Agrociencia

SELECTION OF NATIVE AND CONVENTIONAL COTTON (*Gossypium hirsutum* L.) GENOTYPES BASED ON FIBER QUALITY

Enrique **Hernández-Leal**[1], Iván **Franco-Gaytán**[3], Olga **Bonilla-Barrientos**[1*],
Aurelio **Hernández-Bautista**[2], Arturo **Reyes-González**[3],
Rocío **Toledo-Aguilar**[4], Fernando **López-Morales**[5]

[1] Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Campo Experimental Delicias. Carretera Delicias-Rosales km 2, Colonia Centro, Ciudad Delicias, Chihuahua, Mexico. C. P. 33000.
[2] Colegio de Postgraduados Campus Montecillo. Postgrado de Recursos Genéticos y Productividad-Genética. Carretera México-Texcoco km 36.5, Montecillo, Texcoco, State of Mexico, Mexico. C. P. 56264.
[3] Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Campo Experimental La Laguna. Boulevard José Santos Valdez No. 1200 Pte, Matamoros, Coahuila, Mexico. C. P. 27440.
[4] Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias. Carretera Iguala-Tuxpan km 2.5, Tuxpan, Iguala de la Independencia, Guerrero, Mexico. C. P. 40000.
[5] Benemérita Universidad Autónoma de Puebla, Facultad de Ciencias Agrícolas y Pecuarias, San Juan Acateno, Teziutlán, Puebla, México. C. P. 73965.
* Author for correspondence: bonilla.olga@inifap.gob.mx

ABSTRACT

Cotton (*Gossypium hirsutum* L.) is the main source of natural textile fibers in the world. Properties such as short fiber stickiness, trash content, color, fiber length, and fineness are fiber quality characteristics that determine pricing, profitability, and marketability. Therefore, the description and measurement of all its characters is indispensable to ensure high-quality cotton fiber production. The objective of this work was to evaluate, select, and characterize cotton germplasm (*Gossypium* spp.) with high fiber quality in a randomized complete block experimental design with three replications and 15 plants per replication for the generation of new conventional varieties, based on the hypothesis that genotypes with excellent fiber quality can compete with currently commercialized transgenic varieties. The evaluation was conducted in a greenhouse during the 2019 autumn-winter agricultural cycle at La Laguna Experimental Field of the National Institute of Forestry, Agricultural and Livestock Research (INIFAP-CELALA). Two harvests were carried out, where a random sample of 60 buds was taken from each genotype and the fiber was separated from the seed. A total of 150 g of fiber was taken from each sample and measured for length, strength, fineness, spinnability index, uniformity index, short fiber index, elongation, reflectance, and yellow +b content. Analysis of variance (ANOVA) showed significant differences between genotypes for all variables evaluated, mainly in fiber length, strength, and fineness. The results indicate that TOA-17, TOA-18, GOS-17, GOS-21, and FZ-13 CLON showed outstanding characters of similar quality to the commercial control (DeltaPine®), making these genotypes suitable for the requirements of the textile industry.

Citation: Hernández-Leal E, Franco-Gaytán I, Bonilla-Barrientos O, Hernández-Bautista A, Reyes-González A, Toledo-Aguilar R, López-Morales F. 2025. Selection of native and conventional cotton crop (*Gossypium hirsutum* L.) genotypes based on fiber quality.
Agrociencia. https://doi.org/ 10.47163/agrociencia.v59i1.3197

Editor in Chief:
Dr. Fernando C. Gómez Merino

Received: May 17, 2024.
Approved: November 30, 2024.
Published in Agrociencia:
January 20, 2025.

Key words: genetic diversity, cotton germplasm, selection.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is the dominant natural textile fiber in the world (Lee and Fang, 2015) and the most widely used raw material in the textile industry (Zheng *et al*., 2018) because of its high fiber quality for fabric manufacturing. Due to its wide adaptability and excellent performance, it is grown in more than 80 countries (UNIDO, 2023), producing about 92 % of the world's cotton fiber (Zhang *et al*., 2015) and accounting for 27 % of the fibers consumed in the textile industry (FAO, 2021).

Over the years, breeders have only focused on increasing yield because simultaneously improving complex traits was a major challenge (Li *et al*., 2016). Currently, genetic improvements in yield and fiber quality are being made to meet the demands of the modern textile industry (Zhao *et al*., 2022). However, the genetic basis of fiber quality and yield traits in Native American (upland) cotton needs to be discovered for future improvement (Ning *et al*., 2014).

Around 95 % of the world cotton production corresponds to the *G. hirsutum* (upland) species, as it has excellent yield, good adaptability and fiber quality ("long" category). In some ways, the genetic diversity of these commercial varieties is low, and genetic uniformity poses obstacles to breeders. In addition, it puts the cotton industry at high risk of collapse in the likely event of a disease or pest outbreak or increase (Shim *et al*., 2018).

Cotton fiber has a wide variation among genotypes, so its description is essential to know all of its properties and maintain a high-quality production. Since the late 1960s, researchers have used the High Volume Instrument (HVI) to select plant populations with high fiber quality, as these parameters are critical in determining cotton profitability (Pinnamaneni *et al*., 2021).

Fineness (micronaire), length, strength, elongation, moisture index, short fibers, and color are parameters that determine fiber quality (Tarragó *et al*., 2019) and are mainly controlled by genetic factors (Yehia and El-Hashash, 2022). On the other hand, short fiber stickiness, trash content, color, fiber length, and fineness are fundamental in determining the commercial system of cotton pricing and marketing in the world (Ge *et al*., 2008).

When fiber quality is low, producers assume that cotton bolls were exposed to adverse events in the field, such as unexpected rains, insect secretions, or dust (Pinnamaneni *et al*., 2021), resulting in low-quality fibers or fibers with undesirable qualities. However, selection of good cultivars (Orawu *et al*., 2017), sowing outside optimal dates, fertilization, irrigation (Witt *et al*., 2020), early crop defoliation, harvesting, and dethatching are factors that can also affect final fiber quality (Hernández-Leal *et al*., 2022). To some extent, all these factors are affected by the environment, although fiber quality is mainly controlled by genetic factors (Yehia and El-Hashash, 2022).

Selection of genotypes with good genetic traits for yield and fiber quality is critical in the breeding of high-quality cotton (Liu *et al*., 2020). Yehia and El-Hashash (2022) mention that most genetic variations in yield components and fiber quality are controlled by non-additive genetic effects. Cotton fiber quality parameters prior to the publication of genomes were studied with linkage analysis methods in biparental segregating populations (Liu *et al*., 2020). To date, nearly 1000 quantitative trait loci (QTL) are associated with fiber quality and are distributed on all 26 cotton chromosomes (Said *et al*., 2015).

Therefore, the objective of this study was to evaluate genetic diversity by characterizing the fiber quality of 28 cotton genotypes and a commercial control (DeltaPine®) to select outstanding germplasm. This material can be the basis of a breeding program for the generation of new conventional cotton varieties with excellent fiber quality.

MATERIALS AND METHODS

Area of study, genotypes evaluated, and their characteristics

The work was carried out in a greenhouse at La Laguna Experimental Field of the National Institute of Forestry, Agricultural and Livestock Research (INIFAP-CELALA) in Matamoros, Coahuila, Mexico (25° 32’ 1’’ N, 103° 14’ 79’’ W, at an altitude of 1150 m), in the autumn-winter 2019 agricultural cycle. Twenty-eight cotton genotypes and the commercial control DeltaPine® were evaluated (Table 1).

Table 1. Place of collection, origin, and cotton (*Gossypium hirsutum* L.) population type of derived lines and a commercial control evaluated in Matamoros, Coahuila, Mexico.

Genotype	Place of collection	Origin	Description
FZ-10	La Mojonera, Tepecuacuilco, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native population
FZ-13 CHAMPION	Cuexcontlán, Tepecuacuilco, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native population
FZ-13 CLON	Cuexcontlán, Tepecuacuilco, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native subpopulation
FZ-15	Huitzuco, Huitzuco, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native population
GOS-17	Ixcateopan, Ixcateopan, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native population
GOS-21	El Jordán, Tehuantepec, Oaxaca	INIFAP Iguala Experimental Field Botanical Garden	Native population
GOS-22	Carretera a Mixtequilla, Tehuantepec, Oaxaca	INIFAP Iguala Experimental Field Botanical Garden	Native population
GOS-27	Colonia Centro, Marquelia, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native population
US-023	Vicente Guerrero (Barrio el Torque), Venustiano Carranza, Chiapas	INIFAP Iguala Experimental Field Botanical Garden	Native population

Table 1. Continue

Genotype	Place of collection	Origin	Description
TOA-03	Loma de Coyotes, Carretera Iguala-Teloloapan Iguala, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native population
TOA-04	Casino de la Unión, Taxco de Alarcón, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native population
TOA-06	Teacalco, Amacuzac, Morelos	INIFAP Iguala Experimental Field Botanical Garden	Native population
TOA-11	Cuaulutla, Tehuitzingo, Puebla	INIFAP Iguala Experimental Field Botanical Garden	Native population
TOA-12	Sección Primera, Tehuitzingo, Puebla	INIFAP Iguala Experimental Field Botanical Garden	Native population
TOA-17	Ranchería Guadalupe, Chichimá, Comitán de Domínguez, Chiapas	INIFAP Iguala Experimental Field Botanical Garden	Native population
TOA-18	Colonia 28 de agosto, Comitán de Domínguez, Chiapas	INIFAP Iguala Experimental Field Botanical Garden	Native population
TOA-27	Piedras Negras, Pilcaya, Guerrero	INIFAP Iguala Experimental Field Botanical Garden	Native population
PI-589	-	Germplasm bank of the Chapingo Autonomous University	Native population
P1-583 CHAPIS	-	Germplasm bank of the Chapingo Autonomous University	Native population
P1-873	-	Germplasm bank of the Chapingo Autonomous University	Native population
PI-528748	-	Germplasm bank of the Chapingo Autonomous University	Native population
PI-201584	-	Germplasm bank of the Chapingo Autonomous University	Native population
JUÁREZ-91	-	INIFAP Experimental Field La Laguna	Conventional variety
CIAN-95	-	INIFAP Experimental Field La Laguna	Conventional variety
CIAN PRECOZ	-	INIFAP Experimental Field La Laguna	Conventional variety
NAZAS-87A	-	INIFAP Experimental Field La Laguna	Line
NAZA- 87B	-	INIFAP Experimental Field La Laguna	Line
NAZAS SELECTA	-	INIFAP Experimental Field La Laguna	Conventional variety
DELTAPINE®		Comercial control	Conventional variety

General crop management and experimental design

The experiment was set up on October 22, 2019, in 200-cavity polystyrene trays using Peat Moss as substrate. Transplanting was done under hydroponic conditions at 35 days after sowing (DDS). The 28 genotypes and the control were established in black polyethylene bags with a capacity of 12 L filled with river sand as substrate. Fertilization was carried out with fertigation using amino acids (300 to 500 mL per 200 L of water), seaweed (2 L ha^{-1}), Bayfolan® (0.4 L ha^{-1}), and Push® (10 to 20 L ha^{-1}). The dose was increased according to the phenological stage of the crop, starting with a concentration of 50 % during the vegetative stage, and from flowering until fruiting, the concentration was increased to 100 %. Two applications were made with fungicides Promyl 50® and Previcur® at a dose of 1 kg ha^{-1} to control damping off and Captan® to prevent *Rhizoctonia solani*.

Variables evaluated to determine fiber quality

The first harvest took place on May 20 and the second on June 2. A random sample of 60 buds was taken from 15 plants for each genotype, separating the fiber from the seed. Cotton fiber samples were sent to the INIFAP-CELALA fiber quality laboratory for analysis. Fiber length (LON; mm), strength (RES; g tex^{-1}), fineness (FIN; micronaire index), spinnability index (HI; %), uniformity index (UI; %), short fiber index (SFI; %), elongation (ELG; %), reflectance (RD; %), and yellow +b content (PLUS_B) were determined for each sample.

Statistical analysis

A randomized complete block design with three replications and 15 plants per replication was used. An analysis of variance was performed on each variable; when statistical differences between genotypes were detected ($p \leq 0.05$), Tukey's mean comparison test was applied ($p \leq 0.05$). For the analysis of variance, the following model was applied:

$$y_{ij} + \mu + G_i + B_j + E_{ij}$$

where Y_{ij} is the value of the response variable corresponding to genotype i in block j; μ is the overall mean, G_i is the effect of the genotype i; β_j is the effect of block j; and E_{ij} is the experimental error.

A principal component analysis (PCA) was carried out to appreciate the similarities and differences among the 28 genotypes and the commercial control using the statistical package SAS® v.9.3 (SAS Institute, 2011). Furthermore, a cluster analysis was performed by Euclidean distance using the unweighted pair grouping method with arithmetic mean (UPGMA) with the statistical package NTSYS® (Rohlf, 2000). Finally, Pearson's correlation coefficient was calculated with the SAS® v.9.3 statistical package.

RESULTS AND DISCUSSION

Fiber quality performance

The analysis of variance detected significance ($p \leq 0.05$) among genotypes for all nine fiber quality variables (Table 2). The coefficients of variation (CV) ranged from 0.197 to 1.66 %. In this regard, Patel *et al*. (2001) point out that CV varies according to the type of experiment. For cultivar evaluations, acceptable CV values vary between 6 and 8 %, for fertilization between 10 and 12 %, and for pesticide evaluations between 13 and 15 %. The mean CVs in the various tests ranged from 6.1 to 12 %.

Table 2. Mean squares of the analysis of variance for nine fiber quality variables in 28 cotton genotypes (*Gossypium hirsutum* L.) and one control (DeltaPine®) evaluated in Matamoros, Coahuila, Mexico.

Variable	Genotype		Repetitions	Error	CV (%)
Fineness (micronaire index)	1.73	**	0.0002	0.0002	0.286
Length (mm)	0.047	**	0.000005	0.00003	0.437
Resistance (g tex^{-1})	33.29	**	0.0538	0.165	1.29
Spinnability index (%)	2330.44	**	1.6	4.12	1.37
Short fiber index (%)	18.42	**	0.0006	0.002	0.533
Elongation (%)	1.41	**	0.0001	0.0093	1.66
Reflectance (%)	40.67	**	0.0125	0.0246	0.197
Uniformity index (%)	11.09	**	0.001	0.0376	0.231
PLUS_B	2.52	**	0.0001	0.0004	0.219
DF	28		2	56	

CV: coefficient of variation; DF: degrees of freedom; PLUS_B: yellow +b content. $^{*}p \leq 0.05$; $^{**}p \leq 0.01$.

The comparison of means indicates that genotypes TOA-17, FZ-13 CLON, GOS-17, FZ-17, and PI-589 showed a very coarse fineness according to the classification by HVI. In contrast, the NAZAS-87B genotype showed the lowest value, classifying it as fine. Mexican Standard NMX-A-051-SCFI-2000 (DOF, 2000) establishes that the ideal fineness is 3.7 to 4.2 micronaire, with TOA-06, GOS-22, and FZ-13 CHAMPION falling within this parameter (Table 3).

Of the total genotypes evaluated, 21 had very high resistance (> 31 g tex^{-1}). While GOS-22 and FZ-15 showed low resistance, the rest of the genotypes had high resistance. Gourlot *et al*. (2020) note that, for spinners, fineness is crucial in predicting the spinning ability of cotton. Regarding length, GOS-17, GOS-21, GOS-27, TOA-06, TOA-11, TOA-17, TOA-18, NAZAS SELECTA, CIAN PRECOZ, and CIAN-95 had the highest values and fall into the extra-long fiber category (>1.21 mm), so they can be used for the production of very fine yarns. FZ-15 had the lowest value at 0.86 mm._Length and fineness influence yarn strength, while strength and length influence textile processing, affecting yarn quality (Yang *et al*., 2016).

Table 3. Fiber quality comparison of 28 cotton genotypes (*Gossypium hirsutum* L.) and a commercial control (DeltaPine®) evaluated in Matamoros, Coahuila, Mexico.

Genotype	FIN	LON	RES	HI	SFI	ELG	RD	UI	PLUS_B
TOA-03	4.34 o	1.10 k	31.3 h	138 k	8.69 g	5.2 ijk	79.5 j	83 kl	8 q
TOA-04	4.51 lm	1.06 lm	27.3 j	125 l	8.63 g	6.5 bcd	78.2 l	83.6 jk	8.3 n
TOA-06	4.09 p	1.25 cd	33.4 bg	173 bcd	6.86 q	5.6 h	80 i	85.8 bc	7.4 u
TOA-11	4.70 jk	1.30 j	33.2 cg	139 k	8.1 l	5.1 jk	78.7 k	82.7 l	8.3 n
TOA-12	4.45 n	1.04 n	29 i	122 l	9.57 e	6.4 cde	79.1 jk	82 m	8.2 o
TOA-17	6.51a	1.25 de	34.6 ab	175 bc	6.51 s	6.3 def	76.5 n	85.6 be	10.7a
TOA-18	6.11 c	1.25 cd	32.97 dg	169 cde	7.45 mn	4.97 k	77.7 m	84.6 ghi	10.07 d
TOA-27	4.74 ij	1.09 k	29.7 i	136 k	7.74 k	6.4 cde	77.6 m	84.7 fi	8.5 l
GOS-17	6.13 c	1.40a	32.45 fgh	178 ab	5.81 u	6.8 b	80.6 h	85.3 cf	9.05 i
GOS-21	4.75 i	1.30 b	34.7a	160 ghi	7.26 op	5 k	71.6 q	85.7 bcd	8.2 o
GOS-22	3.87 r	1.05 mn	22.5 m	99 m	14.93 b	5.4 hij	84.2 b	79.1 o	7.9 r
GOS-27	4.78 hi	1.25 cd	33.2 cg	168 def	7.89 j	5.1 jk	83.2 cd	85.3 cf	7.7 s
FZ-10	4.46 n	1.19 gh	32.6 fg	162 fgh	6.59 rs	5.5 hi	80 i	86.6a	7.9 r
FZ-13 CHAMPION	3.97 q	1.23 e	34.7a	171 cde	7.49 lm	5.5 hi	83.4 c	85.3 cf	8.1 p
FZ13 CLON	6.29 b	1.19 gh	33.3 cg	170 cde	6.61 rs	6.7 bc	78 lm	85.5 be	10.4 c
FZ-15	5.40 d	0.86 p	24.9 l	76 n	16.29a	4.5 l	70.4 r	79.5 o	10.6 b
PI-589	5.31 e	0.91 o	25.7 kl	98 m	10.55 d	6.1 ef	76 o	82.4 lm	8.4 m
P1-583 CHAPIS	4.82 h	0.92 o	26.2 jk	98 m	12.71 c	5.4 hij	73.7 p	81.1 n	9.6 f
PI-201584	4.44 n	1.07 l	33.6 a-f	147 j	7.62 kl	6.5 bcd	84.2 b	83.4 k	7.5 t
P1-873	4.36 o	1.11 k	34.4 abc	154 i	7.33 no	5.7 gh	80.2 hi	84.4 hi	7.9 r
P1-528748	4.90 g	1.1 k	29 i	137 k	7.18 p	6.3 def	82 f	85.1 dg	8.2 o
US-023	4.55 l	1.05 mn	33.3 cg	136 k	8.18 l	6 ef	76.9 n	82.6 lm	8.7 k
NAZAS SELECTA	4.48 mn	1.21 f	32.3 hg	157 hi	7.51 lm	5.6 h	82.8 de	85 eh	8.8 j
NAZAS-87A	4.45 n	1.18 h	32.9 df	155 i	8.37 h	5 k	82.5 e	82.4 lm	9 i
NAZAS-87B	3.52 s	1.19 g	33.6 af	158 hi	9.41 f	5.7 gh	84.7a	84.5 ghi	8.5 l
CIAN PRECOZ	4.47 mn	1.21 f	34.1 ae	162 fgh	8.22 i	6 fg	83.4 c	84.8 fi	8.5 l
JUÁREZ	4.47 mn	1.17 i	34.2 ad	157 hi	7.9 j	5.5 hi	82.8 de	84.2 ij	9.8 g
CIAN-95	4.67 k	1.3 b	32.7 fg	182 a	6.73 qr	5.2 ijk	81.5 g	85.9 bc	9.2 h
DELTAPINE®	5.01 f	1.16 i	33.6 af	166 efg	6.26 t	7.2 a	81.1 g	86.1 ab	9.3 g
DSH	0.044	0.016	1.29	6.44	0.141	0.305	0.498	0.615	0.061
RMSE	0.0002	0.00003	0.165	4.12	0.002	0.009	0.025	0.037	0.0004
SE	0.717	0.126	3.33	27.28	2.43	0.659	3.68	1.91	0.914

abc: Mean values per column with different letters are statistically different ($p \leq 0.05$). DSH: honest significant difference; SE: standard error; RMSE: root mean square error; FIN: fineness (micronaire index); LON: fiber length (mm); RES: strength (g tex-1); HI: spinnability index (%); SFI: short fiber index (%); ELG: elongation (%); RD: reflectance (%); UI: uniformity index (%); PLUS_B: yellow content (+b).

For the spinnability index, CIAN-95 reported the highest value with 182 %, surpassing the commercial control (166 %); FZ-15 was the genotype with the lowest value (76 %). FZ-15 had the highest short fiber index (SFI) with 16.29 % and GOS-17 the lowest SFI (5.81 %). The more automated the harvest, the more the fiber is damaged, and therefore, the shorter the fiber is. Eleven genotypes and the commercial control showed a high uniformity index, with values between 85 and 87 % according to the HVI classification. In contrast, only GOS-22 and FZ-15 had a low uniformity index (with values of 79.1 and 79.5 %). The textile industry seeks longer fibers, as this means more lint production and greater cohesion (Frazier *et al*., 2023).

Regarding elongation, DeltaPine® had the highest value, followed by GOS-17 with 7.2 and 6.8 %, respectively, while TOA-18 had the lowest value with 4.97 %. If plants lack water in the period immediately after anthesis, fiber growth, elongation, and final fiber length are strongly affected (Zhang *et al*., 2021).

For the HVI classification system, color is quantified as the degree of reflectance (Rd) and yellowness (+b). The genotypes NAZAS-87B (84.7 %) and PI-201584 (84.2 %) showed higher Rd values, while TOA-17 and FZ-15 had higher yellowness. In contrast, FZ-15 had the lowest value for Rd, with 70.4 %, and TOA-06 for yellowness. Thus, creamy white fibers are considered of higher quality compared to dull, gray, or yellowish fibers, but the application of growth regulators, frost, and drought increase the yellowness (+b) of the fiber due to premature fiber maturation (Zhu *et al*., 2024).

Relationships between fiber quality variables

Four correlations were positive and greater than 0.6. The spinnability index and uniformity index (r = 0.939) had the highest correlation, followed by the length and spinnability index (r = 0.881), length and uniformity index (r = 0.746), and fineness with yellow +b content (r = 0.708) (Table 4). These results have implications for genetic improvement since selection for a higher index of spinnability simultaneously increases the uniformity index and fiber length. In contrast, negative and highly significant ($p \leq 0.01$) correlations were found between the spinnability index and short fiber index (r =

Table 4. Correlation between fiber quality traits in 28 cotton genotypes (*Gossypium hirsutum* L.) and a commercial control (DeltaPine®) evaluated in Matamoros, Coahuila, Mexico.

	FIN	LON	RES	HI	UI	SFI	ELG	RD	PLUS_B
FIN	1								
LON	0.042	1							
RES	-0.501 **	-0.155	1						
HI	0.140	0.881 **	-0.095	1					
UI	0.119	0.746 **	-0.026	0.939 **	1				
SFI	-0.185	-0.811 **	0.106	-0.87 **	-0.752 **	1			
ELG	0.256 *	0.081	-0.308 **	0.177	0.048	-0.406 **	1		
RD	-0.470 **	0.296 **	0.369 **	0.432 **	0.419 **	-0.311 **	0.189	1	
PLUS_B	0.708 **	-0.019	-0.277 **	-0.008	-0.035	0.126	-0.005	-0.426 **	1

*$p \leq 0.05$; **$p \leq 0.01$. FIN: fineness (micronaire index); LON: fiber length (mm); RES: strength (g tex^{-1}); HI: spinnability index (%); SFI: short fiber index (%); ELG: elongation (%); RD: reflectance (%); UI: uniformity index (%); PLUS_B: yellow content +b.

-0.874), length and short fiber index (r = -0.811), and fineness with strength (r = -0.501). As the units of each variable are different, the principal component analysis (PCA) was performed using the correlation matrix. The first three components explained 81.34 % of the total variation, with 41.99, 69.03, and 81.34 %, respectively (Table 5). López and Hidalgo (1994) indicate that components whose eigenvalues explain 70 % or more of the total variance are acceptable. In PC1, the variables included were length, spinnability, short fiber index, and uniformity index. PC2 was composed of fineness, yellow +b content, reflectance, and strength, while PC3 was only composed of the elongation variable. Yehia and El-Hashash (2022) mention that the PCA analysis is very useful to evaluate the relationship and diversity among cotton collections and to know the relationships between yield, its components, and fiber quality.

Table 5. Vectors and eigenvalues of the principal component analysis (PCA) with variables with the highest descriptive value of the total variance evaluated in 28 cotton genotypes and a commercial control (DeltaPine®).

Variable	PC1	PC2	PC3
Fineness (micronaire index)	0.070	**-0.582**	-0.002
Length (mm)	**0.451**	0.000	0.263
Resistance (g tex^{-1})	-0.053	**0.447**	0.273
Spinnability index (%)	**0.492**	0.000	0.175
Short fiber index (%)	**0.473**	-0.035	0.105
Uniformity index (%)	**-0.496**	0.027	0.077
Elongation (%)	0.172	-0.125	**-0.833**
Reflectance (%)	0.214	**0.436**	-0.216
Yellow content +b (PLUS_B)	-0.045	**-0.503**	0.262
Variance explained (%)	41.99	27.03	12.31
Cumulative variance (%)	41.99	69.03	81.34

Genotype clustering according to fiber quality

According to the distribution of the 28 genotypes and the commercial control (DeltaPine®), five groups were identified (Figure 1). Group 1 consists of 14 populations, including all conventional varieties generated by INIFAP, six populations from the botanical garden, and two populations from the Chapingo germplasm bank. This group was characterized by a very strong fiber, average fineness, medium length, acceptable spinnability index, short-low fiber index, and a white fiber (reflectance).

The genotypes GOS-27, FZ-13 CLON, TOA-17, TOA-18, and the control formed Group 2 and were characterized by having a very resistant fiber, fine fineness, and average micronaire. These genotypes are good for yarn formation as they are long-fibered and have a good spinnability index. Genotypes from groups 1 and 2 can be used in crosses to obtain new combinations that can perform even better than their parents due to the

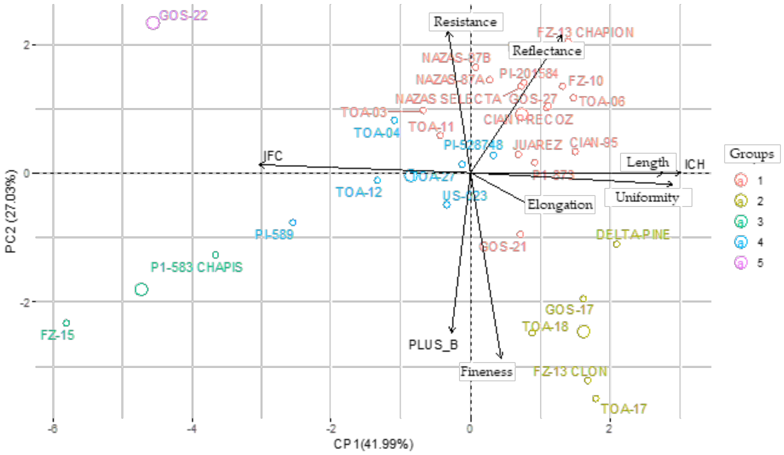

Figure 1. Dispersion of 28 native cotton (*Gossypium hirsutum* L.) and a commercial control (DeltaPine®) on the plane determined by the first two principal components, based on nine variables of the combined analysis. FIN: Fineness (micronaire index); LON: fiber length (mm); RES: strength (g tex-1); ICH: spinnability index (%); UNI: uniformity index (%); IFC: short fiber index (%); ELONG: elongation (%); REF: reflectance (%); PB: yellow content +b (PLUS_B); Rd: reflectance (%).

presence of higher fiber quality in both groups. For example, GOS-27 can be used in regional and/or national trials due to its high fiber quality, which is required by the textile industry.

Meanwhile, Group 3 consisted of genotypes P1-583 CHAPIS and FZ-15, and was characterized by medium fiber length, high strength, and low short fiber index. Genotypes US-023, TOA-04, TOA-12, TOA-27, P1-589, and PI-528748 constituted Group 4 and were characterized by weak and rough fiber strength (micronaire). Finally, Group 5 consisted only of GOS-22. This genotype was characterized by weak fiber strength, average fineness, medium length, high short fiber percentage, weak elongation, and low uniformity index. Alishah (2001) mentions that all this genetic variation can be exploited to obtain varieties with excellent yield and fiber quality.

The cluster analysis produced five groups (Figure 2) that differed in conformation from those obtained by the PCA. This difference results from the PCA only using the variables that explain PC1 and PC2 (69.03 % of the variation), whereas in the cluster analysis, all variables evaluated in the dendrogram are considered. The first two principal components played a key role in describing the main parameters contributing to variability while investigating different traits (Saeed *et al*., 2014).

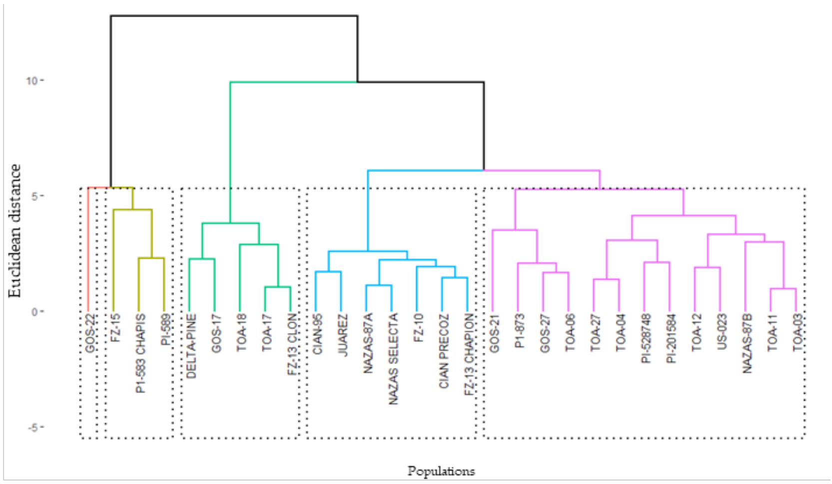

Figure 2. Dendrogram of 28 native cotton genotypes (*Gossypium hirsutum* L.) and a commercial control (DeltaPine®) based on nine variables of the combined analysis.

CONCLUSIONS

Genotypes TOA-17, TOA-18, GOS-17, GOS-27, and FZ-13 CLON showed similar characteristics to the commercial control (DeltaPine®), mainly in the fiber quality traits of fineness, length, resistance, and color (white) required by the textile industry; these genotypes could be used as a source of germplasm for the generation of new commercial varieties and hybrids. Highly significant correlations were found between fineness and strength, spinnability index and short fiber index, and length and short fiber index.

ACKNOWLEDGMENTS

To the National Institute of Forestry, Agricultural and Livestock Research (INIFAP) for financing project number 10242634878 entitled "Characterization, conservation, and regeneration of native cotton (*Gossypium*) accessions as a key phytogenetic resource for the textile industry."

REFERENCES

Alishah E. 2001. Study of morphological traits and genetic variation in different genotypes of upland cotton (*Gossypium hirsutum* L.). Iran Seed and Plant Improvement Journal 17 (1): 44–60. https://doi.org/10.22092/spij.2017.110885

DOF (Diario Oficial de la Federación). 2000. NORMA Oficial Mexicana NMX-A-051-SCFI-2000. Productos agrícolas no industrializados para uso industrial -algodón para hilar- (*Gossypium* spp.), especificaciones (cancela a la NMX-A-051-1964). Gobierno de México. Secretaría de

Economía. Ciudad de México, México. https://www.dof.gob.mx/nota_detalle.php?codigo=5659174&fecha=26/07/2022#gsc.tab=0 (Retrieved: November 2019).

FAO (Food and Agriculture Organization of the United Nations). 2021. Recent trends and prospects in the world cotton market and policy developments. Rome, Italy. 58 p. https://doi.org/10.4060/cb7232en

Frazier RM, Vivas KA, Azuaje I, Vera R, Pifano A, Forfora N, Jameel H, Ford E, Pawlaka JJ, Venditti R, Gonzalez R. 2023. Beyond cotton and polyester: An evaluation of emerging feedstocks and conversion methods for the future of fashion industry. Journal of Bioresources and Bioproducts 9 (2): 130–159. https://doi.org/10.1016/j.jobab.2024.01.001

Ge Y, Thomasson JA, Sui R, Morgan CL, Searcy SW, Parnell CB. 2008. Spatial variation of fiber quality and associated loan rate in a dryland cotton field. Precision Agriculture. 9 (4): 181–194. https://doi.org/10.1007/s11119-008-9064-2

Gourlot JP, Drieling A, Qaud M, Gordon S, Knowlton J, Matusiak M, van der Sluijs M, Martin V, Froese K, Delhom C. 2020. Interpretation and use of SITC measured characteristics. International Cotton Advisory Committee. International Textile Manufacturers Federation. Washington, DC, USA. 75 p.

Hernández-Leal E, Franco-Gaytán I, Maltos-Buendía J, Reyes-Gonzáles A. 2022. Determinación de la calidad de fibra del cultivo de algodón. Folleto Técnico No. 42. Secretaría de Agricultura y Desarrollo Rural. Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias. Matamoros, México. 39 p.

Lee JA, Fang DD. 2015. Cotton as a world crop: Origin, history, and current status. *In* Agronomy Monographs. Madison, WI, USA. 57 p. https://doi.org/10.2134/agronmonogr57.2013.0019

Li C, Dong YT, Zhao TL, Li L, Li C, Yu E, Mei L, Daud MK, He Q, Chen J, Zhu S. 2016. Genome-wide SNP linkage mapping and QTL analysis for fiber quality and yield traits in the upland cotton recombinant inbred lines population. Frontiers in Plant Science 7: 1356. https://doi.org/10.3389/fpls.2016.01356

Liu W, Song C, Ren Z, Zhang Z, Pei X, Liu Y, He K, Zhang F, Zhao J, Zhang J, *et al*. 2020. Genome-wide association study reveals the genetic basis of fiber quality traits in upland cotton (*Gossypium hirsutum* L.). BMC Plant Biology 20 (1): 395. https://doi.org/10.1186/s12870-020-02611-0

López JA, Hidalgo MD. 1994. Análisis de componentes principales y análisis factorial. *In* Ato M, López JJ. (eds.), Fundamentos de Estadística con SYSTAT. Editorial y Publicaciones: Wilmington, DE, USA. 648 p.

Ning ZY, Chen H, Mei HX, Zhang TZ. 2014. Molecular tagging of QTLs for fiber quality and yield in the upland cotton cultivar Acala-Prema. Euphytica 195 (1): 143–156. https://doi.org/10.1007/s10681–013–0990–3

Orawu M, Amoding G, Serunjogi L, Ogwang G, Ogwang C. 2017. Yield stability of cotton genotypes at three diverse agro-ecologies of Uganda. Journal of Plant Breeding and Genetics 5 (3): 101–114.

Patel JK, Patel NM, Shiyani RL. 2001. Coefficient of variation in field experiments and yardstick thereof-an empirical study. Current Science 81 (9): 1163–1164.

Pinnamaneni SR, Anapalli SS, Sui R, Bellaloui N, Reddy K. 2021. Effects of irrigation and planting geometry on cotton (*Gossypium hirsutum* L.) fiber quality and seed composition. Journal of Cotton Research 4 (2): 2–11. https://doi.org/10.1186/s42397-020-00078-w

Rohlf FJ. 2000. NTSYS. Numerical taxonomy and multivariate analysis system. Version 2.0, Exeter Publ. Setauket, NY, USA. 31 p.

Saeed F, Farooq J, Mahmood A, Riaz M, Hussain T, Majeed A. 2014 Assessment of genetic diversity for cotton leaf curl virus (CLCuD), fiber quality and some morphological traits using different statistical procedures in *Gossypium hirsutum* L. Australian Journal of Crop Science 8 (3): 442– 447.

Said JI, Knapka JA, Song M, Zhang J. 2015. Cotton QTLdb: A cotton QTL database for QTL analysis, visualization, and comparison between *Gossypium hirsutum* and *G. hirsutum* x *G. barbadense* populations. Molecular Genetics and Genomics 290 (4): 1615–1625. https://doi.org/10.1007/s00438-015-1021-y

SAS Institute. 2011. SAS/STAT® 9.3 9.3 user's guide. SAS Institute. Cary, NC, USA.

Shim J, Mangat PK, Angeles-Shim RB. 2018. Natural variation in wild *Gossypium* species as a tool to broaden the genetic base of cultivated cotton. HSOA Journal of Plant Science: Current Research 2 (1): 2–9. https://doi.org/10.24966/pscr-3743/100005

Tarragó J, Colli SL, Nadal NJ, Giménez L. 2019. Efecto de diferentes tipos de cosecha sobre la calidad tecnológica de la fibra de algodón en cultivos de alta densidad. Revista de Investigaciones Agropecuarias 45 (2): 225–233.

UNIDO (United Nations Industrial Development Organization). 2023. World Cotton Day 2023. Making cotton fair and sustainable for all, from farm to fashion. Vienna, Austria. 70 p.

Witt TW, Ulloa M, Schwartz RC, Ritchie GL. 2020. Response to deficit irrigation of morphological, yield and fiber quality traits of upland (*Gossypium hirsutum* L.) and Pima (*G. barbadense* L.) cotton in the Texas High Plains. Field Crops Research 249: 107759. https://doi.org/10.1016/j.fcr.2020.107759

Yang H, Zhang D, Li X, Li H, Zhang D, Lan H, Wood AJ, Wang J. 2016. Overexpression of *ScALDH21* gene in cotton improves drought tolerance and growth in greenhouse and field conditions. Molecular Breeding 36 (3). https://doi.org/10.1007/s11032-015-0422-2

Yehia WMB, El-Hashash EF. 2022. Estimates of genetic parameters for cotton yield, its components, and fiber quality traits based on line x tester mating design and principal component analysis. Egyptian Journal of Agricultural Research 100 (3): 302—315. https://doi.org/10.21608/ejar.2022.134192.1228

Zhang T, Hu Y, Jiang W, Fang L, Guan X, Chen J, Zhang J, Saski CA, Scheffler BE, Stelly DM. 2015. Sequencing of allotetraploid cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology 33 (5): 531–537. https://doi.org/10.1038/nbt.3207

Zhang Y, Liu G, Dong H, Li C. 2021. Waterlogging stress in cotton: Damage, adaptability, alleviation strategies, and mechanisms. The Crop Journal 9 (2): 257–270. https://doi.org/10.1016/j.cj.2020.08.005

Zhao Z, Liu Z, Zhou Y, Wang J, Zhang Y, Yu X, Wu R, Guo C, Qin A, Bawa G, Sun X. 2022. Creation of cotton mutant library based on linear electron accelerator radiation mutation. Biochemistry and Biophysics Reports 30: 101228. https://doi.org/10.1016/j.bbrep.2022.101228

Zheng Z, Xie S, Dai HN, Chen X, Wang H. 2018. Blockchain challenges and opportunities: A survey. International Journal of Web and Grid Services 14 (4): 352–375. https://doi.org/10.1504/ijwgs.2018.095647

Zhu H, Hu W, Li Y, Zou J, He J, Wang Y, Meng Y, Chen B, Zhao W, Wang S, Zhou Z. 2024. Drought decreases cotton fiber strength by altering sucrose flow route. Journal of Experimental Botany 75 (11): 3579–3595. https://doi.org/10.1093/jxb/erae108