Completely Distinguishing Individual A-genome Chromosomes and Their Karyotyping Analysis by Multiple BAC-FISH

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Multiple BAC-FISH is a powerful tool for modern cytogenetic researching in both animals and plants. But in cotton, this technique is unavailable due to the high percentage of repetitive sequences. Here, we identified twenty BACs from more than fifty BACs, and successfully demonstrated the use of multiple BAC-FISH for cytogenetic research in a diploid cotton species, *G. arboreum*. The karyotyping should be a basic application of this technique, but the potential usage such as high-resolution physical mapping construction, assisting BAC-by-BAC sequencing will be invaluable.