2004 BELTWIDE COTTON CONFERENCES, SAN ANTONIO, TX – JANUARY 5-9

OVERVIEW OF THE UNIVERSITY OF ARKANSAS COTTON BREEDING PROGRAM

F.M. Bourland
Northeast Research and Extension Center
University of Arkansas
Keiser, AR

Abstract

Approaches and methods used by cotton breeders differ with specific breeding objectives, available equipment and facilities, and level of personnel and financial support. The objective of this paper is to provide an overview of the methods presently being employed by the University of Arkansas Cotton Breeding Program. Development of lines with improved host plant resistance and that are well suited to Arkansas cotton production has been and continues to be the primary emphasis of cotton breeding in Arkansas. Selection criteria include methods to improve host plant resistance (active and passive screens), increase yield parameters (earliness, yield and yield components), and enhance fiber quality. The selection criteria are used to develop breeding lines, which are evaluated in non-replicated tests. Superior breeding lines are promoted to strains and tested in replicated strain tests. Strains are eventually either discarded or released as cultivars or germplasm lines.

Introduction

A major emphasis of cotton breeding research at the University of Arkansas was initially, and continues to be, the development of host plant resistance and development of cotton lines that are highly adapted to Arkansas cotton production areas (Bourland and Waddle, 1988). In the 1920's, research was initiated by the Arkansas Agricultural Experiment Station to develop genotypes and techniques to combat the damages inflicted by a relatively new pest, the cotton boll weevil. Until effective insecticides became available, research efforts were directed toward discovering effective methods to produce cotton in spite of this insect pest. Escape from late season damage by the development of cultivars and systems, which allowed shortening of the production season provided the only means of boll weevil control. The establishment of the Cotton Branch Station at Marianna in 1927 significantly advanced these research efforts. Separate, but cooperating, cotton breeding programs were housed on the main campus at Fayetteville (J.O. Ware followed by B.A. Waddle) and on the Cotton Branch Station at Marianna (C.A. Moosberg followed by C.W. Smith) until the mid-1980's. In 1988, the two programs were merged into one program led by F.M. Bourland. The program was housed at Fayetteville until it was moved to the Northeast Research and Extension Center at Keiser in 1997.

The basic approach used in the present program was initiated in 1988, and has been modified over the years (Bourland, 1988, 1995, 1995). Approaches and methods used by cotton breeders differ with specific breeding objectives, available equipment and facilities, and level of personnel and financial support. The objective of this paper is to summarize the approaches and methods, which are currently used in the University of Arkansas Cotton Breeding Program. The approaches and methods are separated into three sections: selection criteria, development of breeding lines, and testing of strains.

Selection Criteria

The heart of any breeding program is the selection criteria used to evaluate individual plants in segregating populations and to choose superior breeding lines or strains. Selection criteria in this program are primarily concerned with improving host plant resistance, yield and earliness, and fiber quality.

Host Plant Resistance

Both "active" (intentional treatment made to enhance adversity) and "passive" (incidental occurrence of adversity) screens are used to improve host plant resistance. Active screens are presently being conducted for four diseases (seed deterioration, bacterial blight, root knot nematode, and Verticillium wilt) and two insects (thrips and tarnished plant bug). Passive screens are conducted for stress (drought/heat) tolerance and any leaf, plant terminal, or fruiting symptom associated with a known causal factor.

Resistance to Seed Deterioration. Bourland et al. (1988) developed a hot water technique to screen for resistance to seed deterioration. Seed from segregating populations are immersed in 65C (distilled) water for 0, 30 or 40 minutes, then removed and air-dried. The seed are then planted in field plots, and stand counts are made prior to thinning. Selections within populations are made from the highest treatments that provide adequate number of surviving plants.

Bacterial Blight. Inoculation and screening using specific races of *Xanthomonas campestris* pv *malvacearum* (Smith) Dye provide resistance to all known U.S. races of the bacteria (Bird, 1982). When parentage of a segregating population or a seed

increase line includes at least one resistant line, susceptible plants are removed. Progeny rows are inoculated and ones segregating for resistance are discarded.

Root Knot Nematode (RKN). Over the years, lines have been developed from crosses made with RKN resistant lines (Shepherd et al. 1996). With no active screen for RKN resistance, the resistance genes have apparently not been preserved in this material. In 2004, a pit (ca. 12x20x3(depth) foot) was dug and has been filled with sand from a RKN area. Prior to planting, the sand will be inoculated with RKN and covered with a plastic greenhouse. Segregating populations will be screened, and resistant plants will be transplanted for seed production. Also, lines will be evaluated for resistance in the pit and in a field that is naturally infested with RKN.

Verticillium Wilt. Fields at the University of Arkansas Delta Branch Station (Clarksdale) are naturally infested with the causal agent of Verticillium wilt. Reduced plant densities and increased nitrogen rates are employed to encourage incidence of wilt. Wilt tolerance is measured by visually rating the incidence of wilt and by yield in the wilt infested area.

Stress Tolerance. Work has been initiated with Derrick Oosterhuis (Plant Physiologist, University of Arkansas) to develop screens for evaluating stress tolerance. Present work is focusing on seed setting efficiency and on specific plant enzymes.

Yield and Earliness

Development of breeding lines that will produce high yields have been and will continue to be the primary objective of most cotton breeding programs. Attention to maintaining stable yields has increased as lines with higher yield potential have been developed. Presently, we are cooperating with researchers in Missouri and Tennessee to evaluate means to characterize stability of yield by using data pooled from variety tests.

Yield Measurement. Having cotton pickers equipped with load cells to weigh plot yields has facilitated yield determination of lines in early generations. Yields in F_2 through F_4 generations are used to determine the number of individual plants (selection pressure) to be selected in the F_4 generation. Yields of F_5 and F_6 progenies relative to adjacent check cultivars are used to advance progeny to strain status. Strains are evaluated at multiple locations spanning ca. 200 miles (north to south) in the Mississippi River Delta of Arkansas. Strains that yield well over locations and over years are assumed to have high yield stability.

Harvested seedcotton yields multiplied by lint percentage provide estimates of lint yields. In our program, lint percentages are determined from hand-harvested boll samples. We use boll samples, rather than grab samples, because our 10-saw gins are not equipped with burr extractors or lint cleaners. Also, subsequent machine harvest is not complicated by the collection of grab samples. For our boll samples, half of the bolls are collected from each of two rows. Within each row, a site having average or above plant density is chosen. When harvesting samples, all bolls on consecutive plants are harvested until the designated number is achieved. In replicated tests, typically 50-boll samples are collected from two replications. The average lint percentage is then used to convert seedcotton yields to lint yields in all replications.

Yield Components. Lewis et al. (2000) suggested a very simple model for cotton lint yield consisting of two components, number of seed per acre and weight of lint per seed. They suggested that yield stability might be improved by developing cultivars, which rely more heavily on weight of lint per seed rather than number of seed per acre to produce yield. The improved stability would be due to lower physiological requirements to produce fibers than seed.

Number of seed per acre is typically involved in yield models of most agronomic crops, and may be determined by multiplying seed per plant (which is often further broken into plant parts) times plants per acre. Seed yield is then equal to the number of seed per acre times the weight per seed. Cotton is unique among agronomic crops in that seed produce fibers, and these fibers are the primary concern of yield. Lint weight per seed is basically the same measurement as “lint index” (weight of lint per 100 seed), an frequently reported measurement in the early and mid-1900’s. The only measurements needed to calculate seed per acre and lint index are lint yield, gin data, and seed index (weight of 100 seed).

Obviously, lint index tends to increase as seed index increases. Selection primarily based on lint index would cause an increase in seed size, while selection primarily based on lint percentage tends to cause a decrease in seed size. Yield components are now being used in our breeding program from progeny through strain testing. Priority is given to lines, which produce high yields and possess moderate seed index and high lint index.

Earliness. In the past century, short-season concepts of producing cotton have seemed to appear and disappear in regular intervals. In the early 1900's, early production of cotton was seen as a way to escape ravishes of the boll weevil, which had become a new pest of U.S. cotton. Using short-season concepts, yields were increased and production costs declined. When new, more effective insecticides were developed, short-season concepts were generally abandoned - until the insects became resistant and lessened the effectiveness of the insecticide. Each time, the return to using short-season concepts to grow cotton provided increased yields with lower production costs. The advent of boll weevil eradication and the availability of Bt cotton do not negate many of the benefits of earliness and short-season cotton production.

Maturity may be expressed as percentage picked or mean maturity date determined with weights from multiple harvests or as days to physiological cutout determined by counts of nodes-above-white-flower (NAWF) over multiple dates (Bourland et al., 2001). Much labor is required to obtain multiple harvests or multiple counts of NAWF in breeding tests having many entries. In our tests, plant height measured after physiological cutout is used as an indicator of relative maturity of lines. Mepiquat chloride is used sparingly. If used, it is applied early (prior to first flower) and at low dosages so that genetic expression of height may be expressed. Multiple measurements of NAWF on check cultivars (having different expected maturity) are used to determine physiological cutout and manage insecticide termination and timing of defoliation for the entire test.

Fiber Quality

Fiber quality (micronaire, length, strength, and elongation) is determined from lint samples taken from individual plants and from boll samples in breeding tests and replicated strain tests. Typically, fiber quality of progeny is measured by "breeders' test" while "HVI" testing is used for individual plants and strain tests. Advanced strains are characterized by relative HVI fiber measurements over locations and years. Priority is given to high yielding lines that produce relatively long, strong, and fine (low micronaire) fiber.

Lint from smooth leaf cultivars is easier to clean and, consequently, tends to have less trash (improved leaf grades) relative to hairy leaf cultivars (Rayburn and Libours, 1983; Anthony and Rayburn, 1989). Leaf pubescence of progenies and strains are visually rated using a system developed by Bourland et al. (2003). Seed increases are subsequently rogued for specific leaf pubescence. Priority is typically given to lines with reduced leaf pubescence.

Recent work has concentrated on reducing marginal trichomes on bracts as a means of lessening trash in cotton (Hornbeck et al., 2003; Jackson et al. 2003). Significant variation in density of marginal trichomes has been found among smooth-leaf cultivars and among hairy leaf cultivars. Inheritance of marginal trichomes and relation to seed trichomes (fibers) are now being investigated with hopes of being able to reduce marginal bract trichomes independently of leaf and seed trichomes.

Development of Breeding Lines

A common feature of most successful cotton breeding programs is a planned stepwise path that new genetic material must progress through before being released as germplasm line or cultivar. The typical, stepwise path used for the development of breeding lines in the University of Arkansas Cotton Breeding Program is outlined in Table 1. In this paper, the term "breeding line" refers to any genotype after crosses of parents are made and prior to being promoted to strain status. Due to the high number of lines and limited number of available seed, breeding lines are evaluated in non-replicated tests, but are sometimes repeated over locations within a year. The development of breeding lines begins with choosing parents for crosses. Within this program, each cross is made and the respective parents are chosen with a specific goal. Parents are chosen for a specific agronomic or morphological trait that they have demonstrated in previous variety and/or strain tests. Usually, parents of a cross include at least one parent that was developed in the University of Arkansas Cotton Breeding Program. In this way, the base of the program should constantly be improved.

Once crosses are made, the F_1 seed are sent to Mexico for winter increase, and the F_2 generation is increased in the following year (Table 1). After stands are thinned, the F_2 populations are screened for resistance to bacterial blight (if a resistant parent is in the pedigree), rogued for desired morphological traits associated the cross, and mass selected for plant structure and fruit retention. In the following generation, F_3 seed are hot water treated prior to planting, thinned to uniform stands then screened and mass selected as done in the F_2 generation. Additional plantings of the F_3 populations are evaluated for machine harvested yield and fiber quality. Very poor populations may be dropped. The F_4 populations are treated and screened in the same manner as the F_3 populations except that individual plants are selected, rather than employing mass selection. In addition, the F_4 populations are evaluated for yield at two locations. Yield in the F_3 and F_4 generations as well as fiber quality in the F_3 generation are used to determine the number of individual plants that will be selected from each F_4 population.

Progenies (F_5 generation) are evaluated in two-row plots at Keiser and one-row plots at Clarksdale. The progenies are evaluated for bacterial blight resistance, Verticillium wilt tolerance, and morphological traits. These data along with seedcotton yield from Clarksdale and from one of the two-rows at Keiser are used to choose progeny to carry forward. Seed produced on the other row of the plots at Keiser are used to plant advanced progenies (F_6 generation). Testing and selection of advanced progenies are similar to that employed in the F_5 generation except that plot size is increased to two-rows at Rohwer and four-rows (two for yield, two for seed increase) at Keiser. Selected advanced progenies are promoted to strain status.

This general approach to development of breeding line was initiated at the University of Arkansas in 1988 (Bourland, 1988), and is similar to the stepwise plan later outlined by Bourland (1995, 1996). The main strategic change has been the used of mass selection in the F_2 and F_3 generations rather than individual plant selection in the F_2 followed by second cycle of individual plant selections made in the F_5 or F_6 generation of superior strains. This change was incorporated to lessen time from cross to strain release, reduce number of strains to be tested, and to reduce the degree of heterozygosity in individual plant

selections (by advancing the generation). Other minor changes have been made in a number of populations and progenies evaluated and the locations where they are tested.

Exceptions to this approach are made when appropriate. Screening of resistance to root-knot nematode and evaluation of some morphological traits, e.g. enlarged true leaf at emergence (Ortiz and Bourland, 1999) and tufted seed (Girma et al., 1993), are being developed using different strategies.

Testing of Strains

The typical, stepwise path used in the testing of strains is outlined in Table 2. Here, the term "strain" refers to any genotype that has been promoted from progeny (evaluated in non-replicated tests) to strain (evaluated in replicated tests) status. Strain tests usually consist of 18 strains and two check cultivars, evaluated in 2-row plots with four replications. Standard data taken in these tests include stand, plant height, yield, lint percentage, seed index, lint index and fiber quality. Response of New and Advanced Strains to thrips and tarnished plant bugs are evaluated in additional tests.

Depending on the number of progenies promoted to strains, either three or four Preliminary Strain Tests are conducted each year. The best 18 strains in the Preliminary Tests are evaluated in the New Strain Test in the following year. The best strains in the New Strain Test are carried forward to the Advanced Strain Test where they will be evaluated multiple years until they are released or discarded. The best Advanced Strains are entered into regional strain and state variety tests.

Release of Genetic Material

A total of 30 germplasm lines and one cultivar have been released using the general approach outlined above. Five additional lines should be released in 2004. Over the years, seed companies have used this genetic material to develop several different commercial cultivars. In addition, the program has played a role in training new cotton breeders and progress the science of cotton breeding.

References

Anthony, W.S. and S.T. Rayburn. 1989. Cleanability of smooth- and hairy-leaf cottons - quality effects. Trans. ASAE 32:1127-1130.

Bird, L.S. 1982. The MAR (multi-adversity resistance) system for genetic improvement of cotton. Plant Dis. 66:172-176.

Bourland, F. M. 1988. Breeding cotton for enhanced profitability. pp. 45-47. Ark. Agric. Exp. Station. Special Report 132.

Bourland, F.M. 1995. Progress report: The University of Arkansas cotton breeding program, 1993. pp. 115-117. Ark. Agric. Exp. Station. Special Report 166.

Bourland, F.M. 1996. Progress report: The University of Arkansas cotton breeding program, 1994. pp. 79-80. Ark. Agric. Exp. Station. Special Report 172.

Bourland, F.M., N.R. Benson, E.D. Vories, N.P. Tugwell, and D.M. Danforth. 2001. Measuring maturity of cotton using nodes above white flower. J. Cotton Sci. 5:1-8.

Bourland, F. M., J. M. Hornbeck, A. B. McFall, and S. D. Calhoun. 2003. A rating system for leaf pubescence of cotton. J. Cotton Sci. 7:8-15.

Bourland, F.M., G. Kaiser, and E. R. Cabrera. 1988. Rapid deterioration of cotton, *Gossypium hirsutum* L. using hot water. Seed Sci. and Technol. 16:673-683.

Bourland, F.M. and B.A. Waddle. 1988. Cotton research overview: breeding. Arkansas Farm Research 37:7.

Girma, B., B.A. Waddle, and F.M. Bourland. 1993. Breeding behavior of tufted seed character in cotton, Gossypium hirsutum L. p. 630. Proc. Beltwide Cotton Production Research Conferences, New Orleans, LA. 10-14 Jan. 1993. National Cotton Council, Memphis, TN.

Hornbeck, J.M., S. B. Jackson, S.B., J.T. Johnson, and F.M. Bourland. 2003. Variation in marginal bract trichomes among contrasting cotton cultivars. p. 880. *In* Proc. Beltwide Cotton Prod. Res. Conf., Nashville, TN. 6-10 Jan. 2003. National Cotton Council, Memphis, TN.

Jackson, S.B., J.M. Hornbeck, and F.M. Bourland. 2003. Measurement and relationships of leaf, stem and bract trichomes on cotton. p. 879. *In* Proc. Beltwide Cotton Conf., Nashville, TN. 6-10 Jan. 2003. National Cotton Council, Memphis, TN.

Lewis, H., L. May and F. Bourland. 2000. Cotton yield components and yield stability. Pp. 532-537. *In* Proc. Beltwide Cotton Conf., San Antonio, TX. 4-8 Jan. 2000. Natl. Cotton Counc. Am., Memphis, TN.

Ortiz, C.E. and F. M. Bourland. 1999. Comparative early growth of cotton seedlings expressing a visible true leaf at emergence and normal phenotype seedlings. J. Agric. Univ. P.R. 83:19-31.

Rayburn, S.T., Jr., and L. Libous. 1983. Preliminary investigation of cleanability of cotton with varying degrees of plant hairiness. pp. 152-153. *In* Proc. Beltwide Cotton Prod. Res. Conf., San Antonio, TX. 2-6 Jan. 1983. Natl. Cotton Counc. Am., Memphis, TN.

Shepherd, R. L., J. C. McCarty, Jr., J.N. Jenkins, and W. L. Parrott. 1996. Registration of nine cotton germplasm lines resistant to root-knot nematode. Crop Sci. 36:820.

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

Generation	Selections made:	No. / year	Location(s) tested
Parents	Parents selected and crossed	20-30	Keiser
F_1	Generation advanced during winter	20-30	Mexico
F_2	Mass selection (screened for bacterial blight, morphological, fruiting)	20-30	Keiser
F_3	Mass selection (seed deterioration, bacterial blight, morphological, fruiting)	20-30	Keiser, Rohwer
F_4	Plants selected (selection pressure based on yield; fiber quality determined)	800	Keiser, Rohwer
F_5	Progenies to advanced progenies (based on HPR, yield, fiber quality)	200	Keiser, Clarksdale
F_6	Advanced progenies to strains (based on HPR, yield, fiber quality)	54	Keiser, Rohwer

Table 2. Typical testing of strains in the University of Arkansas Cotton Breeding Program.

Generation	Replicated test (selection for HPR, yield and fiber quality)	No. / year	Locations tested
F_7	Preliminary Strain Tests (18 strains + 2 checks in each test)	Ca. 54	Keiser, Rohwer
F_8	New Strain Test (18 strains + 2 checks)	Ca. 18	Keiser, Clarksdale, Marianna, Rohwer
F_{9+}	Advanced Strain Test (18 strains + 2 checks)	Ca. 9	Keiser, Clarksdale, Marianna, Rohwer
F_{10+}	Regional strain tests and state variety tests	Ca. 1-4	Arkansas and other states