## EMERGENCE OF A COTTON SNP CHIP FROM CONSORTIUM-BASED COLLABORATIONS

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## Abstract

A SNP chip for Cotton (Gossypium hirsutum L.) has been developed as the result of an international collaborative effort. The Chip will feature a high-throughput format which will allow for genotyping of up to 90,000 single nucleotide polymorphisms (SNPs) for 24 individual samples simultaneously. Of the 90,000 possible SNP, 70,000 will be available for public use to everyone who purchases the chip, designated as public "Base Content". The remaining 20,000 possible SNP are available for additional cost as "Add-On Content" for private use in typically non-public applications. The chip will include nearly all previously published SNPs and some sets of SNPs that are currently in press. All SNP in the "Base Content" will be public and published upon validation of the chip. As diversity is low among agronomically elite cottons, the overall pool of SNPs is necessarily large and the Base Content will primarily target SNP between cultivated hirsutum (intra-specific). This will strongly support global conventional breeding efforts for Upland cotton. The remaining SNP represent differences relative to hirsutum (inter-specific) in five other Gossypium species: G. barbadense, G. tomentosum, G. mustelinum, G. armourianum, and G. longicalyx. Some of these SNPs will also be useful in other species, e.g. A or D genome species. The inter-specific SNPs will primarily target the other 52-chromosome species and will greatly facilitate introgression breeding and various types of research involving the AD species. The SNP Chip will be a resource that will be used globally by public and private breeders, geneticists, and other researchers to enhance cotton genetic analysis, breeding, genome sequence assembly and many other uses. We report on the results of the computational analyses undertaken to derive the final public Base Content for the Cotton SNP Chip.

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