**Construction, Characterization, and Preliminary BAC-End Sequence Analysis of a Bacterial Artificial Chromosome Library of the Tea Plant (Camellia sinensis)**

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**Abstract**

We describe the construction and characterization of a publicly available BAC library for the tea plant, Camellia sinensis. Using modified methods, the library was constructed with the aim of developing public molecular resources to advance tea plant genomics research. The library consists of a total of 401,280 clones with an average insert size of 135?kb, providing an approximate coverage of 13.5 haploid genome equivalents. No empty vector clones were observed in a random sampling of 576 BAC clones. Further analysis of 182 BAC-end sequences from randomly selected clones revealed a GC content of 40.35% and low chloroplast and mitochondrial contamination. Repetitive sequence analyses indicated that LTR retrotransposons were the most predominant sequence class (86.93%–87.24%), followed by DNA retrotransposons (11.16%–11.69%). Additionally, we found 25 simple sequence repeats (SSRs) that could potentially be used as genetic markers.