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BREEDING AND GENETICS

Seed-score (S-score), a Method for Characterizing Seed and Lint Indices of Cotton Lines

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ABSTRACT

Increased lint yields of cotton (*Gossypium hirsutum* L.) cultivars during recent years have been accompanied by increased lint percentages and decreased seed size. Small seed size can be associated with low seed and seedling vigor and can contribute to ginning problems. In contrast, large seed size can be associated with thin seed coats and lower lint yields. Our objective was to develop an index that would characterize seed size and lint weight per seed. Seed-score (S-score) attempts to normalize seed index (SI) and lint index (LI) into a single index with penalties for both high and low SI values and no penalty for high LI values. Location × cultivar means (6,453 lines) for SI and LI extracted from the 1999 through 2020 Arkansas Cotton Variety Testing program produced mean SI of 10.17 ± 1.07 g and mean LI of 7.01 ± 0.90 g. These data were used to develop the normalization and weighting of factors for S-score. S-score was then calculated for transgenic cultivars evaluated in the 2015 through 2020 Arkansas Cotton Variety Tests. Within each year, cultivar was the major source of variation for SI, LI, and S-score. The 2015-2017 data set and the 2018-2020 data set produced 12 and 15 common cultivars, respectively. S-score among cultivars varied by more than 25 points in each data set and was relatively consistent over years. S-score will most likely be used as a secondary selection criterion in cotton cultivar development programs.

Improving lint yield is the primary objective of most, if not all, cotton breeding programs. Lint yields can be improved by increasing the volume of selection and testing, improving testing precision, employing advanced statistical and molecular tools, and by utilizing yield components. Lewis et al. (2000) proposed the simplest component model for lint yield in cotton to be number of seed per area (SPA) times the weight of lint per seed. Weight of lint per seed is normally expressed as lint index (LI), which is the lint weight per 100 seed. Because more plant energy is required to produce seed than fiber, lint yields produced with relative preference of LI over SPA are preferred. Measurement of seed index (weight of 100 seed, SI) is required to calculate both SPA and LI, as well as other yield component variables, for example, fibers per seed, seed surface area, and fiber density (Groves et al., 2016).

Lint frequency as defined and used by Hodson (1920) measured the weight (g) of fiber of uniform length produced cm^{-2} of seed surface area. This method was used to select for improved yield while standardizing seed size. Thurman (1953) developed a lint density index that measured the weight of fibers 100 cm^{-2} of seed surface area. Lint density index included all lint and removed the fiber length uniformity parameter of lint frequency. Lint density index was positively correlated with lint percentage and lint index. Lint percentage does not require an estimate of seed index or seed surface area and was used by most cotton breeding programs.

Breaux (1954) indicated that high lint density and small- to medium-sized seed offered the best possibility of obtaining high yielding lines. Mechanized harvest equipment provided a more consistent measurement of yield and allowed breeding programs an opportunity to focus on lint yield improvement by directly measuring lint yield rather than yield components. Since harvest mechanization, research has identified multiple combinations of lint and fiber parameters that have served as selection criteria. High lint percentage has been the method most used.

Selection favoring high lint percentage has led to increased lint yield and ultimately, smaller seeded cultivars. Both Miller and Rawlings (1967) and Bridge et al. (1971) found that selection for high lint yields simultaneously increased lint percentage and decreased SI with little change in LI. Selecting for high lint percentages (and lint yields) have effec-

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tively reduced SI over time. Culp and Harrell (1975) indicated that Coker cultivars were noted for their small seed having SI < 12.0 g. Few, if any, of our modern cotton cultivars possess SI that approaches 12.0 g. The primary advantage of lower SI over high SI is the negative association between SI and lint percentage. Harrell and Culp (1976) stated "Until methods for measuring surface area of seed and lint/unit area of seed are developed, we will select for high lint percentage and hope to maintain an acceptable level of lint/seed." Groves and Bourland (2010) established a method of estimating seed surface area based on SI.

Lint index is a function of seed surface area and selection for increased LI results in larger seeds. Large seed size is unfavorable due to its association with lower lint percentages and thinner seed coats. Bechere et al. (2021) indicated that as seed size increased, ginning rate increased but ginning energy requirement decreased. Both germination and seed vigor increase as SI increases (Krieg and Carroll, 1978; Kunze et al., 1969; Minton and Supak, 1980; Snider et al., 2014). Conversely, smaller seeds are related to higher lint percentages, but their smaller cotyledons are often associated with decreased stand and lower seedling vigor (Snider et al., 2016).

Moderate SI has long been considered to be optimum in cotton. Main et al. (2013) observed the highest lint yields on cultivars having medium seed size. Minton and Supak (1980) indicated that cultivars having medium-sized seed produced similar yields as smaller seeded cultivars, but maintained improved germination, stand, and survival that was associated with larger seeded cultivars.

Bednarz et al. (2006) noted that lint percentage increased by as much as 10% since approximately 1950. Their data indicated that fiber quality became less desirable, and SI declined with increased lint percentage. They proposed that selection for increased lint mass per unit seed surface area could be the next reasonable selection criteria. They further indicated that number of fibers per seed and lint mass per unit seed surface area are confounded with SI.

Seed-score (S-score) attempts to reduce the confounding effects of SI and LI by normalizing the two parameters into a single index. The logic of S-score is patterned after the logic of Q-score (Bourland et al., 2010a) with SI handled like micronaire in Q-score (penalties for both high and low values) and LI handled like fiber length in Q-score (no penalty for high values).

MATERIALS AND METHODS

SI and LI Data. In addition to standard data produced from ginning small samples, SI is the only other parameter needed to calculate lint index. We began measuring SI in the Arkansas Cotton Variety Testing and Cotton Breeding Programs in 1999 and have routinely determined SI on boll samples since. Currently, SI is measured by counting and weighing two sets of 25 fuzzy (gin-run) seed from each ginned sample. If the two seed weights differ more than 0.2 g, additional 25-seed sets are counted and weighed. Typically, the 0.2 g tolerance is exceeded in less than 5% of samples. SI is then calculated as the weight of 100 fuzzy seed. LI (weight of lint from 100 seed) is calculated by dividing lint weight from a ginned sample by the number of seed per sample (estimated using average seed weight) then multiplying by 100.

The 1999 through 2020 data from the Arkansas Cotton Variety Testing program produced a total of 6,453 lines of data for SI and LI (Table 1). Each line of data was the mean of two replications, which were the field plots from which boll samples were collected. These data produced mean SI of 10.17 ± 1.07 g and mean LI of 7.01 ± 0.90 g.

Logic and Calculation of S-score. Similar to the Q-score (Bourland et al., 2010a), S-score is an effort to combine data from multiple parameters into a single score between 0 and 100 to facilitate consideration of seed size in genotype evaluations. Q-score combines several fiber quality parameters into a single score to assist cotton breeders in genotype selection and variety characterization. SI is incorporated into S-score in a similar manner as micronaire is in Q-score with penalties for both high and low values. LI in S-score is treated like fiber length and length uniformity are in Q-score with only low values penalized. The equation for S-score is:

$$\text{S-Score} = 100(WF_{LI} * S_{LI} + WF_{SI}*S_{SI})$$

where WF_{LI} and WF_{SI} are the weighting factors for the terms S_{LI} and S_{SI} that represent dimensionless values scaled between 0 and 1; and the subscripts LI and SI indicate the lint index and seed index, respectively. The weighting factors are between 0 and 1 and the two must sum to 1. S-score weightings of the two parameters in this paper were SI = 0.5 and LI = 0.5. These weights reflect equal importance of SI and LI but could be altered by the S-score user.

Table 1. Test sites and number of entries in annual Arkansas Cotton Variety Tests used as sources of data to determine population means and standard deviations for SI and LI

Year	Irrigated sites[z]	Non-irr. sites[z]	No. of entries	T/C[y]	Reference
1999	Kei, Clk, Mar, Roh	Clk, Mar	69[x]	T, C	Bourland et al., 2000
2000	Kei, Clk	Kei	59[x]	T, C	Benson et al., 2001
2000	Mar, Roh	Mar	64[x]	T, C	Benson et al., 2001
2001	Kei, Clk	Kei	61[x]	T, C	Benson et al., 2002
2001	Mar, Roh	Mar	67[x]	T, C	Benson et al., 2002
2002	Kei, Clk, Mar, Roh	Kei, Mar	66[x]	T, C	Bourland et al., 2003
2003	Man, Kei, Clk, Mar, Roh	Kei, Mar	56[x]	T, C	Bourland et al., 2004
2004	Kei, Clk, Mar, Roh	Kei, Mar	54[x]	T, C	Bourland et al., 2005
2005	Man, Kei, JH, Mar, Roh	Kei	96[x]	T, C	Bourland et al., 2006
2006	Kei, JH, Mar, Roh	Kei	78[x]	T, C	Bourland et al., 2007
2007	Kei, JH, Mar, Roh	none	76[x]	T, C	Bourland et al., 2008
2008	Kei, JH, Mar, Roh	none	50[x]	T, C	Bourland et al., 2009
2009	Kei, JH, Mar, Roh	none	50[x]	T, C	Bourland et al., 2010b
2010	Kei, JH, Mar, Roh	none	55[x]	T, C	Bourland et al., 2011
2011	Kei, JH, Mar, Roh	none	48[x]	T, C	Bourland et al., 2012
2012	Kei, JH, Mar, Roh	none	40	T, C	Bourland et al., 2013
2013	Kei, JH, Mar, Roh	none	40	T, C	Bourland et al., 2014
2014	Kei, JH, Mar, Roh	none	40	T, C	Bourland et al., 2015
2015	Man, Kei, JH, Mar, Roh	none	32	T	Bourland et al., 2016
2015	Kei, JH, Mar, Roh	none	10	C	Bourland et al., 2016
2016	Man, Kei, JH, Mar, Roh	none	35	T	Bourland et al., 2017
2016	Kei, JH, Mar, Roh	none	10	C	Bourland et al., 2017
2017	Man, Kei, JH, Mar, Roh	none	41	T	Bourland et al., 2018
2017	Kei, JH, Mar, Roh	none	16	C	Bourland et al., 2018
2018	Man, Kei, JH, Mar, Roh	none	65	T	Bourland et al., 2019
2018	Kei, JH, Mar, Roh	none	15	C	Bourland et al., 2019
2019	Man, Kei, JH, Mar, Roh	none	50	T	Bourland et al., 2020
2019	Kei, JH, Mar, Roh	none	17	C	Bourland et al., 2020
2020	Kei, JH, Mar, Roh	none	51	T	Bourland et al., 2021
2020	Kei, JH, Mar, Roh	none	10	C	Bourland et al., 2021

[z] From north to south (spanning approximately 320 km), tests sites were on Arkansas Agricultural Experiment Stations at Manila (Man), Keiser (Kei), Judd Hill (JH), Clarkedale (Clk), Marianna (Mar), and Rohwer (Roh). Within a year and test, the same entries were evaluated at each test site.

[y] Test included transgenic (T) and/or conventional (C) entries.

[x] First-year entries evaluated in a separate test from, but adjacent to, returning entries.

To determine S_{LI} and S_{SI} in this evaluation, the standard deviation of LI and SI (sd_{LI} and sd_{SI}, respectively) from 6,473 location x cultivar means in University of Arkansas variety trials from 1999 to 2020 (Table 1) were used. For that data set, the mean SI was 10.17 g with a sd_{LI} of 1.07 g and mean LI of 7.01 with a sd_{SI} of 0.90 g. S_{LI} was then determined using the mean LI of a specific trial and setting the lower limit as the trial mean LI minus two times sd_{LI} and the upper limit the trial mean plus two times sd_{LI}. S_{LI} was set 0 for any LI values below the lower threshold and set to 1 for LI values greater than the upper threshold. LI values between the two thresholds were linearly scaled from 0 to 1 as shown in Fig. 1.

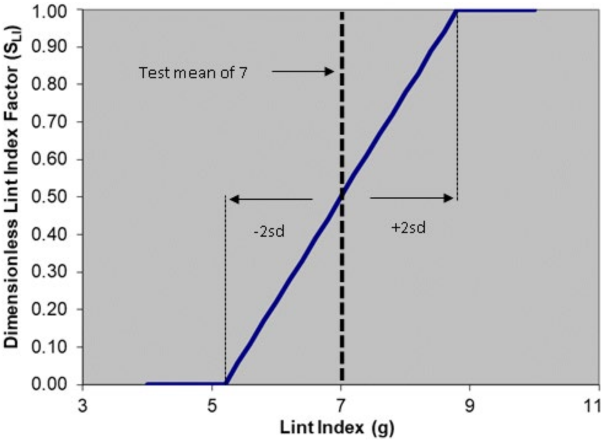

Figure 1. Example of the normalization of Lint Index for a trail with a mean of 7 g, and standard deviation (sd) equal to 0.9 g.

S_{SI} was determined so that the value of 1 was assigned to SI values within one sd_{SI} of the variety trial mean. If SI was less than the trial mean minus two times sd_{SI} or greater than the trial mean plus two sd_{SI}, S_{SI} was set to 0. If SI was between two times ± sd_{SI} of the mean and ± sd_{SI} of the mean, S_{SI} was linearly scaled between 0 and 1 as illustrated in Fig. 2.

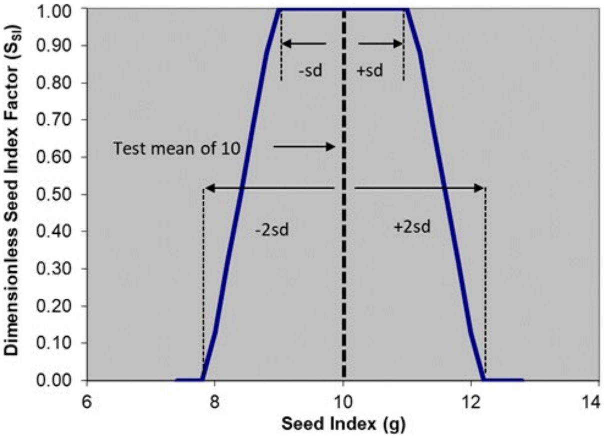

Figure 2. Example of the normalization of Seed Index for a trail with a mean of 7 g, and standard deviation (sd) equal to 1.07 g.

The described S-score calculations were performed in an Excel spreadsheet and macro (Microsoft 365, version 2011). The spreadsheet can be obtained through a request to the third author (DJones@cottoninc.com). S-score weightings of the two parameters in this paper were SI = 50% and LI = 50%. These weightings reflect equal importance of SI and LI but can be altered by the S-score user.

Variation in S-score, SI, and LI. Individual plot data (two replications per location) for SI and LI were extracted from the 2015 through 2020 Arkansas Transgenic Cotton Variety Tests (Bourland et al., 2016, 2017, 2018, 2019, 2020, and 2021). S-scores associated with these plots were determined using the S-score app. SI, LI, and S-score data were analyzed by SAS v. 9.4 PROC GLM (SAS Institute, 2013). For data collected over years and locations, years and replications were considered to be random while entry and location were fixed. Differences among means for each parameter were examined by a protected, two-tailed LSD test at the 0.10 probability level. Carmer (1976) indicated that significance levels in the range of $\alpha = 0.20$ to 0.40 were more defensible than traditional values of $\alpha = 0.05$ or 0.01 for making LSD comparisons among means in most agronomic trials. His logic was that Type II errors are more important that Type I errors in crop performance trials, and that Type II errors are lowered at high probability levels.

The data were first analyzed within years over locations using data from all cultivars in the tests. Data were then extracted for the 12 common entries in the 2015 through 2017 tests, and the 15 common entries in 2018 through 2020 tests. These extracted data were analyzed over years in two separate analyses. The 2015 through 2020 Arkansas Transgenic Cotton Variety Tests had 25 cultivars that were evaluated at least three consecutive years. To observe the variation over years within a cultivar, S-score means over locations for these 25 transgenic cultivars were determined and means and standard deviations were calculated for each cultivar.

RESULTS AND DISCUSSION

Variation in S-score, SI, and LI. Cultivar was the major source of variation and cultivars differed for SI, LI, and S-score within each year of the 2015 through 2020 Arkansas Transgenic Cotton Variety Tests (Table 2). Location effects did not affect S-score but did affect SI and LI in four of the six years. The cultivar × location interaction was significant in two, four, and four of the six years for SI, LI, and S-score, respectively. However, the same cultivars tended to express high and low values for the traits each year.

Table 2. Statistics associated with S-score, seed index, and lint index in Arkansas Transgenic Cotton Variety Tests, 2015-2020

Parameter	2015	2016	2017	2018	2019	2020
No. cultivars (Cult.)	32	35	41	65	50	51
No. locations (Loc.)	5	5	5	5	5	4
Seed-score						
Mean	67.8	69.7	69.1	69.4	69.0	70.8
Low	43.4	40.9	47.9	18.1	43.2	37.4
High	84.7	88.7	84.7	88.6	85.0	91.8
Cult. LSD 0.10	9.0	6.8	8.7	6.6	8.6	8.7
Loc. LSD 0.10	ns	ns	ns	ns	ns	ns
C.V. %	18.0	13.2	17.0	12.9	16.9	14.9
R^2 x 100	71.4	80.0	68.9	82.4	67.8	79.2
Prob (cult x loc)	0.1097	0.3438	0.1162	<.0001	0.8982	0.0283
Seed index						
Mean, g	10.7	10.2	9.9	10.1	9.0	9.5
Low, g	9.1	8.8	8.5	8.2	8.2	8.0
High, g	12.4	12.2	11.9	12.1	11.4	11.5
Cult. LSD 0.10, g	0.4	0.3	0.4	0.3	0.4	0.5
Loc. LSD 0.10, g	0.2	0.1	ns	0.1	ns	0.1
C.V. %	5.0	4.3	5.3	4.4	5.4	5.8
R^2 x 100	90.9	90.8	86.3	91.6	89.4	85.0
Prob (cult × loc)	0.0070	0.1600	0.1850	0.0003	0.0290	0.0760
Lint index						
Mean, g	7.7	7.5	7.7	7.7	7.5	7.4
Low, g	6.4	6.5	6.6	6.1	6.6	6.1
High, g	8.6	8.5	8.6	9.0	8.5	8.4
Cult. LSD 0.10, g	3.0	0.3	0.4	0.3	0.3	0.4
Loc. LSD 0.10, g	0.1	0.1	0.1	ns	ns	0.1
C.V. %	5.5	5.0	6.2	4.7	4.7	5.9
R^2 x 100	84.4	85.7	79.1	85.8	85.8	85.3
Prob (cult × loc)	0.1780	0.0920	0.5370	0.0202	0.0280	0.0080

Yearly means for S-score and LI were relatively similar over years, whereas SI means appeared to decline in 2019 and 2020 (Table 2). A low S-score value (18.1) was found in 2018 and was associated with ‘DG 3433 B2XF’. This cultivar also expressed the lowest SI (8.2 g) and lowest LI (6.1 g) of the 65 cultivars evaluated in 2018 (data not shown). Because this cultivar was only entered into our test in 2018, we were unable to determine if these low cultivar values were consistent over years. The next lowest S-score in the 2018 was 44.2, which was similar the lowest S-score value found each year. The R^2 values for S-score were relatively high, but consistently lower than R^2 values for SI and LI. Because S-score incorporates variability from SI and LI, lower R^2 values might be expected.

The 2015-2017 data set and the 2018-2020 data set produced 12 and 15 common cultivars, respectively. When both data sets were analyzed over years and locations, the greatest source of variation for S-score, SI, and LI was cultivars (Table 3). SI was affected by years and by locations in the 2018-2020 tests, but not in the 2015-2017 data set. S-score and LI were not affected by years or by locations. S-score, SI, and LI were affected by the year × location interaction in 2015-2017 data set but not in the 2018-2020 data set. In contrast, year × cultivar interaction was significant for S-score, SI, and LI in the 2018-2020 data set but not in the 2015-2017 data set. The only significant location × cultivar and three-way interaction for S-score, SI, and LI was a three-way interaction for LI. The different sources of variation were relatively similar for both S-score and Q-score, particularly in the 2018-2020 data set.

Table 3. Probability values associated with sources of variation associated with cultivars in the 2015-2017 and the 2018-2020 Arkansas Transgenic Cotton Variety Tests

Source of variation	S-score	Seed index	Lint index	Q-score
2015-2017 tests – 12 common cultivars				
Year (Y)	**0.5008**	**0.4603**	**0.7377**	**0.2017**
Location (L)	**0.3242**	**0.4311**	**0.5303**	**0.3670**
Y × L	**0.0826**	**0.0013**	**0.0012**	**0.9277**
Cultivar (C)	**<0.0001**	**<0.0001**	**<0.0001**	**<0.0001**
Y × C	**0.2377**	**0.4198**	**0.8038**	**0.3352**
L × C	**0.2393**	**0.1080**	**0.1571**	**0.8599**
Y × L ×C	**0.5364**	**0.3716**	**0.0802**	**0.0653**
2018-2020 tests – 15 common cultivars				
Year (Y)	**0.2980**	**0.0794**	**0.4294**	**0.1778**
Location (L)	**0.1992**	**0.0584**	**0.2593**	**0.2153**
Y × L	**0.8366**	**0.1213**	**0.0109**	**0.8890**
Cultivar (C)	**<0.0001**	**<0.0001**	**<0.0001**	**<0.0001**
Y × C	**0.0360**	**0.0564**	**0.0637**	**0.0220**
L × C	**0.0291**	**0.5228**	**0.3389**	**0.0280**
Y × L ×C	**0.6178**	**0.3785**	**0.7434**	**0.6086**

Considerable variation was found in S-score among cultivars with a range greater than 25 points in each data set (Table 4). Both data sets demonstrated that low S-score values can derived from either very high or very low SI values (Table 4). Most cultivars having the highest S-score values expressed moderate SI and high LI, and most cultivars having the lowest S-score values expressed low SI and LI. However, the lowest three S-score values in both sets of data included cultivars having the lowest and highest SI. This should be expected because S-score favors moderate SI values and penalizes both low and high SI values. Surprisingly the lowest three S-score values in both data sets included cultivars having the lowest and second highest LI. In both data sets, high LI values were negated by the highest ranked SI values.

'DG 3385 B2XF', 'DP 1518 B2XF' and 'DP 1646 B2XF' were common to both the 2015-2017 and the 2018-2020 data sets (Table 4). SI and LI values for DG 3385 B2XF and DP 1646 B2XF were similar in each data set. However, SI for DP 1518 B2XF was higher in the 2015-2017 data set than in 2018-2020 data set. This change in DP 1518 B2XF suggests some subtle, unintentional change might have occurred in the cultivar or might be associated with genotype × environment interaction.

For the 25 cultivars evaluated in three or more years, S-scores were relatively consistent across the 2015 through 2020 tests (Table 5). Standard deviations associated with S-score for 18 of the 25 cultivars were less than 3.9. Even with the shift in SI, the standard deviation associated with S-score for DP 1518 B2XF over the six years was relatively low. The highest standard deviations in S-score were found for 'DP 1614 B2XF', 'PHY 480 W3FE', and DP 1646 B2XF.

Variation in S-score can be visually observed. S-score varied from 33 to 97 in the 2020 Arkansas Transgenic Cotton Variety Test at Marianna (Fig. 3). The three cultivars having the highest S-score exhibited high LI and moderate SI. Two of three low S-score values were associated with cultivars which had the low LI and the lowest SI. The other low S-score cultivar had moderately high LI but was penalized for its very high SI.

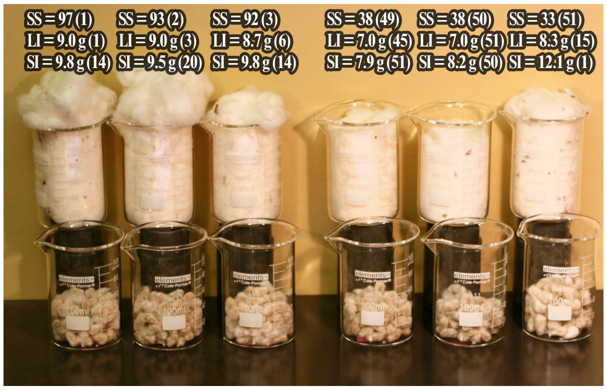

Figure 3. Seed index (SI) and lint index (LI) for cultivars having the three highest (left three) and three lowest (right three) S-scores (SS) in 2020 at Marianna. Numbers in parenthesis are rank out of 51 cultivars.

Table 4. S-score, seed index, and lint index means and ranks over four locations for cultivars common in the 2015-2017 and the 2018-2020 Arkansas Transgenic Cotton Variety Tests

Cultivar	S-score	Rank	Seed index	Rank	Lint index	Rank
2015-2017 tests – 12 common cultivars						
PHY 312 WRF	77.5	1	10.9	3	8.1	3
DG 3385 B2XF	77.0	2	10.3	6	7.8	4
PHY 444 WRF	75.3	3	11.3	2	8.5	1
NG 3406 B2XF	74.0	4	10.4	5	7.5	7
NG 3522 B2XF	74.0	5	10.0	7	7.6	6
DP 1522 B2XF	72.8	6	9.9	9	7.4	8
DP 1639 B2XF	69.1	7	9.2	10	7.6	5
DP 1612 B2XF	68.8	8	10.8	4	7.4	9
DP 1518 B2XF	68.2	9	10.0	8	7.1	11
ST 4946 GLB2	58.7	10	11.7	1	8.1	2
DP 1614 B2XF	56.0	11	8.9	11	7.3	10
DP 1646 B2XF	51.9	12	8.8	12	7.0	12
Cultivar LSD (0.10)	2.9		0.1		0.8	
2018-2020 tests – 15 common cultivars						
DG 3385 B2XF	77.8	1	10.2	3	7.9	2
PHY 400 W3FE	77.1	2	9.3	7	7.6	8
DG 3317 B3XF	76.8	3	9.3	8	7.7	7
PHY 480 W3FE	76.3	4	10.0	4	7.8	4
ST 4550 GLTP	75.4	5	8.9	10	7.7	6
DP 1725 B2XF	74.0	6	8.8	12	7.8	5
PHY 500 W3FE	72.8	7	8.9	11	7.4	9
PHY 350 W3FE	71.9	8	10.2	2	7.8	3
NG 3729 B2XF	71.4	9	9.7	6	7.2	11
NG 4936 B3XF	67.7	10	9.7	5	7.0	13
Armor 9608 B3XF	65.0	11	8.7	13	7.4	10
DP 1518 B2XF	64.3	12	9.2	9	6.9	14
DP 1646 B2XF	62.0	13	8.6	14	7.0	12
PHY 360 W3FE	55.4	14	8.5	15	6.8	15
DG 3520 B3XF	49.4	15	11.4	1	7.9	1
Cultivar LSD (0.10)	6.6		0.3		0.2	

Use of S-score in Cotton Cultivar Development Program. S-score will most likely be used as a secondary selection criterion in cotton cultivar development programs. Primary selection should continue to be placed on lint yield and fiber quality parameters. Without attention to SI, selection for high lint yield tends to be accompanied by increased lint percentage and lower SI. S-score brings attention to seed size by identifying those high performing cultivars that have favorable combinations of SI and LI values. With only two replications sampled per location in the Arkansas tests, a mistake made in one sample can greatly skew S-score values for a cultivar at one location. Like Q-score, the accuracy of S-score increases with number of samples. Thus, Q-score and S-score values averaged over locations should be given more credence than single location values.

Selection based on increased lint percentages results in smaller seed size. In contrast, selection based on increased lint per seed results in larger seed size. S-score provides a quantitative method of identifying cultivars and lines that possess both high lint per seed and moderate seed size.

Table 5. Seed-Score (S-score) for 25 cultivars evaluated in three or more years in the 2015 through 2020 Arkansas Transgenic Cotton Variety Tests

Cultivar	S-score over locations by year[z]						Mean	S.dev.
	2020	2019	2018	2017	2016	2015		
DG 3317 B3XF	78.3	76.0	82.0				78.8	3.0
PHY 400 W3FE	76.6	79.9	79.7				78.7	1.9
DG 3385 B2XF	83.8	78.2	74.2	78.6	76.5	77.6	78.2	3.2
DP 1725 B2XF	82.9	83.1	71.6	73.8	78.5		78.0	5.2
ST 4550GLTP	78.1	78.3	77.5				78.0	0.4
PHY 312 WRF			75.7	71.5	82.4	79.2	77.2	4.7
PHY 444 WRF			78.7	79.6	71.3	78.6	77.1	3.9
PHY 340 W3FE		78.6	76.4	74.7			76.6	2.0
NG 3522 B2XF				72.2	75.2	78.1	75.2	3.0
NG 3406 B2XF				71.9	76.9	76.1	75.0	2.7
PHY 480 W3FE	74.5	79.2	75.5	63.1			73.1	7.0
PHY 500 W3FE	73.8	75.0	70.4				73.1	2.4
DP 1522 B2XF				74.0	73.0	68.7	71.9	2.8
NG 3729 B2XF	69.4	70.7	73.5				71.2	2.1
DP 1823NR B2XF		73.0	67.3	71.6			70.6	3.0
DP 1639 B2XF				72.6	68.2	69.3	70.0	2.3
Armor 9608 B3XF	70.5	75.8	62.4	69.8			69.6	5.5
DP 1612 B2XF				70.0	71.2	67.3	69.5	2.0
DP 1518 B2XF	68.4	63.6	64.6	70.7	69.4	62.8	66.6	3.3
PHY 350 W3FE	66.5	68.9	66.5	62.7			66.2	2.6
DP 1646 B2XF	62.9	66.0	60.1	59.8	59.6	47.6	59.3	6.3
PHY 360 W3FE	60.0	59.2	58.0				59.1	1.0
ST 4946 GLB2				51.1	59.1	58.4	56.2	4.4
DP 1614 B2XF		60.5	62.1	47.9	62.5	43.4	55.3	9.0
DG 3520 B3XF	47.4	39.6	43.6				43.5	3.9

[z] Five locations each year except four in 2020. Two replications were sampled at each location.

SUMMARY

S-score incorporates weighted values of SI and LI into one numerical index. Entries in the Arkansas Cotton Variety Test over multiple locations from 1999 through 2020 produced 6,453 lines of SI and LI data. Each line represented the mean of two replications at each location within each year. Means and standard deviations of these data were used to develop a S-score app, which was patterned after the Q-score app used to index fiber quality. Users of S-score can adjust the relative weights of SI and LI but the weights must total 100%. Weights assigned for calculations of S-score in this paper were 50% SI and 50% LI.

S-score was calculated for entries in the 2015 through 2020 Arkansas Cotton Transgenic Variety Test. When analyzed over years and location, variability among cultivars was the major source of variation for S-score. For 25 cultivars that had been included in the tests for three or more years, average S-score ranged from 43.5 to 78.8. S-score values for cultivars were relatively consistent over years. Within cotton breeding and cultivar testing programs, S-score can be used to identify which lines possess favorable SI and LI.

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