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Potential of ten wild diploid cotton species for the improvement of fiber fineness of upland cotton through interspecific hybridization

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Cotton is the highest source of natural fiber in textile industry worldwide. With the modern spinning technologies, the demand for cotton fiber with higher quality has increased, making the genetic improvement of fiber quality one of the main challenges for cotton breeders. In cotton breeding, wild species are important source of several desirable genes for genetic improvement of the main cultivated cotton *Gossypium hirsutum* L (Upland cotton). Besides length and strength, fineness is one of the most important criteria associated with cotton fiber quality. In this study, ten wild diploid species of cotton were investigated for their fiber fineness and potential to improve fiber fineness of *G. hirsutum* L. The method was measuring of ribbon width after caustic swelling. The results showed the potential of four wild species (*G. longicalyx* Hutch. & Lee, *G. anomalum* Wawra & Peyr., *G. thurberi* Todaro and *G. stocksii* Mast.) to significantly improve the fiber fineness of upland cotton in a hybrid configuration. Among them, *G. longicalyx* stood out for its exceptional fiber fineness, and its remarkable impact on reducing the fiber fineness of *G. hirsutum* L. The wild species highlighted in this study constitute an interesting genetic resource for the development of upland cotton varieties with improved fiber fineness.

Key words: Cotton, fiber fineness, *Gossypium* spp, hybrid, plant breeding, tetraploid species, wild diploid species.

INTRODUCTION

Cotton fiber is the major commercial product from cotton and the most widely used natural fiber in the world's textile industry (Ayubov et al., 2018). This important fiber crop belongs to the genus *Gossypium* which includes 46 diploid (2n = 2× = 26) and 7 tetraploid (2n = 4× = 52) species (Fang et al., 2017). All the diploid *Gossypium* species originated from a common ancestor and diversified into eight genome groups from A to G, and K (Wu et al., 2018). All tetraploid cotton species are allotetraploid and have a genome designated by AD; they come from a natural hybridization event between an A-genome species and a D-genome species, followed by a doubling of the chromosome number 1 to 2 million years ago (Wendel and Grover, 2015; Fang et al., 2017).

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Among the 53 *Gossypium* species, only four species including two diploids (*G. arboreum* L and *G. herbaceum* L) and two tetraploids (*G. hirsutum* L and *G. barbadense* L) are cultivated for their spinnable fibre (Gallagher et al., 2017; Wang et al., 2018; Ijaz et al., 2019). The remaining 46 species are wild.

G. hirsutum L, which is also known as Upland cotton, Long Staple cotton or Mexican cotton, is extensively cultivated due to its wide adaptability to the environment, high production, and better yield potential. It fulfils over 90 % of the output of global cotton fiber yield (Shim et al., 2018; Konan and Mergeai, 2020). *G. barbadense* L, otherwise known as Sea Island cotton, Pima cotton or Egyptian cotton, is known for excellent fiber quality with long, strong, and fine fibers (Avci et al., 2013). It contributes to 8% of the global cotton production (Shim et al., 2018). The cultivated diploid species provide approximately 2% of the world's cotton and are cultivated in the more traditional growing areas of India, Pakistan, China, Bangladesh and Iran (Kulkarni et al., 2009, Wendel et al., 2010; Shim et al., 2018).

Based on genetic hybridization properties, *Gossypium* species are grouped into the primary, secondary and tertiary gene pools. Both the cultivated (*G. hirsutum* L and *G. barbadense* L) and wild allotetraploids (*G. tomentosum* Nuttall ex Seemann*, G. mustelinum* Miers ex Watt and *G. darwinii* Watt) comprise the primary gene pool of cotton. The secondary gene pool includes the diploids having the A, B, D and F genomes, whereas the tertiary gene pool is composed of species with C, E, G and K genomes (Campbell et al., 2010).

Previously, cotton breeders primarily emphasized yield and agronomic characteristics, but with the recent development of high-speed spinning technologies, the demand for cotton fiber with higher quality has increased, making the improvement of fiber quality highly crucial in Upland cotton (Islam et al., 2016; Shang et al., 2016; Ayubov et al., 2018). Faced with this existing demand and the dynamics of modern textile industry, the perpetual need of genetic improvement in fiber quality is one of the main challenges for cotton breeders today. Biologically, cotton fibers are single-celled trichomes that grow from the epidermal cell layer of the ovule in a boll (Miao et al., 2017; Ayubov et al., 2018; Ijaz et al., 2019). Besides the length and the strength, the fineness is one of the most important criteria associated to cotton fiber quality (Bradow and Davidonis, 2000; Konan and Mergeai, 2020).The fineness of mature fiber is critical for fiber processing. It influences the fabric lustre, dye appearance, fabric stiffness, spinning performance, and yarn strength (Rodgers and Thibodeaux, 2012). The better the fineness of cotton, the more would be the number of fibers per cross-section. This would result in higher yarn strength, which improves spinning efficiency and yarn evenness (Ahmad et al. 2003; Islam et al., 2016).

Cotton fiber fineness can be expressed as the perimeter, diameter or ribbon width (RW), cross sectional area, and standard fiber weight (Rodgers and Thibodeaux, 2012). The indirect methods used for its measurements are Advanced Fibre Information System (AFIS), Fibre Maturity Tester (FMT), and Near Infrared (NIR) spectroscopy, Vibroscope, High Volume Instrument (HVI) for micronaire etc; the most common direct measurements of fiber fineness include cross-sectional image analysis and ribbon width measurement after caustic swelling (Rodgers and Thibodeaux, 2012). The most effective way to improve cotton fiber fineness is through breeding (Nacoulima and Mergeai, 2014; Islam et al., 2016).

Previous progress in the improvement of fiber quality of upland cotton has been mainly achieved using the genetic diversity present in the primary gene pool of cotton (especially *G. barbadense* L), but currently, this available diversity has been exhaustively utilized (Gotmare et al., 2000; Ayubov et al., 2018). Accordingly, it has become a necessity to exploit useful genes of wild species from the two other gene pools. Indeed, in cotton breeding, wild species constitute an important resource with several useful traits which can be introgressed into the main cultivated species for improvement (Konan and Mergeai, 2020). The objective of the present study is to detect donor parents for fiber fineness by determining the fiber fineness of a collection of wild diploid species using ribbon width measurement and evaluating their potential to improve fiber fineness of upland cotton through interspecific hybridization.

MATERIALS AND METHODS

Plant material

The plant material included plants from the living cotton collection of the Laboratory of Tropical Agro ecology of Gembloux Agro-Bio Tech (Liège University, Belgium). It was composed of eleven diploid cotton species, their bi-species hybrid with *G. hirsutum*L, one cultivar of the tetraploid species *G. barbadense* L, four cultivars of the tetraploid species *G. hirsutum* L and fifteen second back-cross (BC2) progenies of the HTL tri-species hybrid (*G. hirsutum* L × *G. thurberi* Todaro)² × *G. longicalyx* Hutch. & Lee (Table 1). The crossing scheme used to generate the bi-species hybrid and the BC2 progenies of the HTL tri-species hybrid are presented in Figures 1 and 2, respectively. The crossing procedures used are presented in detail by Konan et al. (2007) and Konan and Mergeai (2020). The plants were maintained in a ventilated greenhouse where the growing conditions during capsule maturation period were 55-60% relative humidity and 35-26°C day-night air temperatures. The plants were grown in 5 L pots filled with a 3:2:1 (v:v:v) sterile mixture of compost, sand and peat. Cotton fibers were harvested at full maturity and used for the analysis of their fineness.

Fiber fineness analysis

Fiber fineness analysis was conducted on all the genotypes studied. For this analysis, the fibers were combed and a tuft of parallel fibers was cut from the seed. Their free points were also cut and the median region was placed on a slide and covered with a cover glass.

Table 1. Presentation of the genotype, genome and status of the plant material used in the study.

Genotype	Genome	Status (distribution)
G. anomalum Wawra & Peyr.	B_1B_1	Wild diploid species (Africa)
G. sturtianum (R.Br.) J. H. Willis	C_1C_1	Wild diploid species (Australia)
G. armourianum Kearney	$D_{2\text{-}1}D_{2\text{-}1}$	Wild diploid species (America)
G. harknessii Brandegee	$D_{2\text{-}2}D_{2\text{-}2}$	Wild diploid species (America)
G. aridum (Rose &Standl.) Skovst.	D_4D_4	Wild diploid species (America)
G. raimondii Ulbr.	D_5D_5	Wild diploid species (America)
G. stocksii Mast.	E_1E_1	Wild diploid species (Arabia)
G. areysianum Deflers	E_3E_3	Wild diploid species (Arabia)
G. thurberi Todaro	D_1D_1	Wild diploid species (America)
G. longicalyx Hutch. & Lee	F_1F_1	Wild diploid species (Africa)
G. arboretum L.	A_2A_2	Cultivated diploid species (Indo-Burma, China and Arab)
G. hirsutum L. (cv. C2)	$(A_hA_hD_hD_h)$	Cultivated tetraploid species
G. hirsutum L. (cv. NC8)	$(A_hA_hD_hD_h)$	Cultivated tetraploid species
G. hirsutum L. (cv. 98M-2983)	$(A_hA_hD_hD_h)$	Cultivated tetraploid species
G. hirsutum L. (cv. 11240-RNR)	$(A_hA_hD_hD_h)$	Cultivated tetraploid species
G. barbadense L. (cv. 353)	$(A_bA_bD_bD_b)$	Cultivated tetraploid species
(*G. hirsutum* cv. C2 × *G. arboreum*)²	$2(A_hD_hA_2)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. anomalum*)²	$2(A_hD_hB_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. sturtianum*)²	$2(A_hD_hC_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. NC8 × *G. australe*)²	$2(A_hD_hC_3)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. harknessii*)²	$2(A_hD_hD_{2\text{-}2})$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. NC8 × *G. aridum*)²	$2(A_hD_hD_4)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. raimondii*)²	$2(A_hD_hD_5)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. NC8 × *G. stocksii*)²	$2(A_hD_hE_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. NC8 × *G. areysianum*)²	$2(A_hD_hE_3)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. thurberi*)²	$2(A_hD_hD_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. longicalyx*)²	$2(A_hD_hF_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. thurberi*)² x *G. longicalyx*	$A_hF_1D_hD_1$	Tri-species tretraploid hybrid
(*G. hirsutum* cv. C2 × *G. thurberi*)² x *G. longicalyx* BC2	$A_hF_1D_hD_1$	Tri-species tretraploid BC2 hybrid

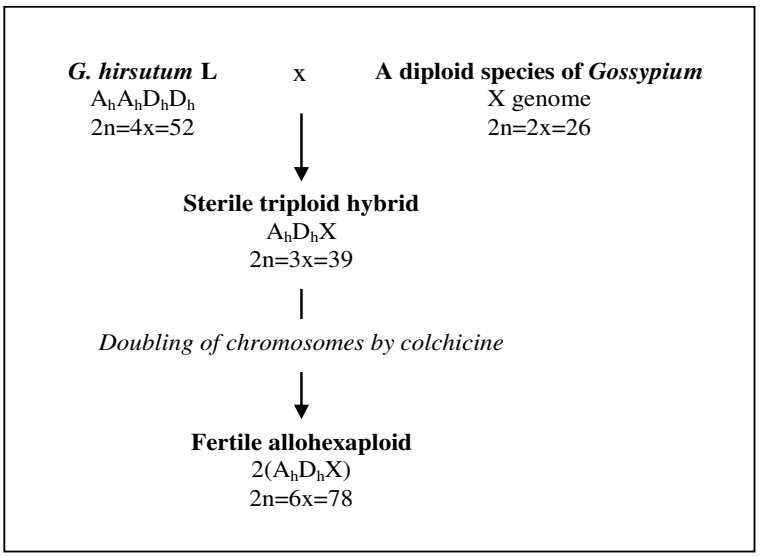

Figure 1. Development scheme of the bi-species hexaploid hybrids. "X" represents a diploid genome (A, B, C, D, E, F, G or K).

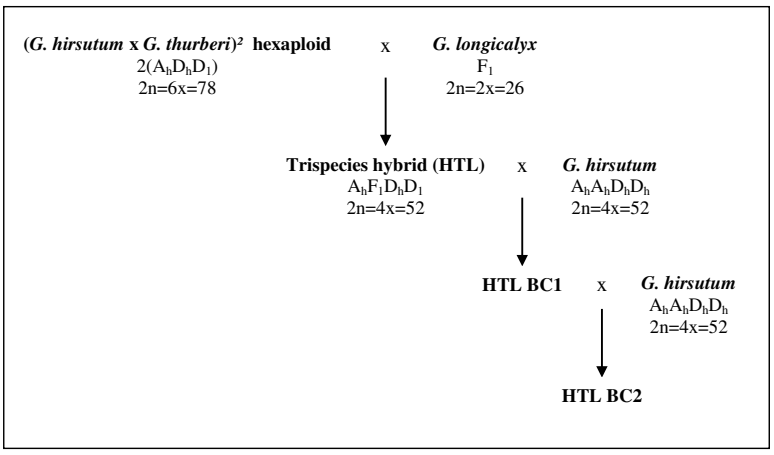

Figure 2. Development scheme of the tri-species BC2 hybrids.

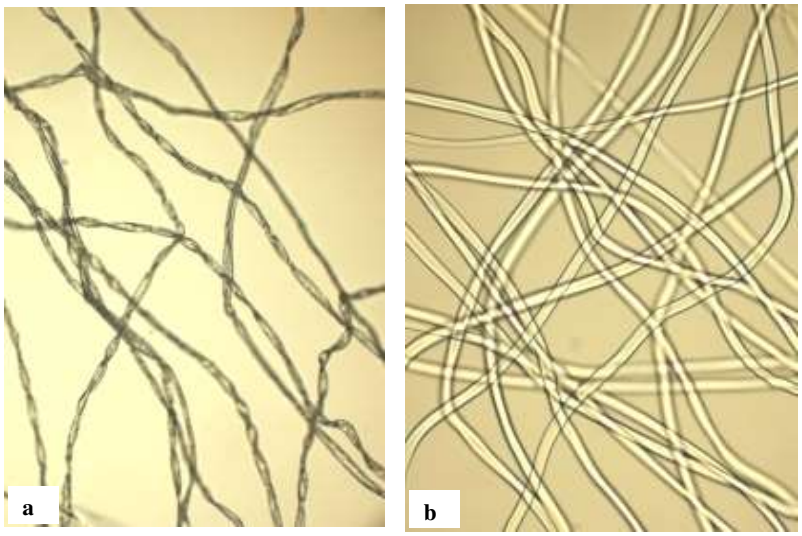

Figure 3. Swelling of cotton fibers after a treatment with 18% NaOH solution: (a) appearance of the fibers before treatment; (b) fibers swollen after treatment (x 200).

One or two drops of 18% NaOH solution was allowed to penetrate into the fibers by capillarity. The NaOH solution swells the fibers (Figure 3). The diameter of at least 100 fibers was then measured with the software NIS-Elements BR 2.30 (Nikon, Japan) using the Nikon Eclipse E800 microscope (Nikon, Tokyo, Japan) equipped with a digital JVC KY-F 58E camera (JVC, Yokohama, Japan). The ribbon width was determined by dividing the mean of the diameters measured by the 1.3 Summers coefficient (Roehrich, 1947; Nacoulima et al., 2016; Konan and Mergeai, 2020).

Statistical analysis

All the data collected were subjected to the analysis of variance (ANOVA) using the software Statistica 7.1 (Stat Soft, France). The least significant difference (LSD) was used to establish the differences between means at P=0.05.

RESULTS AND DISCUSSION

Analysis of fiber fineness of studied diploid and tetraploid cotton species

The results of the analysis of fiber fineness for the studied diploid and tetraploid cotton species are presented in Table 2. The ribbon width of the ten wild diploid species varied from 5.940 µm (*G. longicalyx* Hutch. & Lee) to 15.533 µm (*G. thurberi* Todaro), while that of the cultivated species ranged from 17.765 µm (*G. hirsutum* L cv. C2) to 24.374 µm (*G. arboretum* L). All the wild diploid species had finer fibers than the cultivated species. Their fibers were even finer than the Sea Island cotton (*G. barbadense* L), which is known for its fine

Table 2. Ribbon width of the diploid and tetraploid cotton species studied.

Genotype	Number of fiber analysed	Ribbon widh (µm) ± standard deviation	Min	Max	LSD grouping
G. anomalum	104	6.128 ±0.210	3.738	9.138	A
G. sturtianum	71	10.907 ±0.255	6.877	18.700	D
G. armourianum	102	13.967 ±0.212	7.769	20.438	F
G. harknessii	104	7.772 ±0.210	4.662	12.369	B
G. aridum	100	11.013 ±0.215	7.123	15.931	D
G. raimondii	110	8.570 ±0.205	5.592	11.585	C
G. stocksii	101	11.706 ±0.213	6.069	14.562	E
G. areysianum	102	13.786 ±0.212	7.685	20.085	F
G. thurberi	83	15.533 ±0.235	9.054	21.938	G
G. longicalyx	113	5.940 ±0.202	4.254	8.862	A
G. arboreum	107	24.374 ±0.207	16.338	37.308	K
G. hirsutum (cv. C2)	107	17.765 ±0.207	12.092	24.369	H
G. hirsutum (cv. NC8)	116	18.294 ±0.199	13.885	24.169	H
G. hirsutum (cv. 98M)	114	19.445 ±0.201	13.885	25.785	I
G. hirsutum (cv. 11240)	112	20.036 ±0.203	13.423	25.015	J
G. barbadense (cv. 353)	110	19.117 ±0.205	12.938	26.638	I

fibers (Avci et al., 2013; Ijaz et al., 2019). Regarding the LSD grouping, the finest fibers among the studied wild diploid species were given by *G. longicalyx* Hutch. & Lee (5.940 µm) and *G. anomalum* Wawra & Peyr.(6.128 µm), followed by *G. harknessii* Brandegee (7.772 µm) and *G. raimondii* Ulbr.(8.570 µm). The other wild diploid species presented values of ribbon width ranging from 10.907 to 15.533 10 µm. The very low ribbon width exhibited by the African wild diploid species *G. longicalyx* Hutch. & Lee underlines its potential to improve fiber fineness (Demol et al., 1978; Nacoulima et al., 2016; Konan et al., 2020). The results also highlighted another African wild species, *G. anomalum* Wawra & Peyr., which presented good fiber fineness close to that of *G. longicalyx* Hutch. & Lee, with no significant difference. The good fiber fineness of *G. anomalum* Wawra & Peyr. has also been reported by Mehetre (2010). The American wild species *G. harknessii* showed finer fiber than *G. raimondii* Ulbr, but it is rarely cited as a good source of fiber fineness like *G. raimondii* Ulbr (Gotmare et al., 2000; Islam et al., 2016).*G. harknessii* Brandegee is most often cited for its resistance to Verticillium wilt and Fusarium wilt, and as source of cytoplasmic male sterility and fertility restorer (Ano et al., 1982; Gotmare et al., 2000).

Among the cultivated species, the Upland cotton varieties *G. hirsutum* L (cv. C2) and *G. hirsutum* L (cv. NC8) had the finest fibers with 17.765 and 18.294 µm ribbon width respectively; while *G. barbadense* L presented a ribbon width of 19.117 µm. Although *G. barbadense* L is recognized as having finer fiber than Upland cotton (Avci et al., 2013), the present results showed finer fibers for these two varieties of *G. hirsutum* L. Actually, several varieties of upland cotton resulting from breeding programs for fiber quality have gained in fiber fineness comparable to that of *G. barbadense* L; this is the case for these two varieties of *G. hirsutum* L (cv. C2 and cv. NC8) in the present study.

Of the results presented in Table 2, the cultivated diploid species *G. arboreum* L had the highest ribbon width value. This result showed that not all diploid species produce fine fibers, even if all the other (wild) diploid species studied had finer fibers than the tetraploid cotton studied. It again stresses that wild diploid species can be a source of desirable genes for the genetic improvement of cultivated cotton (Konan and Mergeai, 2020).

Analysis of fiber fineness of the bi-species hexaploid hybrids

To evaluate the influence of the studied diploid genomes on the fiber fineness of upland cotton, hybrids including each of these genomes and genome of *G. hirsutum* L cv C2 or cv NC8 were examined for their fiber fineness. The results of this analysis are shown in Table 3. The mean values of ribbon width of the different hybrid ranged from 12.526 to 26.072 µm. The bi-species hexaploid hybrid (*G. hirsutum* L cv. C2 × *G. longicalyx* Hutch. & Lee)² showed the finest fibers with a mean value of ribbon width of 12.526 µm. It was followed by (*G. hirsutum* L cv. C2 × *G. anomalum* Wawra&Peyr)² with on average 15.833 µm of ribbon width, and then (*G. hirsutum* L cv. C2 × *G. thurberi* Todaro)² and (*G. hirsutum* L cv. NC8 x *G. stocksii* Mast.)² with mean value of 16.835 and 16.852 µm of ribbon width, respectively. The highest value of ribbon width

Table 3. Ribbon width of the bi-species hexaploid and tri-species hybrids studied.

Genotype	Number of fiber analysed	Ribbon widh (µm) ± standard deviation	Min	Max	LSD grouping
(*G. hirsutum* cv. C2 × *G. arboreum*)²	100	22.306 ±0.199	15.615	27.646	H
(*G. hirsutum* cv. C2 × *G. anomalum*)²	110	15.833 ±0.190	11.331	20.523	B
(*G. hirsutum* cv. C2 × *G. sturtianum*)²	106	19.499 ±0.193	12.538	26.338	F
(*G. hirsutum* cv. NC8 × *G. australe*)²	112	26.072 ±0.188	19.877	33.046	J
(*G. hirsutum* cv. C2 × *G. harknessii*)²	116	20.204 ±0.185	14.415	25.446	G
(*G. hirsutum* cv. NC8 × *G. aridum*)²	104	18.183 ±0.195	14.462	21.915	D
(*G. hirsutum* cv. C2 × *G. raimondii*)²	104	18.853 ±0.195	14.415	22.077	E
(*G. hirsutum* cv. NC8 × *G. stocksii*)²	103	16.852 ±0.196	12.069	20.977	C
(*G. hirsutum* cv. NC8 × *G. areysianum*)²	107	22.937 ±0.192	16.500	28.438	I
(*G. hirsutum* cv. C2 × *G. thurberi*)²	117	16.835 ±0.184	12.215	23.208	C
(*G. hirsutum* cv. C2 × *G. longicalyx*)²	122	12.526 ±0.180	8.946	16.008	A
(*G. hirsutum* cv. C2 × *G. thurberi*)²x *G. longicalyx* (HTL)	120	12.649 ±0.182	10.008	15.277	A

was presented by the bi-species hybrid (*G. hirsutum* L cv. NC8 × *G. austral* F.Muell.)². As for the diploid species where *G. longicalyx* Hutch. & Lee and *G. anomalum* Wawra & Peyr had the smallest ribbon width, it was the hexaploid hybrids which contained genomes of *G. longicalyx* Hutch. & Lee or *G. anomalum* Wawra&Peyr which showed the smallest ribbon width. However, the hexaploid hybrid including *G. longicalyx* produced significantly finer fibers than the hybrid including *G. anomalum* Wawra & Peyr. This result indicates the greater impact of the F_1 genome of *G. longicalyx* Hutch. & Lee in the improvement of fiber fineness of upland cotton than the B_1 genome of *G. anomalum* Wawra & Peyr. The results also showed that the D_1 genome of *G. thurberi* Todaroand E_1 genome of *G. stocksii* Mast.reduced the fiber fineness of *G. hirsutum* L as well, but not as much as *G. longicalyx* Hutch. & Lee and *G. anomalum* Wawra & Peyr.

Apart from the four wild diploid species *G. longicalyx* Hutch.& Lee, *G. anomalum* Wawra & Peyr, *G. thurberi* Todaro and *G. stocksii* Mast, all the other diploid species did not bring an interesting improvement in fiber fineness of *G. hirsutum*L. Even some wild diploid species such as *G. harknessii* Brandegee (genome E3) and *G. raimondii*Ulbr. (genome D5) which had good fiber fineness (ribbon width <10 µm) could not reduce the ribbon width of *G. hirsutum* L when combined to it in bi-species hybrids. These results suggest that the genes that control the fineness of the fibers in the different wild diploid species did not have the same action when they are confronted with the genome of upland cotton in a hybrid configuration. The diameter of the cotton fiber is primarily a genetic trait and the genetic mechanisms of fiber traits are complex (Matic-Leigh and Cauthen, 1994; Bradow and Davidonis, 2000; Zhang et al., 2013; Islam et al., 2016). According to Ijaz et al. (2019), cotton fiber quality traits are controlled by multiple genes (polygenic inheritance) with different mechanisms and complex genetic architecture. For instance, in the past decades, studies on cotton fiber quality traits on *G. hirsutum* L and *G. barbadense* L found a significant association between SSRs and fiber quality traits and identified 70 stable loci for target traits including 30 for fiber length, 27 for fiber strength, and 13 for fiber fineness (Zeng et al., 2009; Cai et al., 2014). Later, several studies, on cotton fiber quality traits that focused on both *G. hirsutum*L and *G. hirsutum* L×*G. barbadense*L populations, have mapped fiber QTLs in large genomic regions that may include hundreds or thousands of genes (Said et al., 2013; Fang et al., 2014; Shang et al., 2015; Tang et al., 2015; Tan et al., 2015; Ma et al., 2017, 2018; Ijaz et al., 2019). QTLs are chromosomal regions which contribute cumulatively to a trait with varying percentages of phenotypic variance from each QTL (Said et al., 2015). According to Ijaz et al. (2019),the number of fiber quality trait QTLs over the chromosomes of the cotton genome is not identical, and QTLs associated with cotton fiber quality obtained from Cotton QTL database (http://www.cottonqtldb. org) are distributed unevenly across the 26 chromosomes of the cotton genome.

Analysis of fiber fineness of the tri-species hybrid and its BC2 progenies

The HTL tri-species hybrid (*G. hirsutum* L × *G. thurberi* Todaro)² × *G. longicalyx* Hutch. & Lee (Konan et al., 2007) with a ribbon width of 12.65 µm (Table 3) had the same fiber fineness as *G. hirsutum*L × *G. longiclayx* Hutch. & Lee² hexaploid hybrid (P>0.05).To check the behavior of the genes of *G. longicalyx* Hutch. & Lee responsible for the fiber fineness in the advanced progenies of the tri-species hybrid, HTL/BC2 plants were examined for the fineness of their fibers. The results of

Table 4. Ribbon width of the BC2 progenies of the HTL tri-species hybrid.

Genotype	Number of fiber analysed	Ribbon widh (µm) ± standard deviation	Min	Max	LSD grouping
HTLBC2#1	102	15.332 ±0.171	10.262	20.977	C
HTLBC2#3	110	14.906 ±0.165	10.331	19.554	BC
HTLBC2#9	110	17.388 ±0.165	10.877	21.754	I
HTLBC2#11	102	14.650 ±0.171	11.331	18.292	B
HTLBC2#14	101	16.842 ±0.172	13.692	20.523	GH
HTLBC2#15	100	16.519 ±0.173	12.008	23.838	FG
HTLBC2#17	101	16.931 ±0.172	11.331	21.385	GHI
HTLBC2#18	103	15.977 ±0.171	12.538	20.415	DE
HTLBC2#5	116	13.922 ±0.161	10.723	17.154	A
HTLBC2#6	121	16.356 ±0.157	11.808	20.692	EF
HTLBC2#7	111	13.473 ±0.164	8.038	16.654	A
HTLBC2#10	112	15.876 ±0.164	12.008	22.077	D
HTLBC2#13	122	15.328 ±0.157	9.885	20.523	C
HTLBC2#16	117	17.024 ±0.160	13.400	20.962	HI
HTLBC2#20	109	16.757 ±0.166	10.238	23.154	FGH

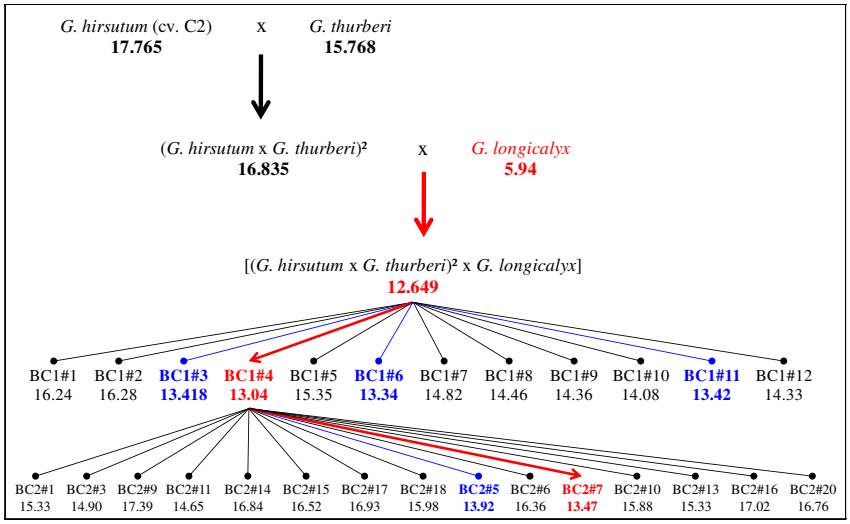

Figure 4. Ribbon width (µm) of parental species and the BC1 and BC2 progenies of the HTL tri-species hybrid. Ribbon width values of the BC1 plants come from the study of Konan et al. (2020).

this analysis are presented in Table 4. The ribbon width of the BC2 plants varied from 13,473 to 17,388 µm. The finest fibers were presented by BC2#7 and BC2#5 with 13.473 µm and 13.922 respectively, while the other BC2 plants had a ribbon width varying from 14.650 to 17.388 µm. These results show the presence of fiber fineness segregation among BC2 plants. Konan and Mergeai (2020), working on twelve BC1 progenies of the tri-species hybrid HTL, reported ribbon width ranging from 13.039 to 16.276 µm with four BC1 plants having the lowest ribbon width (13.039 – 13.416 µm). This fiber fineness segregation among the HTL/BC plants may be due to the segregation of *G. longicalyx* alleles among the BC plants. This suggests the differential presence or absence of this diploid species chromosomes and/or chromosome recombinants as shown by Konan and Mergeai (2020) with genomic *in situ* hybridization (GISH) analysis. The persistence of the outstanding fiber fineness of *G. longicalyx* Hutch. & Lee, in the bi-species hybrid with *G. hirsutum* L, in the HTL tri-species hybrid and in the HTL/BC1 and BC2 derivative plants demonstrates the inheritance of this trait through the crossing scheme (Figure 4). Hence, this finding brings out the good donor status of *G. longicalyx* Hutch. & Lee

for fiber fineness.In addition, according to Demol et al. (1978), the fibers of *G. longicalyx* Hutch. & Lee have exceptional fiber strength and a high molecular weight. Such finer and stronger fibers than those of *G. barbadense* L would undoubtedly be much appreciated by spinners. These results therefore make *G. longicalyx* Hutch. & Lee an interesting source that deserves more attention from breeders for the improvement of cotton fiber quality

Conclusion

The results obtained in the present study show the potential of four wild cotton diploid species (*G. longicalyx* Hutch. & Lee, *G. anomalum* Wawra & Peyr., *G. thurberi* Todaro and *G. stocksii* Mast.) to significantly improve the fineness of the fibers of upland cotton in a hybrid configuration. However, among these wild species, *G. longicalyx* Hutch. & Lee stood out for its exceptional fiber fineness, and its remarkable impact on improving the fiber fineness of *G. hirsutum* L. This wild African diploid species seems to be a good donor for the introgression of this useful trait into upland cotton. In view of the results of this study, the species *G. longicalyx*, and to a lesser extent the three other highlighted wild species, constitute interesting genetic resources for the development of cotton varieties with outstanding fiber fineness.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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