

## Reducing the Genetic Vulnerability of Cotton

Andrew H. Paterson,\* Randal K. Boman, Steven M. Brown, Peng W. Chee, John R. Gannaway, Alan R. Gingle, O. Lloyd May, and C. Wayne Smith

THE U.S. COTTON (*Gossypium* spp.) production system exemplifies the challenges that must be met to reduce the genetic vulnerability of a major crop. As an industrial crop that sustains one of the largest U.S. industries (textiles), more than 400 000 domestic jobs are related to cotton production and processing, with an aggregate impact of over \$40 000 million on the U.S. gross domestic product.

The U.S. cotton gene pool is genetically impoverished. All cottons cultivated in the USA are tetraploid, thought to have arisen in the New World about 1 to 2 million years ago, as a result of an unusual hybridization event between an invasive A-genome diploid genotype and an indigenous D-genome diploid. Polyploid cottons are thought to be monophyletic, with contributions from only two of the eight extant diploid “genome types” in the genus, representing the first genetic bottleneck. A second bottleneck was associated with the domestication of cotton from a small subset of the wild genotypes. A third bottleneck was imposed by human sampling of tetraploid cotton genotypes from their center of diversity in Mexico and Central America, and spread northward into the USA, and also to China, India, Egypt, Australia, and other countries.

Growing concern about genetic vulnerability of the cotton gene pool to a wide range of biotic and abiotic hazards is exemplified by recent investigation of trends in yield improvement. Stagnation in yield improvement of *G. hirsutum* L. recently led the National Cotton Council to form a Blue Ribbon Committee of public and private scientists to determine if there truly was a yield plateau, and if so, how it should be addressed (Helms, 2000). The committee based its findings on current public data, largely from National Cotton Variety Tests (Rayburn et al., 1999) and the National Agricultural Statistics Service, USDA (NASS, 1998). On the basis of a linear model, over the past 39 yr, cotton yields have increased about 6.7 kg ha<sup>-1</sup> yr<sup>-1</sup> (1.3% annual rate). A polynomial model clearly indicates that this increase has not been linear. From 1970 through 1985, the rate of change in cotton yields rose at an increasing level. However, from 1985 through 1998, the rate of change in cotton yields declined and from 1992 through 1998, the actual yields declined. Stated another way, the rate of

change in cotton yields has steadily declined since 1985. By 1998, absolute cotton yields (not just the rate of change) reached a disturbing rate of decline of about 16.8 kg<sup>-1</sup> ha<sup>-1</sup> yr<sup>-1</sup> (3.3% annual rate). Accompanying this yield decline, year-to-year variations in yield were almost four times greater in the period from 1980 to 1998 than in 1960 to 1979. This increased volatility in yield translates directly into higher risk for the grower.

The yield plateau in cotton appears to be closely associated with increasing genetic vulnerability. In addition to the genetic bottlenecks imposed by polyploid formation, domestication, and migration, the U.S. cotton gene pool has been further eroded by the over-exploitation of a few genetic backgrounds during the past 15 yr. Commercial breeding programs repeatedly employ a few closely related genotypes to generate new cultivars (May et al., 1995). Growers are planting large areas to these closely related cultivars, resulting in a high level of field genetic uniformity (Van Esbroeck et al., 1998). This has been exacerbated by the widespread (about 60% of 1999 U.S. hectares) planting of transgenic cultivars that are the result of backcross breeding with an even smaller subset of closely related genotypes.

A solution may lie in the exploration of exotic genotypes. Although there exist five tetraploid *Gossypium* species each including a huge array of feral and wild forms, at present, no exotic cottons appear in the pedigrees of any modern U.S. cultivars or enhanced germplasm (Bowman et al., 1996; Bowman et al., 1997; Calhoun et al., 1997). Our early explorations in a small sampling of these genotypes show many transgressive QTL alleles (P. Chee, X. Draye, A.H. Paterson, in preparation), including some cases in which different taxa appear to have evolved complementary alleles at alternative homeologous loci (Saranga et al., 2001).

However, introgressive breeding involves new challenges that require fundamentally different approaches than mainstream plant breeding, and an equally long-term effort. Particularly prominent among the challenges of introgressive breeding appear to be a high level of epistasis (nonlinear interactions between unlinked loci)—in many cases individual QTL loci in combination with different unlinked introgressed alleles affect a phenotype to very different degrees. In a few cases, the same QTL allele has even shown statistically significant opposite effects in different genetic backgrounds (P. Chee, X. Draye, A.H. Paterson, in preparation). This complication, superimposed on the effects of linkage drag, hybrid breakdown, and other well-known characteristics of wide crosses all highlight the fact that successful introgressive breeding of quantitative traits will require a dedicated effort that is designed to address such challenges, rather than being a ‘side project’ in a mainstream plant breeding program. Further, this will clearly be a high-risk, high-reward activity, in the sense that many promis-

Andrew H. Paterson, Plant Genome Mapping Laboratory, Univ. of Georgia, 111 Riverbend Road, Athens GA 30602; Steven M. Brown, Peng W. Chee, and O. Lloyd May, Dep. of Crop and Soil Sciences, Univ. of Georgia, Coastal Plain Exp. Station, Tifton, GA 31793; Randal K. Boman and John R. Gannaway, Dep. of Soil and Crop Sciences, Texas A&M Research and Extension Center, Lubbock TX 79403; Alan R. Gingle, Center for Applied Genetic Technologies, Univ. of Georgia, 111 Riverbend Road, Athens GA 30602; C. Wayne Smith, Dep. of Soil and Crop Sciences, Texas A&M University, College Station TX 77843. Received 23 July 2003. \*Corresponding author (paterson@plantbio.uga.edu).

ing early leads will not translate into commercially viable products ... but those that do may confer larger incremental gains than are available in the present cultivated gene pool.

Implementing this solution requires integration of research, education, and extension activities. Genetic vulnerability is a complex problem that results from a crop's evolutionary history, trends in breeding and biotechnology practices, and grower decisions based on inadequate information being available, all responding to the inevitable pressures of processor and consumer preferences. Gaining the partnership of stakeholders is key. Toward this end, while the introgressive breeding process proceed, we are working with both researchers and extension personnel to create a Web-based resource to provide objective information about relatedness of genotypes, as a management tool for producers to better deploy the remaining variation in the gene pool to minimize genetic vulnerability of the crop, and a research tool for scientists to glean new information useful for crop improvement.

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## The Role of Genomics Research in Improvement of "Orphan" Crops

Rebecca J. Nelson, Rosamond L. Naylor, and Molly M. Jahn\*

THE IMPORTANCE OF AGRICULTURE to global food security goes beyond the need for total growth in crop yields and production. Agriculture promotes food security because it fulfills nutritional needs and/or contributes to local incomes and employment. Poverty in the developing world remains most pronounced in rural areas where agriculture is one of few sources of income and employment. The world's poorest regions are typically those where agricultural investments by the public and private sectors are extremely low. There is an urgent need for mechanisms to enhance agricultural development poor agrarian societies (Mosher, 1966).

In addition to a small number of well-known major global crops such as maize (*Zea mays* L.), rice (*Oryza sativa* L.), and wheat (*Triticum aestivum* L. em. Thell.), many more crops are regionally or locally important for nutrition and income in poor regions. Crops such as plantain and bananas (*Musa* sp. L.); root and tuber crops such as cassava (*Manihot esculenta* Cranz.), sweet potato [*Ipomoea batatas* (L.) Lam.], and yam (*Dioscorea* sp. L.); millets such as pearl millet [*Pennisetum glaucum* (L.) R. Br.], finger millet [*Eleusine coracana* (L.) Gaertn.], and foxtail millet [*Setaria italica* (L.) Beauv.]; legumes

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such as cowpeas [*Vigna unguiculata* (L.) Walp], groundnut (*Arachis hypogaea* L.) and Bambara groundnut [*Vigna subterranea* (L.) Verdc.]; and tree crops. Moreover, indigenous crops such as tef [*Eragrostis tef* (Zucc.) Trotter], quinoa (*Chenopodium quinoa* Willd.), and many types of vegetables are critical for food security and nutrition on a regional or local basis.

Twenty-five such "orphan" crops within developing countries total some 240 million hectares, with an additional 70 million hectares planted to fruits and vegetables (Naylor et al., 2004). In Sub-Saharan Africa, for example, sorghum [*Sorghum bicolor* (L.) Moench.] and pearl millet are more important than rice and wheat, both in area (41 million ha. vs. 9 million ha.) and in contribution to diet. Roots and tubers are essential staples in Africa, where cassava is the third most important source of calories overall. The underresearched crops are nutritious, valued culturally, adapted to harsh environments, and diverse in terms of their genetic, agroclimatic, and economic niches. Attention to locally important crops takes on added urgency given that 38% of Sub-Saharan Africa's population is undernourished, and the number of undernourished children in that region is expected to increase from present levels by 39% by 2020 (Pinstrup-Anderson et al., 1999).

A large discrepancy exists between the potential role of these crops in improving food security and livelihoods,

R.J. Nelson, Dep. of Plant Pathology, 321 Plant Science, Cornell Univ., Ithaca, NY, 14853; M.M. Jahn, Dep. of Plant Breeding, 313 Bradfield Hall, Cornell Univ., Ithaca, NY, 14853; R.L. Naylor, Center for Environmental Science and Policy, Stanford Univ., Encina Rm. 418E, Stanford, CA, 94305. Received 23 July 2003. \*Corresponding author (mmj9@cornell.edu).

**Abbreviations:** EST, expressed sequence tag; MAS, marker-assisted selection; QTL, quantitative trait loci.