FACILITATING THE USE OF WILD SPECIES GERMPLASM FOR COTTON IMPROVEMENT VIA CS LINES

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Abstract

Many studies have documented that genetic diversity among elite lines of cotton is extremely low. Given that rates of genetic gain depend on levels of selection intensity and genetic diversity, the gains from cotton breeding would increase if genetic diversity were increased, at least theoretically. While infusion of germplasm from non-elite and non-adapted types of *Gossypium hirsutum* would expand genetic diversity, they, too, are insufficiently genetically distinct. Far greater genetic diversification would be achieved if germplasm of other AD species were introgressed into cultivated *G. hirsutum*. The aims of this project are [1] to transfer germplasm from three related AD species, all 2n=52, into *G. hirsutum*, [2] to establish a isogenic true-breeding lines that are amenable to conventional cotton research and breeding operations, and [3] to establish a new platform for germplasm diversification, genetic investigation, and improvements. This multi-decade project, now increasingly multi-investigator and multi-institutional, has increased genetic diversity by creating "Chromosome Substitution" (CS) lines by [1] interspecific hybridization of mostly isogenic hypoaneuploid stocks of *G. hirsutum* with *G. barbadense*, *G. tomentosum*, or *G. mustelinum*, [2] modified backcross-inbred breeding to establish disomic substitution lines, each of which is true breeding and contains a targeted alien chromosome or chromosome segment. The most significant breeding modifications include phenotypic, cytogenetic and marker-based selection for maintenance of hypoaneuploidy (hemizygosity) during backcrossing, or disomy (homozygosity) upon inbreeding. Each CS line contains 500-4000 alien genes, which can have direct effects and/or interactions with any number of other genes in the genome, roughly estimated to number 60,000. The CS lines were studied *per se* and used to create F2s, F3s, sets of topcrosses with cultivars, recombinant inbred lines (RILs) and CSxCS cross combinations. Variations of the AD quantitative genetic model were developed to enable increasingly incisive inferences regarding components of genetic variation. In each case, the studies have revealed beneficial genetic variation for essentially all agronomic, plant and fiber traits tested. For instance, a recent initial screen indicated heritable thrip resistance and/or tolerance exists among CS lines from each of the three alien species donors. Given that the CS lines collectively introduce about an estimated 120,000 or more alien genes into the breeding pool, we expect analogous opportunities for most traits, if not all. Our challenges now are to obtain collaborators and resources to expand and utilize this important new platform for cotton research and improvement.