

Toward an Integrated Physical Map of the Coffee Genome

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SUMMARY

Availability of very large-insert, ordered DNA libraries are crucial for genomics research including physical mapping, map-based cloning of agronomically important genes, and analysis of gene structure and function. The construction of an integrated genetic and physical map of the coffee genome represents therefore an important challenge that has justified a recent initiative. A bacterial artificial chromosome (BAC) library of the allotetraploid species, *Coffea arabica*, was constructed. This large insert DNA library derived from a multi-disease resistance line contains 88 813 clones with an average insert size of 130 kb, and represents approximately 8 *C. arabica* haploid genome equivalents. The undertaken mapping approach combined hybridisation with mapped markers and BAC fingerprinting. We completed hybridisation with both low-copy RFLP markers distributed on the 11 different chromosomes and probes corresponding to disease resistance gene analogues. BAC clones from subgenomes E^a and C^a were assembled into separate contigs. Accuracy of the map was verified using several approaches. These preliminary results represent the first step toward the construction of a physical map of the coffee genome.