

A GLIMPSE INTO THE COTTON GENOME

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Abstract

The large size and tetraploid nature of the *Gossypium hirsutum* genome will make it costly and technically challenging to determine its complete DNA sequence, based on today's technology. Therefore, it has been proposed that *G. raimondii* would be a desirable species to sequence because it may be representative of the D genome and its genome is one-third the size of *G. hirsutum*. An alternative strategy would be to use an approach that would concentrate on gene rich regions. In our pilot study, we used GeneThresher technology (methyl filtration) to evaluate the genome composition of the *G. hirsutum* (AD1), *G. barbadense* (AD2), *G. raimondii* (D5), and *G. arboreum* (A2) genomes. The results from this study demonstrate that there might be an optimal approach for obtaining the maximum gene information for *Gossypium* at the lowest cost, while complementing present efforts on sequencing the *G. raimondii* genome.

A brief discussion on current efforts within the cotton research community to have the cotton genome sequenced will also be presented.