

Sequencing the Cotton Genomes - *Gossypium* spp.

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The genomes of most major crops, including cotton, will be fully sequenced in the next few years. Cotton is unusual, although not unique, in that we will need to sequence not only cultivated (tetraploid) genotypes but their diploid progenitors, to understand how elite cottons have surpassed the productivity and quality of their progenitors. Some technical questions remain about the most efficient approach by which to sequence the *Gossypium* (cotton) genomes, and different members of the genus may require different strategies. The potential benefits of the post-genomic era in cotton are real and large - improved quality, productivity, and stability; reduced input needs that improve sustainability and environmental stewardship of cotton production; and value-added features tailored to human needs. The greatest challenge facing the cotton community is the conversion of 'sequence' to 'knowledge'. We will quickly identify much cotton sequence to be repetitive "junk DNA" -this cannot be dismissed as unimportant, but will be relatively low in unique information content. We will also quickly convert some cotton sequence to information based on similarity to known sequences (from *Arabidopsis* in particular). However, few if any other seedborne epidermal plant cells reach 1-2" in length and >90% cellulose. To understand and manipulate the unique features of cotton will require a host of enabling tools, technologies, and resources to be developed and creatively deployed; in particular targeting portions of the sequence that are substantially different from those of other organisms.