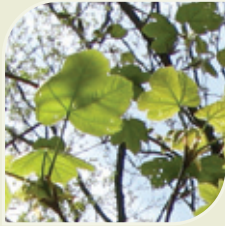


EVOLTREE PARTNERS



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EVOLTREE brings together 25 research groups from 15 European countries in different disciplines from forest ecology to genomics, contributing to the emergence of a new discipline, 'ecosystem genomics', which combines genetics, genomics, ecology and evolutionary biology to study gene-level responses to biotic and abiotic pressures on forests.



For more information on
EVOLTREE please contact:
Project Coordinator, Dr. Antoine Kremer
INRA, Bordeaux, France
E-mail: kremer@pierroton.inra.fr

For information on
EVOLTREE dissemination activities
please contact:
Dr. Barbara Vinceti
Bioersity International, Rome, Italy
E-mail: b.vinceti@cgiar.org

For information on
THE PLANT GENE RESOURCE PLATFORM
please contact:
Silvia Fluch, MSc
AIT Austrian Institute of Technology GmbH, Austria
E-mail: silvia.fluch@ait.ac.at

www.picme.at

www.evoltree.eu



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Photos by: Silvia Fluch and Michael Stierschneider (AIT Austrian Institute of Technology GmbH).



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THE PLANT GENE RESOURCE PLATFORM



EVOLUTION OF TREES AS DRIVERS OF TERRESTRIAL BIODIVERSITY

EVOLTREE IS A LARGE EU-FUNDED NETWORK OF EXCELLENCE LAUNCHED IN APRIL 2006 TO ANALYZE THE IMPACTS OF CLIMATE CHANGE ON FOREST ECOSYSTEMS FROM AN EVOLUTIONARY PERSPECTIVE



REPOSITORY CENTRE

IN THE FRAME OF EVOLTREE, existing plant gene collections available at PICME (www.picme.at) are being further expanded in the frame of EVOLTREE. Over 350,000 reference DNA samples have been gathered and can be used for genetic analysis of populations; the enlarged EST sets enable functional analyses of trees and associated species. Additional samples from forest trees and associated species of insects and fungi are being collected at different sites. They will be maintained as reference material, stored in the centralized repository centre.

THE AVAILABLE RESOURCES include total genomic DNA, BAC enriched libraries and EST collections as well as cDNA arrays for expression profiling. The material is stored in an automated storage and retrieval system, which allows bar-coded sample tracking at -20 and -80°C.



THE INFORMATION RELATED to these resources is searchable through a web-based portal. Genebanks can be searched for pedigree material as well as for phenotypic traits linked to genetic maps. The material stored can be ordered through internet and is made available upon request.

WITH THE ADVANCES OF MODERN BIOLOGY, understanding and exploiting biological systems has become a feasible research task. Scientific research has focused on model organisms for which large amounts of data have been collected. However, it is of major importance to extend the effort to other ecologically important key species and generate knowledge and data on the functioning of entire ecosystems.



IN ORDER TO ADD NOVEL UNDERSTANDING on how entire ecosystems function, large amounts of high quality data need to be generated, assembled and analyzed jointly. The adoption of standardized protocols and the possibility to openly access reference samples are prerequisites for multidisciplinary research and for modelling efforts based on large integrated datasets.



WEB PORTAL-DATA ACCESS

LARGE AMOUNTS OF HETEROGENEOUS INFORMATION, data and knowledge are presently assembled in existing datasets maintained by different research centres across Europe. New data are continuously generated by large collaborative research efforts, such as the EVOLTREE Network of Excellence. One of the main objectives of EVOLTREE is to integrate all these distributed electronic resources into a single information system accessible online through one search portal.



THE E-LAB HAS BEEN DEVELOPED as an online resource providing central access to various distributed and heterogeneous database systems all over Europe. At present, it allows to submit online queries to twelve databases. These are linked to the e-Lab and a query produces a single output, which results from the simultaneous screening of different datasets automatically connected. Issues of data overlaps are autonomously addressed by the information system.

AT PRESENT, THE E-LAB information system covers sequence data, information about mapping pedigrees, association populations, geo-reference information about natural populations, microarray experiments, physical and QTL maps, DNA resources, and investigated phenotypic traits. Species from several genera, including *Fagus*, *Quercus*, *Populus*, *Fraxinus*, *Pinus*, *Picea*, *Abies*, *Glomus*, *Laccaria*, and *Lymantria*, are represented in these data sets.