

2068 Development of phytochrome specific 'candidate-gene' markers to reveal genetic associations of phytochrome gene family with the important QTLs in cotton

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Phytochromes are known to play roles in cotton plant architecture, floral initiation, and fiber elongation. Previously in our laboratory, we characterized the *Gossypium* orthologs of the Arabidopsis *PHYA*, *PHYB*, *PHYE* and *HY5* genes from *G. hirsutum* and *G. barbadense* (AD-genomes), and from *G. herbaceum* (A-genome) and *G. raimondii* (D-genome). Based on SNP sites in *Gossypium*-derived *PHY* genes, several phytochrome-specific CAPs and dCAPs markers were developed for *PHYA1*, *PHYB1*, *PHYB2* and *HY5* genes to reveal their association with important QTLs in interspecific populations of *G. hirsutum* and *G. barbadense*. Using these 'candidate-gene' markers, cotton phytochrome genes were assigned in specific cotton chromosomes using cytogenetic stocks of cotton, and incorporated into the genetic linkage map of cotton derived from the interspecific cross of TM1 (*G. hirsutum*) and 3-79 (*G. barbadense*). Results of both analyses with cytogenetic stocks and linkage mapping revealed that *PHYA* genes located in chromosome 11, *PHYB* genes are in chromosome 10 and *HY5* gene is chromosome 24. The association of these phytochrome-specific 'candidate' gene markers with useful agronomic traits of cotton will be presented.