

What Will We Do with a Cotton Genome Sequence?

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With the publication of "Toward Sequencing Cotton (*Gossypium*) Genomes" [Chen et al. *Plant Physiology*, 2007, 145:1303-1310] a clear consensus emerged from the cotton genomics community not only that cotton genome sequences were a critical resource for research and commercial innovation in cotton genomics, but that there was a logical means of achieving this goal. This consensus emerges at a propitious moment in science. A range of new sequence technologies have reached a level of technical maturity that is allowing sequence data to be generated at unprecedented scales and costs. The first human genome sequence took 13 years and cost US\$ 2.7 billion. The most recent human genome sequence, that of James Watson, took 4.5 months and cost US\$ 1.5 million. Of course, this most recent result required a previous reference sequence, but it is illustrative of the explosion of research possibilities once a reference sequence is in place. As we anticipate the publication of the first cotton genome sequence, we can begin to look ahead to the new research possibilities this will create. Cotton genomics researchers will be able to unravel the genetics of complex traits and genome structure and evolution with increasing levels of resolution and insight. By looking to the organisms that have a genome sequence available, the scope and resolution these possibilities are becoming clear.