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A COMPARISON OF GENOME MAPPING TOOLS IN PLANTS

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Abstract

The rapid expansion of genomics tools in recent years has provided rapid advancement in many areas of genetics research. These tools have provided vast new opportunities to understand genomic structures and apply this knowledge. One on the major hurdles to such advancement in cotton is the lack of an integrated consensus genome map. An overview and comparison of various technologies for genome mapping as they have been applied to cotton reveals several pressing needs. One need is to identify syntenic linkage groups, such that they coalesce to the haploid number. Another is to better map regions where closely linked markers are unresolved by recombination. A third is to provide additional mechanisms through which partially to largely independent linkage mapping efforts can interface their resources can create common map resources and information. A fourth is to increase the absolute physical resolution and coverage provided at the chromosome level by cytogenetic stocks. Physical coverage also needs to be improved over that provided by large-insert libraries and their maps of assembled contigs. Here, we draw attention to the need and usefulness of physical mapping through radiation hybrid mapping, especially wide-cross whole-genome radiation hybrid mapping. To date, all animal genome mapping projects have relied heavily on radiation hybrid mapping. Proof-of-concept experiments on cotton are described for 5- and 8-krad WWRH panels. Support for this project was provided by Cotton Incorporated, the Texas A&M Nuclear Science Center, and the Texas A&M Electron Beam Food Research Facility.