturated fatty acid ratios, 3.13, 3.20, and 3.59 were obtained from genotype DP62, 84033 and 84027, respectively. Other parameters studied also reflected genotypic variability, including crude protein, crude oil, crude fiber, ash, nitrogen free extract, and carbohydrates content. This research may contribute to establishing a relationship between the unsaturated/saturated fatty acid ratio of a particular genotype and its ability to maintain physiological and biochemical functions under salt stress.

**Key words:** Cotton, fatty acid, *Gossypium hirsutum*, chemical, composition

### Introduction

Mature cotton (*Gossypium hirsutum* L.) seeds contain oils and proteins at differing concentrations depending on genotype (Cherry *et al.*, 1878a,b, 1981a,b; Lawhon *et al.*, 1976). These compounds are metabolized to provide energy for embryo germination. The content of such compounds and other biochemical and physiological parameters have been shown to differ among salt tolerant plants (Bowman *et al.*, 1996; Caldwell, 1974; Epstein, 1972). Genetic modifications by breeding and agronomic practices can affect both the physical and chemical properties of cottonseed (Cherry and Leffler, 1984); for example, improvement of oil and fatty acids composition (Cherry, 1983).

Salt-tolerant cotton germplasm lines (84027 and 84033) have been developed from the parental line Deltapine 62 (DP62) through a breeding program carried out by Ledbetter (1986). During germination and emergence under varying NaCl conditions, lines 84027 and 84033 showed superior vigor and higher ribosomal-RNA content in relation to line DP62. Furthermore, the selection process for salt tolerance influenced seed germination and growth rate (Al-Bahrany, 1989). The objective of this study was to determine differences elicited by salt selection breeding program between salt tolerant cotton lines 84027 and 84033 and parental line DP62 in relation to 1) Seed composition of fatty acids and unsaturated/saturated ratios and 2) Proximate analysis for moisture, crude protein, crude oil, crude fiber and ash content.

### Materials and Methods

**Plant material:** Three cotton germplasms used in this study including two lines selected for salt tolerance (lines 84027 and 84033) and their parental cultivar Deltapine 62 (DP62) lines 84027 and 84033 represent the second selection cycle for germination salt tolerance.

**Fatty acids composition:** The methyl esters of the fatty acids were prepared directly from seeds and fatty acids content was determined using gas chromatography as described by Flood (1981) with modifications reported by El-Shintinawy and Selim (1995). Grounded clean and dry seeds, 200 mg, were mixed with 4 ml of 0.66 N KOH in methanol then placed in a 20 ml screw capped tube. The tube was flushed with N<sub>2</sub>, sealed and heated at 100°C for 5 min. The mixture was cooled and 4 ml of boron-trifluoride (BF<sub>3</sub>) in methanol (14% w/v, BDH Co.) was added. The tube was flushed with N<sub>2</sub>, capped and heated

at 100°C for 5 minutes. The mixture was cooled and 4 ml of each of saturated NaCl; water and petroleum ether (b.p. 40-60°C) were added. The supernatant was removed, washed with water, dried over anhydrous N<sub>2</sub>SO<sub>4</sub>, and concentrated by stream of N<sub>2</sub> at room temperature to about 1 ml. Methyl ester of dodecanoic acid (2 was added as internal standard. A sample of 0.5 µl dried supernatant was injected into a GLC variant 6000 with Flame Ionization Detector (HD), 2 m length, 18 inch internal diameter stainless steel column, packed with 15% OV-275. Chrom Placid wash/80-100 mesh stationary phase operated at 175°C. Injection temperature was 230°C. Detector temperature 2513°C with helium carrier gas at a flow rate of 25 ml/min., hydrogen flow 30 ml/min, air flow 300 ml/min. Identification of fatty acid methyl esters was carried out by comparison of their retention times with that of the standard and the quantities were calculated from the areas obtained by the KLB-2220 Recorder Integrator. The unsaturated/saturated fatty acid ratio of each sample was obtained by dividing the summed percentage of unsaturated fatty acids by the summed percentage of saturated fatty acids.

**Proximate analysis:** Proximate analysis for moisture, crude protein, crude oil, crude fiber, and ash were performed in accordance to the methods described in the Association of Official Analytical Chemist (AOAC, 1984). A sample weighing 5 g of seeds was used for analysis. Total carbohydrates were estimated by subtracting the sum of moisture, crude protein, crude oil, and ash content percentages from one hundred. Nitrogen-free extract (NFE content) was determined by subtracting crude fiber percentage from total carbohydrates percentage.

**Statistical analysis:** Three samples per genotype were analyzed, and data were subjected to an analysis of variance end means were separated using least significance difference (LSD), where appropriate, at 5% significance level.

### Results and Discussion

**Fatty acid composition:** The salt selection process was associated with decreasing total saturated fatty acids (myristic, palmitic and stearic) and increasing total unsaturated fatty acids (palmitoleic, oleic and linoleic) (Fig. 1). The principle unsaturated fatty acid of cottonseeds oil in the genotypes tested were linoleic (18:2) followed by oleic (18:1). Palmitic acid (16:0) was the most abundant Saturated fatty

### Al-Bahrany and Al-Khayri: Fatty acid content in cotton

Table 1: Mean fatty acid compositions and unsaturated/saturated fatty acid ratios from hulled cottonseed of genotypes Deltapine 62, line 84027, and line 84033

Genotype	Fatty acids expressed as % of total						Ratio unsaturated/saturated fatty acid
	Myristic 14:0	Palmitic 16:0	Palmitoleic 16:1	Stearic 18:0	Oleic 18:1	Linoleic 18:2	
DP62	0.79a*	20.56b	0.80b	2.89b	14.86e	60.10a	3.13a
84027	0.70a	18.55a	0.70a	2.54a	14.97h	62.54c	3.69c
84033	0.74a	20.59b	0.76b	2.52a	14.60a	60.79b	3.20b

\*Values followed by the same letter in each column are not significantly different at 0.05 level by LSD

Table 2: Proximate analysis of cottonseed of genotypes Deltapine 62, line 84027, and line 84033

Genotype	% Moisture	% Curde protein	% Curde oil	%Curde fiber	% Ash	% Nitrogen free extract	% Carbohydrates
DP62	8.63b	23.47c	20.71e	16.52e	4.00c	27.66b	43.18a
84027	7.34a	21.21b	23.72c	20.13c	3.86b	23.74e	43.87a
84033	7.11a	19.50a	23.19b	18.35b	3.77a	28.41b	46.43B

\*Values followed by the same letter in each column are not significantly different at 0.05 level by LSD

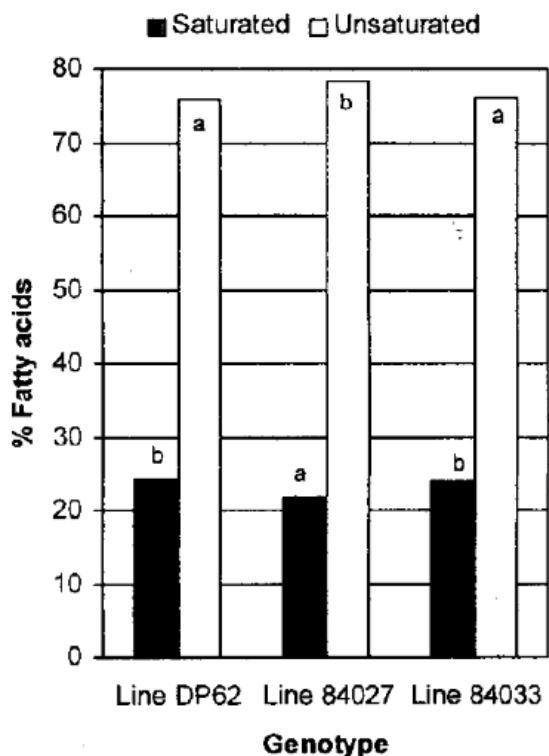


Fig. 1: Total saturated and total unsaturated fatty acids exhibited by cotton genotypes Deltapine 62, line 84027, and line 84033

acid (Table 1). These results in agreement with those obtained by other researchers studying various genotypes (Cherry *et al.*, 1981a; Sawan *et al.*, 1989).

Except for myristic acid (14:0), fatty acid composition differed significantly among genotypes (Table 1). Line 84027 had the highest significant concentration of linoleic acid (62.54%) of all genotypes analyzed followed by line 84033, whereas the parental line DP62 lowest concentration of linoleic acid (60.10%) (Table 1). Palmitic acid was lower in line 84027 than either of the other two genotypes. Stearic acid was significantly lower in

the salt selected lines in comparison to the parental line. Unsaturated/saturated fatty acid ratios differed according to genotype. Lines 84027 and 84033, characterized by salt tolerance, exhibited higher unsaturated/saturated fatty acid ratio than the parental line (DP62). However, line 84027 had significantly higher ratio (3.59) than line 84033 (3.20) (Table 1). The genotypes that were associated with high unsaturated/saturated fatty acids ratios (lines 84027 and 84033) were previously shown to have greater emergence percentage under salt stress and higher ribosomal-RNA than DP62 (Al-Bahrany, 1989). This suggests that there might be a relationship between unsaturated/saturated fatty acid ratios and salt tolerance. It can be noted that the salt selection process could have resulted in genetic modifications, thus affecting the ratio and composition of unsaturated and saturated fats, despite of the common origin of the two lines.

**Proximate analysis:** Apparently the selection process for seed germination salt tolerance resulted in measurable genetic changes and altered chemical composition in all parameters tested (Table 2). The parental line DP62 had a higher protein and ash percentages and lower oil and carbohydrates percentages than the other salt tolerance genotypes (84027 and 84033). The protein content ranged from 19.50 to 23.47%. Protein content in cottonseed of other genotypes ranged from 19.6 to 24.0% (Lawhor *et al.*, 1976) and 25.6 to 27.6% (Cherry *et al.*, 1978a,b, Cherry *et al.*, 1981a,b).

In our study, seed oil content ranged from 20.71 to 23.72%. Salt tolerant line 84027 had the highest increase 13.01 % in oil content followed by line 84033 (2.48%) in relation to the parental line DP62. In comparison, others have shown that oil content ranged from 18.5 to 25.6% (Lawhor *et al.*, 1976) and 23.2 to 25.7% (Cherry *et al.* 1978a,b, 1981a,b).

In conclusion, selection procedures for salt tolerance were effective in altering chemical composition in cottonseed. Salt tolerant lines exhibited higher percentage of unsaturated/saturated fatty acid ratios than parental line. This ratio, however, differed between the two salt tolerant lines. Based upon these observations, it can be assumed that fatty acid composition of the two salt tolerant lines were genetically modified in different ways by salt breeding program, even though they were selected from a single variety.

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