

ICGI Comparative Genomics and Bioinformatics

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In the coming years, researchers in this workshop may assemble the telomere-to-telomere level genome sequences and high-quality graph-based pan-genomes of the cultivated cottons as well as the super pan-genome of the *Gossypium* genus. The comparative genome analysis of the genomic and pan-genomic sequences should clarify the evolutionary history of cotton genome evolution, uncover the missing heritability of some major agronomic traits, retrieve the lost favorable genes during domestication and improvement, and enable genome-based cotton breeding. The cotton genome study should be extended to include but not limited to other fields, such as epigenome and three-dimensional (3D) genome, which may help characterize the Encyclopedia of DNA Elements (ENCODE) in cotton and uncover the dynamic regulome underpinning some important biological processes such as fiber development. To fulfill these projects, researchers should develop new bioinformatic and database tools to assemble and analyze these multi-omics data, and make these resource available publicly to the cotton community. As a co-chair for this workshop, he should organize relevant researchers to promote the implementation of these projects together, make efforts for open access to cotton genome resources, and boost international cotton genome research to achieve a higher level.