



Plant & Animal Genomes XVIII Conference

January 9-13, 2010
Town & Country Convention Center
San Diego, CA

P520 : Forest Trees

Progress On *Eucalyptus* BAC Libraries Characterization

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Eucalyptus species are amongst the most planted hardwoods in the world. However, because of their long generation times as compared to crop species, they are still at the early stages of domestication. Genomic technologies could significantly speed up the process of genetic improvement of *Eucalyptus*. Genomic libraries are important genomic tools suitable for physical mapping, map-based cloning and genome sequencing. Here we present the results of the progress on analysis of BAC libraries for *E. grandis* and *E. globulus*, the two main commercial *Eucalyptus* species. For *E. globulus* *E. grandis* BAC clone, positive for chloroplast genome, was full sequenced with 454 pyrosequencing technology. The *E. grandis* chloroplast consists of 160,137bp and is 99% identical to that of *E. globulus* chloroplast genome sequence. These genomes are very well conserved in gene content and structure. A dedicated *Eucalyptus* genomic database was implemented to stock and manage all data produced. Results on BAC libraries characterization obtained in the frame of GenEglobwq project (FCT funding, Portugal) and within the Portugal-France collaborative research efforts (EUCABAC) will be presented and discussed.