

Registration of RMPAP-C4, a Random-Mated Primitive Race Accession Cotton Germplasm Population

J. C. McCarty Jr.,* J. N. Jenkins, O. A. Gutierrez, and R. W. Hayes

ABSTRACT

A random-mated population involving four cultivars of Upland cotton (*Gossypium hirsutum* L.) and 30 day-neutral primitive accessions, RMPAP-C4 (Reg. No. GP-980, PI 670133) was developed and jointly released by the USDA-ARS and the Mississippi Agricultural and Forestry Experiment Station in 2014. This population involved five cycles of random mating following the cross of 30 day-neutral primitive accessions to the conventional cultivars Sure-Grow 105, DP 393, FM 458, and ST 474. Random mating was facilitated by hand emasculation and bulk pollen methodology. The aim of this project was to incorporate alleles from day-neutral primitive accessions into a population useful to cotton breeding programs for trait improvement and genetic diversity. The mean values for agronomic traits measured following five cycles of random mating were not significantly different from those of cultivars, except for lint percentage, which was lower. Small nonsignificant changes occurred for fiber quality traits, except for fiber uniformity, which increased following random mating. Morphological trait diversity is also present in this population. This unique population should offer new genetic combinations and genetic diversity that may be useful to Upland cotton breeding programs.

THE USDA-ARS and the Mississippi Agricultural and Forestry Experiment Station developed and jointly released RMPAP-C4 (Reg. No. GP-980, PI 670133), a random-mated population of Upland cotton (*Gossypium hirsutum* L.) cultivars and primitive accessions, in 2014. RMPAP-C4 was derived from crossing 30 day-neutral primitive accessions to four cultivars and subsequently random-mating for five cycles. Development of random-mated populations is a useful approach to capture genetic diversity from race accessions.

Useful genetic diversity can be exploited for development of improved cultivars. Several studies indicate that the germplasm base of cotton is narrow and many cultivars are closely related (Bowman et al., 1996, 1997, 2006; Calhoun et al., 1997; Van Esbroeck et al., 1998; Gutierrez et al., 2002). A narrow genetic base will not only limit long-term genetic gain in yield and quality but also reduce environmental stress tolerance and may increase genetic vulnerability (Wallace et al., 2009; Campbell et al., 2010). Therefore, a need exists to expand genetic diversity of Upland cotton breeding programs.

The primitive or wild accessions of Upland cotton contain useful genetic variance for cultivar improvement, with extensive genetic diversity reported for pest resistance, agronomic, morphological, and fiber traits (Percival, 1987; Percival and Kohel, 1990; Meredith, 1991; McCarty and Percy 2001; McCarty et al., 2003; Ragsdale and Smith, 2007). The use of these accessions in breeding programs has been limited by their undesirable short day photoperiod for flowering. A main objective of the ARS cotton research program at Mississippi State, MS, has been the introgression of genes for day-neutrality into primitive accessions (McCarty et al., 1979; McCarty and Jenkins 1993, 2002, 2005). Day neutral-derived primitive accessions provide genetic variation that offers the potential to improve important agronomic and fiber traits and to expand genetic diversity in breeding programs (McCarty et al., 2006, 2007; Wu et al., 2010)

Random mating is a scheme by which individuals are mated together at random or without choice or selection. Breeding

Copyright © Crop Science Society of America. All rights reserved. No part of this periodical may be reproduced or transmitted in any form or by any means, electronic or mechanical, including photocopying, recording, or any information storage and retrieval system, without permission in writing from the publisher. Permission for printing and for reprinting the material contained herein has been obtained by the publisher.

Journal of Plant Registrations 8:313–317 (2014).

doi: 10.3198/jpr2014.01.0004crg

Received 31 Jan. 2014. Registration by CSSA.

5585 Guilford Rd., Madison, WI 53711 USA

*Corresponding author (jack.mccarty@ars.usda.gov)

J.C. McCarty Jr., J.N. Jenkins, and R.W. Hayes, USDA-ARS, P.O. Box 5367, Mississippi State, MS 39762; O.A. Gutierrez, USDA-ARS, 13601 Old Cutler Rd., Miami, FL 33158. Joint contribution of USDA-ARS and Mississippi State University. Journal paper J-12498 of the Mississippi Agricultural and Forestry Experiment Station. Mention of trademark, proprietary products, or vendor does not constitute a guarantee or warranty of the product by United States Department of Agriculture nor any other participating institution and does not imply its approval to the exclusion of other products or vendors that may also be suitable.

methods used following random mating can be flexible and are usually dictated by breeding goals. This breeding strategy has been used successfully to break undesirable linkage blocks in cotton (Miller and Rawlings, 1967; Meredith and Bridge, 1971). Jenkins et al. (2008) developed a random-mated population using 11 diverse cotton cultivars. They reported that correlations between fiber strength and yield were negative in parents but nonsignificant after six cycles of random mating. Hinze et al. (2011) developed a complex race germplasm population composed of 42 non-photoperiodic stocks that would flower at College Station, TX. After making initial crosses, individuals were advanced to the F₃ generation where bulk pollen was used to pollinate individual plants. In the subsequent generation, a male sterile, *MsA*, was introduced into the population to enhance intercrossing, which occurred over seven generations. Their results suggested that intercrossing in a complex population may generate a large amount of potentially useful variability.

The objective of this project was to use random mating to incorporate alleles from primitive accessions into a population useful for trait improvement and genetic diversity in cotton breeding.

Methods

The procedure for developing the day-neutral lines that were used in the random-mated population was to cross each of the 30 photoperiodic primitive race accessions (Table 1) as male to the day-neutral donor ‘Deltapine 61’ (PI 607174). The crosses were made in a winter cotton nursery located in Tecoman, Colima, Mexico during 2004–2005. The F₁ generation was self-pollinated at the winter nursery during 2005–2006, and the F₂ generation was grown in field plots at Mississippi State, MS, in 2006. One open-pollinated boll was harvested from each F₂ plant that set fruit and bulked to provide seed for increase in 2007. In 2008, 30 F₄ day-neutral lines were grown as male parents and crossed to four cultivars selected for specific agronomic traits as follows: earliness, ‘Sure-Grow 105’ (PVP 9900190); productivity, ‘DP 393’ (PVP 200400266); fiber quality, ‘FM 958’ (PVP 200100208); and high lint percentage, ‘ST 474’ (PVP 9400152). The pedigree for the four cultivars can be found in Bowman et al. (2006). Day-length neutral primitive accessions were used originally to develop the cultivars that were grown in the beginning of cotton cultivation in the United States.

Table 1. Accession number, PI number, race classification, country, state, and site of origin, and year collected or donated to the cotton collection.†

Accession no.	PI no.	Race‡	Country	State	Site	Year
1. TEX0028	PI 154038	punctatum	Mexico	Chiapas	Berriozabal	1946
2. TEX0118	PI 163619	latifolium	Guatemala	Jutiapa	El Progreso	1948
3. TEX0184	PI 163642	marie-galante	Guatemala	Jutiapa	Atescatempa	1948
4. TEX0231	PI 163725	punctatum	Guatemala	Zacapaa	Gulan	1948
5. TEX0258	PI 165260	latifolium	Mexico	Oaxaca	Mitla	1948
6. TEX0266	PI 165232	morrili	Mexico	Oaxaca	Tlacolula	1948
7. TEX0306	PI 165383	§	Mexico	Guerrero	Playa de Pie de La Cuesta	1948
8. TEX0310	PI 165354	§	Mexico	Guerrero	Pubelo Nuevo	1948
9. TEX0311	PI 165370	§	Mexico	Guerrero	San Mareos	1948
10. TEX0325	PI 165393	§	Mexico	Guerrero	El Tinguis	1948
11. TEX0342	PI 165328	§	Mexico	Guerrero	Ometepec	1948
12. TEX0378	PI 165321	latifolium	Mexico	Oaxaca	San Francisco	1948
13. TEX0480	PI 158523	punctatum	Mexico	Yuctan	Merida	1947
14. TEX0604	PI 153994	§	Mexico	Puebla	Acatlan	1946
15. TEX0693	PI 265135	§	Honduras		San Lorenzo	1960
16. TEX0695	PI 265137	§	Honduras	Cortes	San Pedro Sula	1960
17. TEX0717	PI 165365	§	Mexico	Guerrero	La Salinas	1948
18. TEX0760	PI 201596	§	Mexico	Veracruz	El Tajin papantila	1952
19. TEX1015	PI 529893	§	Venezuela	Sucre	Cumana	1989
20. TEX1055	PI 529910	§	Mexico	Veracruz	El Capital	1989
21. TEX1076	PI 325780	§	Venezuela	Sucre	Cumana	1968
22. TEX1130	PI 529960	§	Colombia	Tolima	Darmen de Apicala	1971
23. TEX1203	PI 376044	marie-galante	Brazil	R. del Norte	Cruzeta	1972
24. TEX1237	PI 529997	§	U.S. Virgin Islands	St. Thomas	Charlotte	
25. TEX1333	PI 530061	§	Mexico	San Luis Po	Kuelhabitadz	1976
26. TEX1354	PI 530082	§	United States	Puerto Rico	La Pica	
27. TEX1369	PI 530097	§	U.K. Virgin Islands	Tortola Island	Road Town	
28. TEX2167	PI 530706	§	Trinidad	Nariva	Charuma, Biche	1985
29. TEX2431	PI 607736	§	Brazil			1988
30. TEX2434	PI 607739	§	Brazil			1988

† Additional descriptor information can be found in Percival (1987) and the Germplasm Resources Information Network (GRIN) database (www.ars-grin.gov).

‡ Race is the classification below the species level.

§ Not classified.

A structured random-mating scheme was followed because of the varying maturities among the accessions and cultivars. To produce the F_1 crosses, male parents were planted as six groups of five (males 1–5, 6–10, 11–15, 16–20, 21–25, and 26–30; Table 1); each group included five rows of accessions (one of each male) and four rows of cultivars (one of each female). Each row consisted of 60 plants. Mating to produce F_1 seeds was made by crossing two blooms, bagged the previous day, from each of the five male rows and crossed to each of the four female cultivars. Each bloom was used to pollinate one emasculated flower on each cultivar parent (ratio of 1:4). Male plants were tagged and not used again for blooms. Crossing continued until 75 crossed bolls (15 per male) were set on each of the four cultivars. The crossed bolls from the five male parents in a group were harvested by cultivar female parent. This same procedure was followed for each of the six groups of five males. F_1 seed and random-mating cycles C_0 , C_2 , and C_4 were produced at Mississippi State, MS, in 2008, 2009, 2010, and 2011. Random-mating cycles C_1 and C_3 were made at a winter nursery in Mexico in 2009–2010 and 2010–2011.

To produce the first cycle (C_0) of random mating, an equal number F_1 seed from each of the six male parent groups was mixed within a cultivar and planted as four groups (one for each cultivar) in two-row plots, 12 m long in a skip-row pattern (plant two, skip one), with 96.5 cm between rows. Each two-row plot consisted of approximately 120 plants. Therefore, for each cultivar, six two-row plots (one for each male group) were grown and randomly intercrossed using the bulked pollen method. The use of bulked pollen was described by Miravalle (1964) and has been previously used to develop random-mated cotton populations (Gutierrez et al., 2006; Jenkins et al., 2008, 2013). When all plots had flowers present, random intercrossing began, briefly described as follows. Four unopened blooms were bagged on one row of a two-row plot, and 10 flowers were emasculated on the other row of the plot. On the following morning, pollen was collected from bagged blooms (96) across all plots, bulked, and used to pollinate the previous days emasculated flowers. The selection of male flowers and female emasculated flowers was alternated daily between the two rows in each plot. This process was continued each day for 2 wk. An average of 235 cross-pollinated bolls were harvested by cultivar across male groups and bulked to provide four individual family bulks (cycle C_0). To produce subsequent cycles, a random sample of seed from the previous cycle for each of the four cultivar families was planted for crossing. For C_2 and C_4 , each cultivar family was planted in six two-row plots (720 plants) and random mated following the

above procedure except crossing continued for 3 wk. An average of 579 and 500 crossed bolls were harvested for each cultivar family for C_2 and C_4 , respectively.

Cycles C_1 and C_3 were made at the winter nursery in Mexico where about 60 plants were grown for each of the four cultivar families in four plots. When adequate numbers of flowers were present, 10 unopened blooms were bagged and 25 candles were emasculated per cultivar family per day. The following mornings, bagged blooms across families were harvested and pollen was collected, bulked, and used to pollinate the previous day's emasculated flowers. Crossing continued for 2 wk for C_1 and 3 wk for C_3 . An average of 328 and 482 crossed bolls were harvested for each cultivar family for C_1 and C_3 , respectively.

In sum, the number of plants for each cultivar family in each cycle of random mating was 720, 60, 720, 60, and 720, and crossed bolls harvested each cycle was 941, 1313, 2317, 1927, and 1998 for cycles 0 to 4 (Table 2). A total of 8496 crossed bolls were harvested over the four families and five cycles of bulked-pollen crossing. After C_4 , a random sample of seed within each cultivar family was planted as 45 plants in a winter nursery and self-pollinated. An equal number of seed from each of the C_4S_1 cultivar families was bulked together for seed release and designated RMPAP-C4 (Random Mated Primitive Accession Population C4).

After each cycle of random mating, a random sample of cross-pollinated seed from each of the four families was planted as individual plots and self-pollinated to produce C_xS_1 seed. An equal number of C_xS_1 seed from each cultivar family was bulked to provide seed for field evaluations. In 2012, C_0S_1 , C_1S_1 , C_2S_1 , C_3S_1 , C_4S_1 plus the four cultivar parents were planted in replicated plots for determination of agronomic and fiber properties. The entries were planted on the Plant Science Research Farm at Mississippi State, MS (33.4° N, 88.8° W) in a randomized complete block design with four replicates on two soil types. Soil type one was a Leeper silty clay loam (fine smectitic, nonacid thermic Vertic Epiaquepts), and soil type two was a Marietta loam (fine-loamy, siliceous, active thermic Fluvaquentic Eutrudepts) soil. Each plot was a single row 12 m long with a row spacing of 96.5 cm and plant spacing within row of 10 cm. Yield was determined by harvesting with a two-row mechanical cotton picker equipped with load cells for individual rows. Before machine harvest, a 25-boll sample was hand harvested from bolls near the center of the plant for measuring data on fiber traits at STARLAB Inc., Knoxville, TN. Fiber traits measured using high volume instruments (HVI) were length (upper-half mean, mm), uniformity (%), strength (kN m

Table 2. Number of bolls harvested each cycle by cultivar family, year, number of plants grown, and location for development of RMPAP-C4.

	Random-mating cycle					Total
	C_0	C_1	C_2	C_3	C_4	
	Number of cross bolls harvested					
Sure-Grow 105	226	340	526	425	487	2004
DP 393	247	325	571	554	418	2115
ST 474	265	325	623	496	557	2265
FM 958	203	323	597	452	536	2111
Plants grown†	720	60	720	60	720	
Year grown	2009	2009–2010	2010	2010–2011	2011	
Location	Mississippi	Mexico	Mississippi	Mexico	Mississippi	

† Number of plants grown for each cultivar family.

kg⁻¹), fiber elongation (%), micronaire, fiber reflectance (Rd), and fiber yellowness (+b).

Characteristics

Agronomic and fiber data for different cycles of random mating and cultivar parents are given in Tables 3 and 4. Data for Deltapine 393 were not included in the analysis due to a seed quality issue. Data from other field studies show that agronomic and fiber properties of DP 393 are similar to Sure-Grow 105 (unpublished data). Boll weights after different cycles of random mating were similar and fell between the high and low cultivars means. C₄S₁ lint percentage was lower than the other cycles, and all cycles exhibited lower lint percentage than the cultivar parents. Yields tended to be lower than that of cultivar. Seed weights tended to increase, following random mating. Fiber length remained similar to the cultivars following random mating, whereas fiber uniformity increased. No significant changes occurred for fiber strength, elongation, reflectance, and yellowness following five cycles of random mating. The mean values for all traits measured were not greatly different than those for cultivars. Since the random-mated population is a

heterogeneous mixtures of genotypes, one should expect to be able to make plant selections that exceed the population mean for the various traits.

This population has introgression of alleles from *G. hirsutum* primitive accessions into a population of four upland cultivars in new and unique genetic combinations. The primitive accession used in developing this population contained diversity for agronomic, fiber, and morphology traits in addition to being collected from diverse locations (Table 1). We observed diversity for leaf shape, okra leaf type, a range in leaf and stem hairs, petal spot, petal and pollen color, and brown lint color. The approach to capture useful diversity from photoperiodic accession of primitive cotton by random mating with cultivars has not previously been utilized.

We suggest that this introgression population can be used for direct plant-to-row selections or that one boll or lock could be bulk harvested from each plant and planted with individual plant selections made in the S₂ or later generations. We further suggest that breeders who plant this population harvest a large random sample of bolls and maintain this bulk for further research.

Table 3. Mean agronomic properties of cultivar parents and random-mating cycles C₀S₁ through C₄S₁ of a population involving primitive accessions.

Entry†	Boll wt.	Lint	Seed cotton		Seed index
	g	%	kg ha ⁻¹		g
C ₀ S ₁	5.22	39.26	2961	1166	10.50
C ₁ S ₁	5.38	38.51	2904	1115	11.14
C ₂ S ₁	5.48	38.23	3089	1180	11.44
C ₃ S ₁	5.34	38.90	2589	1000	11.50
C ₄ S ₁	5.34	37.68	3021	1130	11.40
Sure-Grow 105	5.12	41.64	2778	1155	10.56
ST 474	4.98	44.13	3257	1432	10.08
FM 958	5.96	42.86	3092	1330	11.16
Entry F	**	**	**	**	**
LSD _{0.05}	0.26	0.90	442	178	0.54

** Significant at the 0.01 level.

† Data for DP393 not included due to poor seed quality.

Table 4. Mean high volume instruments (HVI) fiber properties of cultivar parents and random mating cycles C₀S₁ through C₄S₁ of a population involving primitive accessions.

Entry	Upper-half mean length	Uniformity index	Strength	Elongation	Micronaire	Fiber reflectance	Fiber yellowness
	mm	%	kN m kg ⁻¹	%		Rd†	+b‡
C ₀ S ₁	30.29	84.15	308	7.49	5.08	77.44	7.39
C ₁ S ₁	30.67	84.48	308	7.26	4.78	76.89	7.70
C ₂ S ₁	30.45	84.71	312	7.43	4.94	76.88	7.66
C ₃ S ₁	30.00	84.93	311	7.48	4.83	77.53	7.65
C ₄ S ₁	30.19	85.00	312	7.46	5.01	76.44	7.51
Sure-Grow 105	30.67	85.33	310	7.58	5.03	76.50	7.31
ST 474	29.27	85.04	291	7.75	5.08	76.99	8.43
FM 958	30.26	85.01	328	7.08	5.24	78.31	7.23
Entry F	**	ns§	**	**	**	*	**
LSD _{0.05}	0.77	0.74	10	0.23	0.18	1.09	0.49

* Significant at the 0.05 level.

** Significant at the 0.01 level.

† Rd is the percentage of the reflectance; the higher the value, the lighter the fiber color.

‡ Hunter's +b value is a measure of increasing yellowness of fiber.

§ ns, not significant at the 0.05 level.

Seed Availability

Small amounts of seed, up to 1000, of the random-mated population germplasm are available for distribution to cotton breeders and other research workers until the present supply is exhausted. Written requests should be addressed to Jack C. McCarty, Crop Science Research Laboratory, P.O. Box 5367, Mississippi State, MS 39762-5367 or by email to the corresponding author. Seed of this population has been deposited in the National Plant Germplasm System, where it will be available for research purposes, including development and commercialization of new varieties/cultivars. Although no transgenic lines were used in the development of this population seeds of this release are not warranted by the USDA-ARS to be free of transgenes. We tested 150 seeds from this population for Bollgard II/Roundup Ready (Monstanto) transgenes using QuickStix Combo Strips (EnviroLogix) and none were detected. It is requested that appropriate recognition be made if this germplasm contributes to the development of a new breeding line or variety.

Acknowledgments

The authors thank Deltapine/Monsanto for allowing the use of DP393 in this breeding project. We further thank technician Kim Gourley and the staff at the winter nursery for assistance during the laborious crossing process. This work was supported by USDA-ARS CRIS Project 6406-21000-012-00D.

References

- Bowman, D.T., O.L. May, and D.S. Calhoun. 1996. Genetic base of upland cotton cultivars released between 1970 and 1990. *Crop Sci.* 36:577–581. doi:10.2135/cropsci1996.0011183X003600030008x
- Bowman, D.T., O.L. May, and D.S. Calhoun. 1997. Coefficients of parentage for 260 cotton cultivars released between 1970 and 1990. USDA-ARS Bull. 1852. U.S. Gov. Print. Office, Washington, DC.
- Bowman, D.T., O.A. Gutierrez, R.G. Percy, D.S. Calhoun, and O.L. May. 2006. Pedigrees of Upland and Pima cotton cultivars released between 1970 and 2005. Bull. 1155. Mississippi Agric. Forestry Exp. Stn, Mississippi State, MS.
- Calhoun, D.S., D.T. Bowman, and O.L. May. 1997. Pedigrees of Upland and Pima cotton cultivars released between 1970 and 1995. Bull. 1069. Mississippi Agric. Forestry Exp. Stn, Mississippi State, MS.
- Campbell, B.T., S. Saha, R. Percy, J. Frelichowski, J.N. Jenkins, W. Park, C.D. Mayee, V. Gotmare, D. Dessauw, M. Giband, X. Du, Y. Jia, G. Constable, S. Dillon, I.Y. Abdurakhmonov, A. Abdurakimov, S.M. Rizaeva, A. Adullaey, P.A.V. Barroso, J.G. Padua, L.V. Hoffmann, and L. Podolnaya. 2010. Status of the global cotton germplasm resources. *Crop Sci.* 50:1161–1179. doi:10.2135/cropsci2009.09.0551
- Gutierrez, O.A., S. Basu, S. Saha, J.N. Jenkins, D.B. Shoemaker, C.L. Cheatham, and J.C. McCarty, Jr. 2002. Genetic distance among selected cotton genotypes and its relationship with F_2 performance. *Crop Sci.* 42:1841–1847. doi:10.2135/cropsci2002.1841
- Gutierrez, O.A., D.T. Bowman, C.B. Cole, J.N. Jenkins, J.C. McCarty, Jr., J. Wu, and C.E. Watson. 2006. Development of random-mated populations using bulked pollen methodology: Cotton as a model. *J. Cotton Sci.* 10:175–179.
- Hinze, L.L., R.J. Kohel, B.T. Campbell, and R.G. Percy. 2011. Variability in four diverse cotton (*Gossypium hirsutum* L.) germplasm populations. *Genet. Resour. Crop Evol.* 58:561–570. doi:10.1007/s10722-010-9599-8
- Jenkins, J.N., J.C. McCarty, Jr., O.A. Gutierrez, R.W. Hayes, D.T. Bowman, C.E. Watson, and D.C. Jones. 2008. Registration of RMUP-C5, a random mated population of upland cotton germplasm. *J. Plant Reg.* 2:239–242. doi:10.3198/jpr2008.02.0080crg
- Jenkins, J.N., J.C. McCarty, Jr., O.A. Gutierrez, R.W. Hayes, and D.C. Jones. 2013. Registration of RMBUP-C4, a random-mated population with *Gossypium barbadense* L. alleles introgressed into upland cotton germplasm. *J. Plant Reg.* 7:224–228. doi:10.3198/jpr2012.08.0028crg
- McCarty, J.C., Jr., and J.N. Jenkins. 1993. Registration of 79 day-neutral primitive cotton germplasm lines. *Crop Sci.* 33:351. doi:10.2135/cropsci1993.0011183X003300020035x
- McCarty, J.C., Jr., and J.N. Jenkins. 2002. Registration of 16 day length-neutral flowering primitive cotton germplasm lines. *Crop Sci.* 42:1755–1756. doi:10.2135/cropsci2002.1755
- McCarty, J.C., and J.N. Jenkins. 2005. Registration of 21 day length-neutral flowering primitive cotton germplasm lines. *Crop Sci.* 45:2134. doi:10.2135/cropsci2005.0113
- McCarty, J.C., Jr., J.N. Jenkins, W.L. Parrott, and R.G. Creech. 1979. The conversion of photoperiodic primitive race stocks of cotton to DN stocks. *Mississippi Agric. and Forestry Exp. Stn. Res. Rpt.* 4(19):1–4.
- McCarty, J.C., J.N. Jenkins, and J. Wu. 2003. Use of primitive accessions of cotton as sources of genes for improving yield components and fiber properties. Bull. 1130. Mississippi Agric. Forestry Exp. Stn., Mississippi State, MS.
- McCarty, J.C., and R.G. Percy. 2001. Genes from exotic germplasm and their use in cultivar improvement in *Gossypium hirsutum* L. and *G. barbadense* L. In: J.N. Jenkins and S. Saha, editors, Genetic improvement of cotton emerging technologies. Science Publishers, Enfield, NH. p. 65–80.
- McCarty, J.C., J. Wu, and J.N. Jenkins. 2006. Genetic diversity for agronomic and fiber traits in day-neutral accessions derived from primitive cotton germplasm. *Euphytica* 148:283–293. doi:10.1007/s10681-005-9027-x
- McCarty, J.C., Jr., J. Wu, and J.N. Jenkins. 2007. Use of primitive derived cotton accessions for agronomic and fiber traits improvement: Variance components and genetic effects. *Crop Sci.* 47:100–110. doi:10.2135/cropsci2006.06.0404
- Meredith, W.R., Jr. 1991. Contributions of introductions to cotton improvement. In: H.L. Shands and L.E. Weisner, editors, Use of plant introductions in cultivar development. Part I. CSSA, Madison, WI. p. 127–146.
- Meredith, W.R., Jr., and R.R. Bridge. 1971. Breakup of linkage blocks in cotton, *Gossypium hirsutum* L. *Crop Sci.* 11:695–698. doi:10.2135/cropsci1971.0011183X001100050027x
- Miller, P.A., and J.O. Rawlings. 1967. Breakup of initial linkage blocks through intermating in a cotton breeding population. *Crop Sci.* 7:199–204. doi:10.2135/cropsci1967.0011183X000700030009x
- Miravalle, R.J. 1964. A new bulked-pollen method for cotton cross pollination. *J. Hered.* 6:276–280.
- Percival, A.E. 1987. The national collection of *Gossypium* germplasm. *Southern Coop. Ser. Bull.* 321.
- Percival, A.E., and R.J. Kohel. 1990. Distribution, collection, and evaluation of *Gossypium*. *Adv. Agron.* 44:225–256. doi:10.1016/S0065-2113(08)60823-8
- Ragsdale, P.L., and C.W. Smith. 2007. Germplasm potential for trait improvement in Upland cotton: Diallel analysis of within-boll seed yield components. *Crop Sci.* 47:1013–1017. doi:10.2135/cropsci2006.09.0627
- Van Esbroeck, G., D.T. Bowman, D.S. Calhoun, and O.L. May. 1998. Changes in the genetic diversity in the cotton in the USA from 1970 to 1995. *Crop Sci.* 38:33–37. doi:10.2135/cropsci1998.0011183X003800010006x
- Wallace, T.P., D. Bowman, B.T. Campbell, P. Chee, O.A. Gutierrez, R.J. Kohel, J. McCarty, G. Myers, R. Percy, F. Robinson, W. Smith, D.M. Stelly, J.M. Stewart, P. Thaxton, M. Ulloa, and D.B. Weaver. 2009. Status of the USA cotton germplasm collection and crop vulnerability. *Genet. Resour. Crop Evol.* 56:507–532. doi:10.1007/s10722-008-9382-2
- Wu, J., J.C. McCarty, J.N. Jenkins, and W.R. Meredith. 2010. Breeding potential of introgressions into upland cotton: Genetic effects and heterosis. *Plant Breed.* 129:526–532 doi:10.1111/j.1439-0523.2009.01715.x