ENHANCING UPLAND COTTON BREEDING BY IMPROVING THE INTROGRESSION, DISSECTION AND MANIPULATION OF GERMPLASM FROM *GOSSYPIUM* DIPLOID SPECIES

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Abstract

A key means of alleviating genetic constraints on rates of genetic improvement in crops with low genetic diversity, like cotton, is to expand genetic diversity through interspecific germplasm introgression. We report here new DNA marker resources that can be used to address a number of impediments to the introgression, dissection and manipulation of diploid *Gossypium* germplasm for Upland cotton improvement. For example, backcross introgression projects can be greatly empowered and accelerated using marker-assisted selection (MAS), whether for one or many targeted loci. For applied breeding programs, the choice to use marker-assisted selection methods or not often depends on the time, cost and other resources, especially when large backcross populations are involved. While the high-throughput highly multiplexed CottonSNP63K platform can be used very cost effectively in the early stages of the breeding programs for quickly genotyping small and medium-sized mapping populations, e.g., to develop high-density linkage maps, the cost of genotyping multiple or large populations can be prohibitive for the advance generations. Moreover, it may be ill-suited to needs when the MAS targets are limited in number--for which simplex and low-plex genotyping methods may offer a more effective alternatives.

Whereas the previously reported CottonSNP63K genotyping platform was optimized for automated genotyping of Upland cottons, we report here a customized version of the cluster file optimized for Upland cottons containing germplasm from diploid species of the secondary gene pool. To address the need for targeted MAS, too, we report on rates at which simplex and low-plex KASP assays can be derived from the mapped loci, based on a genome-wide sample set of polymorphic mapped markers. The results demonstrate the ease with which ad hoc simplex SNP assays can be derived for downstream breeding objectives such as MAS-based seed/seedling of rare recombinants and multi-gene combinations.