

ORGANIZING COTTON GENOMICS THROUGH PHYSICAL MAPPING

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Abstract

Large-scale and high-throughput approaches suited to analysis of genomes collectively comprise a new field called “genomics”. Development of cotton genomics is crucial to cotton’s future in the US and elsewhere. Increased amenability to genetic manipulations will ultimately enable cotton to compete successfully for marketshare in the textile world, as well as cottonseed as a source of feed- or food-stuffs. Multiple, well-integrated approaches are required for efficient analysis of the cotton genome, which is both large and complex. The genome of *Gossypium hirsutum* L. contains 26 chromosomes (more than virtually all other economically important plants) and 2,300,000,000 base pairs of DNA. Scientists recognizing the difficulty, need, and resource limitations to advance cotton science formed the International Cotton Genome Initiative (ICGI) and formed a workgroup on each of these five major areas in genomics: Structural Genomics (organization), Functional Genomics (gene expression), Germplasm & Genetic Stocks, Evolutionary & Comparative Genomics, Bioinformatics (data storage, inter-relating, analysis, access). Development of structural genomics entails mapping that is both extensive and comprehensive. Because all mapping methods have analytical strengths and weaknesses, multiple approaches must be used. Linkage mapping is central to not only cotton genomics but also marker-assisted breeding, but we also need to include methods of physical mapping, because these are highly complementary to linkage mapping. We focus herein on three complementary physical mapping methods: [1] Chromosome manipulations, [2] Molecular cytogenetics (in situ hybridization of DNA to actually see locations on chromosomes), and [3] Radiation hybrid mapping. They offer improved resolution in low-recombination regions; facile detection of synteny across high-recombination regions; and “validation”, e.g., a means to detect errors in linkage maps. Physical mapping resources are thus essential to cotton genomics. We see ICGI will be an excellent vehicle for assembling and sharing common resources that will advance cotton domestic and international research, simultaneously promoting domestic research and collaboration. As a result, we will see industry-wide advances that globally enhance cotton fiber as a competitor for textile use. We gratefully acknowledge current or past research support from the following sources: Texas Agricultural Experiment Station, USDA-ARS, USDA-NRICGP, Texas Food & Fiber Commission, TxCot, Texas State Support Committee, Cotton, Incorporated.