NOVEL APPROACHES USED IN THE UNIVERSITY OF ARKANSAS COTTON BREEDING PROGRAM

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Abstract

To remain viable, breeding programs must make adjustments to meet changing needs and to take advantage of new opportunities. The University of Arkansas Division of Agriculture has maintained cotton breeding programs since the 1920's. Currently, the program is housed at the Northeast Research and Extension Center, Keiser, AR. An overview of the procedures used in this program was published in 2004. The objective of this paper was to chronicle modifications to the selection criteria and procedures that have been made since 2004. In addition to changes in some test locations and number of genotypes in different generations, several selection criteria have been added and/or modified. These include changes in the measurements of yield components, in the evaluation of resistance/tolerance to seedling diseases, bacterial blight, Verticillium wilt, root-knot nematode, and tarnished plant bug, and in the characterization of fiber quality. These modifications have aided in the development and descriptions associated with 43 germplasm lines and three cultivars released from the program since 2004.

Introduction

The art of cotton breeding was once described by Dr. Bob Bridge, renowned cotton breeder (now deceased), as trying to get a bunch of monkeys up a tree. Just when you think you have them all there, one will fall out. These "monkeys" (traits) include aspects of seed quality, pest (insect and disease) resistance, temperature (cold and heat) tolerance, various favorable morphological traits, maturity, plant conformation, characteristics associated with harvest and ginning efficiency, yield components and fiber quality. In addition, several transgenic traits have recently been added to some programs.

Maintaining positive expression for these traits in a breeding program requires constant attention and effort. To improve cotton lines, breeders sometimes employ novel traits or new expressions of established traits. To facility such improvement, breeders must find, establish, and maintain variation for important traits in their program, then re-direct selection as demand changes. Barriers that hinder progress include establishing effective and efficient means to measure the traits, identifying useable genetic variation, and dealing with negative relationships of traits. A cotton breeder must constantly deal with a multitude of old traits ("monkeys") and be able to occasionally add new ones.

The basic procedures used in the University of Arkansas Cotton Breeding program remain similar to those presented in 2004 (Bourland, 2004). Logistic changes include moving field tests previously done on the Delta Branch Experiment Station at Clarkedale, AR, to the Judd Hill Cooperative Research Station near to Trumann, AR (located about 30 miles northwest of Clarkedale) in 2005. Both sites are on a Dundee silt loam soil. Other primary test sites remain the Northeast Research and Extension Center at Keiser (Sharkey clay); the Lon Mann Cotton Research Station at Marianna (Calloway silt loam); and the Southeast Branch Experiment Station at Rohwer (Hebert silt loam). All sites are furrow-irrigated, and span approximately 200 miles (north-south) in the Mississippi River Delta of Arkansas. This paper will chronicle other refinements and additions to the selection criteria and procedures used in the program, and document the release of germplasm lines and cultivars from the program since 2004.

Methods to Increase Yield Efficiency

Higher yield efficiency in cotton is generally expressed as producing more fiber using fewer inputs. Inputs can be understood in terms of time, nutrients, water, pest control, and ultimately production costs. The goal of cotton breeders is to develop cultivars that will produce consistently high yields over a wide range of environments and use minimum amounts of inputs. Yield efficiency can be enhanced by selecting lines that produce more favorable expression of yield components, and that are better able to cope with insect pests, diseases, and environmental stress.

Modify yield components

Cotton yields are greatly affected by the environment, and relative yields of cotton cultivars vary greatly in different

environments. To genetically improve yields, cotton breeders evaluate new lines over multiple locations and years. Modifying the basic components of cotton yield may provide a window to effectively select for improved yield efficiency. Most crop models define yield as the product of some determination of "number of seed per area" times the "weight per seed". For cotton yield, the "weight of fiber per seed" must also be considered. Lewis et al. (2000) modeled cotton yield simply as the "number of seed produced per area" multiplied by the "weight of fiber per seed". Obviously, a high number of seed per area is required for high yields, but heavy reliance on producing yield by increasing this component can lead to less stable yields. Reliance on seed production for yield leads to less stable yields because seed production requires more weight (seed makes up about 60% of seedcotton by weight) and energy (oil compared to cellulose production) than does lint production. Slight changes in the partitioning can result in significant lint yield increases. An increase of only 5 milligrams of fiber per seed produces about 75 lb/acre (84 kg/ha) in lint yield. Furthermore, the "weight of fiber per seed" component eliminates many of the possible interactions that normally affect yield (Groves, 2009).

In addition to the ginning and fiber quality measurements normally available in cotton testing, the only other parameter needed to calculate these yield components is seed index (weight of 100 fuzzy seed). Seed surface area (SSA) is then estimated by the regression equation suggested by Groves and Bourland (2010): SSA = 35.74 + 6.59SI, where SI is equal to seed index associated with the sample. We have found that "weight of fiber per seed" and its associated parameters of "number of fibers per seed" and "fiber density" (number of fibers per unit area of seed coat) are much less affected by environment than are lint yield or number of seed per area (Groves, 2009). Selection for high "weight of fiber per seed" alone results in lines with higher lint per seed, but also larger seed. In contrast, selection for high lint percentage will result in lines with higher gin turnout, but also smaller seed. Selecting for high fiber density may be an effective means to increase both yield and yield stability.

Increased resistance to tarnished plant bug

Due to their sheer numbers and diversity, insect pests are dynamic and will often shift with different cropping systems, control tactics, and crop management strategies. Eliminating one pest species or neutralizing it with insecticides often leads to enhanced damage by another pest species. Recent changes in cotton insect control in the U.S. illustrate this scenario. Over the past 15 years, boll weevils have been eradicated in most cotton areas and heliothine species (worms) are largely controlled with Bt cotton. The reduction of insecticide applications has had positive effects on the environment and on maintaining beneficial predators. Unfortunately, the elimination of insecticide applications for weevils and worms has frequently led to increased problems with plant bugs (*Lygus* spp.). Plant bug populations now have documented resistance to organophospate and pyrethroid insecticides. Neonicotinoid insecticides are applied as a seed treatment and as foliar treatments to combat plant bugs in cotton and are frequently used in other crops. With widespread and frequent use, plant bug resistance to this group of insecticides will likely evolve. New transgenic control of plant bugs may soon be available.

Cotton cultivars that are resistant to plant bugs have long been sought. Nectariless [no glands on leaves or bolls that exude nectar, which attracts insects] cottons have been shown to be effective for lowering plant bug populations – a degree of partial resistance. Over the past 40 years, cotton breeders have expended much effort to develop high yielding, nectariless cultivars. The most successful efforts have been 'Stoneville 825' in the 1980's and 'DP 0935 B2RF' in 2009. It is not clear why so few successful nectariless cultivars have been realized.

Using a modification of the method developed by Maredia et al (1994), we annually evaluate cultivars and breeding lines for resistance to tarnished plant bug (TPB). The lines are planted in short 1-row plots (replicated 8 to 12 times) in tests where populations of TPB are encouraged. A highly susceptible Frego bract line is planted (about one month prior to planting tests) in 4-row strips between tests, and is included as a check in each test. After building up in the early fruiting Frego bract strips, TPB populations move to the tests as the Frego bract strips mature. When TPB damage is observed in the Frego bract checks, examination for discoloration of the anthers in white flowers is initiated in each test. In the absence of boll weevils, this damage (called "dirty flowers") is associated with plant bugs. About six flowers per plot are examined for about five sample dates (near consecutive days). Data are accumulated over sample dates to establish "% dirty flowers" for each plot.

Variation in "dirty flowers" among cotton lines tends to be similar over years, suggesting genetic control of this trait. Studebaker and Bourland (2012) found that TPB treatment thresholds were reached at a slower rate (thus, reduced insect control costs) on lines characterized as resistant by our "dirty flowers" measurement. In addition, we have found "dirty flowers" of some nectaried lines to be as low as "dirty flowers" of nectariless lines. This suggests

that sources of resistance to TPB, other than nectariless, are present. We are now working to combine these other sources with nectariless to further improve resistance to TPB.

Increased resistance to diseases

Disease problems in cotton are often localized and generally cause less damage than insect pests. We routinely directly evaluate for four cotton diseases: seedling disease, bacterial blight, Verticillium wilt and root-knot nematode.

Most seedling disease problems can be effectively controlled with fungicides applied to the seed and/or in-furrow at plantings. However, improved genetic resistance can lessen the adverse effects of this disease and reduce reliance on chemical control. We have recently initiated work to evaluate relative resistance of advanced lines to seedling disease. In separate tests, advanced lines are screened for resistance to two major pathogens, *Rhizoctonia solani* and *Pythium* spp. Using large beds in the greenhouse, we plant seed treated to control one of the pathogens, then add inoculum of the other pathogen in the seed furrow. Stand is determined in the inoculated plots, and is evaluated with germination percentage (determined in standard germinator) as a covariant. Variation in stand (corrected for germination percentage) is then assumed to be associated with the inoculated pathogen.

Bacterial blight (also known as angular leaf spot) is not a major disease, but resistance to the disease is well-defined and easily established. Bird (1982) indicated that resistance to bacterial blight is based on multiple genes, and may be related to some degree of resistance to other pests. Most of the crosses in the UA cotton breeding program include at least one resistant parent. After making crosses, plants in subsequent generations in the breeding nursery and seed increases are annually inoculated with multiple races (always including race 18) of *Xanthomonas axonopodis* pv. *malvacearum* (Smith) Dye, the causal agent of bacterial blight, using the field inoculation procedures described by Bird and Blank (1951). Plants resistant to race 18 are resistant to all known races occurring in the U.S. A "MudMaster" (Bowman Manufacturing, Newport, AR) sprayer equipped with a 4-row, front-mounted boom (2 nozzles per row) is used. The nozzles with TX8 cone tips are pointed up into the plant canopy. The 110 gallon tank is filled with non-chlorinated (well) water, 40 to 80 plates of inoculum (removed from petri plates, mixed with water, and strained through cotton cloth), and 750 ml of organosilicone surfactant (Agrisolutions Silkin™). Plants (about 4-leaf stage) are inoculated early in the morning (stomata open) with nozzles pointed upward to the abaxil side of leaves using about 50 psi pressure (approximately 1100 row feet inoculated per gallon). Symptoms are evaluated about two weeks after inoculation. Susceptible plants are removed from the early-generation populations and subsequent seed increases. Progeny rows having susceptible plants are normally discarded. Thus, most lines released from this program are highly resistant to this disease.

Verticillium wilt tends to be localized in areas with specific soils and certain temperature regimes during boll development. Since pre-mature boll opening is one of the symptoms of Verticillium wilt, visual rating of disease symptoms is often confounded with variation in plant maturity. Our Judd Hill (Arkansas) test site is naturally infested with the Verticillium wilt pathogen, but severity of the disease differs greatly from year to year. We assume that cotton lines that produce high relative yields at this location are expressing tolerance to the disease. Due to cool temperatures of irrigation water, disease symptoms are typically most severe in the area nearest to the irrigation pipe. In 2012, we began evaluating Verticillium wilt tolerance at Judd Hill by planting replications of lines adjacent to the irrigation pipe. Plants in these plots were thinned to a uniform stand (approximate 2 plants per row foot), and wilt symptoms were visually rated. Under these conditions, Verticillium wilt symptoms tend to occur earlier and were less confounded with plant maturity. Greenhouse screening for resistance to Verticillium wilt has also been initiated.

The most widespread occurring nematode problems on cotton are the root-knot and reniform nematodes. Columbian, lance and the lesion nematode are important in some areas. Genetic resistance to root-knot nematode is presently available, but it has been difficult to combine resistance with good agronomic performance. Marker DNA technology may facilitate this. For several years, we have attempted to improve resistant to root-knot nematode by screening in the greenhouse. Nematode infested roots are incorporated into large beds filled with soil conducive to the disease. Cotton lines are planted in the beds, and allowed to grow until galls begin to form on the roots. Watering of the beds is then stopped, and plants are evaluated for how well they survive drought conditions. Resistant plants should be able to develop better roots in the nematode infested soil, and consequently be able to better survive the drought conditions.

Increase stress tolerance

Lack of water and excessive heat are frequently the most limiting factors in cotton production. When supplemental irrigation is not available, the effects of drought may be lessened by improved rooting systems. Due to difficulty in observing roots, research on rooting systems is limited. About 30 years ago, we were able to increase the number of lateral roots on cotton seedlings by selection (Bourland et al., 1985). However, simply increasing the number of seedling roots may not necessarily be related to final root mass or effectiveness of the roots. Factors other than root mass determine the plant's ability to absorb water and nutrients. To make progress in this area, a better understanding of the physiology of roots is needed to define the optimum rooting system.

Excessive heat often accompanies drought. In humid areas, high night temperatures are particularly harmful. The ability to tolerate high day temperatures in arid regions may not necessarily be related to the ability to tolerate high night temperatures in humid regions. A simple, quick method to accurately quantify heat stress is needed. Methods, such as membrane leakage and fluorescence before and after heat stress, as well as, examining certain pre-stress antioxidant levels, are presently being examined (Oosterhuis, 2011). The latter is particularly exciting because it can be done relatively quickly in the field. Such a measurement may provide us a method to genetically improve heat tolerance.

Methods to Improve Fiber Quality

Although the first priority for evaluating a cultivar must be its ability to produce competitive high yields, high yields have less value if the cotton is difficult to market. Marketing of low quality cotton may be subject to high price discounts and delayed cash flow. Adverse environmental conditions will always provide an ample supply of low quality cotton. Historically, marketing of low quality cotton has often been supported by governmental marketing loans. Re-structuring or elimination of these loan programs will further weaken marketing opportunities for low quality fibers. Consequently, the development of cotton cultivars possessing enhanced cotton fiber quality is essential for sustaining long-term cotton production in any region. Cultivars possessing a genetic capacity for higher fiber quality can build and sustain greater marketability and price. Even with harsh growing conditions, such cultivars will maintain a better quality than cultivars without a high capacity for quality.

Q-score

Ideally, breeders would like to have one parameter to characterize fiber quality. To address this desire, Bourland et al. (2010) developed "Q-score", a simple numerical index based on up to six HVI fiber parameters. Fiber properties and their relative contributions to Q-score calculations initially used in Q-score included fiber length (50%), micronaire (25%), fiber length uniformity (15%) and fiber strength (10%). These weights were based upon perceived demands of the current cotton market, and were particularly weighted in favor of fibers desirable for ring-spinning technology. Users of Q-score may change the relative weights of these four HVI parameters and add weights for elongation and short fiber content.

Q-score can be effectively used throughout the breeding process beginning with evaluation of non-replicated data from individual plant selections (IPS) and progenies and ending with replicated data used in the release of a genotype. A primary benefit of Q-score with regard to IPS and progeny is the reduced time and effort required to make selections. Breeders typically make hundreds or thousands of IPS each year. Discarding IPS based on relative values for multiple fiber property traits is a daunting task. Without the use of Q-score, a breeder will usually examine each fiber parameter value for an IPS, and determine whether each value is within some arbitrary tolerance limit. Frequently, the breeder must then mentally assign weights to the different parameters to determine which IPS to discard. Sorting the data by Q-score facilitates rapid discard of lower quality lines and recognition of high quality lines. Once Q-score is calculated in a spreadsheet, the IPS can be sorted by their relative Q-score. Lines having low Q-score values can be quickly and painlessly discarded.

The HVI parameters of elongation and short fiber content may be employed in Q-score calculations, but have received little attention. In most tests, genotypes display significant variation for elongation. Since standard values have not been established, elongation values often vary greatly among years and among testing laboratories. Without established premium and discount values for elongation, its use in Q-score is limited. In contrast to the measure of elongation, genotypes seldom display meaningful variation for short fiber content. This may be related to the small laboratory gins employed by breeders. Without meaningful differences in a trait, breeders can make little progress.

Since Q-score does not include consideration of trash or color, it does not completely define fiber quality. Meaningful measures of trash and color are typically not available from small samples that are taken and processed by breeders. Color is primarily affected by field conditions after boll opening and prior to harvest, and by conditions during storage and ginning. Since color has little genetic basis, breeders have little opportunity to improve color grades of cotton.

Reduce leaf trash in cotton fiber

By reducing plant hairiness, breeders can effectively reduce trash content in ginned fiber. Breeders may consider both leaf and bract pubescence ("hairiness") and give preference to breeding lines and cultivars having lower pubescence on leaves and bracts. Reduced pubescence on cotton leaves has been associated with improved seedcotton cleaning efficiency and low foreign matter levels in harvested lint, and thus higher leaf grades in ginned cotton (Novick et al., 1991). To assist with characterizing leaf pubescence, Bourland et al. (2003) developed a rating system that could be easily used to identify less pubescent genotypes. Using this rating system, six random plants from every progeny row and replicated plot are characterized for leaf pubescence by examining the abaxial side of a fully-expanded main stem leaf (approximately 5 nodes from plant apex). By making these ratings near the time of physiological cutout, work fatigue (due to bending over to examine younger plants) is lessened and sampling of partially senescent leaves is avoided. Since genotype by location interaction is not strong, these evaluations are preformed at only one location. Based on these characterizations, off-type plants can be removed from seed increases. We also characterize stem pubescence using this rating system. After plots are defoliated and harvested, the uppermost expanded internodes of six random plants per plot are rated from 1 (glabrous) to 9 (pilose, very hairy).

Pubescence on cotton bracts has received relatively little attention. Bracts are modified leaves surrounding the flower buds and bolls of the cotton plant. Morey et al. (1976) found that bracts are a major contributor to "leaf trash" in harvested cotton. This seems reasonable since bracts are in closer proximity to the cotton fibers than are plant leaves, and most leaves are removed from the plant prior to harvest if defoliation is successful. By examining variation in marginal bract trichomes ("hairs") on different canopy positions and cultivars as well as over time and environments, sampling methods were established by Bourland and Hornbeck (2007). They found that glabrous leaf genotypes tended to have lower marginal bract trichome density than did hairy leaf genotypes, but there was some overlap of bract trichome density among glabrous and hairy leaf genotypes. Of all the Upland cotton genotypes that we have examined, none were found to have glabrous marginal bract surfaces. Hornbeck and Bourland (2007) found significant, but low magnitude ($r = 0.33$ to 0.35), correlations between trichome density on abaxial leaf and marginal bract surfaces. This suggests some degree of independence of the two traits. Preliminary results from a ginning study of contrasting cultivars appear to verify that lower marginal bract trichomes are related to lower trash in ginned cotton (Boykin and Bourland, 2012). We determine bract trichome density for all replicated tests at one location. After physiological cutout, bracts from a mid-canopy, first-position boll are taken from six random plants per plot. The bracts are labeled, and placed in a freezer. At our convenience, the bracts are removed from the freezer and thawed on wetted germination paper. Marginal trichomes are counted in two areas of each bract using a viewing telescope, and expressed as number per cm. Selection preference is given to lines with low bract trichome density – regardless of their leaf pubescence rating.

Advancement of Lines

In most cotton breeding programs, about 10 years is needed from making an initial cross to release of a new cotton cultivar. The required time may increase if transgenes are introgressed. In the University of Arkansas Cotton Breeding Program, crosses are made in year 1 and F_2 seed are increased in a winter nursery (Table 1). Segregating populations are grown in years 2, 3, and 4 with modified single seed descent (SSD) selection made in years 2 and 3. The modifications to SSD are that a single boll (instead of a single seed) is taken from each plant; bolls are not taken from plants deemed to not meet specified selection criteria; and a set number of bolls (150) is harvested from each population. After two years of modified SSD, individual plant selections are made in year 4. Genotypes from the individual plants are evaluated for two years in non-replicated progeny rows at multiple locations. Seedcotton yields for progenies are measured at each location using a cotton picker modified with a weigh system. Priority is given to progenies which have yields that equal or exceed those of check cultivars. Seedcotton is harvested from all progeny planted at Keiser, then ones selected for yield are ginned and processed for fiber and seed samples. For 1st-year progeny, seedcotton is collected by placing a mesh bag over the chute carrying seedcotton from one of the back

drums (harvests inside of two-row plot). For advanced progeny, the inside two rows of 4-row plots are harvested with a picker modified to catch all seedcotton from plot in large mesh bags. Since the Bourland (2004) report, the number of test locations has been reduced from two to one for F_3 and F_4 generations, and increased from two to three for the F_6 generation.

Table 1. Development of breeding lines in the University of Arkansas Cotton Breeding Program.

Year	Gen.	Selections made:	No./yr.	Location(s) tested
1	Parents	Parents selected and crossed	20-30	Keiser
1	F_1	Generation advanced during winter	20-30	Winter nursery
2	F_2	Modified SSD selection (screened for bacterial blight resistance; morphological & fruiting traits)	20-30	Keiser
3	F_3	Modified SSD selection (screened for bacterial blight resistance; morphological & fruiting traits)	20-30	Keiser
4	F_4	Plants selected (selection pressure based on fruiting habit, plant conformation & fiber quality)	1000	Keiser
5	$F_{4:5}$	Progenies to advanced progenies (based on HPR traits, yield, & fiber quality)	200	Keiser, Judd Hill
6	$F_{4:6}$	Advanced progenies to strains (based on HPR traits, yield, & fiber quality)	72	Keiser, Marianna, Rohwer

After screening for yield enhancement and fiber quality traits (noted above), selected advanced progenies are promoted to strain status, and evaluated in replicated strain tests for up to four years (Table 2). In recent years, testing of Preliminary Strains has increased from three to four tests and from two to four locations. To better estimate their adaptation, some advanced strains are typically entered into regional strain tests (Regional Breeders Testing Network and/or Regional High Quality) during the third and fourth year of replicated testing. After four years of replicated tests, strains are usually released (as a germplasm line or cultivar) or are discarded. Seed of strains are increased in 4-row plots at Keiser. The inside two rows of 4-row plots are rogued for off-types, and then harvested with a picker modified to catch all seedcotton from a plot in a large mesh bags.

Table 2. Testing (selection made for yield, host plant resistance traits, and fiber quality in each generation) of strains in the University of Arkansas Cotton Breeding Program.

Year	Gen.	Replicated test (typically 4 reps, 2-row plots)	No./yr.	Locations tested
7	$F_{4:7}$	Preliminary Strain Tests (18 strains + 2 checks in four tests)	72	Keiser, Judd Hill, Marianna, Rohwer
8	$F_{4:8}$	New Strain Test (18 strains + 2 checks), + seed increase in AZ	18	Keiser, Judd Hill, Marianna, Rohwer
9-10	$F_{4:9-10}$	Advanced Strain Test (18 strains + 2 checks)	18	Keiser, Judd Hill, Marianna, Rohwer
9+	$F_{4:9+}$	Regional strain tests and state cultivar tests	1-4	Arkansas and other states

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Overcoming negative associations

Once a trait is defined and a selection method is established, progress can usually be made to improve that trait. However, improvement in one trait can result in a corresponding negative expression in another trait. Negative relationship between yield and fiber quality provides a good example. If improved yield and fiber quality were positively related, fiber quality would be improved as breeders have selected higher yielding cultivars. This obviously has not been the case. Strong negative associations have long been found between lint yield and many fiber traits (Al-Jibouri et al., 1958; Meredith and Bridge, 1971).

Using data sets from both Australia and U.S., Clement et al. (2012) showed that negative associations still exist between yield and fiber quality parameters. In each set of data, they found that fiber length and strength had significant negative associations with yield; fiber maturity had a positive association with yield, while associations of micronaire and fineness with yield were inconsistent. Progress toward weakening the strong negative associations appears to be occurring in the Australian cotton breeding program.

Poor relationships that are not genetically bound together can be broken, but considerable effort and focus is usually required. Historically, one of the strongest negative relationships was between yield and fiber strength. Culp et al. (1979) was successful in breaking the negative association between fiber strength and yield. Their findings and subsequent germplasm releases have led to improved fiber strength among high yielding cultivars, and demonstrate that many negative relationships can be broken.

Placing a high priority on fiber quality traits in early generations is an approach that appears to help break the negative relationships of fiber quality and yield. As noted above, Q-score greatly facilitates the process of discarding individual plant selections and progeny based on fiber quality. Evaluation on the basis of Q-score can be accomplished with little prejudice since limited other data are available and relatively little time and effort have been invested in the genotype. In addition, discarding individual plants prior to planting decreases the time and space required for field evaluation of progeny. Using high selection pressure for fiber quality in early generations insures that only high fiber quality lines will be advanced in a breeding program. The goal then is to find the best yielding line among the selected high fiber quality lines.

The relative yield and fiber quality of UA48 documents the success of this approach. Over years, UA48 produced lint yields equal to two standard conventional cotton cultivars. Its fiber quality greatly exceeded either check cultivar. Moreover, UA48 matures earlier than either DP 393 or SG 105, both of which are considered to be early maturing cultivars. This combination of early maturation, competitive yields, and exceptional fiber quality is unprecedented. Additional information on this cultivar is available in its registration publication (Bourland and Jones, 2012).

Genetic Materials Released Since 2004

Since 2004, the University of Arkansas Cotton Breeding Program has released 43 germplasm lines and three cultivars (Table 3). All are conventional cottons. All, but four (Arkot S23-1 Arkot S23-2, Arkot S23-4, and Arkot JJ46) are resistant to bacterial blight, and most are early maturing lines. The early maturation characteristic of these lines may be related to their selection in the northern range of the U.S. cotton belt. All of the lines have normal leaf shape (except UA103, an okra leaf line) and nectaries (except four with “ne” as suffix in their names). Pubescence on leaves, stems, and bracts vary from glabrous to very hairy. Exception fiber quality is displayed by UA48, UA222, UA103, and Arkot 0111. The other lines generally display values for fiber quality parameters within acceptable commercial ranges. Other characteristics and adaptation of the lines are chronicled in their respective citations.

Table 3. List of germplasm lines and cultivars released from the University of Arkansas Cotton Breeding Program since 2004.

Release date	Line	Citation	GP	PI
2004	Arkot 8712	Crop Sci. 45:1173-1174	791	636101
2004	Arkot 9111	Crop Sci. 45:2127-2128	798	638506
2004	Arkot 9101	Crop Sci. 45:2128-2129	799	638507
2004	Arkot 9108	Crop Sci. 45:2128-2129	800	638508
2005	Arkot 9203-03	Crop Sci. 46:1408-1409	853	641157
2005	Arkot 9203-17	Crop Sci. 46:1408-1409	854	641158
2005	Arkot 9202	Crop Sci. 46:1412	858	641159
2005	Arkot 9208	Crop Sci. 46:1412	859	641160
2005	Arkot S23-1	Crop Sci. 46:1409	855	641161
2005	Arkot S23-2	Crop Sci. 46:1409	865	641162
2005	Arkot S23-4	Crop Sci. 46:1409	857	641163
2005	Arkot 9406ne	Crop Sci. 46:1833-1834	863	641704
2005	Arkot 9605ne	Crop Sci. 46:1833-1834	864	641705
2005	Arkot 9631ne	Crop Sci. 46:1833-1834	865	641706
2005	Arkot 9315	Crop Sci. 46:2333-2334	866	641707
2005	Arkot 9409	Crop Sci. 46:2333-2334	867	641708
2006	Arkot 9304a	J. Plant Reg 1:56-57	870	643438
2006	Arkot 9304b	J. Plant Reg 1:56-57	871	643439
2006	Arkot 9308	J. Plant Reg 1:56-57	872	643440
2006	Arkot 9314	J. Plant Reg 1:56-57	873	643441
2006	Arkot 9506	J. Plant Reg 1:54-55	874	643442
2006	Arkot 9513	J. Plant Reg 1:54-55	875	643443
2006	Arkot RM24	J. Plant Reg 1:149	881	643444
2007	Arkot 9608ne	J. Plant Reg 2:125-128	888	651854
2007	Arkot JJ46	J. Plant Reg 2:235-238	890	651855
2007	Arkot 9610	J. Plant Reg 2:235-238	891	651856
2007	Arkot 9620	J. Plant Reg 2:235-238	892	651857
2008	Arkot 9623	J. Plant Reg 3:69-72	908	651858
2008	Arkot 9625	J. Plant Reg 3:69-72	909	651859
2008	Arkot 9704	J. Plant Reg 3:289-292	914	654509
2008	Arkot 9706	J. Plant Reg 3:289-292	915	654510
2008	Arkot 9721	J. Plant Reg 3:293-296	918	654511
2009	Arkot 9811	J. Plant Reg 4:232-235	919	658215
2009	Arkot 9815	J. Plant Reg 4:232-235	920	658216
2010	Arkot 0008	J. Plant Reg 5:374-378	932	660502
2010	Arkot 0009	J. Plant Reg 5:374-378	933	660503
2010	Arkot 0012	J. Plant Reg 5:374-378	934	660504
2010	Arkot 0015a	J. Plant Reg 5:379-383	935	660505
2010	Arkot 0015b	J. Plant Reg 5:379-383	936	660506
2010	Arkot 0016	J. Plant Reg 5:379-383	937	660507
2010	'UA48'	J. Plant Reg.6:15-18	CV-129	660508
2011	'UA222'	J. Plant Reg. 6:259-262	CV-130	664929
2011	'UA103'	In press		664928
2011	Arkot 0111	In press		664925
2011	Arkot 0113	In press		664926
2011	Arkot 0114	In press		664927

Summary

An overview of the procedures used in the University of Arkansas Cotton Breeding Program was published in 2004 (Bourland, 2004). This paper chronicles some of the modifications to the selection criteria and procedures that have been made since 2004. Logistical changes in the program have included movement of testing previously done at Clarkedale to Judd Hill, reducing the number of test sites associated F_3 and F_4 generation, and increasing the number of tests sites associated with the Advanced Progeny and the Preliminary Strain Tests. Selection criteria have been added and/or modified changes in the measurements of yield components (added estimate of seed surface area to determine fiber per seed and fiber density), in the evaluation of resistance/tolerance to seedling diseases (added greenhouse screening for *R. solani* and *Pythium* spp.), bacterial blight (inoculation procedures modified), Verticillium wilt (added the use of the field range adjacent to irrigation pipe to increase wilt incidence), root-knot nematode (added greenhouse screening), and tarnished plant bug (added field evaluation using "dirty flowers" technique), and in the characterization of fiber quality (developed and added the Q-score index of fiber quality; refined measurement of bract trichomes). These modifications have aided in the development and descriptions associated with 43 germplasm lines and three cultivars released from the program since 2004.

I have worked in cotton breeding either as a graduate student or project leader since 1970. Over the years, I have had the opportunity to work with and view many cotton breeding programs. In my mind, there are at least seven elements common to all successful breeding programs:

1. Accuracy of field measurements and understanding of field variation is given tireless attention.
2. Samples from harvest, ginning and processing of seed for planting are meticulously handled.
3. Novel selection techniques and experimental equipment are imaginatively added.
4. Limited resources – labor, land, time, equipment – are effectively used.
5. Genotypes progress through the program using a systematic (but amendable) plan without bias.
6. A broad, healthy curiosity conditioned by insights into industry needs is maintained.
7. PATIENCE!

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