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FIBER QUALITY OF A NEAR-ISOGENIC INTROGRESSION LINE SERIES FROM AN UPLAND BY PIMA INTERSPECIFIC CROSS

Andrew H. Paterson
University of Georgia
Athens, GA
C. Wayne Smith
Texas A&M University
College Station, TX
Edward L. Lubbers and Peng W. Chee
University of Georgia
Tifton, GA

Abstract

Genetic diversity is needed to help continue the advance of Upland cotton cultivars. Gossypium barbadense is an excellent source of diversity for fiber quality in cotton. The Advanced Backcross-QTL analysis is demonstrated as a tool used to introgress this exotic germplasm into Upland cotton to renew favorable genetic diversity as well as detect QTLs for fiber quality. All the fiber quality traits that were measured have significant variation that can be used to improve the fiber traits of Upland cotton cultivars.

Summary

The cotton industry goals are to have more and better quality lint. This is done by having increased acreage, changing the environment with such things as irrigation, fertilization, or pest control. One can also change the crop via breeding. Cotton breeding will continue to be one of the best, most cost effective ways to improve production and quality.

Genetic diversity is required for breeding. One cannot select without differing traits or markers. Continued breeding as well as the initial domestication inherently decreases available genetic diversity. Obviously we need to replace genetic diversity, but we need favorable diversity, not just any type of diversity. Mother Nature has given us a lot of alternate alleles but we have had centuries of selection that have eliminated much of them. We are now looking at an apparent yield and fiber quality plateau, as seen in the previous presentation by Dr. Bill Meredith, which some have questioned as being caused by lack of diversity. We are also finding a need for improved fiber quality for the United States producer to be competitive in the global cotton market.

To have the required diversity, we need to introduce new germplasm. Germplasm can be described as coming from gene pools depending generally on sexual compatibility and recombination. The primary gene pool for Upland cotton obviously includes the races of *Gossypium hirsutum*. *G. barbadense, G. darwinii, G. mustelinum, and G. tomentosum* are also included here even though there are additional hindrances to introgression. The secondary gene pool includes the Gossypium diploids that can recombine once the sexual incompatibility is overcome and then those diploids that have reduced chromosome homology are in the tertiary gene pool.

The greatest hindrances in introgressing alleles from the related tetraploids are overwhelming allelic deluge, and linkage drag. This is likely to be the greatest reason that breeders avoid using exotic germplasm. One method that has been suggested to overcome these problems is the AB-QTL (Advanced Backcross – Quantitative Trait Loci) analysis. Using molecular markers to monitor QTLs may be a more effective technique to quickly remove the linkage drag as well as sifting out the desirable alleles despite the background noise caused by the environment.

Table 1. AB-QTL Analysis Summary (Tanksley & Nelson, 1996)

- Backcross to elite for BC1 and BC2 populations
  - Can select against undesirable donor alleles using markers and/or phenotypes
- Molecular marker characterization at the BC2 or BC3 level.
- Generate BC3 or BC4 families
- Evaluate for agronomic performance and analyze for QTLs.
- Target valuable genomic regions
- Produce NILs with elite genetic background by employing MAS
- Evaluate the agronomic performance of the NILs and elite parent control in replicated environments

Our research uses Pima S-6, a *G. barbadense*, as the exotic donor parent in an AB-QTL analysis as it is in the primary gene pool, is an excellent source of additional genetic diversity because it is known for high quality fiber, many polymorphic markers are available, and it is domesticated, thereby giving some chance that there are fewer undesirable alleles. Direct use is inefficient because hybrid breakdown, partial sterility, and later maturity than many Upland cultivars, but AB-QTL renders these specific difficulties less relevant.

Our objective to more effectively utilize this resource is to develop a series of near-isogenic introgression lines (NIILs) by interspecific backcross of Pima S-6 into Tamcot 2111 using a modified AB-QTL. The intent is to cover the entire Pima S-6 genome.

We are using RFLPs (262 loci from a map with more than 2500 loci (Jiang et al., 2000)) to monitor the introgression of the Pima S-6 donor DNA into Tamcot 2111, the backcross parent. Fiber quality traits were measured in the first subset of this series to monitor phenotypic effects of these DNA segments (Chee et al., 2005a; Draye et al., 2005; Chee et al., 2005b).

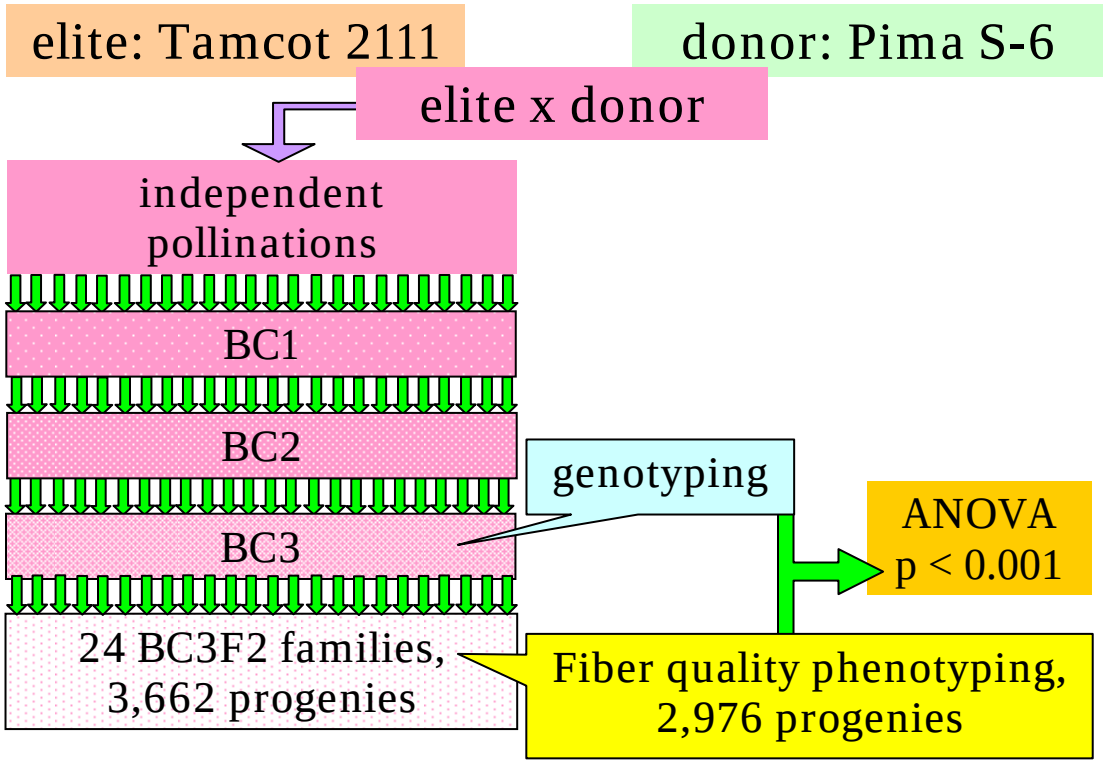


Fig. 1. The Methodology of the QTL Analysis

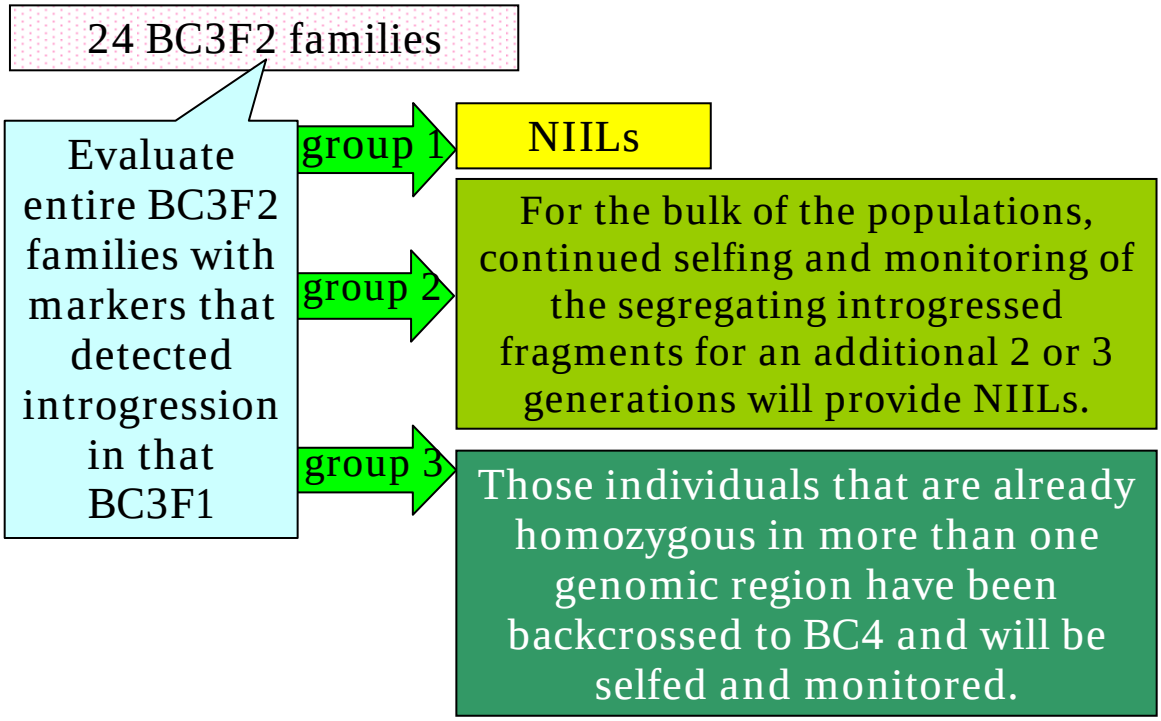
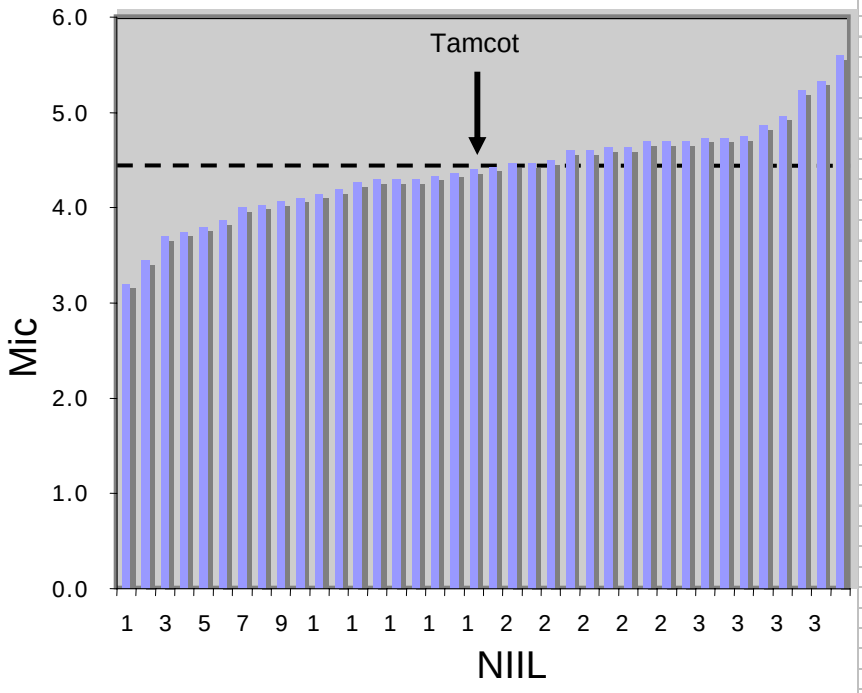


Fig. 2 The Methodology of NIILs Development

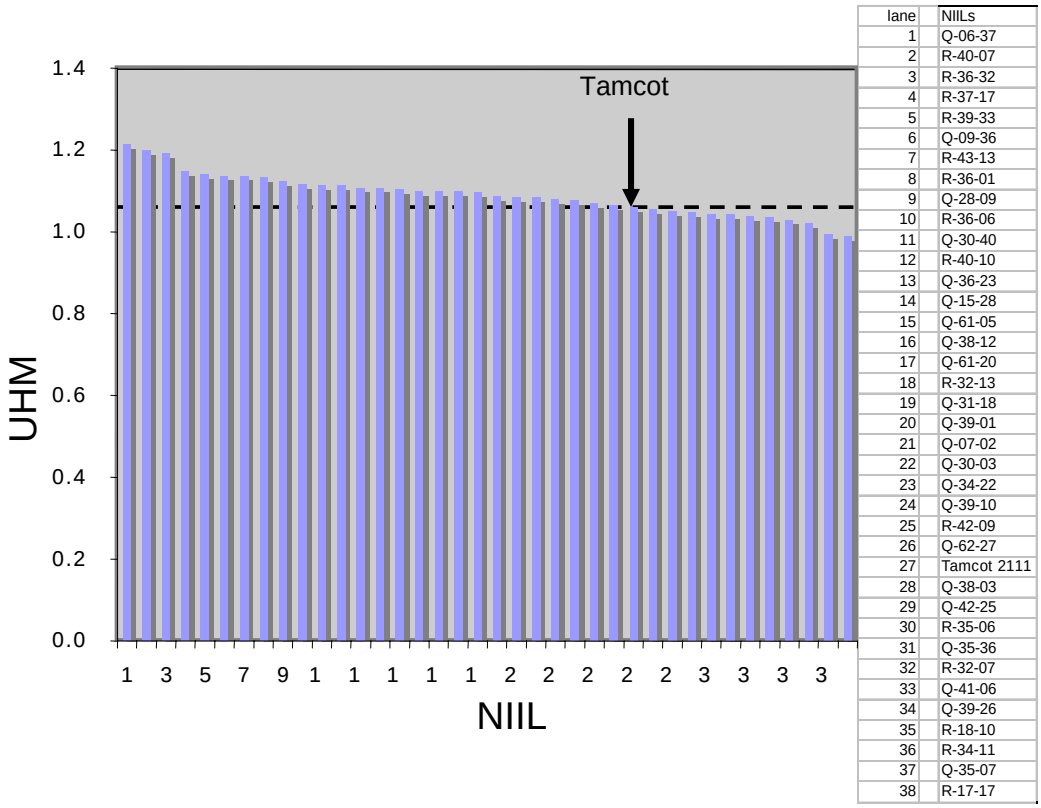
In the NIILs development, we immediately found 37 lines were NIILs. The bulk of the lines (491) are pre-NIILs. Sixty-eight lines were backcrossed again and with selfing and monitoring should provide at least 2 pre-NIILS each for a total of more than 136 pre-NIILs. We should end with a grand total of more than 664 NIILs to select from to cover the Pima S-6 genome. The NIILs in the field look very much like Tamcot 2111.

As we increased seed for the first group of NIILs, we took fiber quality data. With this data from three field plots grown in two years, a single factor ANOVA was performed with F-protected LSD mean separation. All fiber traits reported, as well as HVI Uniformity Index and HVI Elongation, had significant differences between the means. The distribution of the means is graphically reported with the position of Tamcot 2111 emphasized and labeled as Tamcot.



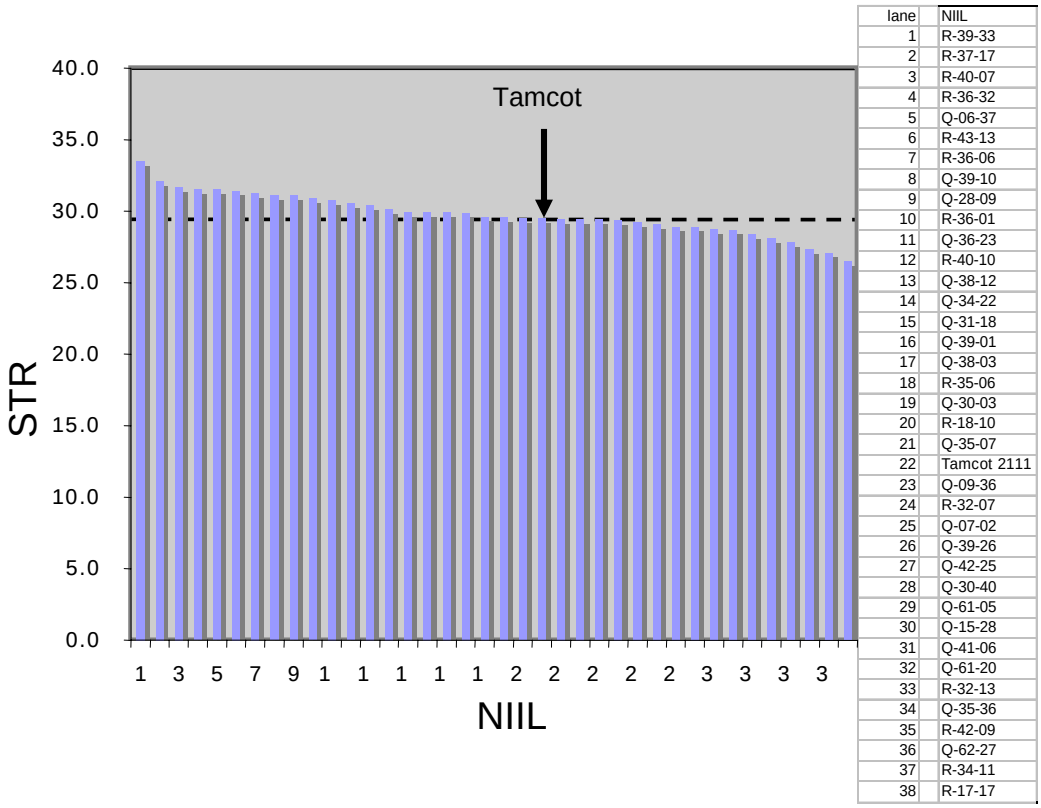
lane	NIIL
1	Q-42-25
2	Q-39-26
3	R-18-10
4	Q-38-03
5	Q-28-09
6	R-37-17
7	Q-39-10
8	Q-15-28
9	R-36-32
10	Q-38-12
11	Q-62-27
12	Q-41-06
13	R-36-01
14	Q-06-37
15	R-39-33
16	R-40-07
17	R-32-13
18	Q-31-18
19	Tamcot 2111
20	R-43-13
21	Q-36-23
22	R-32-07
23	Q-39-01
24	Q-61-05
25	R-40-10
26	Q-07-02
27	R-34-11
28	Q-30-40
29	Q-34-22
30	Q-30-03
31	R-36-06
32	R-42-09
33	Q-61-20
34	Q-35-07
35	Q-35-36
36	R-35-06
37	R-17-17
38	Q-09-36

Fig. 3. The distribution of HVI micronaire of the Group 1 NIILs



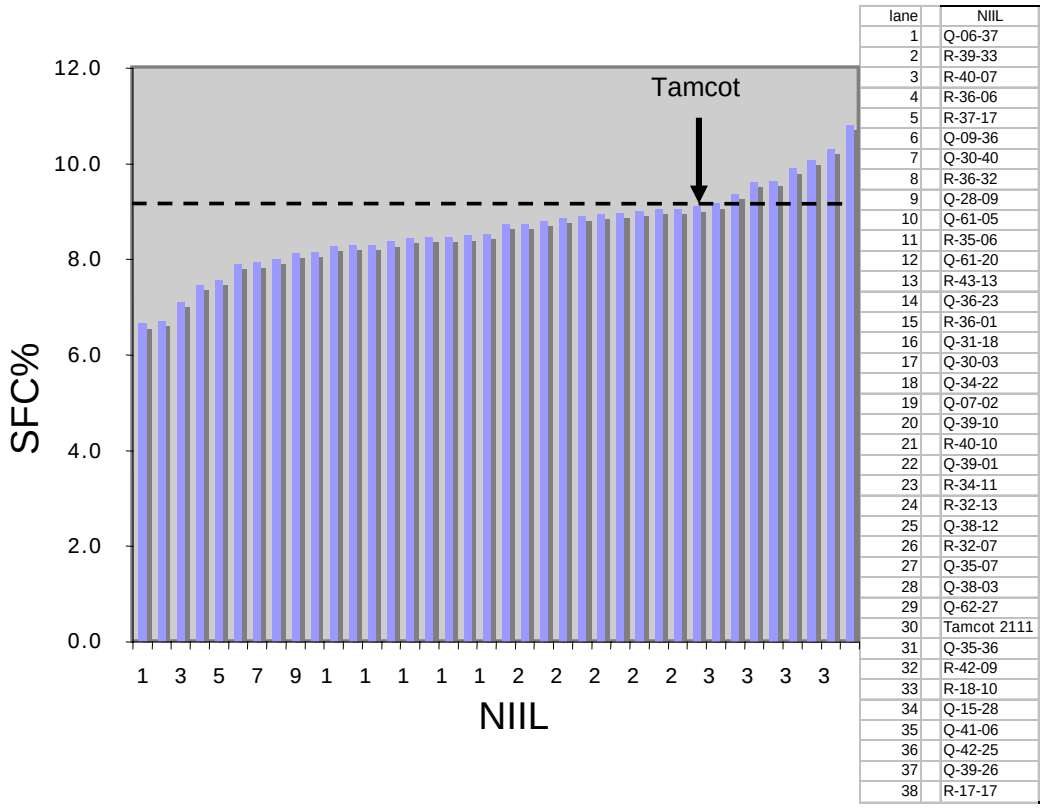
lane	NIILs
1	Q-06-37
2	R-40-07
3	R-36-32
4	R-37-17
5	R-39-33
6	Q-09-36
7	R-43-13
8	R-36-01
9	Q-28-09
10	R-36-06
11	Q-30-40
12	R-40-10
13	Q-36-23
14	Q-15-28
15	Q-61-05
16	Q-38-12
17	Q-61-20
18	R-32-13
19	Q-31-18
20	Q-39-01
21	Q-07-02
22	Q-30-03
23	Q-34-22
24	Q-39-10
25	R-42-09
26	Q-62-27
27	Tamcot 2111
28	Q-38-03
29	Q-42-25
30	R-35-06
31	Q-35-36
32	R-32-07
33	Q-41-06
34	Q-39-26
35	R-18-10
36	R-34-11
37	Q-35-07
38	R-17-17

Fig. 4. The distribution of HVI UHM of the Group 1 NIILs



lane	NIIL
1	R-39-33
2	R-37-17
3	R-40-07
4	R-36-32
5	Q-06-37
6	R-43-13
7	R-36-06
8	Q-39-10
9	Q-28-09
10	R-36-01
11	Q-36-23
12	R-40-10
13	Q-38-12
14	Q-34-22
15	Q-31-18
16	Q-39-01
17	Q-38-03
18	R-35-06
19	Q-30-03
20	R-18-10
21	Q-35-07
22	Tamcot 2111
23	Q-09-36
24	R-32-07
25	Q-07-02
26	Q-39-26
27	Q-42-25
28	Q-30-40
29	Q-61-05
30	Q-15-28
31	Q-41-06
32	Q-61-20
33	R-32-13
34	Q-35-36
35	R-42-09
36	Q-62-27
37	R-34-11
38	R-17-17

Fig. 5. The distribution of HVI Strength of the Group 1 NIILs



lane	NIIL
1	Q-06-37
2	R-39-33
3	R-40-07
4	R-36-06
5	R-37-17
6	Q-09-36
7	Q-30-40
8	R-36-32
9	Q-28-09
10	Q-61-05
11	R-35-06
12	Q-61-20
13	R-43-13
14	Q-36-23
15	R-36-01
16	Q-31-18
17	Q-30-03
18	Q-34-22
19	Q-07-02
20	Q-39-10
21	R-40-10
22	Q-39-01
23	R-34-11
24	R-32-13
25	Q-38-12
26	R-32-07
27	Q-35-07
28	Q-38-03
29	Q-62-27
30	Tamcot 2111
31	Q-35-36
32	R-42-09
33	R-18-10
34	Q-15-28
35	Q-41-06
36	Q-42-25
37	Q-39-26
38	R-17-17

Fig. 6. The distribution of HVI % Short Fiber Content of the Group 1 NIILs

All of the fiber quality traits showed genetic diversity that is available for introgression from these NIILs into elite cultivars. These NIILs are useful in that they are a source of variation with less penalty of linkage drag, they will have a more discrete segregation of the alleles within the genomic segment, and they will allow fine mapping without the clutter of the original cross.

Our future work will include fine mapping of selected genomic regions that are associated with fiber quality traits as well as determining the performance of the QTLs of the NIILs under different genetic backgrounds along with stacking / pyramiding the QTLs to build better quality fiber.

Acknowledements

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References

Chee, P., X. Draye, C-X Jiang, L. Decanini, T.A. Delmonte, R. Bredhauer, C. W. Smith, and A.H. Paterson. 2005a. Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: I. Fiber elongation. Theor. Appl. Genet. 111:757-763.

Chee, P., X. Draye, C-X Jiang, L. Decanini, T.A. Delmonte, R. Bredhauer, C. W. Smith, and A.H. Paterson. 2005b. Molecular dissection of phenotypic variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: III. Fiber length. Theor. Appl. Genet. 111:772-781.

Draye, X., P. Chee, C-X Jiang, L. Decanini, T.A. Delmonte, R. Bredhauer, C. W. Smith, and A.H. Paterson. 2005. Molecular dissection of interspecific variation between *Gossypium hirsutum* and *G. barbadense* (cotton) by a backcross-self approach: II. Fiber fineness. Theor. Appl. Genet. 111: 764-771.

Jiang, C., P. Chee, X. Draye, P. Morrell, C. Smith, and A. Paterson. 2000. Evolution Multi-locus interactions restrict gene flow in advanced-generation interspecific populations of polyploid Gossypium (Cotton). 54:798-814.

Tanksley, S.D. and C.J. Nelson. 1996. Advance backcross QTL analysis: a method for the simultaneous discovery and transfer of valuable QTLs from unadapted germplasm into elite breeding lines. Theor. Appl. Genet. 92:191-203.