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W511: Sequencing of Complex Genomes

Coffea canephora Genome Sequencing, A Tool For Comparative Genomics And Efficient Crop Improvement

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Coffee is the most traded crop by Southern countries and is the main source of income for more than 75 millions small farmers all over the world. Despite its economical importance and the obvious necessity to improve the crop in order to

respond to new environmental constraints and to the consumer demand for quality, the sequencing of its genome only started in late 2009. An international consortium was formed, led by Genoscope, to perform this task. *Coffea canephora*, a diploid cultivated species, was chosen, since *C. arabica* is tetraploid. Furthermore, IRD developed a double haploid plant because *C. canephora* is allogamous. Its genome size is about 695 Mb and whole genome sequencing is being performed using NGS complemented by BAC ends coming from two BAC libraries covering in total 14.8 genome equivalents. SSR markers mined from these sequences are being mapped to establish a consensus genetic map based on the map kindly provided by Nestlé and ICCRI. Both Roche pyrosequencing (454) and Illumina technology are used to provide a 20x coverage by 454 and 50x by Illumina. Direct and paired end sequencing are underway, two, 8kb and 20kb insert libraries have been constructed. In addition to the publicly available EST, more transcriptome sequencing is also planned using 454 to facilitate the annotation. The *Coffea* genome will be one of the first Asterid genome to be sequenced providing information on the proposed ancestral eudicot genome hexaploidization and for comparative genomics among angiosperms. It will also provide information to breeders for relating QTLs to genes.