EXPLOITING AGRICULTURALLY VALUABLE ALLELES FROM GOSSYPIUM MUSTELINUM TO **IMPROVE FIBER OUALITY IN UPLAND COTTON Baohua Wang** Peng W. Chee Limei Liu Zhimin Zhuang **Ed Lubbers O. Llovd Mav Department Of Crop And Soil Sciences** University Of Georgia Tifton, GA Zhengsheng Zhang Susan Auckland **Junkang Rong** Andrew H. Paterson **Plant Genome Mapping Laboratory University Of Georgia** Athens, GA **Tianzhen Zhang** National Key Laboratory of Crop Genetics & Germplasm Enhancement **Cotton Research Institute** Nanjing Agricultural University

Nanjing, China

Abstract

In order to extract agriculturally valuable alleles from *G. mustelinum*, Brazilian endemic cotton representing the first or basal lineage in the polyploidy cotton phylogeny, advanced backcross QTL analysis was used in this research. A total of 35 BC3F1 cotton individuals and the corresponding BC3F2 populations were developed; meanwhile, a genetic linkage map was constructed using an F2 population so as to help get the introgression information of *G. mustelinum* in the BC3F1s. Both DNA marker data and fiber quality data were collected from the BC3F2 populations and QTLs for fiber quality traits were analyzed. The data analysis results showed that fiber quality traits were improved in some of the populations compared to the recurrent parent. Meanwhile, in some populations, quite a few lines demonstrate better fiber quality traits than the recurrent parent. These elite lines may be used as potential germplasm to improve cotton fiber quality.