Article

Diallel Crosses of Cotton (*Gossypium hirsutum* L.) from Burkina Faso and Texas A&M AgriLife Research—1-Analysis of Agronomic Traits to Improve Elite Varieties from Burkina Faso

Larbouga Bourgou [1],*, Jane K. Dever [2],* , Monica Sheehan [2], Carol M. Kelly [2], Sidiki K. Diané [1] and Mahamadou Sawadogo [3]

[1] INERA/Programme Coton, Bobo-Dioulasso 01 BP 208, Burkina Faso; dianeksidiki@yahoo.fr
[2] Texas A&M AgriLife Research, 1102 East Drew, Lubbock, TX 79403, USA; mabellow@ag.tamu.edu (M.S.); cmkelly@ag.tamu.edu (C.M.K.)
[3] Laboratoire de Génétique et Amélioration des Plantes, Département de Biologie Végétale & Phyiologie Végétale, Université Ouaga 1 Joseph Ki-Zerbo, Ouagadougou 09 BP 848, Burkina Faso; sawadogomahamadou@yahoo.fr
* Correspondence: diallabourgou@yahoo.fr (L.B.); jdever@ag.tamu.edu (J.K.D.)

Abstract: Cotton breeding progress stagnation, changing production conditions, and continued high fiber quality demands are challenging the cotton industry in Burkina Faso. The F_1 populations developed by half diallel crosses between germplasm from Texas A&M AgriLife Research and Burkina Faso were evaluated for several agronomic traits. The aim was to identify the most promising parents and hybrids for further varietal improvement. Three AgriLife parents helped improve the most important targeted traits. Parent 15-3-416 reduced days to 50% flowering (-3.14 days) and shortened plant height (-22.25 cm) in hybrids while 16-2-216FQ improved their fiber percentage ($+2.68\%$). Hybrids with Burkina Faso elite cultivar E32 as male parent and the three best AgriLife parents as the females showed good specific combining ability (SCA). FK37 × 15-10-610-7 and FK64 × 15-10-610-7 showed heterosis for earliness by reducing, respectively, days to 50% flowering (-4.27 days) or days to 50% boll opening (-3.95 days) below parent means. E32 × 16-2-216FQ and FK64 × 16-2-216FQ increased fiber percentage by $+1.75\%$ and $+2.06\%$, respectively. FK64 × 15-3-416 increased seed index (SI) ($+0.62$ g) and fiber percentage ($+1.19\%$), while maintaining other traits at the parents' average levels. E32 × 15-3-416 showed the most heterosis for desired improvements, reducing days to 50% flowering (-4) and increasing the number of bolls/vegetative branch ($+3.05$), number of bolls/fruiting branch ($+6.38$), number of bolls/plant ($+13.49$), boll weight ($+1.53$ g), SI ($+0.40$ g), and fiber percentage ($+1.18\%$). Inter-program crosses show the potential to enhance genetic diversity in Burkina Faso's breeding program. Subsequent selection methods must be carefully applied considering the Burkina Faso breeding objectives for future cultivars.

Keywords: half diallel; combining ability; F_1 hybrids; earliness components; architectural traits; production components

1. Introduction

Cotton is a strategic commodity of capital importance for countries and farmers in West Africa. Its production and productivity have generally been low in these countries due to climatic variations, decreasing soil fertility, biotic stress, and poor crop management by farmers [1].

Breeding progress has greatly decreased in recent years, nearly leading to an obsolescence of cultivated varieties. In general, African varieties are agronomically and architecturally tall, vegetative, and late flowering with unstable productivity [2]. Furthermore, water scarcity due to increased climatic variation prevents late-maturing varieties to reach their yield and fiber quality potential. In addition to these environmental and

global climate changes, the industry faces the rising demand for mechanization of cotton production and new emerging diseases and pest insects, for which African varieties are lacking resistance [3].

All national efforts in Burkina Faso are focused on creating cultivars responding to the current agronomic needs and fiber quality demanded by the textile industry. The improved varieties are expected to be short, early maturing (short production cycle), and tolerant to water stress. These varieties must also have less vegetative branches and more fruiting branches with more boll production. However, they must conserve the intrinsic good fiber percentage and fiber property values known to African cottons. Moreover, prospective varieties must be well adapted to the beginning of the mechanization process and to the initiative of the organic cotton production mode led by women. To achieve such objectives, it is possible to combine desirable alleles from diverse germplasm through recombination to develop single superior genotypes [4].

Investigations were conducted with new germplasm introduced from Brazil, but results indicated that they were not suitable for direct cultivation, and further research to use them as parents in crosses was not completed or allowed [5,6]. A collection of germplasm established via local cotton seed acquisition and different investigations by Bourgou et al. [7,8] highlighted potential good material to include in a breeding program. An International Borlaug Fellowship offered an opportunity to partner with Texas A&M AgriLife Research in the United States to develop breeding populations by crossing breeding lines developed at Texas A&M AgriLife Research in Lubbock (LREC) with Burkina Faso cultivars and investigating the potential for the development of future conventional and organic cultivars. At the beginning of cotton production in Africa, American cotton germplasm was exploited and resulted in successful breeding or germplasm enhancement [9]. In this study, we evaluate if modern and enhanced American germplasm may address the current cultivar development needs in Burkina Faso.

To develop genetic populations and new cultivars through their progenies, it is desirable to understand the inheritance of agronomically important traits using a diallel crossing scheme [10]. A diallel mating system has been used and documented in multiple allogamous and autogamous crops, including cotton [11–13]. A half diallel consists of performing all possible combination crosses among parent candidates in one direction only (no reciprocal crosses) to develop multiple hybrid populations [11,12,14]. The use of the half diallel as well as the full diallel (direct and reciprocal crosses) in cotton to evaluate agronomic and fiber properties is based on the analysis of general combining ability (GCA) and specific combining ability (SCA) effects [15–18]. The GCA refers to a parent's overall genetic ability to influence progeny for traits because of additive effects. The SCA refers to the effect of a parent in a specific cross and is due to non-additive genes (dominant or epistatic) [13,19,20]. Then, the hybrid combination that shows high SCA and at least one parent with high GCA will be the most favorable [13,21]. Moreover, diallel analysis highlights, for the cotton breeder, the strategy in screening better combiners and combinations for further enhancement [15,20,22,23].

Our study investigated the opportunity to use cotton germplasm accessed from Texas A&M AgriLife to develop populations and evaluate them for potentially improving Burkina Faso future cultivars. We used a half diallel mating design, using two groups of parents, i.e., six lines from Africa and six lines from the United States, chosen for the way they could respond to the objectives desired for Burkina Faso future cultivars. We aimed (i) to start the development of broad genetic-based populations to increase the chances of identifying expressive gains for further selection procedures, (ii) to highlight the breeding potential, especially via SCA for agro-architectural traits, and (iii) to highlight at an early stage the most promising combination of crosses that could result in earlier crop maturity and high yielding cultivars. The hypothesis is that hybrids with parents from Africa and Texas will introduce positive variation for breeding improved cultivars. The next step will be to evaluate agronomic characteristics as well as fiber properties of segregating populations derived from the hybrids of the present study.

2. Materials and Methods

2.1. Plant Materials

Twelve cotton genotypes were utilized in this study. Three were improved varieties from Burkina Faso, FK37 (BF1) and FK64 (BF2), or introduced from Togo, STAM 59A(BF3). FK37 and FK64 are elite commercial varieties largely produced, so they are well adapted to local production conditions. Three, E9 (BF4), E32 (BF5), and E53(BF6) were selected from the local germplasm collection of Burkina Faso based on good agro-morphological or fiber properties [5,8]. Two were from the USDA National Cotton Germplasm Collection, TX 294, PI 165244 (TX1), and TX 307, PI 165390 (TX2), and four, 16-2-216FQ (TX3), 15-10-610-7 (TX4), 16-2-418BB, and 15-3-416 (TX6) were LREC unreleased breeding lines chosen for characteristics that meet the objectives sought in Burkina Faso future cultivars. Code names for cultivar, accession, or line designation in parentheses are used in the results to simplify discussion and emphasize origin.

2.2. Crosses

A half diallel crossing design, with selected parent mating either as male or as female, was used to develop sets of hybrids at the LREC greenhouse facility. In September 2018, seeds from the twelve genotypes were submerged into an 80 °C hot water bath (Precision 180 series, SN. 698091449; Jouan, Incorporation, Winchester, VA, USA) for 90 s to increase the chances of germination [24], and then they were planted in 18-oz foam cups filled with potting soil media. At 10 days after planting, seedlings were transplanted to 5-gallon pots with potting soil mixed with a slow-release 15-9-12 fertilizer. All seedlings were tested and cleared from any adventitious presence of genetic engineered traits. The number of plants available for crossing after seedling establishment was as follows: 8 plants from each American-originated line (TX1-TX6), 8 plants of Burkina Faso's BK1 and BK4, 8 plants of Togo's BK3, 10 plants of BK2, five plants of BK5, and two plants of BK6. At flowering time, flower buds were emasculated one day before anthesis and pollinated the next day, following the half diallel crossing scheme. All the precautionary measures were observed to prevent alien pollen contamination. F_1 seeds of 66 hybrids were generated.

2.3. Field Experiment

For the evaluation, and as a prelude to estimate heterosis, the seeds of the parents and the 66 F_1 hybrids were sown in randomized complete block designs, with three replications, at the Agricultural Research Station of Farako-Bâ in June 2019. This site is in the western cotton production area of Burkina Faso, between the isohyets 800 and 1200 mm at 405 m of altitude, 4°20′ O of longitude, and 11°06′ N. Seeds were planted 40 cm apart with 80 cm of row spacing. Plots in each replication consisted of four rows of 10 m long each. This study was hand-planted and thinned to two plants per hill. Field management was performed following the national recommendation in terms of fertilization and pest and weed control in conventional cotton production. Ten plants per experimental unit (from the middle rows) were randomly selected for data collection as suggested by Abro et al. [11].

2.4. Agronomic Data Recorded

Important agronomic characteristics, i.e., maturity, plant architectural components, as well as production components, were recorded. Maturity traits included days to 50% flowering (Pfm), days to 50% boll opening (Opcm), and node of the first fruiting branch (NFFB). Pfm and Opcm recording unit is days after emergence (dae). Plant architecture components consisted of the number of vegetative branches per plant (NVB), number of fruiting branches (NFB), and plant height (PH, cm). Production components included number of bolls/vegetative branch (BVB), number of bolls/fruiting branch (BFB), number of bolls/plant (BP), and boll weight (BW). Fiber percentage (FP, %) and seed index (SI, g), weight in grams of 100 seed, were recorded after ginning a 250-g seed-cotton sample from each plot on a 20-saw laboratory saw gin (Baldor Electric Company, Fort Smith, AR, USA).

2.5. Data Analysis

Data collected from parents and hybrids were subjected to analysis of variance using the SISVAR 5.1 Build 72 software. Means separation was conducted by the Scott-Knott test at 0.05 threshold level. The data were further used to determine the combining ability effects according to Griffing's [20] "Method I 'Model II" using DIAL Win 98 software revised 22 September 2002. Correlation analysis was also carried out for GCA effects using the same software.

The relative importance of GCA and SCA effects on inheritance of the studied traits was evaluated using the formula:

$$2GCA/(2GCA + SCA)$$

The closer this ratio is to 1, the more important the additive gene effects are in the inheritance of the trait [10]. Heritability was calculated using the following formula:

$$h^2_n:(\sigma^2_A/\sigma^2_P) \text{ and } h^2_b:(\sigma^2_G/\sigma^2_P)$$

where h^2_n is the narrow sense heritability; h^2_b is the broad sense heritability; σ^2_A is the additive variance; σ^2_G is the genotypic variance; σ^2_P is the phenotypic variance.

3. Results

3.1. Variation of Traits among Parents (ANOVA)

The analysis of variance (Table 1) and the means squares (Table 2) showed that significant differences ($p < 0.05$) were observed between the parents for investigated traits. Despite no genotyping reported herein for these specific lines, significant phenotypic differences are evident for the traits important to future cultivar improvement for Burkina Faso.

Table 1. Analysis of variance (ANOVA) of agronomic traits of 12 cotton lines, six originated from Burkina Faso and six from the United States.

Parent	Pfm	Opcm	NFFB	NVB	BVB	NFB	BFB	BP	PH (cm)	BW (g)	SI (g)	FP (%)
FK 37 (BK1)	$64.67 a_2$	$113.67 a_1$	$7.07 a_1$	$1.73 a_1$	$2.00 a_1$	$16.00 a_1$	$14.70 a_2$	$16.97 a_2$	$120.60 a_3$	$4.44 a_2$	$8.49 a_2$	$40.20 a_2$
FK 64 (BK2)	$64.00 a_2$	$117.67 a_1$	$5.40 a_1$	$1.47 a_1$	$1.33 a_1$	$12.87 a_1$	$8.07 a_1$	$9.87 a_1$	$87.40 a_2$	$4.30 a_2$	$9.08 a_3$	$40.65 a_2$
STAM 59A (BK3)	$64.00 a_2$	$116.33 a_1$	$6.33 a_1$	$2.00 a_1$	$2.93 a_2$	$15.27 a_1$	$11.80 a_2$	$15.60 a_2$	$98.60 a_2$	$4.34 a_2$	$8.55 a_2$	$40.51 a_2$
E32 (BK4)	$70.00 a_2$	$121.00 a_1$	$6.40 a_1$	$1.20 a_1$	$0.30 a_1$	$11.00 a_1$	$11.00 a_2$	$12.50 a_2$	$80.90 a_2$	$3.70 a_1$	$8.18 a_2$	$43.44 a_3$
E53 (BK5)	$63.00 a_2$	$116.33 a_1$	$5.53 a_1$	$2.53 a_1$	$3.60 a_2$	$19.00 a_2$	$13.00 a_2$	$17.20 a_2$	$132.30 a_3$	$4.10 a_1$	$7.74 a_1$	$42.45 a_3$
E9 (BK6)	$80.33 a_3$	$133.50 a_3$	$10.53 a_2$	$4.27 a_2$	$0.40 a_1$	$20.73 a_2$	$7.27 a_1$	$9.40 a_1$	$122.60 a_3$	$2.20 a_1$	$7.69 a_1$	$32.67 a_1$
TX 294 (TX1)	$65.67 a_2$	$118.33 a_1$	$5.80 a_1$	$1.67 a_1$	$1.60 a_1$	$13.07 a_1$	$10.73 a_2$	$13.33 a_2$	$92.93 a_2$	$3.96 a_1$	$9.52 a_4$	$34.28 a_1$
TX 307 (TX2)	$68.33 a_2$	$131.00 a_3$	$7.87 a_1$	$3.53 a_2$	$0.80 a_1$	$27.50 a_3$	$4.00 a_1$	$5.40 a_1$	$153.80 a_4$	$3.65 a_1$	$10.84 a_6$	$33.60 a_1$
15-10-610-7 (TX4)	$70.00 a_2$	$124.33 a_2$	$5.67 a_1$	$0.33 a_1$	$0.20 a_1$	$13.07 a_1$	$7.07 a_1$	$9.07 a_1$	$77.47 a_2$	$3.31 a_1$	$9.49 a_4$	$39.88 a_2$
16-2-216FQ (TX3)	$66.67 a_2$	$116.33 a_1$	$6.60 a_1$	$2.60 a_1$	$4.13 a_2$	$13.53 a_1$	$10.33 a_2$	$15.47 a_2$	$87.30 a_2$	$5.98 a_2$	$7.61 a_1$	$43.43 a_3$
15-3-416 (TX6)	$50.00 a_1$	$119.00 a_1$	$5.47 a_1$	$1.60 a_1$	$0.90 a_1$	$13.00 a_1$	$7.40 a_1$	$10.20 a_1$	$58.60 a_1$	$3.37 a_1$	$10.38 a_5$	$39.26 a_2$
16-2-418BB (TX5)	$66.33 a_2$	$117.00 a_1$	$7.00 a_1$	$2.13 a_1$	$4.40 a_2$	$12.60 a_1$	$12.80 a_2$	$17.60 a_2$	$91.67 a_2$	$4.60 a_2$	$9.11 a_3$	$40.90 a_2$
Mean	66.08	120.38	6.64	2.09	1.88	15.64	9.85	12.72	100.35	4.00	8.89	39.27

Table 1. *Cont.*

Parent	Pfm	Opcm	NFFB	NVB	BVB	NFB	BFB	BP	PH (cm)	BW (g)	SI (g)	FP (%)
CV (%)	6.25	2.89	16.14	34.04	69.40	16.63	27.20	25.52	9.24	19.54	2.46	2.16
p-value	0.0000 **	0.0000 **	0.0003 **	0.0001 **	0.0019 **	0.0000 **	0.0021 **	0.0011 **	0.0000 **	0.0021 **	0.0000 **	0.0000 **

Pfm = first flowering date; Opcm = first boll opening date; NFFB = node of the first fruiting branch; NVB = number of vegetative branches; BVB = bolls of vegetative branches; NFB = number of fruiting branches; BFB = bolls of fruiting branches; BP = all bolls per plant; PH = plant height; BW = boll weight; SI = seed index; FP = fiber percentage. Means within a column followed by the same letter (a) and index number (a_1 or a_2 or a_3, etc.) are not significantly different according to the Scott-Knott test at $p = 0.05$. **: highly significant difference between parents at $p = 0.01$.

Table 2. Mean squares of the agronomic traits of 12 cotton lines originated from Burkina Faso and the United States.

Sources	df	Pfm	Opcm	NFFB	NVB	BVB	NFB	BFB	BP	PH (cm)	BW (g)	SI (g)	FP (%)
Rep (L)	2	130.34 **	93.09 **	0.61	0.82	5.79	176.97 **	21.83	59.42 **	440.09 **	1.21	0.23	0.02
Parent (P)	11	150.87 **	171.85 **	11.43 **	7.87 **	38.43 **	148.65 **	30.36 **	68.01 **	6225.81 **	5.20 **	15.19 **	160.52 **
P × L	22	13.30	6.83	0.74	0.76	1.59	9.54 *	5.80	11.92	79.28	0.31	0.08	0.26
GCA	11	150.87 **	171.85 **	11.43 **	7.87 **	38.43 **	148.65 **	30.36 **	68.01 **	6225.81 **	5.20 **	15.19 **	160.52 **
SCA	66	29.74 **	26.00 **	1.39	0.58	12.08 **	22.23 **	38.28 **	69.99 **	1223.81 **	1.04**	1.67 **	5.32**
2GCA/ (2GCA + SCA)		0.91	0.93	0.94	0.96	0.86	0.93	0.61	0.66	0.91	0.91	0.95	0.98
Error (residuals)	154	14.44	12.97	1.08	0.59	2.04	5.87	7.20	11.65	84.03	0.44	0.11	0.28

Pfm = first flowering date; Opcm = first boll opening date; NFFB = insertion level of the first fruiting branch; NVB = number of vegetative branches; BVB = bolls of vegetative branches; NFB = number of fruiting branches; BFB = bolls of fruiting branches; BP = all bolls per plant; PH = plant height; BW = boll weight; SI = seed index; FP = fiber percentage. *Values followed by ** are significantly different at 0.05 and 0.01, respectively.*

TX6 exhibited the lowest Pfm (50 dae). Most parents flowered between 63 dae and 70 dae. The latest flowering parent was BK4 (83 dae). For Opcm, most parents opened their bolls early (113.67 to 121.0 dae) compared to TX4 (124.33 dae), TX2, and BK4 (131.00 and 133.50 dae, respectively). Most parents similarly initiated the first fruiting branch between 5 to 8 nodes above the cotyledon node, except for BK4 with its first fruiting branch at 10.53 nodes above the cotyledon node. Among the parents, B4 and TX2 produced the largest number of vegetative branches (4.27 and 3.53, respectively); the remaining parents averaged an NVB ranging from 0.33 to 1.60. In terms of boll production on vegetative branches, BK3 (2.93), BK6 (3.60), TX3 (4.13), and TX6 (4.40) produced healthier bolls (harvested, without insect damage) compared to the other varieties. TX2 (27.50) produced the largest number of fruiting branches (NFB), followed by BK4 (20.73) and BK6 (19.0). The other parents produced between 11.0 and 16.0 fruiting branches on average. BK1 (14.70), followed by BK6 (13.00), TX5 (12.80), BK3 (12.80), BK5 (11.0), TX1 (10.73), and TX3 (10.33), recorded similar and significantly healthier bolls on fruiting branches compared to the other genotypes. Parents yielding more bolls on fruiting branches also produced the largest number, including BK3 (15.60), TX3 (15.47), TX1 (13.33), and BK5 (12.50). Parents were separated in four groups for plant height (Table 1). TX2 (TX 307 from the American germplasm collection) was the tallest parent (153.80 cm). Most parents were of medium height (77.47 to 98.60 cm), while TX6 (the 15-3-416 breeding line adapted to mechanical harvest in a short season) was the shortest parent at 58.60 cm. TX3 and TX5 had the largest bolls (5.98 and 4.60 g, respectively) followed by BK1 (4.44 g), BK3 (4.34 g), and BK2 (4.30 g). Parents were further discriminated by SI and were clustered in six different groups. TX2 (10.84 g) and TX6 (10.38 g) produced the heaviest seeds, while the lightest seeds were produced by TX3 (7.61 g), BK4 (7.69 g), and BK6 (7.74 g). Parents were clustered into three groups for the important trait of fiber percent (Table 1). BK5 (43.44%), TX3 (43.43%), and BK6 (42.50%) had the best FP, with most parents intermediate for FP between 39.26 to 40.90%, while the lowest FP were recorded for BK4 (32.67%), TX2 (33.60%), and TX3 (34.28%).

3.2. Analysis of Combining Ability

3.2.1. GCA of Parents—Limited Inference

This project was restricted to only six parent genotypes imported to Texas for crossing from Burkina Faso, and six parent genotypes were imported to Burkina Faso from Texas for F_1 and parent evaluation in the target environment. Thus, the GCA effects calculated are not reliable due to the paucity of genotypes, and they indeed ranged between negative and positive, non-significant, significant, and highly significant for every trait evaluated among the 12 parental lines (Table 3). For days to 50% flowering (Pfm), shorter was desired, and some parents appeared to introduce positive effects (TX6, BK2, and BK1) by reducing the Pfm by 3.14, 1.40, and 1.35 days, respectively. Data indicated that BK4 should be avoided for this trait, as it increased Pfm by more than 4 days. BK1, along with BK6 and TX4, appeared to contribute to earliness by reducing Opcm, while BK4 and TX2 increased Opcm by 5.02 and 3.07 days, respectively. BK4 and TX2 increased NFFB, emphasizing caution in using these parents when earlier crop maturity is desired. BK5 and TX4 showed a desirable tendency to limit excessive vegetative growth with significant impact on their F_1 progeny, reducing NVB by 0.34 and 0.73, while BK4 (1.06) and TX2 (0.34) again demonstrated a trend of later maturity and more rank growth by increasing NVB. Bolls on vegetative branches generally do not contribute significantly to yield in the type of production systems that could be used in the future in Burkina Faso. Elite cultivar FK37 (BK1) and two Texas breeding lines, TX4 and TX6, reduced BVB production, while B6 (0.53), TX 3 (0,69), and again B4 (2.11) and TX2 (0.90) increased boll loading on vegetative branches in F_1.

Table 3. General combining ability (GCA) of 12 ˆ cotton lines originated from Burkina Faso and the United States.

Variety	Pfm	Opcm	NFFB	NVB	BVB	NFB	BFB	BP	PH (cm)	BW (g)	SI (g)	FP (%)
FK 37 (BK1)	−1.35 *	−1.69 **	−0.26	−0.24	−0.69 **	−0.03	1.57 **	1.13 *	7.85 **	0.03	−0.09	0.37 **
FK 64 (BK2)	−1.40 *	−1.05	−0.54 **	−0.11	−0.33	−0.04	0.19	−0.45	6.52 **	0.53 **	0.08	1.44 **
STAM 59A (BK3)	−0.59	−1.03	−0.10	0.18	0.03	0.46	0.77	0.84	1.02	0.09	0.05	0.98 **
E32 (BK5)	0.81	0.00	0.06	−0.34 *	−0.28	−1.31 **	0.47	0.38	−1.85	−0.15	−0.69 **	2.11 **
E53 (BK6)	−1.09	−1.38 *	−0.26	0.10	0.53 *	0.96 *	0.37	0.62	11.56 **	0.12	−0.42 **	1.13 **
E9 (BK4)	4.55 **	5.02 **	1.45 **	1.06 **	2.11 **	0.94 *	−0.09	2.25 **	4.99 **	−0.92 **	−0.69 **	−3.83 **
TX 307 (TX2)	0.79	3.07 **	0.40 *	0.34 *	0.90 **	5.08 **	−0.67	−0.08	23.39 **	−0.10	1.29 **	−2.29 **
TX 294 (TX1)	0.67	−0.57	−0.17	−0.17	−0.64 *	−2.05 **	−1.04 *	−1.36 *	−11.20 **	−0.04	0.18 **	−2.40 **
15-10-610-7 (TX4)	−0.78	−1.34 *	−0.42 *	−0.73 **	−1.32 **	−0.25	0.07	−1.26 *	−12.74 **	−0.12	−0.16 **	0.21 *
16-2-216FQ (TX3)	0.98	0.00	−0.06	0.10	0.69 **	−0.76	−0.74	−0.10	−1.70	0.35 **	−0.68 **	2.68 **
15-3-416 (TX6)	−3.14 **	−1.14	−0.23	−0.14	−1.11 **	−1.58 **	−1.45 **	−2.51 **	−22.25 **	−0.02	0.65 **	−0.48 **
16-2-418BB (TX5)	0.55	0.12	0.11	−0.05	0.10	−1.42 **	0.55	0.54	−5.58 **	0.22 *	0.49 **	0.08

Pfm = first flowering date; Opcm = first boll opening date; NFFB = node of the first fruiting branch; NVB = number of vegetative branches; BVB = bolls of vegetative branches; NFB = number of fruiting branches; BFB = bolls of fruiting branches; BP = all bolls per plant; PH = plant height; BW = boll weight; SI = seed index; FP = fiber percentage. ˆ This project was restricted to 12 genotypes, which is generally not considered a large enough number to adequately infer GCA. *Values followed by * or ** are significantly different at 0.05 and 0.01, respectively.*

Progeny of BK5, TX1, TX5, and TX6 showed significant decreases in NFB in this study, while BK6 and BK4 progeny showed increased NFB. TX2, while demonstrating a negative impact for earliness traits, increased NFB by 5.08 in its F_1 progeny. Parents from Burkina Faso, except for BK4, improved BFB, while AgriLife parents mostly decreased BFB in progeny. Burkina Faso parents, except for BK2, increased the BP total bolls per plant (BVB + BFB), while AgriLife parents, except for TX5, tended to produce progeny with less BP.

All parents, except for BK3, BK5, and TX6, appeared to impact the PH in progeny, negatively or positively. Interestingly, TX2 behaved similar to Burkina Faso parents BK6, BK2, and BK4, increasing PH in their F_1 progeny by 23.39, 11.56, 7.85, 6.52, and 4.99 cm, respectively. TX2 (TX 307) is a non-cultivated accession from the national collection, used in drought and salinity studies. Conversely, other American parents TX6 (−22.25 cm), TX4

(-12.74 cm), TX1 (-11.20 cm), and TX5 (-5.58 cm) significantly decreased plant height in F_1 progeny. Boll weight (BW) in progeny increased or decreased by less than one gram for all parents. SI generally ranged less than one gram smaller or larger among the materials. TX2 (1.29), TX6 (0.65), TX5 (0.49), and TX1 (0.18) increased progeny SI, while BK5 (-0.69 g), BK4 (-0.69 g), TX3 (-0.68 g), BK6 (-0.42 g), and TX4 (-0.16 g) decreased SI. Increasing fiber percent is a primary goal of Burkina Faso's cotton breeding efforts. All parents, except for TX5, significantly impacted, negatively or positively, the FP. Four parents (BK4, TX2, TX1, and TX6) decreased FP by -3.83, -2.29, -2.40, and -0.48%, respectively; progeny from TX3 (2.68%), BK5 (2.11%), BK2 (1.44%), and BK6 (1.13%) showed increases in FP.

3.2.2. SCA Effects

Significant SCA effects are presented in Table 4. SCA effects were non-significant for six of the 66 hybrids, and three other combinations were significant for a single trait. Therefore, they are not presented here. SCA effects were significant for five traits (Pfm, Opcm, NFFB, NVB, and BW) in less than 10 of the combinations. Four of those traits were found to be significantly affected in 10 to 20 of the hybrids. SCA effects were significant for PH, SI, and FP among 37 to 42 hybrids.

Table 4. Specific combining ability (SCA) effects for agronomic traits of 56 cotton hybrids with parental lines from Burkina Faso and the United States.

Hybrid	Pfm	Opcm	NFFB	NVB	BVB	NFB	BFB	BP	PH (cm)	BW (g)	SI(g)	FP (%)
FK 37 × TX 307 (BK1 × TX2)	-2.84	-2.38	-1.11	-0.38	-0.22	1.77	8.36 **	8.22 **	-2.23	0.56	-0.69	1.70 **
FK 37 × TX 294- (BK1 × TX1)	0.28	-0.07	-0.40	-0.06	-0.95	-1.29	-3.84 **	-3.01	-12.84 *	-0.54	0.18	-0.94 **
FK 37 × 15-10-610-7 (BK1 × TX4)	-4.27 *	0.03	-0.68	-0.18	1.02	-0.17	2.83	2.82	14.02 **	0.06	-0.19	0.87 **
FK 37 × 15-3-416 (BK1 × TX6)	2.75	-1.50	0.79	0.30	0.92	-1.36	0.64	0.94	-0.73	0.83 *	-0.34	-0.70 *
FK 37 × 16-2-418BB (BK1 × TX5)	2.40	1.24	-0.09	-0.25	0.11	-0.19	-3.89 **	-3.18	-17.63 **	0.58	-0.18	0.70 *
FK 64 × TX 307 (BK2 × TX2)	-4.79 *	0.31	-0.57	0.23	0.68	5.65 **	3.18 *	4.43 *	47.53 **	0.44	-0.47	1.27 **
FK 64 × 15-10-610-7 (BK2 × TX4)	-2.89	-3.95 *	-0.21	-0.23	-0.64	-0.56	-0.59	-1.70	-6.71	0.10	-0.14	1.94 **
FK 64 × 16-2-216FQ (BK2 × TX3)	-1.99	-3.28	-0.17	-0.06	1.45	0.29	0.12	1.41	11.72 *	-0.39	-0.53	1.75 **
FK 64 × 15-3-416 (BK2 × TX6)	-0.20	-1.47	0.20	-0.35	-0.11	1.98	1.23	0.85	0.06	0.25	0.62	1.19 **
FK 64 × 16-2-418BB (BK2 × TX5)	1.11	-0.07	-0.08	0.09	0.08	-1.18	-0.91	-0.27	-13.27 **	-0.63	-0.63	-1.08 **
STAM 59A × TX 307 (BK3 × TX2)	-0.27	-0.38	2.19 **	-0.13	0.32	-6.39 **	-3.44 *	-3.39	-31.87 **	-0.51	0.80	0.03
STAM 59A × 15-10-610-7 (BK3 × TX4)	-3.37	-0.64	-0.32	-0.33	-1.40	-0.26	-0.87	-2.98	-12.75 *	-0.42	-0.74	1.34 **
STAM 59A × 15-3-416 (BK3 × TX6)	4.32 *	-2.16	-0.18	0.15	-1.50	-1.79	-0.76	-2.40	-17.74 **	0.71	-0.49	1.98 **
STAM 59A × 16-2-418BB (BK3 × TX5)	-1.70	-0.76	-0.12	0.36	-0.42	-0.22	-0.76	-1.02	6.10	-0.15	-0.56	0.58 *
E32 × TX 307 (BK5 × TX2)	-1.34	-2.07	0.36	-1.15 **	-3.03 **	0.48	-1.33	-4.37 *	-12.30 *	-0.96	1.29	-0.59 *

Table 4. *Cont.*

Hybrid	Pfm	Opcm	NFFB	NVB	BVB	NFB	BFB	BP	PH (cm)	BW (g)	SI(g)	FP (%)
E32 × TX 294 (BK5 × TX1)	0.11	3.91 *	0.18	−0.10	−1.56 *	−3.61 **	−4.87 **	−5.60 **	−32.62 **	−0.31	−2.46	3.57 **
E32 × 16-2-216FQ (BK5 × TX3)	−2.53	0.34	0.36	0.36	2.01 *	0.96	−0.02	1.65	11.28 *	−0.22	−0.25	2.06 **
E32 × 15-3-416 (BK5 × TX6)	−4.41 *	−2.52	−0.40	0.07	3.05 **	6.38 **	10.41 **	13.49 **	54.23 **	1.53 **	0.40	1.18 **
E32 × 16-2-418BB (BK5 × TX5)	1.90	0.22	0.72	0.45	1.90 *	0.82	−2.95 *	−1.46	7.36	0.31	0.07	−0.71 *
E53 × TX 307 (BK6 × TX2)	1.56	−2.02	−0.52	−0.65	−1.41	−1.18	2.06	0.80	−8.51	1.19 **	0.45	0.01
E53 × TX 294 (BK6 × TX1)	−2.99	−1.05	0.19	−0.26	3.53 **	1.32	2.37	6.07 **	31.88 **	0.04	0.09	−0.58 *
E53 × 15-10-610-7 (BK6 × TX4)	−2.87	3.05	−0.02	0.22	−1.17	0.31	−1.60	−2.59	−23.99 **	0.23	−0.07	0.79 **
E53 × 16-2-216FQ (BK6 × TX3)	5.04 *	2.38	−0.05	−0.47	−1.01	−1.04	−1.33	−1.98	−12.99 *	0.09	0.06	0.20
E53 × 15-3-416 (BK6 × TX6)	3.82	−0.47	1.12 *	−0.16	−0.10	−2.28	−1.36	−1.88	−12.64 *	−0.27	0.19	−1.42 **
E53 × 16-2-418BB (BK6 × TX5)	2.47	0.26	0.91	0.55	−0.58	−2.11	−3.36 *	−3.53	−24.04 **	−0.16	−0.18	0.85 **
E9 × TX 307 (BK4 × TX2)	2.92	−0.43	0.09	0.56	7.61 **	2.13	−0.01	7.63 **	37.06 **	−0.11	0.72	−0.64 *
E9 × TX 294 (BK4 × TX1)	0.37	−0.45	0.05	0.04	−0.41	−3.60 **	1.29	0.87	−40.85 **	−0.29	−0.66	1.38 **
E9 × 15-10-610-7 (BK4 × TX4)	−1.18	−5.69 **	−1.07	−0.41	1.80 *	4.16 **	8.49 **	10.81 **	16.59 **	−0.52	−0.06	1.13 **
E9 × 16-2-216FQ (BK4 × TX3)	0.06	5.98 **	−1.03	−1.04 *	−0.58	0.57	−1.07	−1.62	10.55 *	0.33	0.55	2.83 **
E9 × 15-3-416 (BK4 × TX6)	4.18 *	1.45	0.97	0.94 *	−0.14	−7.73 **	−5.10 **	−4.91 **	−35.80 **	−0.60	−0.32	−2.58 **
E9 × 16-2-418BB (BK4 × TX5)	−4.51 *	−2.47	−0.54	−1.02 *	2.21 **	3.30 *	7.80 **	9.51 **	20.53 **	0.52	−0.27	0.85 **
FK 37 × FK 64 (BK1 × BK2)	−2.32	0.41	−0.24	0.01	−0.56	0.56	0.40	−0.89	0.57	−0.33	−0.65 **	2.12 **
FK 37 × E32 (BK1 × BK5)	2.47	0.69	−0.24	0.03	−1.44	0.96	−0.28	−1.69	7.33	−0.27	0.52 **	−1.49 **
FK 37 × E53(BK1 × BK6)	1.37	0.07	−0.58	−0.34	0.74	−0.04	−0.91	0.08	5.13	−0.21	0.64 **	−0.95 **
FK 37 × E9 (BK1 × BK4)	−7.60 **	0.34	−0.83	0.03	0.10	−0.15	−2.25	−1.82	6.24	0.23	0.49 **	−0.04
FK 64 × STAM 59A (BK2 × BK3)	1.25	0.41	0.20	0.06	0.41	−2.73 *	−3.06 *	−2.86	−2.70	−0.03	1.74 **	−0.47
FK 64 × E53 (BK2 × BK6)	2.42	1.10	−0.04	−0.26	0.81	−0.76	1.54	2.49	−1.04	−0.29	−0.48 **	−0.77 **
FK 64 × E9 (BK2 × BK4)	1.78	2.69	0.58	0.64	0.94	0.86	1.97	2.53	11.03 *	1.44 **	0.65 **	−1.86 **
STAM 59A × E32 (BK3 × BK5)	−2.29	−1.31	−0.54	0.42	1.07	3.94 **	5.43 **	6.34 **	23.26 **	0.46	0.06	−0.19
STAM 59A × E53 (BK3 × BK6)	−2.39	0.07	−0.48	0.25	0.15	5.54 **	2.92 *	2.61	31.46 **	0.53	−0.28	0.86 **

Table 4. *Cont.*

Hybrid	Pfm	Opcm	NFFB	NVB	BVB	NFB	BFB	BP	PH (cm)	BW (g)	SI(g)	FP (%)
STAM 59A × E9 (BK3 × BK4)	−2.37	−3.66	−0.20	−0.12	3.58 **	2.25	4.88 **	8.44 **	15.23 **	0.16	−0.42 *	−1.16 **
E32 × E53 (BK5 × BK6)	−2.46	−1.62	−0.24	−0.10	2.07 **	−0.59	1.93	3.36	18.62 **	0.04	0.32	−0.49
E32 × E9 (BK5 × BK4)	0.23	−4.69 *	−0.91	−0.48	0.60	−6.17 **	−4.11 **	−3.87 *	−43.60 **	−0.31	−0.92 **	−1.69 **
E53 × E9 (BK6 × BK4)	−5.53 **	−5.31 **	0.23	0.17	−1.92 *	−3.24 *	−2.32	−4.77 *	−16.51 **	−0.27	−0.18	1.11 **
TX 307 × 15-10-610-7 (TX2 × TX4)	−2.08	−5.40 **	−0.28	0.71	3.20 **	1.72	6.70 **	9.64 **	24.29 **	0.83 *	−2.15 **	1.27 **
TX 307 × 16-2-216FQ (TX2 × TX3)	3.16	0.60	−0.45	−0.32	3.33 **	1.53	3.88 **	7.52 **	−0.35	−0.46	0.22	0.36
TX 307 × 15-3-416 (TX2 × TX6)	1.28	−0.93	−0.74	−0.48	0.03	−2.67 *	−3.92 **	−4.21 *	−31.90 **	0.07	−1.07 **	0.63 *
TX 307 × 16-2-418BB (TX2 × TX5)	0.92	0.48	−1.02	−0.76	−2.88 **	−4.90 **	−0.62	−3.33	−28.87 **	−0.59	1.79 **	−0.25
TX 294 × 15-10-610-7 (TX1 × TX4)	2.37	−4.76 *	0.56	−0.24	−0.32	−1.07	−2.40	−2.95	−8.39	0.36	1.00 **	−0.31
TX 294 × 15-3-416 (TX1 × TX6)	2.06	0.05	0.83	0.17	1.27	2.19	0.85	2.03	11.98 *	−0.17	−0.14	−0.66 *
TX 294 × 16-2-418BB TX1 × TX5)	1.04	2.45	−0.25	−0.18	−0.21	2.97 *	2.58	2.18	12.25 *	−0.51	1.29 **	−0.15
15-10-610-7 × 16-22-216FQ (TX4 × TX3)	−1.94	−2.00	1.04	0.42	−0.86	−1.44	−0.82	−2.41	−6.23	0.32	0.47 *	−2.45 *
15-10-610-7 × 16-2-418BB (TX4 × TX5)	1.16	0.88	0.81	0.11	−0.60	−0.84	−1.58	−2.72	−1.68	0.50	0.50 **	−2.69 *
16-22-216FQ × 15-3-416 (TX3 × TX6)	2.75	0.14	−0.41	−0.44	−1.66 *	−0.37	−0.98	−2.76	−0.38	−0.74 *	0.55 **	−0.15
16-22-216FQ × 16-2-418BB (TX3 × TX5)	−3.94	−1.12	−0.43	−0.06	−0.18	0.13	3.36 *	4.12 *	14.02 **	0.16	−0.87 **	0.02
15-3-416 × 16-2-418BB (TX6 × TX3)	−0.49	0.03	−0.85	−0.15	−1.67 *	1.43	1.39	−0.73	25.27 **	0.31	0.50 **	0.42

Pfm = first flowering date; Opcm = first boll opening date; NFFB = node of the first fruiting branch; NVB = number of vegetative branches; BVB = bolls of vegetative branches; NFB = number of fruiting branches; BFB= bolls of fruiting branches; BP = all bolls per plant; PH = plant height; BW = boll weight; SI = seed index; FP = fiber percentage. *Values followed by * or ** are significantly different at 0.05 and 0.01, respectively.*

Earliness of Maturity

The SCA effect was significantly negative for Pfm in five hybrids and indicating time to flowering in these combinations was reduced compared to the average of parents (Table 4). These crosses include at least one parent where the GCA analysis indicated a trend to earliness, except for BK4 × TX5, where both parents trended to later maturity. In opposite, a positive SCA was noted for three hybrids. TX4 was a parent in four out of six hybrids with negative SCA effects, shortening the time to boll opening. The remaining two were BK5 × BK4 (−4.69) and BK6 × BK4 (−5.31). Potential to increase Opcm was observed in BK5 × TX1 (+3.91) and BK4 × TX3 (+5.98). Parents BK4 and TX1 indicated a tendency to increase Opcm (Table 3). For NFFB, SCA effects were only significant for two combinations, BK3 × TX2 (+2.19) and BK6 × TX6 (+1.12). This was not expected for BK6 × TX6, as both parents showed negative GCA effects on NFFB, a strong indication that not enough genotypes were used for robust GCA analysis.

Vegetative and Fruiting Branches

For hybrids BK5 × TX2, BK4 × TX3, and BK4 × TX5 (−1.15, −1.04, and −1.02, respectively), a significantly negative SCA effect showed potential to decrease NVB, even though both BK4 and TX5 showed overall potential to increase NVB among other hybrids. In the cross with TX6, BK4 did indicate an SCA effect (+0.94) with the potential to increase NVB. BVB, NFB, and BFB all showed significant SCA effects in BK5 × TX1, BK5 × TX6, BK4 × TX4, and BK4 × TX5; all were positive in crosses with BK4 as a parent, but they were positive in BK5 × TX6 and negative in BK5 × TX1. A positive significant SCA for BVB in 11 crosses indicated potential from parents to increase the number of healthy bolls harvested on vegetative branches from +1.80 to +7.61. Seven combinations showed heterosis for NFB with values above the means of their two parents, including BK2 × TX2 (+5.65), BK5 × TX6 (+6.38), BK4 × TX4 (+4.16), BK4 × TX5 (+3.30), BK3 × BK5 (+3.94), BK3 × BK6 (+5.54), and TX1 × TX5 (+2.97). No other combination had more NFB than the average of its two parents, as the remaining SCA effects were significantly negative (−2.95 à −5.10). For BFB, TX2, and to a lesser extent BK4, even with negative GCA, they exhibited the potential to increase BFB in their hybrids, i.e., BK1 × TX2 (+8.36), BK2 × TX2 (+3.18), BK4 × TX4 (+8.49), BK4 × TX5 (+7.80), BK3 × BK4 (+4.88), TX2 × TX4 (+6.70), and TX2 × TX3 (+3.88).

Plant Height and Boll Components

SCA effects were significant for BP in 18 of the hybrids, and within them, six had a negative effect (−5.60 to −3.87). SCA effects were positive in twelve of them, mainly influenced by parents TX2 (5) or BK4 (3). PH and FP had the highest number of combinations (38 and 42, respectively) with significant SCA effects, as many parents (9 and 11, respectively) also presented significant GCA effects. For PH, 18 hybrids presented the potential to be significantly shorter than the average of parent lines by −12.30 cm to −43.60 cm. The remaining hybrids showed an increase in plant height compared to the parents (between +10.55 to +54.23 cm). There were 18 hybrids that exhibited a decrease in FP between −0.58% and −2.69%, while 24 increased by +0.58% to +3.57% compared to the parent means. For BW, five out of seven hybrids indicated heavier bolls compared to parents, i.e., BK1 × TX6 (0.83 g), BK5 × TX6 (1.53 g), BK6 × TX2 (1.19 g), BK2 × BK4 (1.44 g), TX2 × TX4 (0.83 g). Conversely, BK5 × TX2 (−0.96 g) and TX3 × TX6 (−0.74 g) resulted in lighter bolls compared to the average of the parents. SCA effects were recorded in the most combinations for seed index and fiber percent. For seed index, 35 hybrids had significant SCA effects, with 16 expressing negative effects (−0.42 g to −2.46 g) and 19 expressing positive effects (+0.40 g to +1.79 g).

3.3. Estimate of Heritability

Heritability (narrow and broad sense) was calculated using additive, genotypic, and phenotypic variances (Table 5). For five traits (BW, NVB, NFFB, SI, and BFB) out of 12, additive variances were under one, while for six others they were under 10; PH additive variance was very high (292.91). A close trend was observed for genotypic variance, with NVB, BW, and NFFB under one, while PH was again very high (644.33). For the remaining traits, genotypic variance was between 1.09 and 17.75. Phenotypic variances were also under one for BW and NVB (0.72 and 0.84, respectively), but in general, they appeared high compared to the other measured variances for the same traits. According to different traits, narrow-sense heritability ranged from 0.05 to 0.81. For two traits, the narrow heritability expressed was over 0.5, i.e., SI (0.51) and FP (0.81). Four traits expressed a narrow heritability lower than 0.30, including BFB, which expressed the lowest (0.05). For the remaining six traits, narrow sense heritability was intermediate, ranging from 0.31 to 0.40. Broad-sense heritability ranged from 0.29 (Pfm) to 0.97 (FP). For seven traits out of 12, broad heritability was expressed up to 0.5, from 0.55 to 0.97 as their genotypic and phenotypic variances appeared closer. Four traits expressed broad heritability from 0.30 to 0.50, while, only for Pfm, it was under 0.30.

Table 5. Heritability estimates for the traits of 12 cotton lines originated from Burkina Faso and the United States.

Characteristics	σ^2_A	σ^2_G	σ^2_P	h^2_n (σ^2_A/σ^2_P)	h^2_b (σ^2_G/σ^2_P)
Pfm	4.74	5.90	20.34	0.23	0.29
Opcm	6.36	6.55	19.53	0.33	0.34
NFFB	0.50	0.50	1.58	0.32	0.32
NVB	0.26	0.26	0.84	0.31	0.31
BVB	2.26	4.64	6.68	0.34	0.69
NFB	6.26	10.38	16.25	0.39	0.64
BFB	0.85	8.88	16.08	0.05	0.55
BP	3.06	17.75	29.40	0.10	0.60
PH (cm)	292.91	644.33	728.36	0.40	0.88
BW (g)	0.19	0.28	0.72	0.26	0.38
SI (g)	0.62	1.09	1.20	0.51	0.91
FP (%)	7.35	8.83	9.11	0.81	0.97

σ^2_A = additive variance; σ^2_G = genotypic variance; σ^2_P = phenotypic variance; h^2_n = heritability in narrow sense; h^2_b = broad-sense heritability. Pfm = first flowering date; Opcm = first boll opening date; NFFB = node of the first fruiting branch; NVB = number of vegetative branches; BVB = bolls of vegetative branches; NFB = number of fruiting branches; BFB = bolls of fruiting branches; BP = all bolls per plant; PH = plant height; BW = boll weight; SI = seed index; FP = fiber percentage.

3.4. Correlation Analysis of GCA Effects

Relationships among GCA effects for the observed traits specific to the limited number of lines in this study are summarized in Table 6. The seed index (SI) trait was not correlated to any other trait. Significant positive correlations were observed among maturity traits (Pfm, Opcm, and NFFB) and traits related to vegetative branches (NVB and BVB). The most highly significant correlation was recorded between Opcm and NFFB (0.94). Total bolls per plant and plant height were positively correlated, and both correlated with many other traits. BP correlated with Pfm (0.62), NFFB (0.60), NVB (0.61), BVB (0.72), BFB (0.67), and PH (0.63). PH was correlated with BVB (0.61), NFB (0.83), and BP (0.63). Highly significant correlations were observed between BP and BVB or between PH and NFB. Boll weight was negatively correlated to Pfm, Opcm, and NFFB; these values were −0.65, −0.71, and −0.81, in this order. Negative correlations were found between FP and Opcm (−0.67) and between FP and NFFB (−0.71), while BW and FP were positively correlated (0.72).

Table 6. Correlation coefficients between GCA effects on the traits of 12 cotton lines originated from Burkina Faso and the United States.

Characteristics	Pfm	Opcm	NFFB	NVB	BVB	NFB	BFB	BP	PH (cm)	BW (g)	SI(g)	FP (%)
Pfm	1											
Opcm	0.841 **	1										
NFFB	0.863 **	0.943 **	1									
NVB	0.671 *	0.810 **	0.844 **	1								
BVB	0.786 **	0.821 **	0.823 **	0.919 **	1							
NFB	0.211	0.520	0.350	0.461	0.516	1						
BFB	−0.025	−0.235	−0.095	−0.115	−0.013	0.043	1					
BP	0.624 *	0.469	0.600 *	0.609 *	0.715 **	0.324	0.668 *	1				
PH (cm)	0.292	0.398	0.284	0.468	0.606 *	0.824 **	0.376	0.626 *	1			
BW (g)	−0.647 *	−0.706 *	−0.815 **	−0.521	−0.442	−0.205	0.077	−0.372	−0.020	1		
SI(g)	−0.353	0.038	−0.135	−0.064	−0.213	0.391	−0.308	−0.432	0.085	0.205	1	
FP (%)	−0.477	−0.673 *	−0.653 *	−0.528	−0.347	−0.322	0.335	−0.086	−0.077	0.719 **	−0.360	1

Pfm = first flowering date; Opcm = first boll opening date; NFFB = node of the first fruiting branch; NVB = number of vegetative branches; BVB = bolls of vegetative branches; NFB= number of fruiting branches; BFB= bolls of fruiting branches; BP= all bolls per plant; PH = plant height; BW = boll weight; SI = seed index; FP = fiber percentage. *Values followed by * or ** are significantly different at 0.05 and 0.01, respectively.*

4. Discussion

Research efforts in Burkina Faso are focused on providing suitable cotton varieties to mitigate the challenges of climatic variations, labor scarcity, and higher fiber quality

required by the textile industry. The aim of this study is to investigate the potential, via prospection, collection, exchange, and introduction, of new germplasm material to generate genetic diversity and develop enhanced cultivars with needed characteristics for Burkina Faso's future industry direction.

4.1. Potentialities of Crosses as Revealed by ANOVA, GCA, Heritability Estimates, and Correlations

The ANOVA revealed highly significant differences for all the agronomic traits studied, indicating considerable phenotypic diversity among the parents. Elite varieties from Burkina Faso (FK, BK1-BK2) expressed, in general, an average performance for almost all the agronomic traits evaluated. The other African materials exhibited useful potentialities, justifying their choice in this diallel to generate populations with a broad genetic base [8]. Elite materials as well as other African types also showed some undesirable traits, such as late maturity. African cotton breeding programs used to select late flowering and maturing varieties, with a tendency to more vegetative growth [2]. Among American breeding lines, TX5 showed the potential to reduce days to 50% flowering, decrease plant height, and increase seed size. TX1, TX2, and TX4 had higher seed indexes and TX3 was a good source for BW and FP compared to African varieties, which was unexpected. In the past, varieties introduced from the United States were found to have inferior FP compared to African varieties, which are among the best worldwide for fiber percent [25,26].

Combining ability describes the breeding value of parental lines and subsequently helps to identify desirable parents for hybridization and population development to expand the genetic variability for the selection of superior genotypes essential in a systematic breeding program [11]. Therefore, GCA was analyzed, even though the present study was limited in the number of lines that could be included in the crossing scheme and showed that selected parent lines varied significantly (Table 3). Results indicated that African lines FK37 (BK1), FK64 (BK2), and E53 (BK6), along with American lines TX6 and TX4, have interesting potential for improving components of maturity (Pfm, Opcm, and NFFB). Populations created from these groups of parents could potentially be used to develop early flowering and early boll maturing cultivars eventually. Conversely, E9 (BK4) and TX 307 (BK2) would contribute to developing late maturing cultivars. A previous study reported that American genotypes are good top-cross candidates to reduce the maturity period [27]. The analysis of the ratio of mean squares, using the formula 2GCA/(2GCA + SCA) by Baker [28], revealed that all the earliness traits are quantitatively inherited traits. Similar results were reported by Simon et al. [29]. Other studies reported that days to 50% flowering is controlled by additive genes [12,30], or additive gene effects is most important for flowering [13]. For traits related to the plant architecture (NVB, NFB, and PH), results indicate that most of the genotypes did not exhibit excessive vegetative growth except for E9 (BK4), Stam 59A (BK3), and TX 307 (TX2). American parents, except for TX1, were shorter in height compared to African parents, which were tall and vegetative. Within a context of climate changes, with water scarcity and cropping season shortening, most of the American lines studied here have characteristics to be exploited in breeding future Burkina Faso cultivars. Potential improvement of architectural traits, i.e., shorter plant height, early maturing, and lodging resistance, would allow mechanization and reduce the water demand. The ratio of mean squares indicated that these traits are all under the predominance of additive gene effects. Simon et al. [29] and Raza et al. [31] also mentioned that plant height is predominantly controlled by additive genes, while Vasconcelos et al. [13] concluded on the prevalence of dominance effects for plant height in water stress condition.

Traits such as BVB, BFB, BP, and BW could be clustered as yield components. Most Burkina Faso materials exhibited positive GCA effects, while most American materials presented undesirable and negative GCA effects when evaluated in Burkina Faso. Only TX5 was similar, even better than African materials. It is obvious that, in their own conditions of production, most adapted cultivars are favored compared to foreign materials [5]. However, this study suggests that crossing Burkina Faso materials with TX5 will likely result in hybrids with a greater number of bolls per plant, larger boll size, and, therefore, more yield.

The analysis of the ratio of mean squares showed that BW is under additive effects, such as stated in the findings of Raza et al. [31]. For bolls per vegetative branch, bolls per plant, and to some lesser extent bolls per fruiting branch, we concluded, in agreement with previous studies, on the presence of both additive and dominance gene effects, with additive being higher than dominance [13,23,30]. For these traits, the selection should be based upon evaluation in several environments [32].

Most Burkina Faso materials are better general combiners compared to American ones for fiber percent. Older accessions from the USDA NCGC (TX 307-TX2 and TX 294–TX1) reduced FP more than 2% in hybrids. However, newer breeding materials TX3 and TX4 are among the best contributors to improve FP. These two lines crossed with African materials (except for E9-BK4) would likely produce populations from which to select new cultivars with enhanced FP. Fiber percent is an effective breeding target in cotton, as it is solidly reported to be controlled by additive gene effects [10,12,13,23,31], in agreement with results of the present study.

Heritability estimates (h^2) were classified as high (>0.50), medium (0.30–0.50), and low (<0.30) according to Bhateria et al. [33]. In our study, two maturity traits (Pfm and Opcm) expressed both medium narrow-sense heritability (0.23 and 0.33) and broad-sense heritability (0.29 and 0.34), while NFFB was both low narrow-sense heritability (0.15) and broad-sense heritability (0.21). The selection for earliness based on NFFB appeared less effective than selection for other traits such as FP and SI [10], requiring evaluation in multiple environments [32]. Except for NVB (both medium narrow-sense and broad-sense heritability), architectural traits were both medium narrow-sense heritability and high broad-sense heritability. This means NFB and PH should be easily inherited in progenies; Lançon [2] found similar results. Yield components expressed medium (BVB) to low (BFB, BP, and BW) narrow-sense heritability and medium (BW) to high (BVB, BFB, and BP) broad-sense heritability. These results concur with those reported by Cheatham et al. [32], indicating complexity in breeding for these traits. FP and SI expressed both very high narrow-sense heritability (0.51 and 0.81) and broad-sense heritability (0.91 and 0.97). Lu and Meyers [10] reported similar results for FP, confirming the relative ease to change this trait through breeding.

In general, many significant and positive correlations were observed among maturity, architectural, and production components. Lu and Meyers [10] reported a positive and significant correlation between number of bolls per plant and boll weight with seed index. They also reported the number of bolls per plant to be significantly and negatively correlated with boll weight and seed index, which is not in accordance with our findings. Moreover, BW and FP were most often negatively correlated with the other traits. Correlation results indicated that it is theoretically possible to breed for many agronomic traits related to earliness, plant architecture, and yield simultaneously. With the other traits, it is possible to cause some potential antagonist effects; therefore, in an improvement program, the best parents for BW, FP, and SI might be exploited separately in different cross combinations.

4.2. Highlighting the Most Promising Combination of Crosses Based on SCA

SCA effects are usually used to identify the best cross combinations for hybrid production. SCA refers to dominance effects and non-additive interactions of genes, resulting from gene complementation between parents, as dominant or epistatic [11].

When analyzing hybrids derived from parents with significant SCA, E9 (BK4) was the least favorable parent. Crosses between E9 and American parents (with E9 as the male parent), as well as between E9 and other Burkina Faso materials (with E9 as both the female and male parent), did not produce hybrids with desired characteristics. E9 is a primitive accession, known to be not as well adapted as the improved cultivars [7,8]. E9 appears to carry both negative trait associations into its hybrids and/or inhibit positive effects from the other parent. Cheatham et al. [32] reported similar effects from an Australian converted wild accession, which tended to decrease most of the positive agronomic properties when

it was used as a parent in crosses with American cultivars. The cross FK37 x E9, however, showed interesting effects by potentially reducing Pfm over seven days, increasing SI by 0.49 g and not influencing significantly the other parental means; it could be kept for an advanced improvement process by back crossing these desired genes into the FK37 parent.

Combinations within the remaining Burkina Faso materials exclusively, as well as within American materials exclusively, did not produce many hybrids with desired characteristics. When the elite FK37 cultivar was included as a male parent, SCA effects were significant only for SI and FP but in an antagonistic way (Table 4). The elite FK64 cultivar resulted in significant SCA effects in hybrids only with two other parents, STAM 59A and E53, by decreasing important characteristics, i.e., NFB and BFB (−2.73 and −3.06, respectively) or SI and FP (−0.48 g and −0.77%, respectively). Parents affecting important characteristics in progenies were also reported by Simon et al. [29]. Crosses between STAM 59A, E32, and E53 resulted in the only positive significant SCA effect, primarily for PH (Table 4). The cross between the old cultivar STAM 59A and accession E32 appeared interesting, increasing PH (+23.36 cm) then NFB (+3.94) and BP (+6.34), while the other traits remained the same as the parents.

Crosses within American materials resulted in both positive and negative SCA effects, but no hybrid had enough interesting genetic gains to be considered promising for Burkina Faso. Previous studies reported that a narrow genetic base, with parents coming from a common origin or sharing common parents in their pedigree leading to insignificant or unfavorable SCA effects [29,32]. In other words, when selecting the genetic base to be used in diallel crosses, it is important to increase the frequency of favorable alleles in the traits of interest, allowing the development of top lines and genetic gain [13]. Materials from Burkina Faso clustered in the same group in a study using molecular SSR markers [7].

In the present study, the most promising hybrids predicted by SCA involved those resulting from crosses with Burkina Faso materials as male parents and American ones as female parents. The SCA effects revealed that seven hybrids, combinations between three Burkina Faso materials (FK37, FK64, and E32) and three American ones (improved breeding lines 15-10-610-7, 15-3-416, and 16-2-216FQ) showed potential for interesting improvements. Those parents in this study have higher parental values for the desired traits. FK37 × 15-10-610-7 F_1 showed improved Pfm (−4.27 days) and FP (+0.87%), while PH was undesirably increased, and the remaining traits were not impacted. These two parents were also contributors in two other promising hybrids, FK37 × 15-3-416 and FK64 × 15-10-610-7. Hybrid FK37 × 15-3-416 is considered promising since no impact on most investigated traits was noticed, while important traits were improved, i.e., BW (+0.83 g). The low decline in FP (−0.70%) could be improved in backcrosses with FK37, which is good for this trait. Moreover, 15-3-416 is a desired parent in terms of earliness components, SI, and short stature.

FK64 × 15-10-610-7 improved the main traits desired of Burkina Faso's future cultivars, i.e., reducing Opcm (−3.95 days) and increasing FP (+0.94%), while not significantly impacting other traits. This combination is interesting since FP and Opcm overall were found to be negatively correlated in this study. Cultivar FK64 is a parent in two other promising hybrids (FK64 × 16-2-216FQ and FK64 × 15-3-416). FK64 × 16-2-216FQ increased in FP (+1.75%), and it could be ranked among the best combination for FP; 16-2-216FQ was found to be a good parent to improve FP. However, PH was increased, and SI decreased, implying that backcrosses are required to address these issues. Abro et al. [11], Khan [12], and Ekenci and Basbag [23] also recommended this process to improve hybrids after diallel crosses.

Hybrid FK64 × 15-3-416 increased SI (+0.62 g) and FP (1.19%) over the parent means while the other traits were maintained at parents' average levels. This increase in SI will put the hybrid among the best for the trait, as 15-3-416 (10.38 g) was the highest ranked parent for SI and FK64 was also at a good level (9.08 g). This is an interesting observation since FP and SI can be negatively correlated.

E32 (BK5) was a parent in two of the most promising hybrids. E32 × 16-2-216FQ (TX3) increased BVB, PH, and FP by 2.01, 11.28 cm, and 2.06%, respectively, while maintaining

the other traits the same as the parents. This hybrid is potentially the best for FP as its parents have higher parental values for this trait. E32 × 15-3-416 exhibited the widest range of desired SCA effects. Although PH undesirably increased (54.23 cm), the combination reduced Pfm over four days and increased BVB (+3.05 bolls), NFB (6.38 branches), BP (13.49 bolls), BW (1.53 g), SI (0.40 g), and FP (1.18%).

As a summary, the present study revealed that all hybrid combinations expressing desired SCA effects involved at least one or both high general combiners as parents, in accordance with many previous studies [10,11,23,29]. The possibilities to realize value from these populations exist through careful selection and carefully considering differences in germplasm materials and environmental effects [10,13,29,34,35].

5. Conclusions

Varietal improvement is imperative for Burkina Faso to address challenges such as irregular rainfall, mechanization of farming, fiber quality requirements, and competitiveness as a cotton producing country. Our study investigated the opportunity to use cotton germplasm accessed from Texas A&M AgriLife through an International Borlaug Fellow program to develop populations and evaluate them for potentially improving Burkina Faso future cultivars. After evaluating parents and F_1 generation in this study, we concluded that USDA NCGC's older accessions (TX 307-TX2 and TX 294-TX1) did not add genetic gains for any agronomic trait in Burkina Faso elite varieties. However, the country's breeding program could benefit from using American materials with characteristics such as the three AgriLife improved breeding lines used in this study with good potential to improve specific agronomic traits in local elite cultivars (FK37 and FK64). The breeding lines 15-10-610-7 (TX4) and 15-3-416 (TX6) contributed positive earliness traits, with 15-3-416 reducing Pfm and PH and 16-2-216FQ improving FP. Most F_1 hybrids expressing desired target objectives were crosses with Burkina Faso elite cultivars and had E32 as male parents and the three best American parents as female. Agronomic characteristics, as well as fiber properties of segregating populations derived from the hybrids of this study, must be further investigated. Evaluation of the F_2 generation will be conducted in at least two location trials when seed and required permissions are available. Open-pollinated parent seed is being multiplied to complete the other half of a full diallel to investigate possible differences in SCA among reciprocal crosses, according to which parent is male or female.

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Data Availability Statement: Data on parental lines and crossing scheme are available from J.D. (jdever@ag.tamu.edu), and data on agronomic characteristics are available from L.B. (diallabourgou@yahoo.fr).

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