

BUILDING RESOURCES FOR MOLECULAR BREEDING OF EUCALYPTUS: THE GENOLYPTUS PROJECT

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We have been building a suite of genomic, field and information resources to discover, sequence, map, validate and understand the underlying variation of genes and genomic regions of economic importance in Eucalyptus with a focus on wood and disease resistance. Conceived to establish a foundation to understand the molecular basis of economically important phenotypes in Eucalyptus, the Genolyptus project aims to translate genomic knowledge into improved tree breeding technologies. This pre-competitive project involving several tens of scientists is based on a partnership among the Brazilian Ministry of Science and Technology, the academic/research sector represented by seven Universities and Embrapa and industry represented by thirteen forest based industries. Our driving principle is that there is plenty of genetic variation within the genus Eucalyptus to allow profound genetic modification of the current planting stock in the tropics. While genomic resources should become increasingly available in the future, biological resources and precise phenotyping could represent the real limitation for the effective advancement of many genomic projects into operational applications. Especially in forest trees, where generation times and phenotype assessment can take years, the construction and evaluation of ideal experimental populations should be one of the first targets in a genomic project. Even with more powerful tools that potentially allow a global and integrated view of genetic processes, genomics will only succeed in contributing to the development of improved eucalypt forests if deeply interconnected with intensive fieldwork and creative breeding. The Genolyptus project therefore differs from other plant genome initiatives in the intensity, refinements and scope of the effort devoted to field experiments to generate the diversity and planned structure of phenotypes necessary to study gene function. QTL detection, association mapping and the development of an EST rich, BAC fingerprint based physical map for the Eucalyptus genome is moving toward linking phenotypes to genes that control processes of wood formation that define industrial level traits. The gene discovery effort based on massive EST sequencing and expression profiling technologies, is focused more on looking transversally at the interspecific allelic variation in relevant genes than longitudinally at the total number of genes. A brief overview of the main advancements in the project since its start in February 2002 will be presented.