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BREEDING AND GENETICS

History and Progress in Cotton Breeding, Genetics, and Genomics in New Mexico

Jinfa Zhang*

ABSTRACT

The New Mexico Cotton Breeding Program was established in 1926 and has been led by five generations of breeders. The program has released 37 Acala 1517 and one short-staple Upland cotton (*Gossypium hirsutum* L.) cultivars and numerous germplasm lines. Two Sea-Island *G. barbadense* L. cultivars have been released for production in the Mesilla Valley, NM. New Mexico germplasm has contributed to the development of 45% of the commercial cotton cultivars including almost all Acala cultivars in California, and has contributed to the improvement in fiber length and strength in U.S. cottons. Many Acala 1517 cultivars are tolerant or resistant to Verticillium wilt and bacterial blight. The recent releases include three transgenic Acala 1517 cultivars, one conventional and two glandless cultivars. The current research program focuses on fiber and seed quality (glandless) to develop elite germplasm with high yields and superior fiber quality and with resistance to Verticillium and Fusarium wilt, thrips, bacterial blight, leaf spot, cotton rust, and tolerance to drought and salinity. Upland × Pima introgression and development of the hybrid seed production system based on cytoplasmic male sterility and the haploid-producing system based on semigamy are also important aspects of the program. Extensive applications of genomic tools and approaches in the program include DNA marker and population development, linkage map construction, and quantitative trait locus mapping. In recent years, reduction in funding and lack of institutional support has hampered the program in delivering solutions to challenging issues such as Fusarium wilt race 4 faced by the cotton farmer.

Cotton is one of the most important field crops grown in New Mexico. However, according to Staten (1971), only until World War I did cotton become a modern commercial crop in the state, despite the early cotton culture for hundreds of years in New Mexico. Cotton was grown historically in New Mexico for a niche market, to which Acala 1517 played an important role. Acala 1517 fiber was sold at a price premium of approximately $.08 higher than other short-staple cotton. However, because its price premium did not compensate for its yield disadvantages over commercial transgenic cotton cultivars and the demise of specific American and European textile mills that used Acala 1517 to make high-end quality textiles that led to reduced demand, Acala acreage in New Mexico declined and the much larger Acala market in California also decreased. Furthermore, strong marketing in transgenic insect-resistant and herbicide-tolerant cotton (> 95% cotton acreage) by several large seed companies exacerbated this situation. The first insect-resistant Bt Acala 1517, Acala 1517-99W, was released by New Mexico State University (NMSU) through Dow AgroSciences in 2005 (Zhang et al., 2008b) and accounted for 14 and 7% of the cotton acreage in New Mexico in 2006 and 2007, respectively (Zhang et al., 2016a). High yield has become the top priority for the Southwest and West cotton growers in the U.S. This has dictated changes in cotton breeding objectives and priorities. However, the NMSU Cotton Breeding Program remains the only public Acala cotton breeding program developing cultivars for high fiber quality.

With limited resources for breeding programs from the public sector, competing with large seed companies in commercial cultivar development is difficult if not impossible. Currently no public cotton breeding program has any commercial cultivars grown on a large scale in the U.S. (http://www.cotton.org/econ/cropinfo/varieties). Because of the commercialization of transgenic cotton in the U.S. in the mid-1990s, most of the public cotton breeding programs have redirected their focus to germplasm improvement instead of releasing cultivars.

Because public breeding programs could not access commercial biotech traits due to intellectual

Zhang, J.F.*, Dept. of Plant and Environ. Sci., Box 30003, New Mexico State University, Las Cruces, NM 88003
*Corresponding author: jinzhang@nmsu.edu

proprietary issues (Zhang, 2015), non-transgenic cotton found its place in cotton production in the U.S., thanks to the success of boll weevil (*Anthonomus grandis* Boheman) and pink bollworm [*Pectinophora gossypiella* (Saund.)] eradication programs and the wide use of Lepidoptera-resistant Bt cotton. One of the non-transgenic cottons is glandless. Currently, cottonseed, traditionally treated as a by-product in cotton production, is primarily used for oil and animal feed, and produces approximately 14 to 19% of the farm-gate value in cotton production (http://www.cotton.org/econ/cropinfo/costsreturns/usa.cfm). Developing and growing glandless cotton as a food crop (in addition to a fiber crop and an oilseed crop) will increase significantly the income for the cotton producer and revitalize the utilization of glandless cottonseed as a valuable source for food.

In the irrigated southwestern region, abiotic stresses such as drought and salinity have become a serious issue in cotton production. In addition, infestation of thrips (*Thrips* and *Frankliniella* spp.) early in the growing season is a threat. Other biotic stresses such as Verticillium wilt (*Verticillium dahlia* Kleb.), Fusarium wilt (*Fusarium oxysporum* f. sp. *vasinfectum* W.C. Snyder & H.N. Hans) and southwestern cotton rust (*Puccinia cacabata* Arthur & Holw.) can reduce cotton growth and production. There are no resistant or tolerant commercial cultivars against these stresses in the U.S., and no active cotton breeding and genetic program for resistance to cotton rust is currently existent. Although root-knot nematodes [*Meloidogyne incognita* (Kofoid &White)] is a production issue in cotton in New Mexico, highly resistant cultivars against this pest have been developed and grown in the U.S. in the last a few years and also contain transgenes for insect resistance and herbicide tolerance.

Currently, the New Mexico Cotton Breeding Program has a major breeding nursery near campus with 5 to 10 ha for 4,000 to 5,000 field plots each year. The program tests 1,000 to 2,500 progeny rows, 200 to 300 preliminary breeding lines, and 90 to 120 advanced breeding lines in the main location at Las Cruces, NM. There are also 1 to 2 ha of testing plots (3-6 replicated tests) with Robert Flynn in Artesia, NM. The program has been annually participating in the annual National Upland Cotton Cultivar Test, National Pima Cotton Cultivar Test, Regional High Fiber Quality Test, and Regional Breeders' Testing Network in 10 to 15 testing locations across the Cotton Belt. The program also performs an Official Cotton Cultivar Test each year to provide unbiased data to seed companies, USDA, extension agencies, and producers.

COTTON BREEDING HISTORY IN NEW MEXICO

The New Mexico Cotton Breeding Program has been led by five generations of cotton breeders (Fig. 1). Although NMSU had cotton cultivar tests on Acala cotton and other cultivars from 1921 to 1927, a breeding program for Acala cotton was first established by the USDA in a cotton field station near the Las Cruces campus in 1926, followed by the hiring of G. N. Stroman as the first cotton breeder by NMSU in 1928. Until the early 1970s, a number of people contributed their efforts to cotton breeding through the cooperative state-federal program, leading to an impressive list of cultivar releases (Table 1).

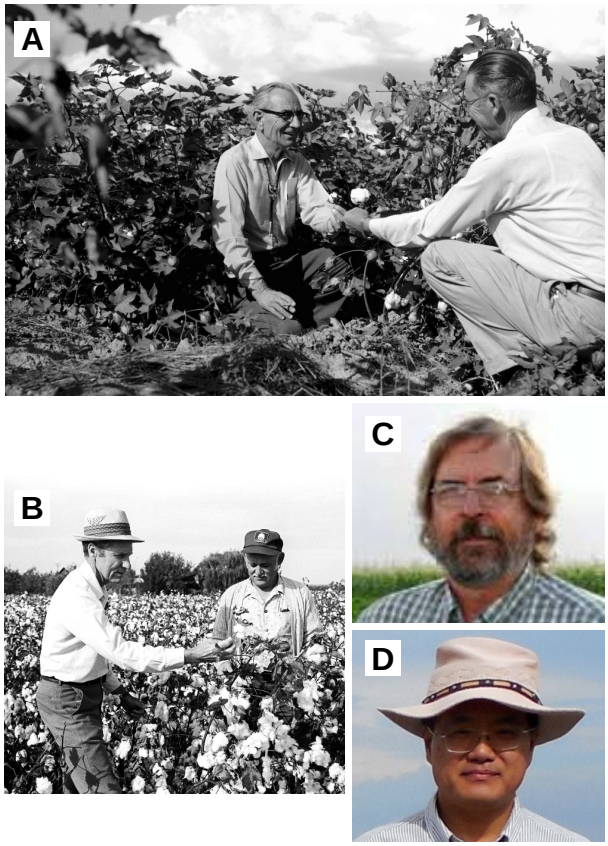

Figure 1. Cotton breeders who have led the Cotton Breeding Program at New Mexico State University. A. Glen Staten (right) from the 1950s to 1972. B. Dick Davis (left) and Norman Malm (right) from the early 1970s to late 1980s. C. Roy. G. Cantrell from the early 1990s to 2001. D. Jinfa Zhang from 2002 to present.

Table 1. Acala 1517 cotton cultivars released from the New Mexico Cotton Breeding Program

Cultivar	Year released	Pedigree	Reference
Acala Young	1929	Watson's	Staten, 1970
College Acala	1930	Acala P12	Staten, 1970
Acala 1064	1937	Acala Young	Stroman, 1938; Staten, 1970
Acala 1517	1939	Acala 1064	Stroman, 1938; Staten, 1970
Acala 1517A (2815)	1941	Acala 1064	Stroman, 1948c; Staten, 1970
Acala 1517WR	1946	Acala 1517	Stroman, 1948c; Staten, 1970
Acala 1517B	1949	Watson's Acala	Staten, 1970
Acala 1517C (7133)	1951	NM 1544 × NM 1577	Staten, 1970; Davis et al., 1978c
Acala 1517C (8893)	1954	Reselection from 7133	Staten, 1970
Acala 1517BR	1954	ST 20/Acala/1517WR/Acala 1517B	Staten, 1970
Acala 1517-BR1	1957	Acala 1517BR/Acala 1517C	Staten, 1970
Acala 1517C (1028)	1958	Reselection from 7133	Staten, 1970; Davis et al., 1978c
Acala 1517D	1960	A cross of two strains of unknown parentage	Staten, 1970
Acala 1517-BR2	1961	(8373/ST 20)/Acala 216/(Acala 49/Hartsville)	Staten, 1970
Acala 1517V (6612)	1964	Acala 2503/Coquette	Staten, 1970; Malm et al., 1978a
Acala 1517-BR (60-209B)	1965	Reselection from Acala 1517-BR2	Staten, 1970
Hopicala	1965	Acala 1517 selection 5-12/HA76	Staten, 1970
Acala 3080	1968	9136/49W	Staten, 1970
Acala 1517V (9450)	1969	Acala 2503/Coquette	Staten, 1970
Acala 1517-70	1970	B1413/Hopicala	Staten, 1970; Davis et al., 1978b
Acala 1517-75	1975	Acala 688/Acala 9608	Malm et al., 1978b
Acala 1517-77	1977	Reselection from Acala 1517-70	Barnes et al., 1980
Acala 1517E-1	1976	Acala 3080/PD 2165	Davis et al., 1978c
Acala 1517E-2	1978	Selection from Acala 1517E-1	Davis et al., 1980
Acala 1517-77BR	1982	Selection from Acala 1517-77	Roberts et al., 1982
Acala 1517-SR1	1982	Acala 1517-E1/Unknown storm-proof	Malm et al., 1984
Acala 1517-SR2	1986	Acala 1517-E1/Unknown storm-proof	Malm et al., 1987
Acala 1517-88	1988	Acala 1517-77BR/DP 70	Roberts et al., 1988
Acala 1517-SR3	1990	Acala 1517-E1/Unknown storm-proof	Cantrell et al., 1992b
Acala 1517-91	1991	Acala 8130/Acala 8874	Cantrell et al., 1992a
Acala 1517-95	1995	From 1517-E2 (3080/PD2165)	Cantrell et al., 1995
Acala 1517-99	1999	B742/E1141	Cantrell et al., 2000
Acala 1517-99W	2006	Acala 1517-99 BC3/ Bt gene donor	Zhang et al., 2008b
Acala 1517-08	2010	B7636/LA 887	Zhang et al., 2011b
Acala 1517-09R	2010	Acala 1517-99 BC3/RR gene donor	Zhang et al., 2011c
Acala 1517-16B2RF	2015	NM 97123 BC3/B2RF donor	Zhang et al., 2016a
NuMex COT 15GLS*	2015	CRI 12 BC5/Bahtim 110/CRI 35	Zhang et al., 2016b
Acala 1517-18 GLS	2017	Acala 1517-08/Acala GLS	Zhang et al., 2018a

***not Acala as it does not have the Acala type fiber quality.**

Stroman directed the cotton breeding program until the early 1950s. Several Acala 1517 cultivars were released by his effort through collaboration with scientists in the USDA. His several years of selection from Young's Acala resulted in the release of Acala 1064 in 1937, followed by Acala 1517 in 1939, a selection from Acala 1064 (Stroman, 1938). It is said that "1517" was the progeny-row number from which the cultivar Acala 1517 was tested, but the name has been retained in all the following Acala cotton cultivars released from the NMSU Cotton Breeding Program. Acala 1517A (2815) with larger bolls from a reselection of Acala 1064 was released in 1941 to replace Acala 1064 and Verticillium-wilt-resistant 1517WR in 1946 to replace Acala 1517 (Stroman, 1948c). Acala 1517B was selected from Watson's Acala and released for commercial production in the Mesilla Valley in 1949 as a replacement for Acala 1517WR. Acala 1517C was released from a cross of the Acala 1517 family in 1951 to replace both Acala 1517A and Acala 1517B. Because of the focus on fiber quality, Stroman dedicated extensive efforts to develop instrumentation to measure fiber quality such as a laboratory mechanical cotton comber (Stroman, 1948a), a rolling table holder (Stroman, 1948b), and a hand cotton fiber sorter (Stroman, 1958).

Glen Staten came from alfalfa breeding and led the program from the early 1950s to 1972 when he retired. He played a key role in developing Acala 1517 while maintaining and improving its superior fiber quality. A number of cultivars, including bacterial-blight-[*Xanthomonas citri* spp.*malvacearum* (ex Smith 1901)]-resistant Acala 1517BR, Acala 1517BR-1, Acala 1517BR-2, Acala 1517-70, Acala 1517D, Verticillium-wilt-resistant Acala 1517V, Acala 3080, and Hopicala were released under his direction, representing significant advances in yield, disease tolerance, fiber quality, and harvesting efficiency. Staten received the 1997 Cotton Genetics Research Award for his outstanding achievements. Notably, Acala 1517D of an unknown parentage had obvious *G. barbadense* L. introgression as shown by its boll shape, pigmentation, and superior fiber and yarn strength. Many of these historically important cultivars were retroactively registered in Crop Science Society of America (CSSA) by Davis et al. (1978a, b) and Malm et al. (1978a, b).

Dick Davis and Norman Malm were the cotton breeders and geneticists between the early 1970s and the late1980s when the USDA terminated its cooperative effort in cotton breeding in New Mexico. Malm led the effort to develop Acala 1517-75 (Malm et al., 1978b) and storm-resistant Acala cultivars including Acala 1517-SR1 (Malm et al., 1984) and Acala 1517-SR2 (Malm et al., 1987) for the Pecos Valley and the Eastern Plains. Davis released several early-maturing Acala cultivars (Acala 1517E-1, Davis et al., 1978c and Acala 1517E-2, Davis et al., 1980) and an interspecific cotton hybrid NX-1. Davis received the 1992 Cotton Genetics Research Award. Carl Roberts, a senior research specialist assisting the program, contributed to the development of Acala 1517-77BR (Roberts et al., 1982), Acala 1517-88 (Roberts et al., 1988), and other Acala cultivars. C. E. Barnes, Superintendent of the Artesia Agricultural Science Center, was active in cotton varietal testing and was responsible for the release of Acala 1517-77 (Barnes et al., 1980). While maintaining the Acala 1517 fiber quality, yield potential, earliness, storm-proof, and bacterial blight resistance were further improved during this period.

Roy G. Cantrell came to NMSU from wheat breeding and led the program in the 1990s and released four Acala 1517 cultivars: Acala 1517-91, Acala 1517-SR3, Acala 1517-95, and Acala 1517-99 (Cantrell et al., 1992a, b, 1995, 2000). One of his significant contributions to the program was his effort to establish a molecular platform and his early use of molecular markers in the cotton breeding community. He became the first vice president in Agricultural Research at Cotton Incorporated in 2001 and received the 2002 Cotton Genetics Research Award for his cotton breeding and genetics work. He then moved to Monsanto in 2007 to lead its global cotton breeding program until his retirement in 2016.

I came to NMSU in 2002 from Monsanto as a molecular cotton breeder. To continue the legacy of developing Acala 1517 cultivars with superior fiber quality, I have fostered a close collaborative effort with Ed Hughs (Research Leader, retired in 2017) of the USDA Southwestern Ginning Research Laboratory to evaluate ginning and spinning properties of advanced breeding lines before their releases. I have expanded the use of genomic tools including structural and functional genomics in the program and continued an extensive introgression breeding effort between Upland and *G. barbadense*. Substantial efforts have been dedicated to study cotton for resistance or tolerance to Verticillium wilt, Fusarium wilt, thrips, bacterial blight, leaf spot [*Alternaria alternata* (Fr.) Keissl.], drought, and salt. Considerable amount of time also has been spent on a hybrid production system based on cytoplasmic male sterility (CMS) and a haploid-

producing system based on semigamy. The program also has maintained activities in breeding for extra-long staple cotton (*G. barbadense*) on a small scale.

COMMERCIAL CULTIVARS RELEASED

Since 1929, 38 commercial Upland cotton cultivars (3-5 cultivars in each decade) have been released and/or registered from the New Mexico Cotton Breeding Program (Table 1), all of which except for one, NuMex COT 15GLS (Zhang et al., 2016b), are Acala cotton with superior fiber quality traits in Upland. The Acala cultivars released since the late 1930s were named with the prefix 1517 followed by a number indicating the year when a cultivar was released: WR refers to wilt resistance, V to Verticillium resistance, BR to bacterial blight resistance, E to earliness, and SR to storm resistance. Before transgenic cotton dominated the U.S. cotton production, Acala 1517 cultivars released in the program were exclusively and extensively grown in New Mexico and neighboring areas such as far-west Texas (El Paso County) and eastern Arizona.

In the early 2000s, an agreement between NMSU and Dow/Phytogen was reached to transfer Dow's Bt genes, Widestrike (W), into Acala 1517-99. In 2003, NMSU participated in the Cotton States Program offered by Monsanto. Through collaborations, Dow's Widestrike (W) and Monsanto's Roundup Ready (R), Bollgard II (BGII or B2), and Roundup-Ready Flex (RF) genes have been transferred into the Acala 1517 background through backcross introgression (Zhang et al., 2008c). The most recent releases are conventional Acala 1517-08 (Zhang et al., 2011b), insect-resistant Acala 1517-99W (Zhang et al., 2008b), herbicide-tolerant Acala 1517-09R (Zhang et al., 2011c), insect-resistant and herbicide-tolerant Acala 1517-16 B2RF (Zhang et al., 2016a), and glandless NuMex COT 15 GLS (Zhang et al., 2016b) and Acala 1517-18 GLS (Zhang et al., 2018a) (Table 1). Acala 1517-08 out-yielded Acala 1517-99 by 15% when tested in New Mexico, 16% in the Southeast and Mid-south, and 29% in Arizona and the Texas High Plains over more than 30 tests in different locations/years. The commercialization of Acala 1517-09R was not realized due to the termination of the biotech trait registration by Monsanto.

Additionally, two Sea-Island cotton cultivars, NMSI 1331 (Robert et al., 1997) and NMSI 2032 (Zhang et al., unpublished) were released for commercialization including organic production in southern New Mexico and El Paso County, Texas. NMSI 1331 was selected from Montserrat Sea Island introduced into New Mexico in 1988 and had longer, finer but weaker fibers than Pima S-6. NMSI 2032 has similar fiber quality traits to Pima S-7 and other Pima cultivars, but higher lint yield potential.

GERMPLASM LINES DEVELOPED AND RELEASED

New Mexico Acala cotton germplasm, known for its high fiber quality, good Verticillium wilt tolerance, and large boll size, is adapted to the semiarid southwestern growing region of the U.S. Cotton Belt. However, the most important impact of the New Mexico Cotton Breeding Program has been the broad use of its germplasm lines in the development of commercial cultivars in the U.S. Even though they are tall and late-maturing with low yield when grown in other regions, they have been used extensively as parental lines for developing other types of cotton cultivars. According to Bowman et al. (1996), approximately 45% of the cotton cultivars released in the U.S. from 1950 to 1990 contained New Mexico germplasm in their pedigrees. Bowman and Gutierrez (2003) further showed that half of the gains in fiber strength of the U.S. cotton cultivars between 1970 and 1990 could be attributed to the cotton breeding program at NMSU. Kuraparthy and Bowman (2013) also reported that much of the improvement in fiber length in the U.S. cotton cultivars between 1980 and 2010 could be traced to germplasm developed at NMSU.

Almost all the Acala cultivars released in California before the 2000s were exclusively derived from germplasm lines developed in New Mexico (Cooper, 1998; Smith et al., 1999). Acala 1517 was first introduced to USDA, Shafter, CA, and yielded Acala 4-42 after one generation of selection by George Harrison. Acala 4-42 dominated cotton production in the San Joaquin Valley until 1967 when it was replaced by Acala SJ-1, which was developed by John Turner from a cross between Acala 1517D (i.e., NM2302) and an experimental line ATE-1. Further selection by H. B. Cooper produced Acala SJ-2 in 1973. Cooper first became interested in cotton breeding as a NMSU student in 1947 while working with G. N. Stroman; he returned to NMSU in 1960 as a faculty member and cotton breeder after earning an M.S. at Colorado State University and a Ph.D. at the University of Wisconsin. In 1964 he joined the USDA at the U.S. Cotton Research Station in Shafter,

CA. Cooper was responsible for the development of every major cotton cultivar in the San Joaquin Valley since 1973, and he used New Mexico germplasm in all the Acala cultivars he developed. For example, NM7378 crossed with C6TE gave rise to Acala SJ-3 in 1974, and the hybrid between this single cross and an experimental line 12304-4 in a cross with another single cross (NM1900-1 × S196) gave rise to Maxxa in 1990. Acala Maxxa represented a breakthrough for growers, combining earliness and high yield with high-quality fiber and spinning characteristics. The single cross between NMB3080 (Acala 3080) and C6TE gave rise to Acala SJ-4 in 1975 and Acala SJ-5 in 1977, whereas its double cross with a single cross (Acala 4-42 × NM7403) gave rise to Acala SJC-1 in 1982 and GC510 in 1984; its cross with another single cross (ATE11 × NM49-2) yielded Prema in 1989; and with the third single cross (ATE1 × Tex E364) yielded Royale in 1990. Steve Oakley contributed to the release of Maxxa, Prema, and Royale. Acala 1517 was also introduced to the Arizona Agricultural Experiment Station and produced Acala 44 in a cross with Santan Acala.

Most of the above germplasm lines were not formally released and registered in CSSA. Since 2000, in addition to free germplasm exchanges with other breeding programs including seed companies, five Acala type germplasm lines (Cantrell and Davis, 2000; Cantrell and Waddell, 2001; Zhang et al., 2018b), six Pima germplasm lines (Percy et al., 2009; Ulloa et al., 2009), and a genetic population of 95 recombinant inbred lines (RILs) were released and registered in CSSA (Gore et al., 2012). In addition, 21 other elite Acala type breeding lines were reported (Zhang et al., 2007c), 16 of which are being publicly released (Zhang et al., 2018b, c, d) (Table 2).

Table 2. Cotton germplasm lines released from the New Mexico Cotton Breeding Program

Line	Year released	Pedigree	Reference
NM24016	2000	H12156/2/77-505/Russian 5904	Cantrell and Davis, 2000
NM970513	2001	Acala 1517-95/NM24052	Cantrell and Waddell, 2001
NM01 to 99 (95 lines)	2006	TM-1/NM24016	Percy et al., 2006; Gore et al., 2012
PSI 113	2009	8810/NMSI 1601	Percy et al., 2009
PSI 425	2009	8810/NMSI 1601	Percy et al., 2009
SJ-07P-FR01	2008	8810/NMSI 1601	Ulloa et al., 2009
SJ-07P-FR02	2008	8810/NMSI 1601	Ulloa et al., 2009
SJ-07P-FR03	2008	8810/NMSI 1601	Ulloa et al., 2009
SJ-07P-FR04	2008	8810/NMSI 1601	Ulloa et al., 2009
NM 970123	2016	Acala Prema/W5250	Zhang et al., 2018b
NM W1218	2016	B4222/Hartz 1014	Zhang et al., 2018b
NM 990813	2016	Acala 1517-95/87D3-24	Zhang et al., 2018b
NM 990649	2018	B5527/DD1920P	Zhang et al., 2018c
NM 990764	2018	'Acala 1517-91'/NM 24052	Zhang et al., 2018c
NM 990815	2018	TAM 87D3-24/'Acala 1517-95'	Zhang et al., 2018c
NM 990827	2018	B7034/B4222	Zhang et al., 2018c
NM 010094	2018	1158/6138	Zhang et al., 2018c
NM 010113	2018	1158/'Acala 1517-95'	Zhang et al., 2018d
NM 010122	2018	1158/1236	Zhang et al., 2018d
NM 010311	2018	B4219/B614	Zhang et al., 2018d
NM 010341	2018	4072/6138	Zhang et al., 2018d
NM 010454	2018	1158/4096	Zhang et al., 2018d
NM 010460	2018	1158/4096	Zhang et al., 2018d
NM 010462	2018	1158/4096	Zhang et al., 2018d
NM 010504	2018	1158/W5250	Zhang et al., 2018d

OTHER STUDIES BEFORE 1990

In addition to cotton breeding, genetic and other related research activities became increasingly important. These activities included anther color (Stroman, 1935), correlations of traits (Stroman, 1949), combining abilities of hybrids (Barnes and Staten, 1961), and inheritance of the following traits based mainly on diallel analyses: Verticillium wilt resistance (Barrow, 1970a,b, 1973; Cano-Rios and Davis, 1981; Roberts and Staten, 1972), earliness (Cano-Rios and Davis, 1981), short branch and clustering (Coffey and Davis, 1985), gossypol content (Yang and Davis, 1976, 1977), and seed yield (Malm and Gwartney, 1979). Woodward and Malm (1976) showed that, among three groups with the same seed cotton yields, the high lint percentage group produced a significantly higher lint yield with more lint per plant, lint per boll, and lint per seed and a greater fiber elongation than did the low lint percentage group. The high lint percentage group had significantly less seed per boll, seed cotton per boll, and five-lock bolls and smaller seed.

In addition to his work on Verticillium wilt resistance and haploid production using semigamy (Barrow and Chaudhari, 1976; Barrow and Dunford, 1975; Barrow et al., 1973; Chaudhari and Barrow, 1975), Jerry Barrow of USDA extensively studied pollen viability, its measuring methods (Barrow, 1981, 1983), and use in selecting pollen for heat tolerance (Rodríguez-Garay and Barrow, 1988). He also studied the conditions for short-term storage of pollen (Rodríguez-Garay and Barrow, 1986), and the techniques for isolating viable microspores (Barrow, 1986) and anther culture (Barrow et al., 1978).

GENETIC GAINS IN LINT YIELD, YIELD COMPONENTS, FIBER QUALITY, AND OTHER TRAITS OF ACALA 1517 CULTIVARS

Yield and Fiber Quality. Based on the data available from annual yield trials, Zhang et al. (2005b) showed that lint yield in Acala 1517 cultivars has increased at an average rate of 1.4% $yr^{-1}$and lint percentage at a rate of 0.12% yr^{-1}since 1930 to 1940, whereas boll size (-0.05 g yr^{-1}) and seed index (-0.10 g yr^{-1}) have been reduced gradually since the 1960s. Fiber strength has been enhanced since the 1960s, which has been accompanied by a steady increase in micronaire. However, fiber length in Acala 1517 cultivars tended to shorten from 31.0 mm to 30.0 mm from 1960 to 1990, whereas newly released Acala 1517 cultivars (Acala 1517-95, 1517-99, 1517-08, and 1517-09R) have fiber lengths greater than 30.5 mm.

Our first year's field comparative testing results in Las Cruces in 2005 (Gatica-Palermo et al., 2006) confirmed that, except for Acala 1064, which had a low boll weight (< 4.0 g $boll^{-1}$), earlier Acala 1517 cultivars had heavier bolls (6.3-6.8 g $boll^{-1}$). However, the boll weight has decreased to < 6 g $boll^{-1}$ over time with an increment rate of -0.02 g $boll^{-1}$ yr^{-1}. For seed index, except for Acala 1064, the earliest Acala cultivars had a large seed. The cultivars released in the 1960s also had large seed (12-13 g of seed index). Since then, the seed size has been reduced gradually at a rate of 0.02 g yr^{-1}. Lint percentage in the cultivars released before the 1960s ranged from 37 to 38%. Since then, lint percentage in Acala 1517 cultivars has improved steadily at a rate of 0.05% yr^{-1}. The most recently released cultivars have even higher lint percentage (> 42%).

Most Acala 1517 cultivars released before the 1960s were shorter in 2.5% span length (26.4-29.5 mm), whereas most of the 1517 cultivars released after the 1980s had longer fiber lengths (27.9-29.7 mm). Several 1517 cultivars released in the 1970s had even longer fibers (> 30.5 mm). The tendency for 50% span length was similar to 2.5% span length, but the increment rate (0.015 mm yr^{-1}) was significant. The early 1517 cultivars had weaker fiber (210.7-230.3 kN m kg^{-1}), whereas recent released Acala 1517 cultivars had improved fiber strength over time at a rate of 0.45kN m kg^{-1} yr^{-1}. The trend in fiber elongation was similar to fiber strength at a rate of 0.0097 % yr^{-1}. Micronaire in Acala 1517 cultivars has increased steadily over years from 3.8 to 4.6 at a rate of 0.008 yr^{-1}.

The Acala 1517 cultivars were further tested in Las Cruces, NM under normal irrigation conditions and in Artesia, NM under Verticillium wilt and non-wilt conditions, and similar results were obtained (Zhang et al., 2007b,c). The yield improvement was 12.3 kg ha^{-1} yr^{-1} ($r^2 = 0.48$, $p < 0.01$) between 1930 and 1975 and 18.8 kg ha^{-1} yr^{-1} ($r^2 = 0.61$, $p < 0.01$) between 1975 and 1999. The yield improvement was accompanied by an increase in lint percentage and micronaire, and a reduction in boll weight. Fiber length, strength, and elongation in Acala 1517 cultivars also have gradually improved.

Verticillium Wilt Resistance. Representative Acala cultivars released from New Mexico and California since the 1930s were screened for Verticillium wilt (VW) resistance in both the greenhouse (2007) and

the fields (2006 and 2007). In comparison to one of the earliest Acala genotypes—Acala Original (Zhang et al., 2012)—Acala Young, Acala 1517-E2, Acala 1517-95, Acala 5, Acala SJ-3, and Acala SJ-4 displayed significantly higher levels of VW resistance in both 2006 and 2007. Acala 1517-SR3, Acala 1517-99, Acala Tex, Acala 1517-77BR in 2006, and Acala 1517-75, 1517-88, 1517-91, 1517-95, 1517-SR2, and Acala 29 in 2007 also showed some levels of VW resistance. However, in the greenhouse when roots were mechanically wounded immediately after inoculation at seedling emergence, Acala 1517-88 and 1517-70 had the lowest disease severity ratings. Acala 1517-77BR, 1517C, and Acala SJ-2 also showed significantly lower VW incidences than Acala Original. Acala Young and 1517C had significantly lower disease severity ratings. Again, Acala germplasm and cultivars from New Mexico and California contain Verticillium wilt resistance, but not all of them are resistant.

Bacterial Blight Resistance. Acala 1517BR received its bacterial blight resistance from the resistant donor parent Stoneville 20, and its cross with Acala 1517C resulted in Acala 1517-BR1. Both were resistant to race 1 but susceptible to race 2. Acala 1517BR-2 was resistant to both races with its resistance to race 2 coming from NM8738, which contained introgression of Arizona Long Staple 120 (*G. barbadense*) in its background. Acala 1517-70 was resistant to races 1, 2, and 10 with resistance from the Acala 9136 parent being derived from *G. barbadense* cv. Tanguis. Acala 1517-77BR was a selection from Acala 1517-77, which was also derived from a single plant selection in Acala 1517-70, and its cross breeding line Acala 1517-88 was also resistant to races 1, 2, and 10. Acala 1517-95 was resistant to races 2 and 10, and Acala 1517-99 was resistant to race 1, 2, and 10, both of which had the resistance also derived from Acala 9136.

Salt Tolerance and Growth Rate. The Acala 1517 cultivars were evaluated for salt tolerance in the greenhouse, some of which were more tolerant (Bajaj et al., 2008). We also measured biomass in field plots and found that more recent developed Acala 1517 cultivars had higher growth rates in both early and late flowering stages (Bajaj et al., 2009).

BREEDING FOR SEED QUALITY

In the mid-2000s, an obsolete Acala glandless line was evaluated in the field in New Mexico, and its yield was much inferior to the glanded control Acala 1517-99. Breeding for improved glandless Acala cotton was consequently initiated, aiming at improving both lint yield and fiber quality (Zhang et al., 2016c). In 2010, an Acala glandless (Acala GLS) released in California in 1999 was introduced and tested together with Acala 1517-99 and Acala 1517-08 in a national cotton cultivar test in Las Cruces, NM. To further enrich the glandless germplasm collection and evaluate their yield potential, obsolete and exotic glandless germplasm were collected and observed in the field in 2011 and 2012. Because there was noticeable phenotypic variation in the field performance and segregation of the glanded trait, only a subset of the glandless lines and their selections were advanced to replicated field tests.

In multiple field tests (Idowu et al., 2014; Zhang et al., 2014b), the glandless Acala GLS yielded only 65 to 80% lint of the glanded control Acala 1517-08 and 46 to 75% lint of commercial transgenic cultivars. Most of the obsolete glandless germplasm and their selections yielded less than 70% of Acala 1517-08 and only three selections yielded 82 to 89% of the control. Genetic variation in yield and fiber quality traits was seen from significant differences between selections within the same glandless germplasm, indicating the existence of residual genetic variation.

In another study (Zhang et al., 2014c), 3 to 29 glandless cotton lines were compared with the glanded control, Acala 1517-08, and other lines in four replicated field tests each containing 32 genotypes. In the same field, 28 glanded commercial cultivars and 78 glanded breeding lines were compared with glanded Acala 1517-08 and Acala 1517-99 in three other tests of 32 genotypes each. The experimental layouts allowed a comprehensive comparative analysis of thrips resistance within and between glandless and glanded cotton. Overall, glandless cotton had lower field damage by thrips than glanded cotton, indicating that the glandless trait could serve as a genetic factor for suppressing thrips damage. As compared with Acala 1517-08, which represented one of the most thrips-resistant genotypes among glanded cottons tested, glandless GLS and many selections from glandless germplasm were more resistant, whereas some were similar to Acala 1517-08, indicating that genetic factors other than the glandless trait also affect thrips resistance in cotton. Through a cross between Acala 1517-08 and Acala GLS, thrips resistance has been transferred to many glandless lines including Acala 1517-18 GLS. Recently, we (Zhu et al., 2018) also found in several field studies that glandless cotton was more resistant to leaf spot than glanded cotton.

Acala 1517-18 GLS carrying the double recessive glandless genes (gl_2gl_3) brings the lint yield level to 90% of that in Acala 1517-08 with a similar fiber quality (Zhang et al., 2018a). Another glandless cultivar NuMex COT 15 GLS carrying the dominant glandless gene (Gl_2^e) was derived from a backcross progeny between a *G. barbadense* Gl_2^e gene donor and Chinese Upland cotton, and it was released from the program in 2015 (Zhang et al., 2016b). Both new glandless cultivars have had limited commercial production in New Mexico and Texas.

BREEDING AND GENETIC RESEARCH FOR TOLERANCE OR RESISTANCE TO ABIOTIC AND BIOTIC STRESSES

A highly *V. dahliae*-infected field nursery has been established in the Artesia Agricultural Science Center, Artesia, NM since 2003 for screening advanced breeding lines for Verticillium wilt resistance on an annual basis. A greenhouse screening technique using artificial inoculation also was established at the same time. Between 2003 and 2009, 357 cultivars and germplasm lines were screened for Verticillium wilt resistance in the field, while 267 cultivars and germplasm lines were screened in the greenhouse (Zhang et al., 2008d, 2012; Zhou et al., 2014). Between 2005 and 2009, more than 200 germplasm lines were also evaluated for salt tolerance in the greenhouse. Since 2010, a number of commercial cultivars, obsolete and new germplasm lines have been evaluated for resistance to Verticillium wilt, bacterial blight (Elassbli et al., 2017), Alternaria leaf spot, and southwestern cotton rust (Zhang et al., 2017) through collaborations with Soum Sanogo (a Plant Pathologist at NMSU). Resistance to thrips (Zhang et al., 2013, 2014c) and tolerance to salt and drought stresses (Higbie et al., 2005, 2010; Niu et al., 2013; Sun et al., 2015) have been evaluated in the greenhouse and field plots. Many genotypes with high levels of resistance or tolerance were identified for further studies in cotton breeding, genetics, and genomics. For example, studies on root-knot nematode resistance led to the development of a quick and reliable greenhouse screening method for resistance (Zhang et al., 2006), and its use in a quantitative genetic analysis for root-knot nematode resistance (Zhang et al., 2007a). Numerous progress reports have been presented at annual Beltwide Cotton Conferences and papers or abstracts published in the proceedings. Comprehensive literature reviews for Verticillium and Fusarium wilt resistance can be found in Zhang et al. (2014d, 2015a) and Sanogo and Zhang (2016).

Most notable is that introgression lines with a *G. barbadense* level of resistance to Verticillium wilt and thrips were developed (Zhang et al., 2012, 2013). Quantitative trait loci (QTL) for Verticillium wilt resistance and a major resistance gene for thrips were identified in a backcross inbred line (BIL) population derived from Upland × *G. barbadense*. BILs with similar salt tolerance to their *G. barbadense* parent at seed germination and salt and drought tolerance in plant growth were also developed (Barrick et al., 2015; Sun et al., 2015; Tiwari et al., 2013a, b). Several glandless lines carrying the dominant Gl_2^e gene were found to be highly resistant to race 4 of Fusarium wilt in California (Zhang et al., 2018e), and collaborative genetic studies are under way (Hutmacher et al., 2013; Dr. M. Ulloa, personal communication).

INTROGRESSION BREEDING AND GENETICS

Although natural introgression of *G. barbadense* in some Acala 1517 cultivars was suspected, no intentional introgression was made until Dick Davis made interspecific crosses to transfer the restorer gene Rf_1 to *G. barbadense* (Davis, 1993a, b), and the effort was continued by Roy Cantrell leading to the release of introgression Upland line NM24016. Parallel, I started introgression breeding in China in the mid-1980s, when I employed interspecific crossing to introduce desirable genes for resistance to spider mites (*Tetranychus urticae* Koch) and Verticillium wilt from *G. barbadense* to Upland cotton. Breeding objectives were then expanded to include fiber quality, sub-okra leaf shape, and heterosis. This resulted in the development of high-yielding breeding lines with sub-okra leaf or cleistagamous flowers, and lines with high fiber quality in the mid-1990s (Zhang, 2011).

Since the early 2000s at NMSU, molecular markers and gene expression profiling have been used to map QTL or differentially expressed genes in interspecific populations or introgression genotypes. Meanwhile, new introgression lines with higher yield potential and/or improved fiber quality than Upland parents have been developed, indicating a simultaneous introduction of desirable genes for yield and fiber quality from Pima into Upland cotton (Zhang, unpublished). A few

introgression lines have shown significantly higher lint yields than their Upland parent Acala 1517-99 and the commercial check Acala 1517-08. Tolerance to drought and salt stresses and resistance to Verticillium wilt and thrips also have been evaluated in these introgression lines (Abdelraheem et al., 2015b; Adams et al., 2010; Sun et al., 2015; Tiwari et al., 2013a, b; Zhang et al., 2012). Progress and difficulties in introgression breeding were reviewed by Zhang and Percy (2007) and Zhang et al. (2014a). Although transferring of Pima fiber strength into Upland is difficult and simultaneous transferring of Pima fiber length, strength, and fineness into Upland cotton without a yield penalty is almost impossible, Upland cotton yield and fiber quality can be improved simultaneously by breeding between Upland and Pima. The success in introgression breeding depends on the population size, time a breeder can invest, persistency, selection pressure, and how lucky the breeder is.

CYTOPLASMIC MALE STERILITY AND HYBRID COTTON

NMSU had a strong hybrid cotton research program based on cytoplasmic male sterility (CMS-D2/Rf_1 from *G. harknessii* Brandagee) in the 1970 to 1980s. However, its potential was not realized in the farmer's field. After Meyer's CMS-D2 and restoration system was released (Meyer, 1975), Davis used it to develop Upland CMS A lines and Pima or Upland restorer R lines, resulting in the release of an interspecific F1 hybrid NX-1 (Palomo and Davis, 1983), five Upland A lines (Davis, 1993a), and six Upland R lines, some of which had *G. barbadense* introgression but were still not stable (Davis, 1993b). Interspecific hybrids between Upland and Pima are usually late maturing with excessive vegetative growth. But Davis (1974, 1979) demonstrated that a dwarf Upland parent increased lint yield of interspecific hybrids by 30% over a commercial Upland cotton while maintaining the plant height and maturity to the levels of normal commercial Upland cotton. The interspecific F1 hybrid, NX-1, from a cross between a CMS-D2 Upland A line and a *G. barbadense* R line, was tested in 32 tests at eight locations in four seasons before its release in 1979 (Palomo and Davis, 1983). Under different planting densities and nitrogen levels, it produced flowers earlier and at a higher rate, and yielded 40 to 50% more lint than its Upland B-line 5-1 and commercial checks. It had smaller bolls with fewer seeds, lower lint percentage but a higher seed index, and longer and stronger fibers (Palomo and Davis, 1983, 1984). The lower micronaire in interspecific F1 was independent of late maturity and could be improved through the use of coarse-fibered parents (Davis, 1978). Although the interspecific hybrid did not gain significant commercialization due to the inability to efficiently produce hybrid seeds, the lines developed in New Mexico were believed to have contributed to the successful development of several interspecific Hazera hybrids in Israel and their commercialization in California. A recent study involving hybrids from two Upland cotton cultivars and six introgression lines (developed from an interspecific crossing and backcrossing between Upland cotton and *G. barbadense*) showed that increased mid-parent heterosis was manifested in several hybrids which also out-yielded the high-yielding Upland cultivar parent (Zhang et al., 2016d).

In collaboration with the late Mac Stewart at the University of Arkansas, I have continued the studies on the gametophytic CMS-D8 and its restoration system at NMSU. The work has led to the elaboration of the genetic basis of its fertility restoration by restorer gene Rf_2 and the allelic relationship with another restorer gene Rf_1 for CMS-D2 (Zhang and Stewart, 2001a, b), the chromosomal location of both restorer genes Rf_1 and Rf_2 based on molecular markers (Feng et al., 2005; Wang et al., 2007, 2009; Wu et al., 2014; Zhang and Stewart, 2004b), mitochondrial genes *atp1* and *atp6* that are possibly associated with CMS (Wang et al., 2010, Wu et al. 2011), and molecular mechanisms underlying the fertility restoration based on gene expression studies (Suzuki et al., 2013a, b, c; Yang et al., 2018; Zhang et al., 2008a). A candidate pentatricopeptide repeat (PPR) gene marker was developed for Rf_1 of the CMS-D2 system. Although a map-based cloning strategy was successful to clone and isolate a restorer gene *Rfo* in radish (Brown et al., 2003), the exotic chromosome introgression to the Upland cotton genome appeared to cause difficulties in pinpointing the Rf_1 or Rf_2 gene. Although no difference in RNA editing was identified among CMS-D8, its maintainer and restorer line, several single nucleotide polymorphic (SNP) markers were developed for mtDNA genes to differentiate CMS-D8 cytoplasm from others (Suzuki et al., 2013c). Several A and R lines for the CMS-D8 have been developed (Zhang, unpublished). However, no commercial hybrids based on the CMS-D8 system have been released so far.

SEMIGAMY

Semigamy is an interesting and important phenomenon as it provides a potential system to study reproductive biology and offers an alternative way to generate haploids in cotton breeding. Semigamy in cotton is controlled by one gene, *Se*, and it appears to be associated with chlorophyll content (Zhang and Stewart, 2004a). The gene functions sporophytically and gametophytically, resulting in incomplete dominance in nature. To analyze the genes and gene products associated with semigamy, we used the Affymetrix GeneChip microarray technology to identify differentially expressed genes by comparing semigamatic (57-4) and non-semigamatic (Pima S-1) anthers and ovaries (Curtiss et al., 2011). Line 57-4 was a doubled haploid semigamy mutant isolated from Pima S-1 in the field. As compared with Pima S-1, 284 differentially expressed genes in semigamatic 57-4 anthers were identified, with 232 being down-regulated and 52 being up-regulated. In the semigamatic 57-4 ovaries, 1,827 differentially expressed genes were identified, with 1,678 being down-regulated and 149 being up-regulated. Upon a comparison of the two tissues, 81 common differentially expressed genes were identified in both tissues of the semigamatic genotype, and the expression levels between the two tissues were significantly and positively correlated. One common finding upon analyzing the expression data was the down-regulation of genes associated with the production of transcription and translation factors. Additionally, we were able to find several genes associated with embryo growth and development through mRNA differential display (Curtiss et al., 2012a). A further work developed several molecular markers associated with the semigamy gene (Curtiss et al., 2012b). The ultimate goal of our research is to identify the underlying gene(s) and protein(s) associated with semigamy.

GENOMICS AND MOLECULAR BREEDING

This area of research encompasses marker development, breeding/genetic population development, linkage map construction, and gene and quantitative trait locus (QTL) identification.

DNA Markers. RAPD and SSR markers were first used for germplasm evaluation in the NMSU Cotton Breeding Program by Roy Cantrell (Liu et al., 2000; Tatineni et al., 1996) and then Zhang et al. (2005a, b). DNA markers were developed to tag somatic embryogenesis (Zhang et al., 2011a), miRNA genes (Chen et al., 2013; Pang et al., 2011), a CMS cytoplasm (Suzuki et al., 2013c), male fertility restoration (Wang et al., 2007, 2009; Zhang and Stewart, 2004b), semigamy (Curtiss et al., 2012b), resistance gene analogs (RGA) (Hinchliffe et al., 2005; Niu et al., 2011; Zhang et al., 2007e), root-knot nematode resistance (*Mi2*) (Niu et al., 2007, 2011), differentially expressed genes during fiber development (Li et al., 2013), and cellulose synthase genes (Lin et al., 2012). Many different marker systems have been developed, including promoter-anchored markers (PAAP-RAPD and PAAP-AFLP, Pang et al., 2009), cleaved AFLP (Zhang et al., 2005c), and other AFLP-based gene-targeted markers (GT-AFLP) including ATG-AFLP (Lu et al., 2008), TF-AFLP (Zhang et al., 2007d), miRNA-AFLP (Pang et al., 2011), PPR-AFLP (Wang et al., 2009), and RGA-AFLP (Fang et al., 2014a; Niu et al., 2011; Zhang et al., 2007e). Gene specific markers were developed for fiber genes (Lu et al., 2009) and drought responsive genes (Rodriguez-Uribe et al., 2014).

Development of Large Breeding/Mapping Populations. To facilitate QTL mapping toward isolation of candidate genes, many different genetic and breeding populations have been developed in the New Mexico Cotton Breeding Program. From Roy Cantrell's work, the first was the release of a recombinant inbred line (RIL) population derived from a cross between TM-1 and NM24016 (Gore et al., 2012; Percy et al., 2006), and it was used to map QTL for yield and fiber quality traits and disease resistance (Fang et al., 2014b; Gore et al., 2014). Next was the establishment of another RIL population from 3-79 × NM24016 (Lu et al., 2004), which was again initiated by Roy Cantrell. But this population was not extensively evaluated for QTL mapping for agronomic and fiber quality traits due to its poor performance in the field. To circumvent the hybrid breakdown problem in interspecific hybrid populations, backcrosses were used for the development of two backcross inbred line (BIL) populations from two interspecific hybrids (SG 747 × Pima S-7 and SG 747 × Giza 75), and the two populations were used to identify QTL for yield, seed and fiber quality (Adams et al., 2010; Yu et al., 2012a, 2013), Verticillium wilt resistance (Fang et al., 2013; Zhang et al., 2015b), and tolerance to drought (Abdelraheem et al., 2015b, 2018; Adams et al., 2010). More recently, more than 1,500 RILs were developed from

a cross of Acala 1517-99 × Pima PHY 76 (Zhang, unpublished). Furthermore, an introgression line population of 700 RILs was reconstituted from the registered RMBUP-C4 population, which was a random mated population derived from multiple crosses between 18 chromosome substitution lines each with a chromosome pair from *G. barbadense* 3-79 and three Upland cotton cultivars (Jenkins et al., 2013). Another multi-parent advanced generation inter-cross (MAGIC) population of 650 lines was also constructed from the registered RMUP-C5 population, which was a random mated germplasm population of Upland cotton involving six cycles of random mating beginning with an 11 parent half diallel (Jenkins et al., 2008). These two large populations have been tested in the field in at least two years and will serve as the germplasm pool for selection breeding and association mapping of QTL; in addition, one population was also tested in the greenhouse for Verticillium wilt resistance (Martinez et al., 2018) and salt and drought tolerance (Hooks et al., 2017). Two populations each with 120 and 170 RILs were developed for *G. barbadense* cotton and have been tested for salt and drought tolerance in greenhouse conditions and for agronomic performance in two locations for two years for QTL mapping (Abdelraheem et al., 2015a).

QTL Mapping. Based on several linkage maps constructed (e.g., Abdelraheem et al., 2015a, b, 2017, 2018; Fang et al., 2013, 2014a; Gore et al., 2014; Yu et al., 2007, 2012a, b, 2013; Zhang et al., 2015b), we have mapped more than 400 QTL for yield, fiber quality, seed quality, and resistance/tolerance to Verticillium wilt, drought, and salt, based on two interspecific BIL populations, two RIL populations, and one association mapping population tested in multiple environments or the greenhouse, accounting for approximately 10% of the cotton QTL reported in the world. Notably, a comprehensive meta-analysis of QTL was performed for all reported QTL in cotton, leading to identification of QTL clusters and hotspots (Said et al., 2013, 2015a). A QTL database (www.cottonqtldb.org) was established for cotton breeders and geneticists and launched in January 2015 (Said et al., 2015b), and it has been updated with more than 10,000 accesses at the end of September 2018. Currently no QTL for fiber quality or yield in cotton has been reportedly cloned. However, the work of Pei Yan at Southwest University of China, elegantly demonstrated that a bacterial IAA synthase gene driven by a petunia promoter to express and synthesize IAA at the fiber initiation stage greatly increased the fiber initials and therefore lint percentage and yield while decreasing micronaire (Zhang et al., 2011d).

Functional Genomics. Different gene expression platforms (including cDNA-AFLP, microarray, RNA-seq, and proteomics) have been used to identify genes/proteins associated with responses to Verticillium wilt infection (Mo et al., 2015); drought and salt stresses (Rodriguez-Uribe et al., 2011, 2014); anther, fiber, and boll development (Ma et al., 2012, 2014, 2016a,b; Pang et al., 2012a,b;Wu et al., 2016); male sterility and restoration (Suzuki et al., 2013a,b; Wei et al., 2013;Zhang et al., 2008a); and semigamy (Curtiss et al., 2011, 2012a).

OTHER PERSONNEL WHO CONTRIBUTED TO THE NEW MEXICO COTTON BREEDING PROGRAM

In addition to the lead cotton breeders and geneticists and those who were previously mentioned from 1929 to present, many scientists worked together in cotton breeding in New Mexico. According to Staten (1971), between the late 1920s and the early 1970s, these individual included: A. R. Leding and L. R. Lytton, of the USDA, who worked on developing College Acala and Acala 1517WR; J. R. Cotton of the USDA, who built an extensive germplasm pool for Verticillium wilt tolerance and released the first Upland cultivar with an appreciable level of VW tolerance; W. P. Sappenfield and P. A. Fryxell were Stroman's associates in the early 1950s. L. M. Blank of the USDA and R. F. Hunter, J. D. Adams, H. B. Cooper, and Dick Davis of NMSU developed the bacterial-blight-resistant series of cultivars; R. L. Wood of NMSU evaluated strains and cultivars and supervised cotton seed production; and J. H. Porter and C. R. Roberts of NMSU evaluated fiber quality. After 2002, the following individuals contributed to the cotton breeding program and are listed in chronological order. Four postdoctoral research associates: Doug Hinchliffe, Chen Niu, Sarah Higbie, and Zhongxu Lin; six research specialists: Cindy Waddell, Yingzhi Lu, Jit Baral, Sanjay Bajaj, HenryGatica-Palermo, and Laura Rodriguez-Uribe; 19 graduate students: Fei Wang, Mingxiong Pang, Wu Wang, Jessica Curtiss, Nick Adams, Rashmi Tiwari, Hideaki Suzuki, Hui Fang, Huiping Zhou, Brian Barrick, Joseph Said, Abdelraheem Abdelraheem, Zachary Larson, Triston Hooks, Hanan Elissbi, Yi

Zhu, Gasper Martinez, Feng Liu, and Jie Chen; and 25 international cotton breeders and geneticists from eight countries: Youlu Yuan (China), Wu Wang (China), R. M. Esmail (Egypt), Ysabel Montoya (Peru), James Bokosi (Malawi), Amadou Aly Yattara (Mali), Bouré Ouéyé Gaouna (Chad), Moussibaou Djaboutou (Benin), Claude Tiemtore (Burkina Faso), Chaozhu Xing (China), Shuli Fan (China), Hongmei Wang (China), Daigang Yang (China), Zhongxu Lin (China), Abdelraheem R. T. Abdelraheem (Egypt), Jiwen Yu (China), Yanying Qu (China), Liping Wang (China), Yuzhen Shi (China), Zongfu Han (China), Jie Chen (China), Sujun Zhang (China), Jina Chi (China), Jinhua Wu (China), and Zhonghua Teng (China).

SUMMARY AND PERSPECTIVE

The contribution of the New Mexico Cotton Breeding Program to the U.S. cotton industry can be gauged by the following: (1) 38 Acala cultivars (3-5 per decade) released since 1929 as listed in Table 1; (2) numerous germplasm lines released for use in other breeding programs; (3) 45% of the commercial U.S. cotton cultivars with pedigrees from the New Mexico germplasm as documented by Bowman et al. (1996); and (4) the impact of New Mexico germplasm on improvement of fiber length and strength of the U.S. commercial cotton cultivars as reported by Bowman and Gutierrez (2003) and Kuraparthy and Bowman (2013).

Since I took over the program in 2002, we have delivered six Upland cultivars including one conventional Acala 1517-08, one glandless Acala 1517-18 GLS, one short-staple glandless cultivar NuMex COT 15 GLS, three transgenic cultivars with insect and/or herbicide resistance, and one *G. barbadense* Sea-Island cultivar. Acala 1517-08, Acala 1517-18 GLS, and NuMex COT 15 GLS are currently in limited commercial production in New Mexico and Texas. In addition, a number of new germplasm lines with Acala fiber quality traits have been released. We have published more than 120 refereed articles in cotton breeding, genetics, and genomics, more than 40 proceeding papers, and more than 60 proceeding abstracts. During this period of time, the program has trained 4 postdocs, 6 research specialists, 19 graduate students, and 25 cotton breeders and geneticists from 8 countries.

In the Southwest and West region of the Cotton Belt, there are more environmental challenges than our predecessors faced in cotton production that require solutions from breeding, such as abiotic stresses including drought, salinity, and heat, and biotic stresses including Verticillium wilt, Fusarium wilt, leaf spot, bacterial blight, and thrips. Farmers continue to demand high-yielding cultivars with better fiber and seed quality to compete in the international market. Between the 1930s and the 1980s NMSU and the USDA combined had 3 to 4 fulltime cotton breeders and geneticists. However, after Davis and Malm retired in the late 1980s, only one breeder position was refilled with a fulltime support specialist. In 2011, the technical support position was taken away, which has greatly constrained the personnel involved in the breeding effort, and the current level of research productivity cannot be sustained in the long run. The erosion of Hatch funding and termination of a special cooperative project funded by the USDA have made matters worse. All these factors have made it difficult for the breeding program to respond and to meet the needs of cotton producers in New Mexico and the neighboring areas. It is uncertain if the worsening situation will continue or be reversed.

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