

YIELD AND FIBER QUALITY BALANCE IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.) BREEDING

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Abstract

The main aim of cotton breeding is to combine yield and fiber quality by broadening the genetic base of the genotypes. The performance of multi-parent hybrid populations and the association among yield attributes and quality parameters were investigated by biometrical techniques, i.e., principal component analysis (PCA), correlation analysis and decision tree. The mean and range of crosses were higher for seed cotton yield and ginning out-turn; similar for fiber strength and length; coarse for fiber fineness compared to their parents. Significantly negative correlations were recorded between seed cotton yield and fiber length; ginning out-turn and fiber fineness. PCA analysis indicated that fiber fineness and ginning out-turn were on the same platform, whereas seed cotton yield per plant with fiber length and fiber fineness were on opposite platforms. The decision tree model showed that fiber fineness (4.60 mic.) within commercial limits depends on the optimization of seed cotton yield per plant of approximately 54.27 g and ginning out-turn of 42.60% in single plant selection.

Introduction

Turkey is one of the most important cotton-producing and exporting countries in the world. World's cotton production was approximately 24.98 million tons of fiber cotton production in 2022, and Türkiye provided 1.1 million tons, 3.6 per cent of this production. Combining yield and improved fiber quality is indispensable for cotton growing, the textile industry and high-speed fiber spinning technology (Campbell *et al.* 2011). Therefore, there is intense pressure on cotton breeding programs to increase the yield and fiber quality. Parental selection is one of the most critical strategies for genetic improvement in all breeding methods (Campbell *et al.* 2013).

The success of cotton breeding has been limited to a narrow genetic base in any breeding program designed to improve the yield and quality parameters. The methods or breeding strategies such as multi-parent crosses (Cavanagh *et al.* 2008), recurrent selection (Gokidi *et al.* 2016, Balci *et al.* 2021) and double-crosses are proposed to overcome the narrow genetic basis. In early generations of pedigree or bulk methods, inbreeding depression is high due to rapid homozygosity in self-pollinated crops such as cotton, wheat and soybean. Thus, increasing the favorable gene frequency and widening the variation is necessary for successful selection in a later generation.

Yu *et al.* (2013), Yehia *et al.* (2019) emphasized the negative associations between yield and fiber quality, and unfavorable relationships limited cotton breeding efforts to enhance multiple fiber properties. In breeding studies, it was observed that the fiber thickness increased with the increase in yield and ginning (Ibragimov 1989). However, there are findings in which the correlations between fiber quality characteristics and yield and ginning yield are not significant (Balci *et al.* 2021, Palabiyik *et al.* 2022).

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The techniques such as principal component and correlation analysis help to identify the phenotypic variability and to allow a complex assessment of the relations between the characteristics in breeding populations. Previously, studies were performed regarding genotypic diversity and similarity for bi-parental populations. Thus, the present study was aimed to explain the divergence of cotton characteristics and determine the selection criteria for optimizing agronomic performance and fiber quality in multi-parent populations. In addition, tree algorithms were performed to optimize the effect of yield components and ginning out-turn on fiber quality parameters.

Materials and Methods

Esperya and Genotype I were crossed with 7 F₃ populations obtained from previous breeding studies to increase the ginning out-turn, and 14 F₁ hybrids were created in 2020. The grandparents of F₁ hybrids were commercial varieties inc., Claudia, Carisma, Carmen, Gloria, Flash, ST-468 and Julia, included as parents in the pedigree of F₃ populations in which the best 10 F₂ plants were crossed by diallel mating design. The most recently used parents were Esperya and Genotype I, having high ginning out-turn.

Twenty-three genotypes, including 14 F₁ hybrids and 9 parents, were planted in Randomized Complete Block Design with 3 replications in May 2021. The planting of seeds was performed in 70 cm row spacing and 12 cm plant-to-plant. Plots were 6 m long with a single row. Recommended agronomic practices were applied for the standard cotton growing of the Aegean Region.

The biometrical characters were measured in randomly selected 10 plants from each plot. The days of first squaring (DFS), days of first flowering (DFF), days of first boll opening (DFB) and boll number per plant (BN) were observed before harvest. Seed cotton yield per plant (SCY) and boll weight (BW) were recorded, and samples were ginned by roller gin (laboratory type) to determine ginning out-turn (GOT) and seed index (SI). The fiber length (FL; cm), fiber fineness (FF; mic.), fiber strength (FS; g/tex), and elongation (%) were determined using Uster HVI 1000, and then the spinning consistency index (SCI) was calculated.

Grouped boxplots were created in R studio via 'tidyverse' (Wickham *et al.* 2019), 'ggplot2' (Wickham *et al.* 2016) and 'gapminder' (Bryan 2022) packages. Correlations between all pairs of measured characters were calculated in R studio using the 'metan' package (Olivoto *et al.* 2020). A principal component analysis (PCA) was used to estimate and rank the principal components contributing to the variation in data by consolidating the relationships among observed characters. PCA was performed in PAST statistics software (Hammer *et al.* 2001). The decision tree, a machine learning method, was built in JMP 14[®] statistical programme (SAS Institute Inc. 2018).

Results and Discussion

Significant differences among genotypes for all observed characters except fiber length indicated the presence of sufficient genetic variability (Table 1). The genotypic mean of earliness characters, such as days to first squaring, first flowering, and boll opening, were 41.78, 56.70 and 120.13 days, respectively (Fig. 1). The number of monopodial and sympodial branches recorded a mean of 0.62 and 10.21, respectively. The maximum boll number per plant of parents was higher than that of crosses (15.73 vs 14.27), whereas the highest boll weight (5.36 g) and seed cotton yield per plant (73.89 g) were recorded in crosses. Ginning out-turn of crosses varied between 43.32 - 48.00%, while the range of parents was 40.73 - 46.11%. The seed index was between 8.86 and 10.23 g for crosses; 8.60 g and 10.45 g for parents. There were no significant differences among genotypes for fiber length. In the present population, fibers of crosses (5.34 mic.) were

coarser than that of parents (4.91 mic.). Although minimum values of crosses for fiber strength (29.60 g/tex), elongation (7.17%) and SCI (126.0) were similar to parents, higher maximum values were recorded in parents (Fig. 1).

Table 1. Mean squares of genotypes for the traits studied.

Traits	Mean squares for genotype
Days of first squaring (DFS)	2.44**
Days of first flowering (DFF)	4.21**
Days of first boll opening (DFB)	9.90**
Monopodial branch number per plant (MBN)	0.46**
Sympodial branch number per plant (SBN)	3.12**
Plant height (PH)	64.43**
Boll number per plant (BN)	7.28**
Boll weight (BW)	0.22**
Seed cotton yield per plant (SCY)	149.01**
Ginning out-turn (GOT)	12.14**
Seed index (SI)	0.98**
Fiber length (FL)	1.48
Fiber fineness (FF)	0.22**
Fiber strength (FS)	3.44*
Elongation	0.49**
Spinning consistency index (SCI)	138.99**

*, **; significant at 5% and 1% probability level, respectively.

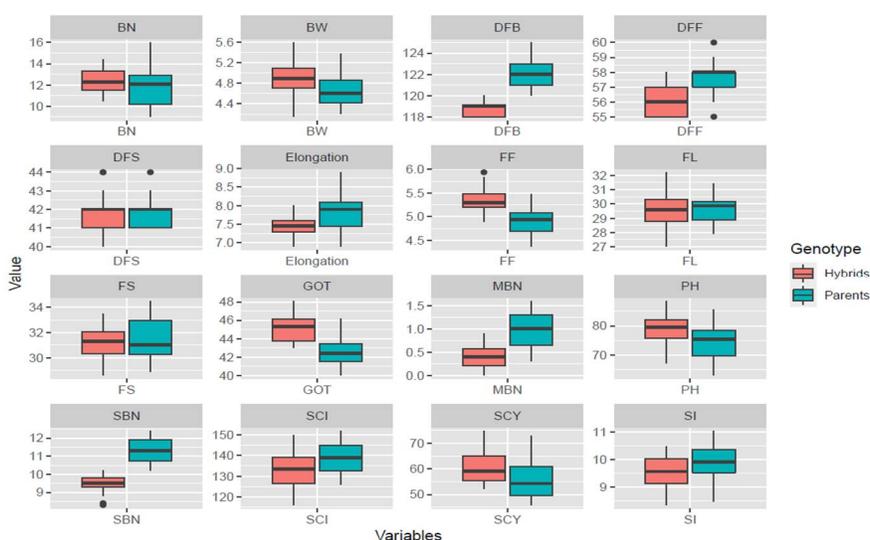


Fig. 1. Grouped boxplots showing variations in observed traits.

Seed cotton yield per plant significantly positively correlated with boll number per plant, whereas the significantly negative correlations were determined between seed cotton yield per plant and days to first flowering, days to first boll opening, sympodial branch number, fiber length and SCI (Fig. 2). Although the findings of Sarwar *et al.* (2021) confirmed the results of a negative correlation of earliness with seed cotton yield, Memon *et al.* (2016) revealed a positive correlation between seed cotton yield and days to first squaring. On the other hand, a significant and positive association between seed cotton yield per plant and boll number per plant was emphasized by many researchers (Ahmad *et al.* 2016, Rehman *et al.* 2020).

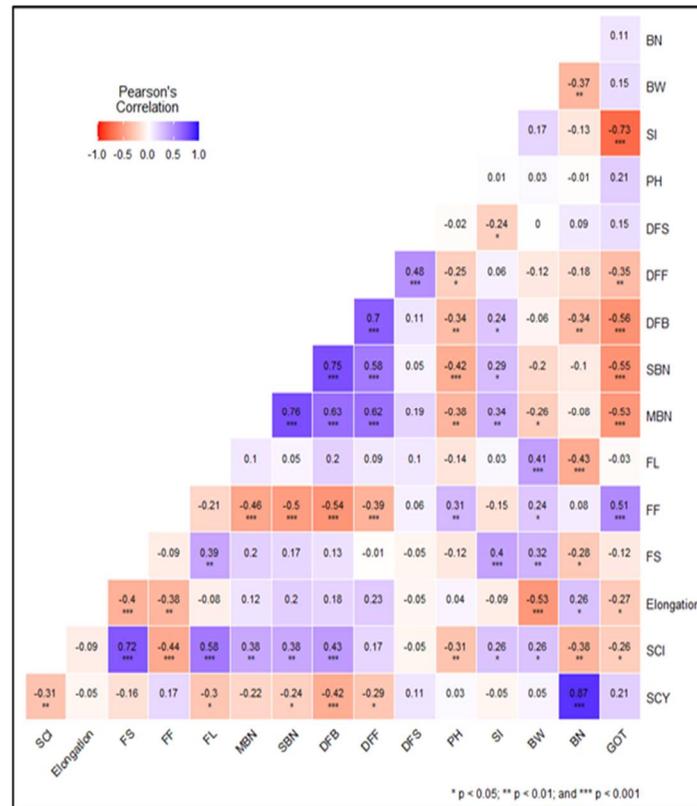


Fig. 2. The matrix colored by the degree of correlation coefficients.

Similarly, the significant and negative associations between ginning out-turn and monopodial branch number, sympodial branch number, days to first flowering and days to first boll opening indicated that yielding genotypes with higher ginning out-turn were those that develop their reproductive organs early, such as flower and boll and branchless. Moreover, ginning out-turn significant and negatively correlated with SCI and elongation, whereas it is significant and positively correlated with fiber fineness. The unfavorable association between ginning out-turn and fiber fineness in the direction of coarsening of the fibers was also stressed in previous studies (Desalegn *et al.* 2009, Yaqoob *et al.* 2016.) The relationships clearly show that genotypes with higher yield and ginning out-turn had unfavorable fiber quality. In addition, negative and significant associations between boll number and SCI, fiber strength and fiber length confirmed these findings.

Jarwar *et al.* (2019) and Ullah *et al.* (2022) took attempt to evaluate the high genetic variability among the yield and its components in cotton. Associations among different components using multivariate analysis were evaluated. Biplot graphics based on cotton genotypes for observed characters presented in Figs 3 and 4 showed that three components had extracted Eigenvalue of >1 as the findings cited (Ullah *et al.* 2019). PC1 carried 34.73%, the second one (PC2) 21.49%, and the third one (PC3) 12.11% of the supply of information input variables. The crosses, parents and variables were positioned on the plot as vectors in PC biplot (Figs 3 and 4). The correlations among observed characters were also visible on the biplot graph. All characters except days to first flower, seed index and plant height exhibited high variability. A similar result of high variability seed cotton yield per plant, boll weight, fiber length, fiber fineness and number of sympodial per plant was reported by Rathinavel (2018). It can be clearly seen that finer fineness and ginning out-turn were opposite to days to first squaring, flowering, boll opening, sympodial and monopodial branch number. Similarly, seed cotton yield per plant and fiber length and fiber fineness were on opposite sides. As illustrated in both biplot, crosses and their parents evolved against each other. Especially Julia, Carmen and Claudia exhibited high performances for fiber length, fiber strength and SCI, while only the 10th cross was in quality group, and the 9th cross was closest to the center in order to all observed characters. These findings clearly indicated that although genotypes with longer, finer and stronger fibers can be bred, the main strategy is combining optimum values for these traits.

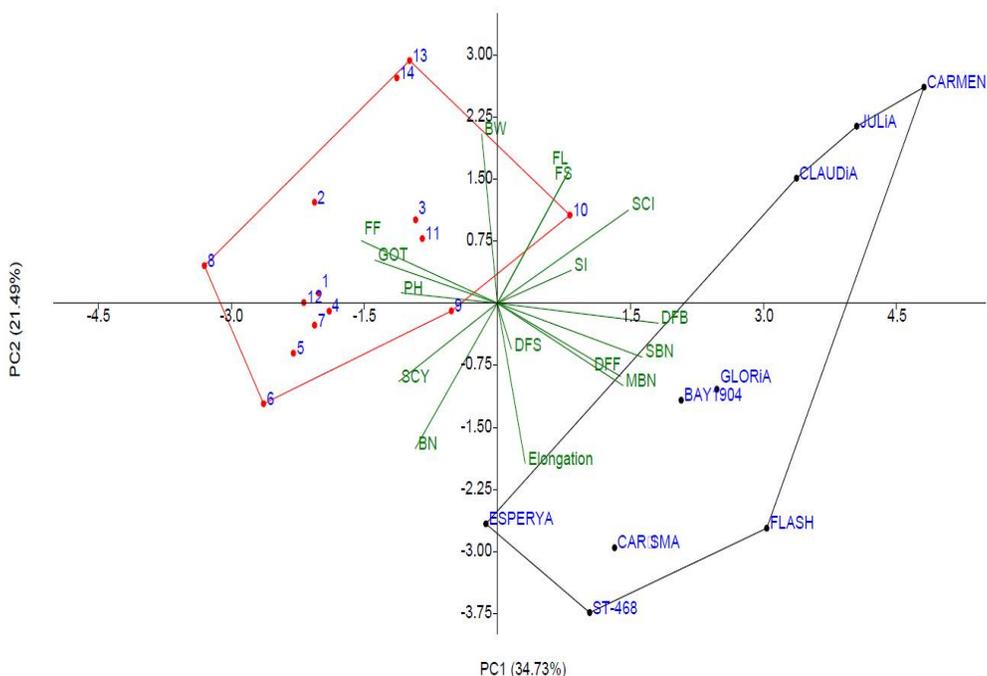


Fig. 3. Biplot between PC1 and PC2.

Chakraborty *et al.* (2018) performed the decision tree to identify the most predominant property affecting the spinnability of cotton fibers. Results of the present study regarding fiber fineness showed that fiber fineness developed in a rather coarse direction and was above

commercial limits. Fiber strength, uniformity index, fiber fineness and reflectance degree are responsible for higher yarn strength and SCI would increase with higher values of fiber strength, uniformity index, upper half mean length and reflectance degree, and its value would decrease with increasing fiber fineness and yellowness (Sarker *et al.* 2022). From the present study it is hypothesized that fiber fineness could be bred at commercial limits by optimizing the associated

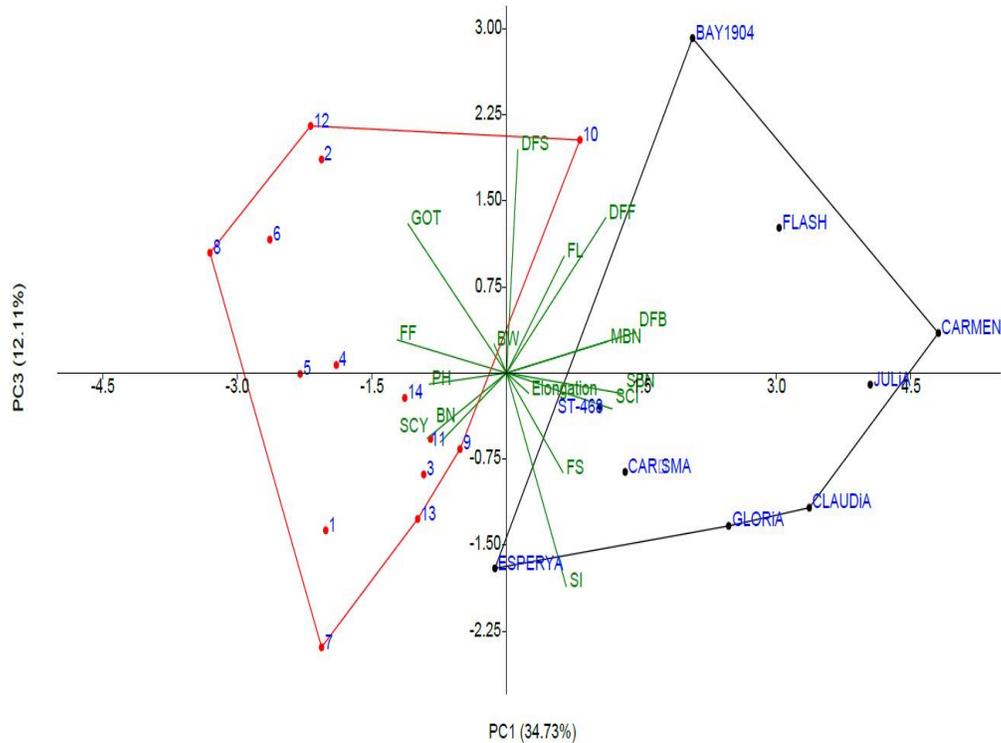


Fig. 4. Biplot between PC1 and PC3.

traits. Therefore, separate model trees were built for fiber fineness. Ginning out-turn was the most significant factor affecting fiber fineness by regression tree (Fig. 5), while seed cotton yield per plant was the second factor. The R^2 adjusted value of the model was 0.48. There were forty-six observations (training 70%, test 30%, totally 69 observations) in the root node at the top of the tree, and separated two main nodes according to fiber fineness. Ginning out-turn was assigned to two different group including 43.59% > and 43.59% <. When ginning out-turn was below 43.59%, fiber fineness was predicted as 4.93 mic., which was close to upper commercial limits. Then, there were two sub-nodes. In the first group (ginning out-turn below 42.6%), fiber fineness was 4.66 mic. within commercial limits. Fiber fineness could be 4.58 mic. depending on if the seed cotton yield per plant is above 54.27 g.

Finally, data mining apparatus such as principal components analysis and decision tree were performed to optimize the yield, ginning out-turn and fiber quality parameters. The negative associations among seed cotton yield, ginning out-turn, and fiber quality were also reported in

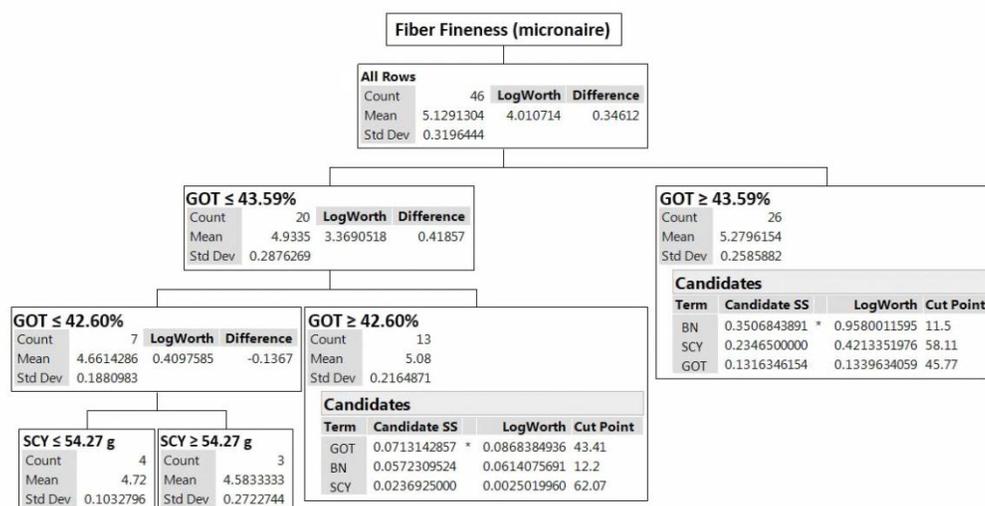


Fig. 5. Decision tree explaining the most appropriate fiber fineness value.

multi-parent populations enriched with high ginning out-turn parents, as confirmed by the PCA results. The decision tree indicated that fiber fineness could be within commercial limits when ginning out-turn and seed cotton yield were kept at a certain level. The present results revealed that the optimum values of the traits should be used in the selection stage in the segregated generations.

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