FATTY ACID PROFILE OF UPLAND COTTON GENOTYPES THROUGH NIR-NEAR-INFRARED SPECTROSCOPY

S. F. Kazmi[*], N. U. Khan[*], S. Gul[*] and I. Ali[**]

[*]Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar – Pakistan
[**]Nuclear Institute for Food and Agriculture, Peshawar – Pakistan
Corresponding Author E-mail: nukmarwat@yahoo.com; nukmarwat@aup.edu.pk

ABSTRACT

The research work comprising genetic studies for oil, fatty acid profile, seed cotton yield and lint percentage in eight parental lines (SLH-284, CIM-446, CIM-473, CIM-496, CIM-499, CIM-506, CIM-554, CIM-707) and their F_3 populations was carried out during 2011 and 2012 at The University of Agriculture, Peshawar and Nuclear Institute for Food and Agriculture, Peshawar - Pakistan. The genetic potential of genotypes in terms of genotypic (GCV) and phenotypic coefficient of variance (PCV), heritability (broad sense), and genetic gain were determined for all the traits. Mean squares revealed significant ($p\ 0.01$) variations among parental cultivars and F_3 population for all the traits, indicating greater genetic variability in the breeding material. Overall, the F_3 populations revealed greater mean values than parental genotypes for oil content, linoleic acid, stearic acid and ratio of unsaturated/saturated fatty acids while for other traits the average mean values were comparable. Genotypic variances were found greater than environmental variances for all traits. The GCV and PCV for all the traits ranged from 1.62 to 37.41 and 1.87 to 39.21, respectively. Broad sense heritability was high for all the traits ranging from 0.75 (lint percentage) to 0.99 (saturated fatty acids) with maximum genetic gain for seed cotton yield (19.73 g). Seed cotton yield revealed positive correlation with all traits, however, it was highly significant with stearic acid and saturated fatty acids, significant ($p\ 0.05$) with oil content, linoleic acid, unsaturated fatty acids and lint percentage indicating that increase in fatty acids had positive impact on seed cotton yield. The parental lines CIM-707, CIM-554, SLH-284 and CIM-496 performed well for all traits. The F_3 populations CIM-707 × CIM-554 and CIM-707 × CIM-499 revealed best performance for oil content and fatty acids profile. The F_3 populations CIM-446 × SLH-284 and CIM-496 × CIM-499 excelled other F_3 populations and parental cultivars for seed cotton yield and lint percentage with desirable oil quality traits. These promising F_3 populations can be used in future breeding for enhancement in fatty acid profile and yield traits.

Keywords: Cottonseed oil, fatty acid profile, lint percentage, seed cotton yield, genetic variability, correlation, upland cotton.

INTRODUCTION

Cotton being major cash crop, and an important source of foreign exchange, worldwide 90% cotton produced by species *Gossypium hirsutum* L. (Khan *et al*., 2009a; Khan and Hassan, 2011). It earns 45-60% foreign exchange depending upon the production and consumption (Khan 2011, 2013; Gul *et al*., 2014). Besides earning huge amount of foreign exchange through export it also provides fiber for inland textile industry. Apart from the great economic significance of cotton as a fiber crop, it shares 65-70% to the local edible oil industry (Khan *et al*., 2009c, d). Cotton, though mainly grown for fiber is also ranked as major oil seed crop after soybean in the international market (Jones and Kersey, 2002). Cotton seed oil is of premium quality vegetable oil and has no cholesterol (Khan *et al*., 2007; Nagappa and Khadi, 2011).

Cottonseed oil and seed cotton yield are the complex characters and directly affected by the various seed and yield related traits. Crop development needs the ability to observe and choose high performing genotypes in a population. Therefore, genetic potential of the various genotypes, and heritability in the targeted traits are required for selection of parental cultivars for breeding (Khan *et al*., 2009b, 2010a; Batool *et al*., 2010, 2013). A thorough study about the nature and genetic potential of different genotypes, heritability pattern of various traits and correlation of yield with oil and fatty acids traits is necessary for successful breeding (Khan *et al*., 2009e; Ahmad *et al*., 2011; Makhdoom *et al*., 2010). Quantitative genetics is of great interest because of complex nature of oil traits, seed cotton and lint yields. As compared to qualitative traits, quantitative traits have distinction in a population and can be altered significantly by the environment (Batool *et al*., 2013; Khan *et al*., 2013).

Cottonseed oil is cooking oil extracted from cottonseed of different species, mainly *G. hirsutum* L. as grown worldwide on larger area. Cottonseed has similar structure as other oil seeds such as sunflower, having an oil bearing kernel covered by a hard outer hull; in processing, the oil is extracted from the kernel.

Because of its flavor stability, cottonseed oil is used for salad oil, mayonnaise, salad dressing, and similar products. The cottonseed oil undergoes comprehensive treatment after extraction to minimize the level of toxic compound i.e. gossypol found in untreated cottonseed oil, the consumption of which may cause undesirable side-effects. The fatty acid profile of cottonseed showed that it consists of 70% unsaturated fatty acids including 18% monounsaturated (oleic), and 52% polyunsaturated (linoleic and linolenic) and 30% saturated fatty acids (Daniel, 2007).

Near-infrared reflectance (NIR) is exploited worldwide for the rapid quantitative determination of proteins, lipids, carbohydrates, moisture and fiber in cereals, grains, feeds, meats and dairy products (Bewig *et al.*, 1994). NIR technique is based on the absorbance of light energy at a given frequency by molecules (or radicals) containing a permanent dipole which vibrates at the same frequency. The said technology was designed in 1964 for the determination of moisture (Panford and deMan, 1990). The NIR spectroscopy was evaluated as a rapid method for prediction of *trans*-fatty acid in ground cereal products without the need for oil extraction (Kim and Kays, 2009). With all these ideas in view, the present investigations were planned to determine the genetic variability in parental cultivars and their F_3 populations of upland cotton for oil content and fatty acids profile (through NIR), seed cotton yield and lint percentage, and correlation of yield with fatty acid profile and lint percentage.

MATERIALS AND METHODS

Plant materials and experimental design: The breeding materials consisted of eight upland cotton genotypes (SLH-284, CIM-446, CIM-473, CIM-496, CIM-499, CIM-506, CIM-554 and CIM-707) which had been crossed in a complete diallel fashion during 2008 and were carried out to F_3 generation (Table 1). The field experiment (comprising of parental cultivars and their F_3 populations) was carried out during 2011 at The University of Agriculture, Peshawar - Pakistan. The quantification of oil content and fatty acids profile in cottonseed was conducted during 2012 at Nuclear Institute for Food and Agriculture, Peshawar - Pakistan. Peshawar lies between 34°, 02 North latitude and 71°, 37 East longitude. The seeds of parental genotypes and F_3 populations were hand sown during May, 2011 in a randomized complete block (RCB) design with three replications. Each treatment consisted of four rows having five meter length with 30 and 75 cm plant and row spacing, respectively. Recommended cultural practices and inputs including land preparation, fertilizers, hoeing, irrigation and pest control were applied uniformly for all the entries from sowing till harvesting and the crop was grown under identical conditions to reduce the environmental variations. On an individual plant basis, two hand pickings were made during the month of November, and ginning was done with eight saw gins.

Traits measurement

Seed cotton yield and lint percentage: Ten plants were randomly selected for data recording and a total of two picks at regular interval were taken from each tagged plant and were weighed on electric balance in grams as seed cotton yield plant^{-1}. The ginning was made with 8-saw gin, and the fiber obtained from each sample of seed cotton was weighed and lint percentage was calculated.

Oil content and fatty acids measurement: An NIRS instrument of "*NIRSYSTEMS (FOSS 6500)*" was used for oil content and fatty acids analyses. The clean cottonseed samples were dried until they were stable for long time storage (max. 9% residual moisture) at a temperature of max 40-60°C. Before the analysis, the sample cups (used in routine analysis) were filled with a single standard sample and scanned on the NIRS instrument. The spectra of these scans were standardized and predicted with standard calibration. In first step the standard deviation of the analysis over all sample cups was calculated. In the final step of z-test using the limits was run to mark bad sample cups. In routine measurements, the samples were analyzed with three repeats to minimize sampling error. During scanning, the moisture of the seed sample was kept below 10% for oil and glucosinolates (GSL) analyses (Anonymous, 1998). In fatty acid profile, the following oil quality traits were measured through NIRS, viz. percentage of oil content, protein content, oleic acid, linoleic acid, palmitic acid, stearic acid, saturated and unsaturated fatty acids. The ratios of unsaturated to saturated fatty acids and oleic to linoleic acids were also computed, however, not included in the analysis of variance.

Statistical analyses: All the data were subjected to analysis of variance according to Steel *et al.* (1997) and Panse and Sukhatme (1967). After getting the significant variations among the genotypes for various traits, the means for each variable were further separated and compared through Duncan's Multiple Range (DMR) test at 5% level of probability (Duncan, 1955). Genotypic (GCV) and phenotypic coefficient of variations (PCV) were computed according to Burton and Devane (1953). According to Hanson *et al.* (1965), the broad sense heritability was estimated based on the ratio of genotypic to phenotypic variance. According to Stansfield (1986), heritability estimate were grouped into low (20%) moderate (20-50%) and high (50%). Genetic gain was estimated according to Allard (1999). However, the genetic gain as percent of the population mean was categorized as high (20% and above), moderate (10-20) and low (0-10%) as outlined by Johnson *et al.* (1955).

The correlation of seed cotton yield with oil quality traits and lint percentage was calculated through MstatC program (Bricker, 1991).

RESULTS

Highly significant (*p 0.01*) differences were observed among parental cultivars and F_3 populations for all traits (Table 2) and the results of these traits are discussed herein.

Oil content: The range in parental cultivars for oil content was 18.84 to 26.20% and F_3 populations ranged from 17.56 to 26.05% (Table 3). The parental genotype CIM-496 (26.20%) showed maximum oil content. However, it was found similar with seven other genotypes including six F_3 populations (CIM-707 × CIM-499, CIM-707 × CIM-554, CIM-496 × SLH-284, CIM-707 × CIM-473, CIM-554 × CIM-499 and CIM-707 × SLH-284) and one parental cultivar (SLH-284) ranging from 24.91 to 26.05%. Minimum oil % was observed in F_3 population SLH-284 × CIM-496 (17.56%) and it was alike with ten other genotypes including two parental cultivars (CIM-473, CIM-499) and eight F_3 populations ranging from 17.75 to 19.06%. Medium oil content was recorded in all other genotypes. On average, F_3 populations revealed increased mean values (21.77%) for oil content than parental cultivars (21.46%) (Table 3). Genotypic variance (5.54) was greater than environmental variance (0.23), however, these variances were smaller than phenotypic variance (5.76), and the GCV was also low (10.83%) than PCV (11.04%) (Table 6). The broad sense heritability (0.96) was high with desirable genetic gain (4.75%) and as percent of population mean the value was 21.86%. Oil content showed significant positive correlation with seed cotton yield (Table 7).

Protein content: For protein content, the parental cultivars were ranging from 15.07 to 25.78% while the F_3 populations varied from 15.01 to 24.35% (Table 3). Maximum protein content were observed in two parental cultivars CIM-473 (25.78%), however, it was found at par with parental cultivars i.e. SLH-284 (25.26%), CIM-499 (24.81%) and CIM-496 (24.42%) and F_3 populations CIM-707 × CIM-554 (24.35%) and CIM-554 × CIM-496 (24.09%). The parental genotype CIM-446 and three F_3 populations (SLH-284 × CIM-473, CIM-707 × CIM-499 and CIM-707 × CIM-506) revealed minimum and analogous protein content ranging from 15.01 to 15.18%. All other genotypes showed medium values for protein content. Overall, the F_3 populations (19.03%) and parental genotypes (22.62%) revealed comparable mean values for protein content and having no significant differences (Table 3). Genotypic variance (7.66) was greater than environmental variance (0.47), while GCV (14.21%) was also low than PCV (14.64%) (Table 6).

Broad sense heritability (0.94) was high for protein content, and genetic advance was 5.53%, while its value as percent of population mean was 28.40%. The correlation of protein content with seed cotton yield was positive but non-significant (Table 7).

Oleic acid: For oleic acid, the parental cultivars were ranging from 7.03 to 17.54% while in F_3 populations the said range was 6.98 to 17.38% (Table 3). Maximum and similar oleic acid was indicated by F_3 population CIM-707 × CIM-554 and five parental cultivars (SLH-284, CIM-496, CIM-499, CIM-506, CIM-707) with range of 17.20 to 17.54%. However, the promising genotypes were closely followed by three F_3 populations viz., CIM-499 × CIM-473, SLH-284 × CIM-446 and SLH-284 × CIM-496 ranging from 14.75 to 15.51%. In case of minimum values for oleic acid, four genotypes including one parental cultivar (CIM-446) and three F_3 populations (SLH-284 × CIM-473, CIM-707 × CIM-506 and CIM-707 × CIM-499) showed least values for oleic acid ranged from 6.98 to 7.15%. All other genotypes revealed medium values for oleic acid content. On average, parental genotypes (14.90%) produced more oleic acid than F_3 populations (11.11%) (Table 6). Genotypic variance (8.56) was greater than environmental variance (0.37), although high PCV (25.81%) was observed than GCV (25.26%) (Table 3). High broad sense heritability (0.96) with genetic advance (5.90%, 50.94%) were observed for oleic acid. Non-significant positive correlation was observed between oleic acid and seed cotton yield (Table 7).

Linoleic acid: For linoleic acid, in parental cultivars the range was 42.80 to 53.30% while F_3 populations varied from 41.89 to 53.85% (Table 3). The linoleic acid was maximum in F_3 population CIM-707 × CIM-554 (53.85%), however, it was found equivalent with fifteen F_3 populations and two parental cultivars (SLH-282 and CIM-496) ranging from 50.00 to 53.71%. In case of least values, the F_3 population CIM-446 × CIM-707 revealed minimum value of linoleic acid (41.89%). Medium linoleic acid was recorded in all other parental genotypes and F_3 populations. Overall, the F_3 populations (47.73%) revealed increased mean values than parental genotypes (46.46%) for linoleic acid. Genotypic variance (9.49) was greater than environmental variance (1.40), while PCV (6.94%) value was greater than GCV (6.48%) (Table 6). High broad sense heritability (0.87) was observed with moderate genetic advance (5.92%) and its value as percent of population mean (12.45%). Linoleic acid had significant positive correlation with the seed cotton yield (Table 7).

Palmitic acid: For palmitic acid, in parental cultivars the range was 13.22 to 23.84% while F_3 populations varied from 13.17 to 23.68% (Table 4). Maximum and equal palmitic acid content was observed in F_3 population CIM-

707 × CIM-554 and five parental cultivars (CIM-473, CIM-496, CIM-506, CIM-499, SLH-284) ranging from 23.50 to 23.84%. Palmitic acid mean values were minimum and similar in parental cultivar (CIM-446) and two F3 populations (CIM-707 × CIM-499 and CIM-707 × CIM-496) ranged from 13.17 to 13.22%. Medium palmitic acid content was recorded for all other parental genotypes and F3 populations. On average, F3 populations (17.23%) and parental genotypes (21.07%) revealed comparable mean values for palmitic acid. High genotypic variance (8.24) was observed as compared to environmental variance (0.69), and the PCV (16.88%) was also greater than GCV (16.21%) (Table 6). Palmitic acid content revealed high broad sense heritability (0.92), genetic gain (5.68%) and genetic gain as population mean (32.07%). Non-significant positive correlation was noted between palmitic acid and seed cotton yield (Table 7).

Stearic acid: For stearic acid, the parental cultivars were 2.97 to 10.26% while in F3 populations the range was 2.90 to 10.39% (Table 4). The minimum and equal values for strearic acid were observed in eight F3 populations (SLH-284 × CIM-446, SLH-284 × CIM-496, SLH-284 × CIM-506, CIM-554 × CIM-446, CIM-707 × CIM-473, CIM-707 × CIM-496, CIM-707 × CIM-499, CIM-707 × CIM-506) and five parental cultivars (CIM-446, CIM-473, CIM-499, CIM-506, CIM-707) ranging from 2.90 to 3.24%. However, the F3 population CIM-707 × CIM-554 (10.39%) showed maximum stearic acid content, and it was found similar with F3 population SLH-284 × CIM-473 (9.97%) and two parental cultivars CIM-496 (10.26%) and SLH-284 (10.10%). All other genotypes revealed medium stearic acid content. Overall, the F3 populations (6.22%) revealed increased mean values than parental genotypes (5.70%) for stearic acid (Table 4). Genotypic variance (5.31) was found greater than environmental variance (0.52), and GCV (37.41%) was lower than PCV (39.21%) (Table 6). High broad sense heritability (0.91) was observed for stearic acid. Genetic gain was 4.53% while its value as percent of population mean was 73.53%. Correlation of stearic acid was highly significant positive with seed cotton yield (Table 7).

Saturated fatty acids: In saturated fatty acids, the parental cultivars were ranging from 16.30 to 33.94% while F3 populations ranged from 16.08 to 34.07% (Table 4). Maximum and alike saturated fatty acids values were observed in F3 population (CIM-707 × CIM-554) and two parental cultivars (CIM-496, SLH-284) ranging from 33.60 to 34.07%. The saturated fatty acids values were least in parental genotype (CIM-446) and three F3 populations (CIM-707 × CIM-506, CIM-707 × CIM-496, CIM-707 × CIM-499) ranged from 16.08 to 16.42%. Medium saturated fatty acids values were obtained for other genotypes. Overall, F3 populations (23.45%) and parental genotypes (26.76%) showed comparable average mean values for saturated fatty acids (Table 4). High

genotypic variance (9.89) than environmental variances (0.07) was recorded, and PCV (13.22%) was also greater than GCV (13.18%) (Table 6). Heritability was high (0.99) with genetic advance of 6.45%, while its value as population mean was 27.05%. Correlation of saturated fatty acids with seed cotton yield was positive and highly significant (Table 7).

Unsaturated fatty acids: For unsaturated fatty acids, the parental cultivars and F3 populations ranged from 50.49 to 70.50% and 53.24 to 71.23%, respectively (Table 4). The unsaturated fatty acids were maximum in F3 population (CIM-707 × CIM-554) and two parental genotypes (SLH-284, CIM-496) ranged from 70.32 to 71.23%. Minimum unsaturated fatty acids were observed in parental cultivar CIM-446, however, it was found equal in performance with five other F3 populations and one parental cultivar ranged from 53.24 to 54.94%. All other genotypes revealed medium values for unsaturated fatty acids. On average, the F3 populations (58.84%) and parental genotypes (61.36%) showed same mean values for unsaturated fatty acids (Table 4). Genotypic variance (9.91) was greater than environmental variance (2.06), and low GCV (5.32%) was obtained than PCV (5.85%) (Table 6). High broad sense heritability (0.83) was observed. The genetic advance and its value as population means were 5.90% and 9.98%, respectively. Unsaturated fatty acids showed significant positive correlation with seed cotton yield (Table 7).

Ratio of unsaturated to saturated fatty acids: The ratio of unsaturated to saturated fatty acids were obtained by dividing the unsaturated fatty acids with saturated fatty acids. The parental cultivars ranged from 2.05 to 3.10% while in F3 populations the range was 2.06 to 3.76% for the ratio of unsaturated to saturated fatty acid (Table 5). The three F3 populations (CIM-707 × CIM-499, CIM-707 × CIM-496 and CIM-707 × CIM-506) and one parental genotype (SLH-284) showed maximum ratios ranging from 3.10 to 3.76%. The parental cultivars CIM-554 and CIM-496 and F3 population (CIM-707 × CIM-554) showed minimum ratio (2.05 to 2.10) for unsaturated/saturated fatty acids. Overall, the F3 populations (2.53%) revealed increased ratios than parental genotypes (2.35%) for unsaturated/saturated fatty acids.

Ratio of oleic to linoleic acids: For the ratio of oleic to linoleic fatty acids, the parental cultivars and F3 populations ranged from 0.16 to 0.41% and 0.13 to 0.35%, respectively (Table 5). The parental cultivars (CIM-707, CIM-499 and CIM-506) revealed maximum ratios ranged from 0.38 to 0.41% for mono-unsaturated fatty acid to poly-unsaturated fatty acid. The five F3 populations (SLH-284 × CIM-473, CIM-707 × CIM-506, CIM-707 × CIM-473, CIM-473 × CIM-707, CIM-496 × SLH-284) showed minimum ratios (0.13 to 0.16%).

Overall, the F_3 populations (0.24%) and parental genotypes (0.32%) showed comparable average mean ratios for oleic/linoleic acids.

Seed cotton yield: Seed cotton yield being complex and polygenic trait, and the variations in yield are managed by various morphological and yield contributing traits and environment. The parental cultivars ranged from 58.32 to 80.96 g while in F_3 populations the range was 41.14 to 93.68 g for seed cotton yield (Table 5). The seed cotton yield was maximum in F_3 populations CIM-707 × CIM-554 (93.68 g), however, it was found alike with six promising F_3 populations i.e. SLH-284 × CIM-473, SLH-284 × CIM-446, CIM-496 × CIM-446, CIM-473 × CIM-496, CIM-506 × SLH-284 and CIM-554 × CIM-499 ranging from 84.22 to 86.41 g. The seed cotton yield was minimum in F_3 populations CIM-446 × CIM-506 (41.14 g), however, it was equivalent with thirteen other F_3 populations ranged from 43.04 to 61.46 g. All other genotypes have medium values for seed cotton yield. Overall, the F_3 populations (69.14 g) and parental genotypes (73.29 g) recorded with similar average mean values for seed cotton yield (Table 5). The genetic variance (121.17) was more than environmental variance (38.85), and the GCV value (15.57%) was also smaller than PCV (17.90%) (Table 6). Broad sense heritability for seed cotton yield was high (0.76). The genetic gain was 19.73 g and its value as percent of population mean was 27.92%.

Lint percentage: Cotton is mainly grown for fibers (lint), which is the focal trait and major outcome after ginning the seed cotton and edible oil is extracted as byproduct from cotton seeds. For lint percentage, the parental cultivars varied from 36.67 to 38.25% while F_3 populations ranged from 34.27 to 38.46% (Table 5). The F_3 populations i.e. CIM-446 × SLH-284 and CIM-496 × CIM-499 showed maximum lint percentage of 38.46% and 38.24%, respectively. However, these populations were found similar with 46 other F_3 population and seven parental cultivars ranging from 36.76 to 38.25% lint percentage. Minimum lint percentage was recorded in F_3 population CIM-446 × CIM-506 (34.27%), followed by F_3 population CIM-499 × CIM-473 (35.69%). All other parental cultivars and F_3 populations showed medium values for lint percentage. On average, the F_3 populations (37.27%) and parental genotypes (37.61%) revealed similar average mean values for lint percentage (Table 5). Least genotypic variance (0.36) and GCV (1.62%) were observed than environmental variance (0.12) and PCV (1.87%) (Table 6). The heritability (bs) was high (0.75) with genetic gain values of 1.07% and 2.87%, respectively. Lint percentage showed significant positive association with seed cotton yield (Table 7).

DISCUSSION

For initiation of any breeding program, the genetic variability, heritability and genetic advance of the germplasm and correlation among various traits are the basic steps. Such type of information is very helpful to the breeders for selecting the superior parents and their cross combinations for development of improved lines. Cottonseed oil is of premium quality as it has no cholesterol, *trans*-free and highly stable vegetable oil with low flavor reversion. It is a good source of essential fatty acids and vitamin E. Cottonseed oil has a fatty acid profile that makes acceptable as healthful oil and very useful as cooking and frying oil (Nagappa and Khadi, 2011). Overall, the F_3 populations revealed increased mean values for oil content, linoleic acid, stearic acid and ratio of unsaturated/saturated fatty acids, while for other traits the mean values were not significantly different.

In present studies, the F_3 populations and their parental lines revealed varied values for oil content. In past studies, the chemical composition of cottonseed revealed 52% oil in cottonseed (O'Brien, 2004; O'Brien and Wakelyn, 2005). The previous findings revealed varying genetic potential and high heritability (0.89) for cottonseed oil in upland cultivars and their F_1 populations which differentiated the genotypes into high and low oil types (Khan *et al.*, 2007, 2010b). Significant variations with highest genetic variability were observed among upland cultivars for cottonseed oil (Dani, 1988, 1991). The cottonseed oil content ranged from 27.55% (BH-36) to 29.32% (CIM-240) in *G. hirsutum* L. cultivars (Khan *et al.*, 2007). Kohel (1998, 1980) measured cottonseed oil content through NIRS and found significant differences among genotypes for cottonseed oil. In various populations of F_1, F_2 and F_3, significant variations were reported for cottonseed oil content (Avtonomov *et al.*, 1981). However, Voitenok *et al.* (1983) and Dani (1989) reported maximum GCA variances than SCA with significant variations among the cotton genotypes for oil content.

Protein is an important constituent of cottonseed which is necessary for living organisms for their growth and development. In present studies, varied values of protein content were obtained in parental cultivars and their F_3 populations, and through selection improvement could be made. Protein content was studied in cotton hybrids and their respective parental cultivars and significant varied values were reported for protein and oil contents (Nergiz *et al.*, 1997; Anonymous, 2003). Chemical composition of six cotton cultivars revealed significant differences for protein components of cottonseed (Pettigrew and Dowd, 2012). For cottonseed oil, in Egyptian cotton genotypes the varied values for fatty acid-composition and protein content were observed (Hamza *et al.*, 1988). Aytac and Kinaci (2009) reported moderate heritability with low genetic advance for

protein content in Brassica genotypes and suggested that protein contents could be improved through selection.

Oleic acid occurs as the esters, commonly the triglycerides, which are the greasy materials in cottonseed oil. Results revealed varied values of oleic acid among F_3 populations and their parental lines and through selection the desired level of the said acid could be achieved. In present studies, the oleic acid was decreased in F_3 populations (11.11%) than parental genotypes (14.90%). A study was carried out to decrease the oleic acid content and increase the stearic acid content in upland cotton genotypes by Hairpin RNA-mediated post-transcriptional gene silencing, and oleic acid content was reduced from 13 to 4% with mean values of 15.0 to 19.2% (Lawhon *et al.*, 1977). However, Lukonge *et al.* (2007) and Dowd *et al.* (2010) reported an increase in oleic acid with average values of 17.02% and 17.20%, respectively which may be due to different genetic make-up of the cotton genotypes and the environment. Linoleic acid is an unsaturated omega-6 fatty acid, colorless liquid at room temperature, and is an important element of cottonseed oil. The F_3 populations and parental cultivars revealed varied values of linoleic acid and through selection the desired level of the said acid can be adjusted. Anonymous (2003) reported 53.8 to 56.5% linoleic acid in BT and non-BT cotton genotypes, respectively and significant variations were observed for fatty acid profiles and omega fatty acid elements of chosen vegetable oil. However, Ergonul and Ergonul (2008) noted 56.01% of linoleic acid in upland cotton genotypes.

Palmitic acid is the most common fatty acid found in plants, microorganisms and animals. In present studies, varied values for palmitic acid were observed in F_3 populations and their parental lines. For palmitic acid the range of 19.10 to 29.10% with an average value of 24.45% was reported in upland cotton (Hall, 2003; Sharma *et al.* (2009). Hamza *et al.* (1988) studied fatty acid composition and protein pattern in Egyptian cotton and found average values of 23.0 to 25.5% among cotton genotypes. Stearic acid is classified as neutral saturated fatty acid because it does not raise the level of low density lipoprotein (LDL) cholesterol in blood. Present findings revealed varied values for stearic acid contents in parental cultivars and their F_3 populations. O'Brien *et al.* (2005a, b) findings revealed that cottonseed oil contains enough saturated fatty acids (25 to 26%: palmitic ~22%, stearic~3%, myristic~1%) to make it a relatively stable vegetable oil without partial hydrogenation as well as enough unsaturates (oleic~22%, linoleic~52%, and linolenic usually <1%) to make it a heart healthy oil. In previous studies, the stearic acid content rose from 2 to 4% and the mean values range was 1.9 to 2.5% (Lawhon *et al.*, 1977), however, in other studies 3% of stearic acid was noted in cottonseed oil (O'Brien, 2004; O'Brien and Wakelyn, 2005).

Saturated fatty acids contain only single carbon-to-carbon bonds and are chemically the least reactive. The saturated fatty acids have higher melting point than corresponding fatty acids of the same chain length with one or more double bonds (unsaturated fatty acids). Natural saturated fatty acids mostly have an un-branched structure with an even number of carbon atoms. Palmitic and stearic acids collectively constitute the saturated fatty acid. In past studies, the cotton genotypes and their hybrids were analyzed for fatty acid composition and significant variation was observed in their mean values for fatty acids ranging from 23.2 to 45.3% (Yunusova *et al.*, 1991). Hall (2003) evaluated eleven cotton genotypes and reported greater genetic variability among the genotypes for fatty acids composition (ranged from 30.30 to 24.80%) and that range could be used to screen the cotton germplasm for various environments. Dowd *et al.* (2010) studied fatty acid profile in 20 cotton genotypes at two different locations, and recorded significant differences among cotton genotypes for saturated fatty acids. Nagappa and Khadi (2011) studied fatty acids composition in upland cotton hybrids through NIRS and observed varied values for fatty acids ranging from 33.96 to 39.72%.

The unsaturated fatty acids contain one or more carbon double bonds and chemically more reactive than saturated fatty acids and this activity increases as the number of double bonds increase. Cottonseed oil generally consists of 70% unsaturated fatty acids. These acids are liquid at room temperature but begin to solidify at low temperature. In comparison, the unsaturated fatty acids solidify at more low temperature than saturated fatty acids. Oleic and linoleic acid collectively make the unsaturated fatty acid. Lukonge *et al.* (2007) evaluated 24 upland cotton genotypes for fatty acid profile and noted significant differences among genotypes for unsaturated fatty acids ranging from 70.2 to 74.9%. Lawhon *et al.* (1977) studied seed composition of eight each glanded and glandless cotton genotypes and observed varied values for unsaturated fatty acids (70.0 to 79.6%). In present studies, the F_3 populations revealed increased values than parental genotypes for oil content, linoleic acid, stearic acid and ratio of unsaturated/saturated fatty acids, and selection in these populations can be used in breeding for improvement of fatty acids profile.

In present studies, greater genetic variability was observed in parental cultivars and their F_3 populations for seed cotton yield and lint percentage. Seed cotton yield showed positive correlation with lint percentage and fatty acid profile. Khan *et al.* (2009c, 2010a) and Ahmad *et al.* (2011) observed maximum genetic variability for seed cotton yield and lint percentage, and reported positive correlation between seed cotton yield and lint percentage in various upland cotton populations. Genetic variability and heritability was found to be moderate for yield and lint percentage in upland cotton (Khan and Hassan, 2011;

Khan *et al*., 2011). In various upland cotton cultivars, significantly varied mean values were observed for yield and lint percentage (Batool *et al*., 2013; Khan, 2011, 2013). Different upland cotton genotypes were evaluated for yield and yield components and observed significant differences (Khan *et al*., 2009c; Gul *et al*., 2014). Soomro *et al*. (2008) and Panni *et al*. (2012) studied various *G. hirsutum* L. genotypes for yield and lint traits and recorded significant differences in mean values for yield and yield contributing traits. Moderate to high genetic variation, heritability and genetic gain were observed for

variables i.e. bolls per plant, boll weight and seed cotton yield in various upland cotton populations (Basal *et al*., 2011; Bibi *et al*., 2011a, b). Seed cotton yield has significant positive correlation with lint percentage and fatty acid profile, and therefore, there is more scope of improvement. On average, the seed cotton yield and lint percentage of parental cultivars and F_3 populations were comparable, however, individually some F_3 populations showed best performance and surpassed the parental cultivars, which can be used in future breeding for enhancement in seed cotton and lint yields.

Table 1. Parental cultivars used in F_3 populations of upland cotton.

Cultivars	Parentage	Breeding Centre	Release (year)	Seed cotton yield (kg ha^{-1})	GOT (%)	Staple length (mm)
SLH-284	Not yet released	CRS, Sahiwal	-	3,707	39.0	28.5
CIM-446	CP-15/2 × S-12	CCRI, Multan	1998	3,000	36.1	27.0
CIM-473	CIM-402 × LRA-5166	CCRI, Multan	2002	3,000	39.7	29.5
CIM-496	CIM-425 × 755-6/93	CCRI, Multan	2005	3,000	41.1	29.7
CIM-499	CIM-433 × 755-6/93	CCRI, Multan	2003	3,000	40.0	29.6
CIM-506	CIM-360 × CP-15/2	CCRI, Multan	2004	3,000	38.6	28.7
CIM-554	2579-04/97 × W-1103	CCRI, Multan	2009	4,241	41.5	28.5
CIM-707	CIM-243 × 738-6/93	CCRI, Multan	2004	3,000	39.0	32.2

Table 2. Mean squares and CV% for various traits of upland cotton.

Variables	Mean squares			CV (%)
	Replications	Genotypes	Error	
Degree of freedom	2	63	126	-
Oil content	0.067	17.281**	0.676	3.78
Protein content	2.741	24.403**	1.424	6.13
Oleic acid	0.114	26.808**	1.118	2.59
Linoleic acid	2.064	32.663**	4.196	4.31
Palmitic acid	0.134	26.790**	2.078	1.77
Stearic acid	0.135	17.494**	1.571	4.04
Saturated fatty acids	0.044	29.872**	0.213	1.93
Unsaturated fatty acids	0.355	35.921**	6.178	4.20
Seed cotton yield plant^{-1}	116.537	480.048**	116.541	15.27
Lint percentage	1.146	1.462**	0.372	1.63

** = *significant at p 0.01.*

Table 3. Mean performance of parental cultivars and F_3 populations for various traits in upland cotton.

Parental cultivars & F_3 populations	Oil (%)	Protein (%)	Oleic acid (%)	Linoleic acid (%)
SLH-284	25.92 ab	25.26 ab	17.20 a	53.30 abc
CIM-446	19.58 r-u	15.07 t	7.03 r	43.46 p-v
CIM-473	18.98 s-w	25.78 a	14.72 c	46.67 j-u
CIM-496	26.20 a	24.42 a-d	17.38 a	52.94 a-d
CIM-499	18.84 s-w	24.81 abc	17.27 a	45.22 m-v
CIM-506	19.37 r-u	19.68 h-m	17.37 a	44.26 o-v
CIM-554	23.42 f-k	23.35 b-e	10.72 i	43.01 r-v
CIM-707	19.34 r-v	22.58 c-f	17.54 a	42.80 s-v
Parental means	21.46	22.62	14.90	46.46
SLH-284 × CIM-446	18.56 t-w	22.73 c-f	14.87 c	44.51 n-v
SLH-284 × CIM-473	17.75 vw	15.01 t	6.98 r	53.71 ab

SLH-284 × CIM-496	17.56 w	22.62 c-f	14.75 c	45.59 l-v
SLH-284 × CIM-499	18.39 uvw	16.75 o-t	8.76 mn	51.36 a-g
SLH-284 × CIM-506	18.33 uvw	22.28 d-g	14.42 c	44.21 o-v
SLH-284 × CIM-554	19.77 q-u	21.48 e-h	13.59 d	44.07 o-v
SLH-284 × CIM-707	19.32 r-v	18.73 i-p	10.78 i	48.17 g-o
CIM-446 × SLH-284	22.43 i-n	21.71 e-h	13.83 d	43.32 q-v
CIM-446 × CIM-473	18.34 uvw	16.99 o-t	9.01 mn	49.73 b-l
CIM-446 × CIM-496	22.08 k-o	21.74 e-h	10.85 i	45.23 m-v
CIM-446 × CIM-499	19.16 s-v	21.53 e-h	13.65 d	44.00 o-v
CIM-446 × CIM-506	20.08 p-t	20.69 f-k	12.79 e	46.16 k-u
CIM-446 × CIM-554	20.02 p-t	20.81 f-k	12.91 e	44.65 n-v
CIM-446 × CIM-707	20.41 p-s	20.96 f-i	13.06 e	41.89 v
CIM-473 × SLH-284	23.51 e-k	17.76 l-s	9.78 k	50.00 a-k
CIM-473 × CIM-446	20.42 p-s	20.62 f-k	12.78 e	45.31 m-v
CIM-473 × CIM-496	20.22 p-s	20.66 f-k	12.76 e	45.13 m-v
CIM-473 × CIM-499	21.53 l-p	20.06 g-l	13.80 d	45.62 l-v
CIM-473 × CIM-506	20.94 n-r	19.82 h-m	11.89 fg	46.10 k-u
CIM-473 × CIM-554	21.29 m-q	19.84 h-m	11.45 gh	43.02 r-v
CIM-473 × CIM-707	24.11 c-h	16.15 q-t	8.14 opq	49.59 c-l
CIM-496 × SLH-284	25.20 a-d	16.24 q-t	8.23 op	52.94 a-d
CIM-496 × CIM-446	20.89 n-r	19.62 h-m	11.70 fg	46.70 i-u
CIM-496 × CIM-473	22.13 k-o	18.84 i-p	10.95 hi	47.00 h-r
CIM-496 × CIM-499	21.46 l-p	19.38 h-n	12.14 f	46.80 i-t
CIM-496 × CIM-506	22.32 j-o	18.97 i-o	7.83 pq	46.06 k-u
CIM-496 × CIM-554	22.25 k-o	18.80 i-p	13.80 d	47.60 g-p
CIM-496 × CIM-707	18.34 uvw	21.68 e-h	11.91 fg	42.61 uv
CIM-499 × SLH-284	22.45 i-n	18.85 i-p	10.90 i	47.82 g-o
CIM-499 × CIM-446	22.42 i-n	18.50 j-q	10.54 ij	49.53 c-l
CIM-499 × CIM-473	19.03 s-w	18.67 i-p	15.51 b	47.07 h-r
CIM-499 × CIM-496	22.71 h-m	18.43 k-q	10.47 ij	48.44 f-n
CIM-499 × CIM-506	22.97 g-l	17.76 l-s	9.79 k	46.86 i-s
CIM-499 × CIM-554	23.45 f-k	17.90 l-s	9.93 k	47.54 g-p
CIM-499 × CIM-707	22.97 g-l	18.15 l-r	10.18 jk	51.00 a-h
CIM-506 × SLH-284	20.10 p-t	16.04 rst	8.03 opq	52.47 a-f
CIM-506 × CIM-446	22.72 h-m	17.66 m-s	9.68 kl	50.61 a-j
CIM-506 × CIM-473	20.00 p-t	20.82 f-j	12.92 e	47.18 h-r
CIM-506 × CIM-496	23.67 d-k	17.22 n-t	9.24 lm	48.81 e-m
CIM-506 × CIM-499	23.37 f-k	16.78 o-t	8.79 mn	49.13 d-m
CIM-506 × CIM-554	23.91 d-j	21.66 e-h	13.77 d	46.32 k-u
CIM-506 × CIM-707	24.34 c-g	16.89 o-t	8.91 mn	50.69 a-j
CIM-554 × SLH-284	23.88 d-j	16.93 o-t	8.94 mn	51.59 a-g
CIM-554 × CIM-446	24.19 c-h	22.59 c-f	14.73 c	42.65 tuv
CIM-554 × CIM-473	24.00 d-i	16.54 p-t	8.54 no	51.51 a-g
CIM-554 × CIM-496	21.54 l-p	24.09 a-d	11.76 fg	47.21 h-q
CIM-554 × CIM-499	24.98 a-f	15.98 rst	7.97 pq	50.81 a-i
CIM-554 × CIM-506	24.36 c-g	17.69 l-s	9.71 kl	50.04 a-k
CIM-554 × CIM-707	20.80 o-r	19.64 h-n	11.72 fg	46.76 i-u
CIM-707 × SLH-284	24.91 a-f	15.78 rst	7.76 pq	51.30 a-g
CIM-707 × CIM-446	24.54 b-g	15.85 rst	11.02 hi	44.44 n-v
CIM-707 × CIM-473	25.06 a-e	15.67 st	7.64 q	52.74 a-e
CIM-707 × CIM-496	19.34 r-v	22.59 c-f	14.72 c	45.93 k-v
CIM-707 × CIM-499	26.05 ab	15.02 t	6.99 r	53.42 abc
CIM-707 × CIM-506	19.06 s-w	15.18 t	7.15 r	46.09 k-u
CIM-707 × CIM-554	25.65 abc	24.35 a-d	17.38 a	53.85 a
F$_3$ population means	21.77	19.03	11.11	47.73
DMRT LSD$_{0.05}$	1.329	1.928	0.4847	3.310

Table 4. Mean performance of parental cultivars and F₃ populations for various traits in upland cotton.

Parental cultivars & F₃ populations	Palmitic acid (%)	Stearic acid (%)	Saturated fatty acids	Unsaturated fatty acids
SLH-284	23.50 a	10.10 abc	33.60 a	70.50 a
CIM-446	13.22 u	3.08 z	16.30 i	50.49 m
CIM-473	23.84 a	3.24 z	27.09 b	61.39 bcd
CIM-496	23.68 a	10.26 ab	33.94 a	70.32 a
CIM-499	23.57 a	2.97 z	26.53 bc	62.49 bc
CIM-506	23.67 a	3.07 z	26.75 bc	61.63 bcd
CIM-554	16.30 jkl	9.89 b-d	26.19 c	53.73 klm
CIM-707	20.74 c	2.97 z	23.71 e	60.34 b-f
Parental means	21.07	5.70	26.76	61.36
SLH-284 × CIM-446	20.89 c	3.12 z	24.01 e	59.38 b-i
SLH-284 × CIM-473	13.82 st	9.97 a-d	23.79 e	60.70 b-e
SLH-284 × CIM-496	20.77 c	3.01 z	23.78 e	60.34 b-f
SLH-284 × CIM-499	14.91 nop	8.64 hi	23.55 ef	60.12 b-f
SLH-284 × CIM-506	20.44 c	2.98 z	23.43 ef	58.63 b-k
SLH-284 × CIM-554	19.64 d	3.71 y	23.34 ef	57.67 b-l
SLH-284 × CIM-707	16.88 i	6.46 qr	23.34 ef	58.94 b-j
CIM-446 × SLH-284	19.87 d	6.84 pq	26.71 bc	57.14 d-l
CIM-446 × CIM-473	15.15 no	3.89 y	19.04 h	58.74 b-k
CIM-446 × CIM-496	19.84 d	3.91 y	23.75 e	56.09 e-l
CIM-446 × CIM-499	19.69 d	3.77 y	23.46 ef	57.65 b-l
CIM-446 × CIM-506	18.85 e	4.39 x	23.24 ef	58.95 b-j
CIM-446 × CIM-554	18.97 e	4.75 wx	23.73 e	57.55 b-l
CIM-446 × CIM-707	21.62 b	5.03 vw	26.65 bc	54.94 g-m
CIM-473 × SLH-284	15.92 lm	7.85 lmn	23.76 e	59.78 b-g
CIM-473 × CIM-446	18.85 e	4.75 wx	23.60 ef	58.09 b-l
CIM-473 × CIM-496	18.82 e	4.73 wx	23.55 ef	57.89 b-l
CIM-473 × CIM-499	18.22 f	5.11 uw	23.32 ef	59.41 b-i
CIM-473 × CIM-506	17.97 fg	5.23 uv	23.20 ef	57.99 b-l
CIM-473 × CIM-554	18.00 fg	5.74 st	23.74 e	54.46 i-m
CIM-473 × CIM-707	14.31 qrs	9.08 fg	23.39 ef	57.73 b-l
CIM-496 × SLH-284	14.40 pqr	9.61 de	24.01 e	61.17 b-e
CIM-496 × CIM-446	17.78 fg	5.68 t	23.46 ef	58.39 b-k
CIM-496 × CIM-473	17.04 hi	5.68 t	22.72 f	57.94 b-l
CIM-496 × CIM-499	17.54 gh	6.14 rs	23.68 e	58.94 b-j
CIM-496 × CIM-506	17.13 hi	6.55 qr	23.68 e	53.90 j-m
CIM-496 × CIM-554	16.96 i	6.54 qr	23.50 ef	61.40 bcd
CIM-496 × CIM-707	19.84 d	3.91 y	23.74 e	54.52 h-m
CIM-499 × SLH-284	17.01 hi	6.71 q	23.71 e	58.72 b-k
CIM-499 × CIM-446	16.65 ij	8.40 hij	25.05 d	60.07 b-f
CIM-499 × CIM-473	16.83 ij	6.84 pq	23.67 e	62.58 b
CIM-499 × CIM-496	16.59 ijk	7.24 op	23.82 e	58.92 b-j
CIM-499 × CIM-506	15.92 lm	7.21 op	23.12 ef	56.65 d-l
CIM-499 × CIM-554	16.06 kl	7.47 no	23.53 ef	57.47 b-l
CIM-499 × CIM-707	19.12 e	7.72 mn	26.84 bc	61.18 b-e
CIM-506 × SLH-284	15.79 lm	9.28 ef	25.07 d	60.50 b-f
CIM-506 × CIM-446	15.82 lm	7.72 mn	23.54 ef	60.30 b-f
CIM-506 × CIM-473	18.98 e	4.89 uw	23.87 e	60.10 b-f
CIM-506 × CIM-496	15.38 mn	7.96 klm	23.34 ef	58.05 b-l
CIM-506 × CIM-499	14.94 nop	8.19 jkl	23.13 ef	57.92 b-l
CIM-506 × CIM-554	19.82 d	3.94 y	23.75 e	60.09 b-f
CIM-506 × CIM-707	15.05 no	8.30 ijk	23.35 ef	59.60 b-h
CIM-554 × SLH-284	15.09 no	8.70 ghi	23.79 e	60.53 b-f
CIM-554 × CIM-446	20.68 c	2.99 z	23.67 e	57.38 c-l
CIM-554 × CIM-473	14.70 opq	8.83 fgh	23.53 ef	60.05 b-f
CIM-554 × CIM-496	17.84 fg	5.58 tu	23.42 ef	58.97 b-j

CIM-554 × CIM-499	14.14 qrs	9.22 ef	23.36 ef	58.78 b-j
CIM-554 × CIM-506	14.20 qrs	7.56 mno	21.76 g	59.75 b-g
CIM-554 × CIM-707	17.80 fg	5.55 tu	23.36 ef	58.48 b-k
CIM-707 × SLH-284	13.94 rs	9.17 ef	23.11 ef	59.07 b-i
CIM-707 × CIM-446	14.01 rs	9.74 cd	23.75 e	55.46 f-l
CIM-707 × CIM-473	20.74 c	2.91 z	23.65 ef	60.38 b-f
CIM-707 × CIM-496	13.17 u	2.98 z	16.15 i	60.65 b-e
CIM-707 × CIM-499	13.18 u	2.90 z	16.08 i	60.41 b-f
CIM-707 × CIM-506	13.34 tu	3.08 z	16.42 i	53.24 lm
CIM-707 × CIM-554	23.68 a	10.39 a	34.07 a	71.23 a
F_3 population means	17.23	6.22	23.45	58.84
DMRT LSD$_{0.05}$	0.5058	0.4023	0.7457	4.016

Table 5. Mean performance of parental cultivars and F_3 populations for various traits in upland cotton.

Parental cultivars & F_3 populations	Unsat. / Sat. fatty acids ratio	Oleic / Linoleic acids ratio	Seed cotton yield plant^{-1} (g)	Lint %
SLH-284	2.10	0.32	80.24 a-f	36.93 a-g
CIM-446	3.10	0.16	58.32 f-m	37.78 a-f
CIM-473	2.27	0.32	74.39 a-j	37.58 a-f
CIM-496	2.07	0.33	78.94 a-g	38.23 abc
CIM-499	2.36	0.38	65.43 b-k	38.23 abc
CIM-506	2.30	0.39	70.62 b-j	38.25 ab
CIM-554	2.05	0.25	77.42 a-h	36.67 b-g
CIM-707	2.54	0.41	80.96 a-e	37.22 a-g
Parental means	2.35	0.32	73.29	37.61
SLH-284 × CIM-446	2.47	0.33	85.20 abc	36.30 efg
SLH-284 × CIM-473	2.55	0.13	86.41 ab	36.01 fg
SLH-284 × CIM-496	2.54	0.32	44.75 klm	37.76 a-f
SLH-284 × CIM-499	2.55	0.17	72.02 a-j	37.71 a-f
SLH-284 × CIM-506	2.50	0.33	54.70 i-m	37.11 a-g
SLH-284 × CIM-554	2.44	0.31	71.92 a-j	36.40 d-g
SLH-284 × CIM-707	2.53	0.22	76.00 a-j	37.80 a-e
CIM-446 × SLH-284	2.14	0.32	67.53 b-j	38.46 a
CIM-446 × CIM-473	3.08	0.18	70.39 b-j	37.82 a-e
CIM-446 × CIM-496	2.36	0.24	68.06 b-j	37.49 a-f
CIM-446 × CIM-499	2.46	0.31	59.20 e-m	37.92 a-e
CIM-446 × CIM-506	2.54	0.28	41.14 m	34.27 h
CIM-446 × CIM-554	2.43	0.29	57.58 g-m	38.13 a-d
CIM-446 × CIM-707	2.06	0.31	58.74 e-m	37.44 a-f
CIM-473 × SLH-284	2.52	0.20	63.73 c-l	37.08 a-g
CIM-473 × CIM-446	2.46	0.28	71.26 b-j	37.11 a-g
CIM-473 × CIM-496	2.46	0.28	84.36 abc	37.91 a-e
CIM-473 × CIM-499	2.55	0.30	68.82 b-j	38.16 a-d
CIM-473 × CIM-506	2.50	0.26	77.48 a-h	37.70 a-f
CIM-473 × CIM-554	2.29	0.27	66.45 b-j	37.89 a-e
CIM-473 × CIM-707	2.47	0.16	72.62 a-j	37.79 a-e
CIM-496 × SLH-284	2.55	0.16	67.39 b-j	37.59 a-f
CIM-496 × CIM-446	2.49	0.25	84.64 abc	37.58 a-f
CIM-496 × CIM-473	2.55	0.23	57.60 g-m	37.42 a-g
CIM-496 × CIM-499	2.49	0.26	74.13 a-j	38.24 ab
CIM-496 × CIM-506	2.28	0.17	62.91 c-l	37.84 a-e
CIM-496 × CIM-554	2.61	0.29	63.07 c-l	37.43 a-g
CIM-496 × CIM-707	2.30	0.28	67.98 b-j	37.42 a-g
CIM-499 × SLH-284	2.38	0.23	77.92 a-h	36.21 efg
CIM-499 × CIM-446	2.40	0.21	60.01 e-m	37.53 a-f
CIM-499 × CIM-473	2.64	0.33	55.86 h-m	35.69 g
CIM-499 × CIM-496	2.47	0.22	67.59 b-j	37.49 a-f
CIM-499 × CIM-506	2.45	0.21	66.49 b-j	37.28 a-g

CIM-499 × CIM-554	2.44	0.21	78.53 a-g	37.31 a-g
CIM-499 × CIM-707	2.28	0.20	76.83 a-i	37.56 a-f
CIM-506 × SLH-284	2.41	0.15	84.26 abc	37.17 a-g
CIM-506 × CIM-446	2.56	0.19	78.82 a-g	37.39 a-g
CIM-506 × CIM-473	2.52	0.27	43.04 lm	36.86 a-g
CIM-506 × CIM-496	2.49	0.19	63.12 c-l	36.76 a-g
CIM-506 × CIM-499	2.50	0.18	78.50 a-g	36.87 a-g
CIM-506 × CIM-554	2.53	0.30	73.09 a-j	37.22 a-g
CIM-506 × CIM-707	2.55	0.18	79.74 a-g	37.22 a-g
CIM-554 × SLH-284	2.55	0.17	63.30 c-l	36.84 a-g
CIM-554 × CIM-446	2.42	0.35	70.50 b-j	37.67 a-f
CIM-554 × CIM-473	2.55	0.17	64.95 b-k	37.03 a-g
CIM-554 × CIM-496	2.52	0.25	59.22 e-m	36.63 b-g
CIM-554 × CIM-499	2.52	0.16	53.78 j-m	36.45 c-g
CIM-554 × CIM-506	2.75	0.19	84.22 abc	37.86 a-e
CIM-554 × CIM-707	2.50	0.25	83.71 a-d	37.14 a-g
CIM-707 × SLH-284	2.56	0.15	76.94 a-i	37.28 a-g
CIM-707 × CIM-446	2.34	0.25	67.37 b-j	37.82 a-e
CIM-707 × CIM-473	2.55	0.14	66.11 b-k	37.84 a-e
CIM-707 × CIM-496	3.75	0.32	63.41 c-l	36.54 b-g
CIM-707 × CIM-499	3.76	0.13	61.46 d-m	37.50 a-f
CIM-707 × CIM-506	3.24	0.16	83.44 a-d	37.06 a-g
CIM-707 × CIM-554	2.09	0.32	93.68 a	37.35 a-g
F_3 population means	2.53	0.24	69.14	37.27
DMRT LSD$_{0.05}$	-	-	17.44	1.385

Table 6. Genotypic, phenotypic & environmental variances, GCV, PCV, heritability (bs) and genetic advance in F_3 populations for various traits of upland cotton.

Variables	V_g	V_p	V_e	GCV (%)	PCV (%)	h^2	G.A.[*]	G.A. (%)[**]
Oil content	5.54	5.76	0.23	10.83	11.04	0.96	4.75%	21.86
Protein content	7.66	8.13	0.47	14.21	14.64	0.94	5.53%	28.40
Oleic acid	8.56	8.94	0.37	25.26	25.81	0.96	5.90%	50.94
Linoleic acid	9.49	10.89	1.40	6.48	6.94	0.87	5.92%	12.45
Palmitic acid	8.24	8.93	0.69	16.21	16.88	0.92	5.68%	32.07
Stearic acid	5.31	5.83	0.52	37.41	39.21	0.91	4.53%	73.53
Saturated fatty acids	9.89	9.96	0.07	13.18	13.22	0.99	6.45%	27.05
Unsaturated fatty acids	9.91	11.97	2.06	5.32	5.85	0.83	5.90%	9.98
Seed cotton yield plant^{-1}	121.17	160.02	38.85	15.57	17.90	0.76	19.73 g	27.92
Lint percentage	0.36	0.49	0.12	1.62	1.87	0.75	1.07%	2.87

_V_g = Genotypic variance, V_p = Phenotypic variance, V_e = Environmental variance, GCV & PCV = Genotypic and phenotypic coefficient of variation, h^2 = Broad sense heritability, G.A.[*] = Genetic advance, G.A. (%)[**] = Genetic advance as percent of population mean_

Table 7. Correlation of seed cotton yield with various traits in upland cotton.

Variables	Correlation of seed cotton yield with other traits	Probability (P 0.05)
Oil content	0.182[*]	0.011
Protein content	0.089[N.S.]	0.218
Oleic acid	0.054[N.S.]	0.458
Linoleic acid	0.164[*]	0.023
Palmitic acid	0.066[N.S.]	0.366
Stearic acid	0.298[**]	0.000
Saturated fatty acids	0.289[**]	0.000
Unsaturated fatty acids	0.172[*]	0.017
Lint percentage	0.139[*]	0.054

[**],[*] = significant at p 0.01 and p 0.05, respectively N.S. = Non-significant

Conclusion: Overall, the F_3 populations revealed increased values than parental genotypes for oil content, linoleic acid, stearic acid and ratio of unsaturated/saturated fatty acids, while for other traits the

mean values were comparable. The F₃ population CIM-707 × CIM-554 followed by CIM-707 × CIM-499 exhibited best performance for oil content and fatty acids profile. The F₃ populations CIM-446 × SLH-284 and CIM-496 × CIM-499 excelled all other F₃ populations and parental cultivars and showed best performance for seed cotton and lint yields with desirable oil quality traits.

REFERENCES

Ahmad, M., N.U. Khan, F. Mohammad, S.A. Khan, I. Munir, Z. Bibi and S. Shaheen (2011). Genetic potential and heritability studies for some polygenic traits in cotton (*G. hirsutum* L.). Pakistan J. Bot. 43(3): 1713-1718.

Allard, R.W. (1999). Principles of Plant Breeding, 2ⁿᵈ edition, John Wiley and sons, New York, USA.

Anonymous (1998). NIR calibration in practice. http://dx.doi.org/1-:1051/analusis: 19982604 0038.

Anonymous (2003). Comparative studies on the chemical composition of cottonseed of BGII cotton hybrids and their non-BGII counterparts. Report submitted to Review Committee on Genetic Manipulation (RCGM).

Avtonomov, V., T. Sokolova, S. Rakhmankulov and L. Sydykhodzhaeva (1981). Seed oil content in distant interspecific hybrids (Pl. Br. Absts., 52(4): 3151; 1982).

Aytac, Z. and G. Kinaci (2009). Genetic variability and association studies of some quantitative characters in winter rapeseed. Afr. J. Biotechnol. 8(15): 3547-3554.

Basal, H., O. Canavar, N.U. Khan and C.S. Cerit (2011). Combining ability and heterotic studies through line × tester in local and exotic upland cotton genotypes. Pakistan J. Bot. 43(3): 1699-1706.

Batool, S., N.U. Khan, K. Makhdoom, Z. Bibi, G. Hassan, K.B. Marwat, Farhatullah, F. Mohammad, Raziuddin and I.A. Khan (2010). Heritability and genetic potential of upland cotton genotypes for morpho-yield traits. Pakistan J. Bot. 42(2): 1057-1064.

Batool, S., N.U. Khan, S. Gul, M.J. Baloch, N.A. Turi, S.A. Taran and M. Saeed (2013). Genetic analysis for yield and yield contributing variables in upland cotton. J. Food, Agri. Environ. 11(3&4): 624-630.

Bewig, K.M., A.D. Clarke, C. Roberts and N. Unklesbay (1994). Discriminant analysis of vegetable oils by near-infrared reflectance spectroscopy. J. Am. Oil Chem. Soc. 71: 195-200.

Bibi, M., N.U. Khan, F. Mohammad, R. Gul, A.A. Khakwani and O.U. Sayal (2011a). Genetic divergence and association among polygenic

characters in *G. hirsutum* L. Pakistan J. Bot. 43(6): 2751-2758.

Bibi, M., N.U. Khan, F. Mohammad, R. Gul, A.A. Khakwani, O.U. Sayal, I.A. Khan and M. Idrees (2011b). Genetic disparity and relationship among quantitatively inherited yield related traits in diallel crosses of upland cotton. Pakistan J. Bot. 43(5): 2543-2550.

Bricker, B. (1991). MstatC: A microcomputer programme for design management and analysis of agronomic research experiments. Michigan State University (MSU), East Lansing, Michigan, USA.

Burton, G.W. and E.M. Devane (1953). Estimating heritability in fall fescue (*Festecd cirunclindcede*) from replicated clonal material. Agron. J. 45: 478-481.

Dani, R.G. (1988). Heterosis for oil content in cotton. [Pl. Br. Absts., 59(9):7672; 1989].

Dani, R.G. (1989). Heterosis and combining ability for oil content and other agronomic traits in cotton (*G. hirsutum* L.). [Pl. Br. Absts., 60(11): 11237; 1990].

Dani, R.G. (1991). Analysis of combining ability for seed oil content in cotton (*G. hirsutum* L). [PL. Br. Absts., 62(8): 7373; 1992].

Daniel, D.R. (2007). The chemical and functional properties of cottonseed oil as a deep-fat frying medium. Ph.D Thesis, T & M Univ. Texas, USA.

Dowd, M.K., D.L. Boykin, W.R. Meredith, Jr., and B.T. Campbell (2010). Fatty acid profiles of cottonseed genotypes from the national cotton variety trials. The J. Cotton Sci. 14: 64-73.

Duncan, D. (1955). Multiple range and multiple F-tests. Biometrics 11: 1-42.

Ergonul, P.G., and B. Ergonul (2008). Changes in fatty acid profiles and omega fatty acid contents of selected vegetable oil during refining process. J. Environ. Agric. Food Chem. 7(13): 2655-2660.

Gul, S., N.U. Khan, S. Batool, M.J. Baloch, M. Munir, M. Sajid, A.A. Khakwani, S.H. Ghaloo, Z.A. Soomro and S.F. Kazmi (2014). Genotype by environment interaction and association of morpho-yield variables in upland cotton. J. Animal & Plant Sci. 24(1): 262-271.

Hall, A.J. (2003). Evaluation of fatty acid composition of cotton germplasm and association with cold tolerance. M.Sc. Thesis, T & M Univ. Texas, USA.

Hamza, M.A., M.H. Abdel-Aal and M.M. Khalil (1988). Studies on Egyptian cottonseeds: Fatty acid-composition and protein patterns. Nahrung 32: 255-259.

Hanson, C.H., H.F. Robinson and R.E. Comstock (1965). Biometrical studies of yield in segregating

populations of Korean Lespedeza. Agron. J. 48: 267-282.

Johnson, H.W., H.F. Robinson and R.E. Comstock (1955). Genotypic and phenotypic correlation in soybean and their implications in selection. Agron. J. 47: 477-483.

Jones, L.A. and J.H. Kersey (2002). Cottonseed article. National Cottonseed Products Association (NCPA), USA (http://www.cottonseed.com/publication/csobro.asp).

Khan, N.U. (2011). Economic heterosis for morpho-yield traits in F_1 and F_2 diallel crosses of upland cotton. SABRAO J. Breed. Genet. 43(2): 144-164.

Khan, N.U. (2013). Diallel analysis of cotton leaf curl virus (CLCuV) disease, earliness, yield and fiber traits under CLCuV infestation in upland cotton. Aust. J. Crop Sci. 7(12): 1955-1966.

Khan, N.U. and G. Hassan (2011). Genetic effects on morphological and yield traits in cotton (*G. hirsutum* L.). Span. J. Agric. Res. 9(2): 460-472.

Khan, N.U., G. Hassan, K.B. Marwat, Farhatullah, M.B. Kumbhar, A. Parveen, U. Aiman, M.Z. Khan and Z.A. Soomro (2009a). Diallel analysis of some quantitative traits in *G. hirsutum* L. Pakistan J. Bot. 41(6): 3009-3022.

Khan, N.U., G. Hassan, K.B. Marwat, Farhatullah, S. Batool, K. Makhdoom, W. Ahmad I. Khan, I.A. Khan and W. Ahmad (2009b). Genetic variability and heritability in upland cotton. Pakistan J. Bot. 41(4): 1695-1705.

Khan, N.U., G. Hassan, K.B. Marwat, M.B. Kumbhar, I. Khan, Z.A. Soomro, M.J. Baloch, and M.Z. Khan (2009c). Legacy study of cottonseed traits in upland cotton using Griffing's combining ability model. Pakistan J. Bot. 41(1): 131-142.

Khan, N.U., G. Hassan, M.B. Kumbhar, A. Parveen, U. Aiman, W. Ahmad, S.A. Shah and S. Ahmad (2007). Gene action of seed traits and its oil content in upland cotton (*G. hirsutum* L.). SABRAO J. Breed. Genet. 39: 17-29.

Khan, N.U., G. Hassan, M.B. Kumbhar, K.B. Marwat, M.A. Khan, A. Parveen, U. Aiman and M. Saeed (2009d). Combining ability analysis to identify suitable parents for heterosis in seed cotton yield, its components and lint % in upland cotton. Ind. Crops Prod. 29: 108-115.

Khan, N.U., H. Basal and G. Hassan (2010a). Cottonseed oil and yield assessment via economic heterosis and heritability in intra-specific cotton populations. Afr. J. Biotechnol. 9(44): 7418-7428.

Khan, N.U., K.B. Marwat, G. Hassan, Farhatullah, S. Batool, K. Makhdoom, W. Ahmad and H.U. Khan (2010b). Genetic variation and heritability

for cottonseed, fiber and oil traits in *G. hirsutum* L. Pakistan J. Bot. 42(1): 615-625.

Khan, N.U., K.B. Marwat, G. Hassan, M.B. Kumbhar, Farhatullah, Z.A. Soomro, N. Khan, A. Parveen and U. Aiman (2009e). Study of fiber quality traits in upland cotton using additive dominance model. Pakistan J. Bot. 41(3): 1271-1283.

Khan, S.A., N.U. Khan, F. Mohammad, M. Ahmad, I.A. Khan, Z. Bibi and I.U. Khan (2011). Combining ability analysis in intraspecific F_1 diallel cross of upland cotton. Pakistan J. Bot. 43(3): 1719-1723.

Kim, Y. and S.E. Kays (2009). Near-Infrared (NIR) prediction of *trans*-fatty acids in ground cereal foods. J. Agric. Food Chem. 57(18): 8187-8193.

Kohel, R.J. (1980). Genetic studies of seed oil in cotton. Crop Sci. 20(6): 684-686.

Kohel, R.J. (1998). Evaluation of near infrared reflectance for oil content of cottonseed. J. Cotton Sci. 2: 23-26.

Lawhon, J.T., C.M. Cater and K.F. Mattil (1977). Evaluation of the food potential of sixteen varieties of cottonseed. J. Am. Oil Chem. Soc. 54: 75-80.

Lukonge, E., M.T. Labuschagne and A. Hugo (2007). The evaluation of oil and fatty acid composition in seed of cotton accessions from various countries. J. Sci. Food Agric. 87: 340-347.

Makhdoom, K., N.U. Khan, S. Batool, Z. Bibi, Farhatullah, S. Khan, F. Mohammad, D. Hussain, Raziuddin, M. Sajjad and N. Khan (2010). Genetic aptitude and correlation studies in *G. hirsutum* L. Pakistan J. Bot. 42(3): 2011-2017.

Nagappa, H. and B.M. Khadi (2011). Studies on composition of oil and fatty acid in Bt and non Bt cotton (*G. hirsutum* L.). World Cotton Res. Conf. 5, India. pp. 568-571.

Nergiz, C., H. Yalçin and H. Yildiz (1997). Some analytical characters of cottonseed varieties grown in Turkey. Grasas y Aceites 48: 411-414.

O'Brien, R.D. (2004). Fats and oils: Formulating and processing for application. CRC Press, Boca Raton, pp 16-18.

O'Brien, R.D., L.A. Jones, C.C. King, P.J. Wakelyn and P.J. Wan (2005a). Cottonseed Oil, 2, Chap. 5, Bailey's Industrial Oil & Fat Products, Sixth Edition, F. Shahidi, ed., John Wiley & Sons, Inc. Hoboken, NJ, USA, 2005, pp.173-279.

O'Brien, R.D. and P.J. Walkelyn (2005). Cotton seed oil: An oil for transfer options. Inform. Nov. 2005, 16(11): 667-679.

O'Brien, R.D., P.J. Wakelyn and P.J. Wan (2005b). Cottonseed Oil: Alternative to *Trans* Fatty Acid-Containing Oils. Oil Mill Gazetteer, 111, pp. 2-4.

Panford, J.A. and J.M. deMan (1990). Determination of oil content of seeds by NIR: Influence of fatty acid composition on wavelength selection. J. Am. Oil Chem. Soc. 67(8): 473-478.

Panni, M.K., N.U. Khan, Fitmawati, S. Batool and M. Bibi (2012). Heterotic studies and inbreeding depression in F_2 populations of upland cotton. Pakistan J. Bot. 44(3): 1013-1020.

Panse, V.G. and P.V. Sukhatme (1967). Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi, p. 381.

Pettigrew, W.T. and M.K. Dowd (2012). Interactions between irrigation regimes and varieties result in altered cottonseed composition. The J. Cotton Sci. 16: 42-52.

Sharma, D.H., D. Pathaki, A.K. Atwal and M.K. Sangha (2009). Genetic variation for some chemical and biochemical characteristics in cotton seed oil. Cotton Res. Dev. 23(1): 1-7.

Soomro, Z.A., A.S. Larik, N.U. Khan, S. Mari, S. Memon and N.A. Panhwar (2008). Genetic variability studies on quantitative traits in upland cotton. Sarhad J. Agric. 24(4): 202-205.

Stansfield, W.D. (1986). Theory and Problems of Genetics. McGraw-Hill Pub. Co. New York, USA. pp 220-221.

Steel, R.G.D., J.H. Torrie and D. A. Dickey (1997). Principles and Procedures of Statistics - A Biometrical Approach, 3rd ed. McGraw-Hill Pub. Co. New York, USA.

Tomar, S.K., S.P. Singh and S.R.S. Tomar (1992). Genetic variability of yield and its components over environments in desi cotton (*G. arboreum* L.). Crop Res. 5(2): 290-293.

Voitenok, F.V., T.B. Sokolova, P. Nematova and L.A. SydKodzhaeva (1983). Inheritance of oil content in the seed of cotton and possible methods of enhancing this character. [Pl. Br. Absts., 56(1): 495; 1986].

Yunusova, S.G., S.D. Gusakova, A.I. Glushenkova, U.K. Nadzhimov, S. Turabekov and S.A. Musaev (1991). A comparative investigation of the fatty acid compositions of the seeds of a number of lines of a genetic collection of *G. hirsutum* L. Chem. Nat. Compd. 27 (2): 147-150.