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., 2009b; 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 F₁ 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 F₁ generation (Table 1). The field experiment (comprising of parental cultivars and their F₁ 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 F₁ 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 F1 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 F1 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 F1 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 F1 population SLH-284 × CIM-496 (17.56%) and it was a like with ten other genotypes including two parental cultivars (CIM-473, CIM-499) and eight F1 populations ranging from 17.75 to 19.06%. Medium oil content was recorded in all other genotypes. On average, F1 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 F1 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 F1 populations CIM-707 × CIM-554 (24.35%) and CIM-554 × CIM-496 (24.09%). The parental genotype CIM-446 and three F1 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 F3 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 F1 populations the said range was 6.98 to 17.38% (Table 3). Maximum and similar oleic acid was indicated by F1 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 F3 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 F3 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 F3 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 F1 populations varied from 41.89 to 53.85% (Table 3). The linoleic acid was maximum in F3 population CIM-707 × CIM-554 (53.85%), however, it was found equivalent with fifteen F3 populations and two parental cultivars (SLH-282 and CIM-496) ranging from 50.00 to 53.71%. In case of least values, the F3 population CIM-446 × CIM-707 revealed minimum value of linoleic acid (41.89%). Medium linoleic acid was recorded in all other parental genotypes and F1 populations. Overall, the F3 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 F1 populations varied from 13.17 to 23.68% (Table 4). Maximum and equal palmitic acid content was observed in F3 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 stearic acid were observed in eight F₂ 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 F₂ 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 F₁ 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 F₃ 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 F₃ populations the range was 41.14 to 93.68 g for seed cotton yield (Table 5). The seed cotton yield was maximum in F₃ populations CIM-707 × CIM-554 (93.68 g), however, it was found alike with six promising F₃ 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 F₃ populations CIM-446 × CIM-506 (41.14 g), however, it was equivalent with thirteen other F₃ populations ranged from 43.04 to 61.46 g. All other genotypes have medium values for seed cotton yield. Overall, the F₃ 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 F₃ populations ranged from 34.27 to 38.46% (Table 5). The F₃ 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 F₃ population and seven parental cultivars ranging from 36.76 to 38.25% lint percentage. Minimum lint percentage was recorded in F₃ population CIM-446 × CIM-506 (34.27%), followed by F₃ population CIM-499 × CIM-473 (35.69%). All other parental cultivars and F₃ populations showed medium values for lint percentage. On average, the F₃ 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 F₃ 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 F₃ 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 F₃ 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 F₁, F₂ and F₃, 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 F₃ 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<sub>1</sub> 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<sub>2</sub> 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<sub>1</sub> 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<sub>2</sub> 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. Saturated 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<sub>2</sub> 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. Cottons 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 ginned and glandless cotton genotypes and observed varied values for unsaturated fatty acids (70.0 to 79.6%). In present studies, the F<sub>3</sub> 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<sub>2</sub> 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 F₃ populations were comparable, however, individually some F₃ 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 F₃ populations of upland cotton.

<table>
<thead>
<tr>
<th>Cultivars</th>
<th>Parentage</th>
<th>Breeding Centre</th>
<th>Release (year)</th>
<th>Seed cotton yield (kg ha⁻¹)</th>
<th>GOT (%)</th>
<th>Staple length (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLH-284</td>
<td>Not yet released</td>
<td>CRS, Sahiwal</td>
<td>-</td>
<td>3,707</td>
<td>39.0</td>
<td>28.5</td>
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<tr>
<td>CIM-446</td>
<td>CP-15/2 × S-12</td>
<td>CCRI, Multan</td>
<td>1998</td>
<td>3,000</td>
<td>36.1</td>
<td>27.0</td>
</tr>
<tr>
<td>CIM-473</td>
<td>CIM-402 × LRA-5166</td>
<td>CCRI, Multan</td>
<td>2002</td>
<td>3,000</td>
<td>39.7</td>
<td>29.5</td>
</tr>
<tr>
<td>CIM-496</td>
<td>CIM-425 × 755-693</td>
<td>CCRI, Multan</td>
<td>2005</td>
<td>3,000</td>
<td>41.1</td>
<td>29.7</td>
</tr>
<tr>
<td>CIM-499</td>
<td>CIM-402 × 755-693</td>
<td>CCRI, Multan</td>
<td>2003</td>
<td>3,000</td>
<td>40.0</td>
<td>29.6</td>
</tr>
<tr>
<td>CIM-506</td>
<td>CIM-433 × S-12</td>
<td>CCRI, Multan</td>
<td>2004</td>
<td>3,000</td>
<td>38.6</td>
<td>28.7</td>
</tr>
<tr>
<td>CIM-554</td>
<td>2579-04/97 × W-1103</td>
<td>CCRI, Multan</td>
<td>2009</td>
<td>4,241</td>
<td>41.5</td>
<td>28.5</td>
</tr>
<tr>
<td>CIM-707</td>
<td>CIM-243 × 738-693</td>
<td>CCRI, Multan</td>
<td>2004</td>
<td>3,000</td>
<td>39.0</td>
<td>32.2</td>
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</table>

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

<table>
<thead>
<tr>
<th>Variables</th>
<th>Mean squares</th>
<th>CV (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replications</td>
<td>Genotypes</td>
<td>Error</td>
</tr>
<tr>
<td>Degree of freedom</td>
<td>2</td>
<td>63</td>
</tr>
<tr>
<td>Oil content</td>
<td>0.067</td>
<td>17.281**</td>
</tr>
<tr>
<td>Protein content</td>
<td>2.741</td>
<td>24.403**</td>
</tr>
<tr>
<td>Oleic acid</td>
<td>0.114</td>
<td>26.808**</td>
</tr>
<tr>
<td>Linoleic acid</td>
<td>2.064</td>
<td>32.663**</td>
</tr>
<tr>
<td>Palmitic acid</td>
<td>0.134</td>
<td>26.790**</td>
</tr>
<tr>
<td>Stearic acid</td>
<td>0.135</td>
<td>17.494**</td>
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<tr>
<td>Saturated fatty acids</td>
<td>0.044</td>
<td>29.872**</td>
</tr>
<tr>
<td>Unsaturated fatty acids</td>
<td>0.355</td>
<td>35.921**</td>
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<tr>
<td>Seed cotton yield plant¹</td>
<td>116.537</td>
<td>480.048**</td>
</tr>
<tr>
<td>Lint percentage</td>
<td>1.146</td>
<td>1.462**</td>
</tr>
</tbody>
</table>

** = significant at p ≤ 0.01.

### Table 3. Mean performance of parental cultivars and F₃ populations for various traits in upland cotton.

<table>
<thead>
<tr>
<th>Parental cultivars &amp; F₃ populations</th>
<th>Oil (%)</th>
<th>Protein (%)</th>
<th>Oleic acid (%)</th>
<th>Linoleic acid (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLH-284</td>
<td>25.92 ab</td>
<td>25.26 ab</td>
<td>17.20 a</td>
<td>53.30 abc</td>
</tr>
<tr>
<td>CIM-446</td>
<td>19.58 ru</td>
<td>15.07 t</td>
<td>7.03 r</td>
<td>43.46 p-v</td>
</tr>
<tr>
<td>CIM-473</td>
<td>18.98 sw</td>
<td>25.78 a</td>
<td>14.72 c</td>
<td>46.67 j-u</td>
</tr>
<tr>
<td>CIM-496</td>
<td>26.20 a</td>
<td>24.42 a-d</td>
<td>17.38 a</td>
<td>52.94 a-d</td>
</tr>
<tr>
<td>CIM-499</td>
<td>18.84 sw</td>
<td>24.81 abc</td>
<td>17.27 a</td>
<td>45.22 m-v</td>
</tr>
<tr>
<td>CIM-506</td>
<td>19.37 ru</td>
<td>19.68 b-m</td>
<td>17.37 a</td>
<td>44.26 o-v</td>
</tr>
<tr>
<td>CIM-554</td>
<td>23.42 f-k</td>
<td>23.35 b-e</td>
<td>10.72 i</td>
<td>43.01 r-v</td>
</tr>
<tr>
<td>CIM-707</td>
<td>19.34 r-v</td>
<td>22.58 c-f</td>
<td>17.54 a</td>
<td>42.80 s-v</td>
</tr>
<tr>
<td>Parental means</td>
<td>21.46</td>
<td>22.62</td>
<td>14.90</td>
<td>46.46</td>
</tr>
<tr>
<td>SLH-284 × CIM-446</td>
<td>18.56 t-w</td>
<td>22.73 c-f</td>
<td>14.87 c</td>
<td>44.51 n-v</td>
</tr>
<tr>
<td>SLH-284 × CIM-473</td>
<td>17.75 vV</td>
<td>15.01 t</td>
<td>6.98 r</td>
<td>53.71 ab</td>
</tr>
</tbody>
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<table>
<thead>
<tr>
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<tbody>
<tr>
<td></td>
<td>17.56 w</td>
<td>18.39 uvw</td>
<td>18.33 uvw</td>
<td>19.77 q-u</td>
<td>19.32 r-v</td>
<td>22.43 i-n</td>
<td>18.34 uvw</td>
<td>22.08 k-o</td>
<td>19.16 s-v</td>
<td>20.08 p-t</td>
<td>20.42 p-s</td>
<td>20.22 p-s</td>
<td>21.53 l-p</td>
<td>20.94 n-r</td>
<td>21.99 m-q</td>
<td>24.11 c-h</td>
<td>25.20 a-d</td>
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<td>21.46 l-p</td>
<td>22.32 j-o</td>
<td>22.25 k-o</td>
<td>18.34 uvw</td>
<td>22.45 i-n</td>
<td>22.42 i-n</td>
<td>19.03 s-w</td>
<td>22.71 h-m</td>
<td>22.97 g-l</td>
<td>23.45 f-k</td>
<td>22.97 g-l</td>
<td>20.10 p-t</td>
<td>17.66 m-s</td>
<td>9.68 kl</td>
<td>50.61 a-j</td>
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<tr>
<td></td>
<td>22.62 c-f</td>
<td>16.75 o-t</td>
<td>22.28 d-g</td>
<td>21.48 e-h</td>
<td>18.73 i-p</td>
<td>21.71 e-h</td>
<td>16.99 o-t</td>
<td>21.74 e-h</td>
<td>21.53 e-h</td>
<td>20.69 f-k</td>
<td>20.62 f-k</td>
<td>20.66 f-k</td>
<td>20.06 g-l</td>
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<td>19.84 h-m</td>
<td>16.15 q-t</td>
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<td>18.67 i-p</td>
<td>18.43 k-q</td>
<td>17.76 l-s</td>
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<td>18.15 l-r</td>
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<td>47.18 h-r</td>
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<tr>
<td></td>
<td>45.59 l-v</td>
<td>51.36 a-g</td>
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<td>43.32 q-v</td>
<td>49.73 b-l</td>
<td>45.23 m-v</td>
<td>44.00 o-v</td>
<td>46.16 k-u</td>
<td>43.81 m-v</td>
<td>45.13 m-v</td>
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<td>46.06 k-u</td>
<td>42.61 uv</td>
<td>47.82 g-o</td>
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</tr>
</tbody>
</table>
Table 4. Mean performance of parental cultivars and F3 populations for various traits in upland cotton.

<table>
<thead>
<tr>
<th>Parental cultivars &amp; F3 populations</th>
<th>Palmitic acid (%)</th>
<th>Stearic acid (%)</th>
<th>Saturated fatty acids</th>
<th>Unsaturated fatty acids</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLH-284</td>
<td>23.50 a</td>
<td>10.10 abc</td>
<td>33.60 a</td>
<td>70.50 a</td>
</tr>
<tr>
<td>CIM-446</td>
<td>13.22 u</td>
<td>3.08 z</td>
<td>16.30 i</td>
<td>50.49 m</td>
</tr>
<tr>
<td>CIM-473</td>
<td>23.84 a</td>
<td>3.24 z</td>
<td>27.09 b</td>
<td>61.39 bcd</td>
</tr>
<tr>
<td>CIM-496</td>
<td>23.68 a</td>
<td>10.26 ab</td>
<td>33.94 a</td>
<td>70.32 a</td>
</tr>
<tr>
<td>CIM-499</td>
<td>23.57 a</td>
<td>2.97 z</td>
<td>26.53 bc</td>
<td>62.49 bc</td>
</tr>
<tr>
<td>CIM-506</td>
<td>23.67 a</td>
<td>3.07 z</td>
<td>26.75 bc</td>
<td>61.63 bcd</td>
</tr>
<tr>
<td>CIM-554</td>
<td>16.30 jkl</td>
<td>9.89 b-d</td>
<td>26.19 c</td>
<td>53.73 klm</td>
</tr>
<tr>
<td>CIM-707</td>
<td>20.74 c</td>
<td>2.97 z</td>
<td>23.71 e</td>
<td>60.34 b-f</td>
</tr>
</tbody>
</table>

Parental means: 21.07 5.70 26.76 61.36
Table 5. Mean performance of parental cultivars and F3 populations for various traits in upland cotton.

<table>
<thead>
<tr>
<th>Parental cultivars &amp; F3 populations</th>
<th>Unsat. / Sat. fatty acids ratio</th>
<th>Oleic / Linoleic acids ratio</th>
<th>Seed cotton yield plant(^1) (g)</th>
<th>Lint %</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLH-284</td>
<td>2.10</td>
<td>0.32</td>
<td>80.24 a-f</td>
<td>36.93 a-g</td>
</tr>
<tr>
<td>CIM-446</td>
<td>3.10</td>
<td>0.16</td>
<td>58.32 f-m</td>
<td>37.78 a-f</td>
</tr>
<tr>
<td>CIM-473</td>
<td>2.27</td>
<td>0.32</td>
<td>74.39 a-j</td>
<td>37.58 a-f</td>
</tr>
<tr>
<td>CIM-496</td>
<td>2.07</td>
<td>0.33</td>
<td>78.94 a-g</td>
<td>38.23 abc</td>
</tr>
<tr>
<td>CIM-499</td>
<td>2.36</td>
<td>0.38</td>
<td>65.43 b-k</td>
<td>38.23 abc</td>
</tr>
<tr>
<td>CIM-506</td>
<td>2.30</td>
<td>0.39</td>
<td>70.62 b-j</td>
<td>38.25 ab</td>
</tr>
<tr>
<td>CIM-554</td>
<td>2.05</td>
<td>0.25</td>
<td>77.42 a-h</td>
<td>36.67 b-g</td>
</tr>
<tr>
<td>CIM-707</td>
<td>2.54</td>
<td>0.41</td>
<td>80.96 a-e</td>
<td>37.22 a-g</td>
</tr>
</tbody>
</table>

Parental means

<table>
<thead>
<tr>
<th>Unsat. / Sat. fatty acids ratio</th>
<th>Oleic / Linoleic acids ratio</th>
<th>Seed cotton yield plant(^1) (g)</th>
<th>Lint %</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.35</td>
<td>0.32</td>
<td>73.29</td>
<td>37.61</td>
</tr>
</tbody>
</table>

\(^1\) Seed cotton yield was recorded at 105 days after planting.

DMRT LSD\(_{0.05}\) 0.5058 0.4023 0.7457 4.016
Table 6. Genotypic, phenotypic & environmental variances, GCV, PCV, heritability (h²) and genetic advance in F₃ populations for various traits of upland cotton.

<table>
<thead>
<tr>
<th>Variables</th>
<th>Vₑ</th>
<th>Vₛ</th>
<th>Vₚ</th>
<th>GCV (%)</th>
<th>PCV (%)</th>
<th>h²</th>
<th>G.A. (%)</th>
<th>G.A. (%)*²</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oil content</td>
<td>5.54</td>
<td>5.76</td>
<td>0.21</td>
<td>10.83</td>
<td>11.04</td>
<td>0.96</td>
<td>4.75%</td>
<td>21.86</td>
</tr>
<tr>
<td>Protein content</td>
<td>7.66</td>
<td>8.13</td>
<td>0.47</td>
<td>14.21</td>
<td>14.64</td>
<td>0.94</td>
<td>5.53%</td>
<td>28.40</td>
</tr>
<tr>
<td>Oleic acid</td>
<td>8.56</td>
<td>8.94</td>
<td>0.37</td>
<td>25.26</td>
<td>25.81</td>
<td>0.96</td>
<td>5.90%</td>
<td>59.04</td>
</tr>
<tr>
<td>Linoleic acid</td>
<td>9.49</td>
<td>10.89</td>
<td>1.40</td>
<td>6.48</td>
<td>6.94</td>
<td>0.87</td>
<td>5.92%</td>
<td>12.45</td>
</tr>
<tr>
<td>Palmitic acid</td>
<td>8.24</td>
<td>8.93</td>
<td>0.69</td>
<td>16.21</td>
<td>16.88</td>
<td>0.92</td>
<td>5.68%</td>
<td>32.07</td>
</tr>
<tr>
<td>Stearic acid</td>
<td>5.31</td>
<td>5.83</td>
<td>0.52</td>
<td>37.41</td>
<td>39.21</td>
<td>0.91</td>
<td>4.53%</td>
<td>73.53</td>
</tr>
<tr>
<td>Saturated fatty acids</td>
<td>9.89</td>
<td>9.96</td>
<td>0.07</td>
<td>13.18</td>
<td>13.22</td>
<td>0.99</td>
<td>6.45%</td>
<td>27.05</td>
</tr>
<tr>
<td>Unsaturated fatty acids</td>
<td>9.91</td>
<td>11.97</td>
<td>2.06</td>
<td>5.32</td>
<td>5.85</td>
<td>0.83</td>
<td>5.90%</td>
<td>9.98</td>
</tr>
<tr>
<td>Seed cotton yield plant¹</td>
<td>121.17</td>
<td>160.02</td>
<td>38.85</td>
<td>15.57</td>
<td>17.90</td>
<td>0.76</td>
<td>19.73%</td>
<td>27.92</td>
</tr>
<tr>
<td>Lint percentage</td>
<td>0.36</td>
<td>0.49</td>
<td>0.12</td>
<td>1.62</td>
<td>1.87</td>
<td>0.75</td>
<td>1.07%</td>
<td>2.87</td>
</tr>
</tbody>
</table>

Vₑ = Genotypic variance, Vₛ = Phenotypic variance, Vₚ = Environmental variance, GCV & PCV = Genotypic and phenotypic coefficient of variation, h² = Broad sense heritability, G.A. = Genetic advance, G.A. (%)*² = Genetic advance as percent of population mean

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

<table>
<thead>
<tr>
<th>Variables</th>
<th>Correlation of seed cotton yield with other traits</th>
<th>Probability (P ≤ 0.05)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oil content</td>
<td>0.182</td>
<td>0.011</td>
</tr>
<tr>
<td>Protein content</td>
<td>0.089N.S.</td>
<td>0.218</td>
</tr>
<tr>
<td>Oleic acid</td>
<td>0.054N.S.</td>
<td>0.458</td>
</tr>
<tr>
<td>Linoleic acid</td>
<td>0.164N.S.</td>
<td>0.023</td>
</tr>
<tr>
<td>Palmitic acid</td>
<td>0.066N.S.</td>
<td>0.366</td>
</tr>
<tr>
<td>Stearic acid</td>
<td>0.298N.S.</td>
<td>0.000</td>
</tr>
<tr>
<td>Saturated fatty acids</td>
<td>0.289N.S.</td>
<td>0.000</td>
</tr>
<tr>
<td>Unsaturated fatty acids</td>
<td>0.172N.S.</td>
<td>0.017</td>
</tr>
<tr>
<td>Lint percentage</td>
<td>0.139N.S.</td>
<td>0.054</td>
</tr>
</tbody>
</table>

N.S. = Non-significant

Conclusion: Overall, the F₃ 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 F$_3$ population CIM-707 × CIM-554 followed by CIM-707 × CIM-499 exhibited best performance for oil content and fatty acids profile. The F$_3$ populations CIM-446 × SLH-284 and CIM-496 × CIM-499 excelled all other F$_3$ populations and parental cultivars and showed best performance for seed cotton and lint yields with desirable oil quality traits.

REFERENCES


