

## EVOLTREE EXTERNAL NEWSLETTER

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### A. INTRODUCTION

**EVOLTREE** is a Network of Excellence established to address research questions related to the evolution of biodiversity in forest ecosystems at different scales, from genes to ecosystems, by linking various disciplines: ecology, evolutionary studies, genetics and genomics, and examining not just trees but also associated organisms (fungi and insects).

The consortium, formed by 25 research centers and about 20 associated parties, across 15 European countries, was established in April 2006 through a contribution of 14.3 million euros from the European Commission.

The analyses of long-term empirical data are revealing that evolution induced by climatic change is already taking place and that trees have started to adapt to increasing atmospheric carbon dioxide concentrations, both at individual and population levels. European forest trees, for example, have experienced extinctions in the past and the remaining tree species have been selected based on their adaptation and dispersal efficiency.

It is of primary importance to assess the vulnerability of tree populations, species and ecosystems to both contemporary climate change and other anthropogenic stresses, and to evaluate the prospect for mitigating these impacts. However, predicting responses of forest ecosystems is a difficult challenge due to the variability of adaptive strategies observed and the complex feedback mechanisms and interactions between climate, land use and biodiversity.

All these considerations demonstrate there is a need to integrate ecology and genetics in further experiments as currently there is limited data available on the fitness of tree species facing simultaneously competition from evolving species.

The rapid pace of genomic research has opened up

tremendous opportunities and prospects for the entire community of biologists, with genomic techniques and information being applied in an increasing number of scientific fields. Genomics has arisen as a new science that studies the whole genome by integrating traditional genetic disciplines with new technologies in molecular biology. Different genomic tools and approaches have been developed to achieve different goals: to understand the genome structure (genetic and physical maps, tree BAC -bacterial artificial chromosome libraries), to investigate the genetic control of complex adaptive traits (eg., quantitative trait loci - QTL, association mapping), to contribute to gene discovery and to analyze gene function (e.g., sequencing of expressed sequence tags - EST, gene expression profiling).

Among the various genomics sub-disciplines, one emerging field is ecosystem genomics, which promises substantial breakthroughs in ecology and environmental science by investigating links between genes and ecosystem functioning, looking at the genetic basis of ecosystem process.

New methodological and conceptual developments have enabled to study heritable traits with effects on entire communities and ecosystems, moving away from the traditional efforts focused mainly on understanding spatial patterns of 'neutral' genetic marker variation or heritable growth-related characters in single tree species.

The best documented genetic analyses of complex communities refer to riparian forest ecosystems in which foundation tree species play a key role in affecting



community composition via genetic controlled traits. For example, the amount of condensed tannin in the bark of poplar species, a genetically controlled trait varying among individual trees, has been found to affect and structure the arthropod community in the soil. Furthermore, the amount of condensed tannin has been found to correlate with the selective felling of poplars by beavers, discriminating against individuals with high amounts of condensed tannins in the bark.

## B. PROGRESS IN INTEGRATION ACTIVITIES

EVOLTREE partners are active in an area of research that is characterized, as far as molecular genetics is concerned, by increasing automation. In order to access the function of the genes, there is a need of well characterized biological material and field sites with equipment to perform a range of sophisticated treatments. The benefits derived from integration of resources and research infrastructure are manifold, including enabling studies otherwise impossible to carry out, more efficient use of investments in expensive equipment, faster completion and improved quality of scientific studies.

Throughout Europe, different research teams are investigating aspects related to population genetics and functional genomics in a wide range of species and naturally occurring populations and ecosystems, thus producing valuable data and research material.

The published findings are of high interest but assembling all this material and data is often too time consuming and costly to be dealt with by the respective research groups. In addition, the prompt availability, management as well as standardization of resources and data is a key factor for successful research. Unfortunately most of the raw data and resources remain inaccessible because of the unsolved problem of resource management.

EVOLTREE's integration activities focus on the installation and management of common infrastructures, to make them accessible to the European research community in a simple way, to store, manage, and provide resources or data needed by the consortium, to integrate the necessary information related to these infrastructures and resources in the form of databases.

### First-year achievements

The NoE has already taken steps towards durable integration. Three main achievements can be mentioned in this respect:

1. The creation of one unique **centralized repository centre** for genomic resources is underway. The legal agreement

regarding the purchase of a centralized repository centre is being finalized after a long negotiation.

The centre is being installed at Austrian Research Centers GmbH (<http://www.arcs.ac.at/>) (Seibersdorf, Austria, partner of Evoltree) and will host various resources extending from tissues, genomic DNA extracts, EST libraries and clones, BAC libraries (eg artificial chromosomes) of trees and species associated to trees. This new facility will be ISO 9001 certified and will allow quality, traceability, safe long term storage of the samples. More than 340.000 individual samples will be available from the different EVOLTREE partners. EVOLTREE has granted a 354000 Euros support.



The approval is conditional to the accessibility to the facility during 10 years, which is well beyond the duration of the network. A framework agreement describing rules of access to the repository centre is being reviewed by the partners. This agreement is meant to regulate transfer and access to the jointly generated material during and after the end of the project (until 2016). Storing this valuable research material at one site will generate high impact in forest ecology research not only in Europe and during the course of the project, but will also serve as reference site internationally, as resources will be continuously available after the end of the project and publicly accessible to researchers outside EVOLTREE on a cost basis. Rules for accessing the material are being defined.

2. A **multicentre gene bank** database is being created. A large database is being built with information related to those genetic resources managed by the various partner institutions and for which material transfer is inappropriate: eg., mapping pedigrees, reference natural or breeding populations that are mostly available in the form of collections, field trials, seed banks or mother stocks. The database contains data on identification of genetic resources, material ownership, geographical origin, conservation strategy in the centre of maintenance and other information of interest to

develop further investigations, in a standardized format. Inventory of existing genetic, genomic and population genetic resources has been undertaken and a common database is being built with data from three groups of species belonging to the following families: Fagaceae, Pinaceae, Salicaceae. The information collected on mapping populations and association populations will be used to evaluate nucleotide diversity, evaluate linkage disequilibrium, and develop association studies.

Being perennial material, the Evoltree Gene bank database was created to provide resources and information in the long term and the initiative is regulated by a framework agreement similar in principle to the one prepared to regulate transfer and access to the common repository centre.

3. **Seven Intensive Study Sites (ISSs)** have been set up across Europe. They are large scale ecosystem plots (a few thousands of hectares) where trees and selected associated species are mapped, genotyped and phenotyped. The sites comprise entire portions of landscapes (agricultural land and forests) where trees are present in different configurations.

The ISSs cover boreal, temperate, Mediterranean, alpine and riparian ecosystems, as well as one untouched ecosystem and one intensively managed site. The objective is to install a European network of sites for long term research on the evolution of biodiversity at different hierarchical levels (from genes to ecosystems).

The ISSs will also enable to monitor the population dynamics through demographic and genetic approaches, in trees and their regulated by associated species, over different spatial scales, and to monitor interaction between species (trees, other plants, vertebrates, insects and microorganism).

Finally, the ISSs will provide a large-scale support for training, education and dissemination activities. As for the repository centre, ISSs are intended to serve as experimental sites for the long term, beyond the duration of EVOLTREE. Access to the sites will be regulated by a legal agreement. For each ISS, one partner will be responsible for the development, maintenance and update of a comprehensive database linked to a Geographic Information System.

In addition to the installation of common infrastructures, EVOLTREE has undertaken an inventory of facilities and infrastructures used by the different partners. EVOLTREE will facilitate access to these infrastructures through convenient deals standard administrative procedures. In this perspective, the definition and adoption of common protocols have been promoted.

### C. RESEARCH HIGHLIGHTS

The following list reminds the objectives of the scientific activities undertaken by the EVOLTREE consortium:

- To identify genes of adaptive significance in the face of global change, in three model species of trees (Pinus, Populus and Quercus), phytophagous insects (Limantria) and mycorrhizal fungi (Laccaria and Glomus) (JERA 1).

As "genomic studies require a reductionist approach, genomic resources and tools can only be developed for very few species (model species), but the objectives is to transfer these tools to a larger range of species (target species).

- To assess the level and distribution of nucleotide diversity in genes of adaptive significance in trees, insects and mycorrhizal fungi (JERA 2)



#### LOCATION OF THE EVOLTREE INTENSIVE STUDY SITES IN DIFFERENT FOREST ECOSYSTEMS

- **Boreal:** Punkaharju (Finland)
- **Temperate:** Solling (Germany)
- **Untouched:** Bliżyn (Poland)
- **Riparian:** Loire (France)
- **Alpine:** Valais (Switzerland)
- **Intensively managed:** Landes (France)
- **Mediterranean:** Ventoux (France)

The countries in darker green are members of EVOLTREE

- To assess the impact of trees on the composition of communities by studying interactions between trees and their associated species (JERA 3).
- To investigate the evolutionary rate of trees by reconstructing their past history and predicting their future response to global change (JERA 4).

### Progress in JERA1 – Ecological genomics

The genomics revolution of the last 10 years has improved our understanding of the genetic make up of living organisms. However, even if the relationships between complex trait variation and molecular diversity of genes can be studied based on a genomic approach, the identification of genes responsible for the variation remains a slow and time consuming process, especially in long lived organisms such as trees.

This research package is making progress in the identification of sets of sequences for genes that are qualified as being putatively involved in the determination of phenotypic variation for the traits that are of interest to the network, in the model species identified.

In the area of the identification of genes of ecological significance, candidate genes have been identified in all model species, including fungi and insects, for a variety of traits of adaptive significance, such as phenology and drought resistance. In the area of neutral marker development, microsatellite markers for the nuclear genome and chloroplast and mitochondrial markers are being developed for both model and target species.

In the area of transferability of genes and markers from model species to target species, a very comprehensive work is underway to carry out the comparative mapping of genes and markers in three major tree families: Fagaceae, Salicaceae and Pinaceae.

### Progress in JERA2 – Genomic diversity in natural populations

Phenotypic variation in traits such as phenology, cold or drought tolerance determines the viability of organisms and thus the ability of the species to adapt to new environmental conditions. This phenotypic diversity is based on variation at the nucleotide level, regulation of the genes, environmental conditions, and ultimately, interactions between genotype and environment.

Advances such as sequencing of full genomes or development of extensive sets of Expressed Sequence Tags (ESTs) and new analytical methods (linkage disequilibrium) make it possible to identify the functional loci that are responsible for the phenotypic variation and to identify areas of the genome where natural selection has been especially important.

However, few studies are available for natural

populations of forest trees, of insects other than *Drosophila*, or fungi, because these studies would require considerable genomic resources, maps, EST sequences or genomic sequences. Only one tree species, *Populus*, has been fully sequenced (<http://genome.jgi-psf.org/Poptr1/Poptr1.home.html>), but the increasing numbers of EST sequences will significantly aid in the studies of population genomics in other species. Genomic resources are also improving for the associated species, the mycorrhizal fungi and the insects.

The aim of this work package is to obtain a view of the nucleotide variation and linkage disequilibrium in many European tree species, in some model insects, and in some fungi. The studies have first been directed to a limited number of species, where some of the necessary genomic resources, such as EST sequences, are available. These include *Pinus pinaster*, *P. sylvestris*, *P. halepensis*, *Picea abies*, *Populus* sp. *Quercus petraea*, the insect *Lymantria* and the fungus *Laccaria*. The first stage has been to select populations for detecting loci with an adaptive role, mainly in the timing of growth, or drought and cold tolerance.

Candidate loci have been chosen based on existing physiological information on pathways in model species, partly on colocation with QTLs, partly on patterns of gene expression. The goal has been to obtain sequences of full length genes, and where possible, also regulatory regions.

Another component has been the study of linkage disequilibrium in two populations, with larger sample sizes. Work has started for choosing and developing suitable populations for association mapping. With some delay, work is starting on the meta-analysis of existing data on molecular and quantitative diversity.



### Progress in JERA3 – Community structure and dynamics

This work package is dedicated to the study of the structure and dynamics of the communities of associated organisms and links the different research programs in EVOLTREE. Its general objective is to study "how the genetic diversity of

trees shapes the species diversity of associated organisms". As a preliminary step, a literature report was produced on the relationships among host tree genetic diversity and genetic/species diversity in associated organisms,

in particular phytophagous insects and ectomycorrhizal fungi (ECM). This data serves as a background for identifying the current state of knowledge in community genetics of host tree– insect/ECM systems, but should also highlight gaps and promising avenues for future efforts in this field of research.

The literature search revealed a limited set of studies published in referenced journals. Furthermore, very few taxa have been studied and the research has been carried by a limited number of research teams that play a key role in this field. In addition, while phylogeographic studies of host tree species are widely available, phylogeographic studies on associated insects and ECM are very limited. Likewise, geographical representation in terms of study locations and ranges is unevenly distributed, with a focus on North America and on local or regional assessments. Community genetics is still in its infancy and represents a rather promising scientific playground in many aspects.

The literature review guided the definition of new research proposal that will focus on intimately associated communities in which strong interdependencies between trees and associated organisms are present, and the respective genetic diversities play a more prominent role in shaping interactions.

A series of research proposals was formulated with the objective to address the specific research question of this work package. They were presented and discussed in a Symposium and Workshop on 'Community Structure and Dynamics' held in Marburg, on 12-13 October 2006.

#### **Progress in JERA4 – Dynamics of biodiversity and evolution of populations**

This activity builds on the understanding of the past evolution of trees, and of their current dynamics, in order to predict their future evolution with the help of modelling. Adaptation has been studied by measuring polygenic phenotypic traits in traditional provenance tests. There have been only few studies carried out with presumably adaptive molecular gene markers.

EVOLTREE's objective is to monitor the effect of past climate and human activities on genetic structures of tree species at all scales (up to the whole range). The methods adopted combine established tools from the field of palaeobotany and genetics as well as innovative methods: pollen and plant macrofossil analyses, dynamic vegetation models using palaeoclimatic reconstructions, and data-model comparisons. The application of newly developed tools based on genomic approaches (JERA1)

allows investigating the different ways by which trees will respond to environmental changes (gene expression, epigenetic responses, and changes in gene frequencies).

A component of this research package is focusing on past dynamics of diversity. European forests established as a consequence of climate improvement after the last ice age, which reached its climax 25,000 to 17,000 years ago. Postglacial colonization continued and from the Neolithic period, human effects on the forests became increasingly significant.

Recent work in the field of phylogeography and population genetics has shown that the early phase of forest establishment played a critical role in determining the current distribution of genetic diversity. This heritage is particularly clear in forest trees due to their long generation time. Humans have modified this structure in many ways, the most obvious being through simple extirpation of populations due to land-use changes and through reshuffling and mixing of populations through planting.

Several modelling approaches have been implemented to better understand the dynamics of the distribution of tree species in the past and to forecast genetic consequences of global change.

Preparations have been made to analyze ancient DNA from tree macrofossils to improve our understanding of past vegetation dynamics, and the European Pollen Database has been re-launched. A new dynamic website for the European Pollen Database has been created (<http://www.europeanpollendatabase.net/>) and opened to palynologists contributions. Its structure will be presented at AFLP Symposium (October 2007 in Toulouse) and the 12th International Palynological Congress, August 2008.

Furthermore, phenotypic responses of pines and beech to different environmental conditions have been assessed in field trials and common garden experiments. Preparation has been made to study the adaptation of poplars to environmental stress and to clarify the role of mycorrhizal fungi in this context. The genetic basis of phenotypic responses and adaptation of poplars to draught, elevated CO<sub>2</sub>, and aluminium toxicity is studied in strictly controlled environments. The genetic consequences of changing population structures and densities are studied for *Fagus*, *Quercus*, and *Picea*. Information concerning different models developed by EVOLTREE partners is being compiled. A site to commonly test and use these models has been selected.

#### D. OUTPUTS OF MEETINGS AND TRAINING

A series of meetings, workshops, and training courses have been co-sponsored and co-organized by EVOLTREE, since its inception. A summary list is presented below:

- Community Structure and Dynamics (symposium and internal workshop), October 11, 2006
- o Microarray And QPCR Course (training course), March 26, 2007
- Open Scientific Meeting of the European Pollen Database, May 08, 2007
- Advance Course on Fungal Genome Annotation (training course), May 15, 2007
- Evolutionary Inferences and the Coalescent (training course), June 11, 2007
- Training module at the European Institute In Statistical Genetics (training course), September 03, 2007
- Summer School: Global Change and Challenges For Genetic And Ecological Research Of Forest Ecosystems, September 10, 2007

#### **Governing Board Meeting, 24th October 2007, in Rome (Italy)**

The ultimate objective of Networks of Excellence in FP6 is to achieve durable integration. Despite uncertainties, EVOLTREE partners have clearly expressed their willingness to extend their network activities beyond the duration of the EVOLTREE and they are exploring the legal and financial structures, circumstances and possibilities for durable integration in order to: (i) set up of a legal framework representing all participating organizations in the network, (ii) decrease the dependence on Community funding and (iii) search for external funding sources (both public and private) beyond the duration of financial support by the EU. There are important requirements that the consortium should fulfill to ensure durable integration. Five milestones were identified as part of the process and of the effort EVOLTREE is investing in achieving long-term integration:

1. Identify long term research priorities
2. Identify common purposes and expectations
3. Search for funding sources
4. Stimulate support of stakeholders
5. Search for a status of the future entity

These issues have been discussed during the meeting of the Governing Board of EVOLTREE, which took place on the 24th of October in Rome (Italy) at Bioversity International. For additional details, see this website: <http://news.bioversityinternational.org/index.php?itemid=1996>

#### E. FORTHCOMING EVENTS AND ANNOUNCEMENTS

#### **Next annual meeting, 4-7 February 2008, Mandelieu-Nice (France)**

The next annual meeting will take place in Mandelieu (near Nice, southeast of France) from Monday February 4th to Thursday February 7th 2008. Annual meetings are events designed to develop work plans and represent an opportunity to see the whole community gathering to discuss the implementation of activities.

#### **First Stakeholder Group meeting, 7-8 February 2008, Mandelieu-Nice (France)**

An European workshop, organized by Bioversity International (formerly IPGRI), the International Union of Forest Research Organizations (IUFRO) in collaboration with the MCPFE Liaison Unit Warsaw, on climate change and forest genetic diversity was held in Paris, France, 15-16 March 2006, as one of the pan-European actions for implementation of Vienna Resolution 5 (Climate change and sustainable forest management in Europe) of the MCPFE process (Ministerial Conferences on the Protection of Forests in Europe) (see the summary report on EUFORGEN's webpage: [www.euforgen.org](http://www.euforgen.org)).

As discussed during the workshop, the practical implications of the new developments in forest genomics are expected to help understanding tree adaptation mechanisms and assist in the development of guidelines for continent-scale transfer and use of forest reproductive material in the face of climate change,. Moreover, the understanding of the patterns of distribution of adaptive diversity will support the location of areas suitable for the establishment of gene conservation measures.

In addition, genomic information will contribute to better measure genetic diversity and to better interpret measures of effective population size, supporting management of tree populations for conservation and production purposes. Finally, the mapping of the genetic diversity of tree populations is expected to also support the traceability of traded wood products and the implementation of certification schemes.

Network partners will take a proactive role in ensuring that the practical recommendations that can be derived from research findings are discussed with and communicated to stakeholders.

A tentative list of topics has been proposed for discussion during the first meeting of the EVOLTREE Stakeholder Group which will take place on the 7th and 8th of February 2008, in Mandelieu (France), back to back with the next EVOLTREE annual meeting:

- Principles of genetically sustainable forest management. Expected insights from a new discipline: ecosystem genomics.
- Evoltree's common repository of DNA and other integrated infrastructures. Potential benefits deriving from integration and synergies within the EU.
- Labeling and tracing the origin of timber, based on molecular markers. Implication in certification schemes and in combating illegal logging.
- Use of appropriate reproductive material for afforestation and reforestation in the face of climate change. Current understanding from studying adaptive diversity.

#### Other meetings and training

- Meeting JERA 3 and IA 2.3 (internal planning meeting), November 14, 2007
- Second Microarray and QPCR Course (training course), December 10, 2007



## F. PUBLICATIONS AND OTHER PRODUCTS

### Reviews and books

The following reviews were recently published. They concern "comparative genetic mapping of trees" (Activity JERA1) and "responses of forest trees to climate change" (Activity JERA4). Many partners of EVOLTREE have contributed to these reviews:

1. Kole, C.R. (ed.) 2007 Genome Mapping & Molecular Breeding. Vol. 7: Forest Trees. Springer Verlag, Berlin, Heidelberg, 221pp.
2. Koskela, J., Buck, A. & E. Teissier du Cross (eds.) 2007 Climate change and forest genetic diversity: Implications for sustainable forest management in Europe. Bioersivity International, Rome, 111pp.

### Publications

1. Buiteveld, J., Vendramin, G.G., Leonardi, S., Kramer, K. & T. Geburek (2007) Genetic diversity and differentiation in European beech (*Fagus sylvatica* L.) stands varying in management history. *Forest Ecology and Management* 247:98-106.
2. Hänninen, H. & K. Kramer (2007) A framework for modelling the annual cycle of trees in boreal and temperate regions. *Silva Fennica* 41(1):167-205.
3. Kremer, A., M. Casasoli, T. Barreneche, C. Bodénès, P. Sisco, T. Kubisiak, M. Scalfi, S. Leonardi, E.G. Bakker, J. Buiteveld, J. Romero-Severson, K. Arumuganathan, J. Derory, C. Scotti-Saintagne, G. Roussel, M.E. Bertocchi, C. Lexer, I. Porth, F. Hebard, C. Clark, J. Carlson, C. Plomion, H. Koelewijn, and F. Villani, 2007. *Fagaceae*(pp. 161-187) in *Genome Mapping & Molecular Breeding. Vol. 7: Forest Trees*, C.R. Kole, Editor. 2007, Springer-Verlag, Berlin, Heidelberg, New York, Tokyo, 221p.
4. Plomion Ch, Chagné D., Pot, D., Kumar S., Wilcox P.L., Burdon R.D., Prat D., Peterson D.G., Paiva J., Chaumeil P., Vendramin G.G., Sebastiani F., Nelson C.D., Echt C.S., Savolainen O., Kubisiak T.L., Cervera M.T., De Maria N., Islam-Faridi M., N. (2007). *Pines* (pp.29-92), in *Genome Mapping & Molecular Breeding. Vol. 7: Forest Trees*, C.R. Kole, Editor. 2007, Springer-Verlag, Berlin, Heidelberg, New York, Tokyo, 221 pp.
5. Rae A.M., Street N.R., Rodriguez-Acosta M. (2007). *Populus Trees* (pp.2-28), in *Genome Mapping & Molecular Breeding. Vol. 7: Forest Trees*, C.R. Kole, Editor. 2007, Springer-Verlag, Berlin, Heidelberg, New York, Tokyo, 221pp.
6. Rowe R, Street NR, Taylor G. (2007). Identifying potential environmental impacts of large scale deployment of dedicated bioenergy crops in the UK. *Renewable and sustainable energy reviews*, In Press.
7. Taylor G., Tallis MJ, Giardona CP, Kevin EP, F Miglietta, Pooja S. Gupta, B. Gioli, C.Calfapietra, B.Gielen, M.E. Kubiske, G.E. Scarascia-Mugnozza, K. Kets, S.P. Long and D.F. Karnosky (2007). Future atmospheric CO<sub>2</sub> leads to delayed autumnal senescence in *Populus* over two continents *Global Change Biology*, In Press.
8. AM. Rae, M.P.C. Pinel, C.Bastien, M.Sabatti, N.R. Street, J.Tucker, C.Dixon N.Marron, S.Y. Dillen and G.Taylor (2007). QTL for yield in bioenergy *Populus*. Identifying G x E interactions influencing growth at three contrasting sites *Tree Genetics and Genomes*, In Press.
9. Rae, AM, Tricker PJ, Bunn SM and Taylor G (2007). Adaptation of tree growth to elevated CO<sub>2</sub>: QTL for biomass in *Populus*. *New Phytologist*, 175, 59-69.

## GLOSSARY

### Genome

All the genetic material in the chromosomes of a particular organism; its size is generally given as its total number of base pairs. Genomics is the study of genes and their function.

### Genomic library

A collection of clones made from a set of randomly generated overlapping DNA fragments that represent the entire genome of an organism.

### DNA sequencing

The relative order of base pairs, whether in a DNA fragment, gene, chromosome, or an entire genome. Sequencing means determining the order of nucleotides (base sequences) in a DNA or RNA molecule or the order of amino acids in a protein. Sequencing technology is the instrumentation and procedures used to determine the order of nucleotides in DNA.

### Genetic map or linkage map

A map of the relative positions of genetic loci on a chromosome, determined on the basis of how often the loci are inherited together. Distance is measured in centimorgans (cM). A genetic linkage map shows the relative locations of specific DNA markers along the chromosome. Any inherited physical or molecular characteristic that differs among individuals and is easily detectable is a potential genetic marker. Markers can be expressed DNA regions (genes) or DNA segments that have no known coding function but whose inheritance pattern can be followed. DNA sequence differences are especially useful markers because they are plentiful and easy to characterize precisely. Markers must be polymorphic to be useful in mapping; that is, alternative forms (alleles) must exist among individuals so that they are detectable among different members in the mapping population.

### Physical map

A map of the locations of identifiable landmarks on DNA (e.g., restriction-enzyme cutting sites, genes), regardless of inheritance. Distance is measured in base pairs.

### Bacterial artificial chromosome (BAC)

A laboratory creation involving an artificially constructed chromosome in which medium-sized segments of DNA (100,000 to 300,000 bases in length) that come from another species are cloned into bacteria. Once the foreign DNA has been cloned into the bacteria's chromosome, many copies of it can be made (amplified) and sequenced.

### Expressed sequence tags (ESTs)

They are short strands of DNA that can act as identifier of a gene. Used in locating and mapping genes.

**Quantitative trait loci (QTLs):** Quantitative traits refer to phenotypic characteristic that varies in degree and can be attributed to the interactions between two or more genes and their environment (also called polygenic inheritance). Though not necessarily genes themselves, quantitative trait loci (QTLs) are stretches of DNA that are closely linked to the genes that underlie the trait in question. QTLs can be molecularly identified to help map regions of the genome that contain genes involved in specifying a quantitative trait. This can be an early step in identifying and sequencing these genes.

### Association mapping

It is a methodological approach used to find the genes responsible for naturally occurring phenotypic variation, advocated as the method of choice for identifying loci involved in the inheritance of complex traits. In association mapping, researchers seek to identify regions of the genome where individuals that are phenotypically similar are also unusually closely related. A statistical association between genotypes at a marker locus and the phenotype is usually considered to be evidence of close physical linkage between the marker and a disease locus. A potentially serious problem is that spurious correlations may arise if the population is structured so that members of a subgroup tend to be much more closely related. Because few genome-wide association studies have been carried out, it is not yet known how important this problem will be in practice.

### Gene-expression profiling

A genomic technique that based on the fact that only a fraction of the genes encoded in the genome of a cell are expressed by being transcribed into messenger RNA (mRNA). The complement of mRNAs in a cell largely dictates its complement of proteins. Consequently, gene expression is a major determinant of the biology of both normal and malignant cells.

### Library

An unordered collection of clones (i.e., cloned DNA from a particular organism) whose relationship to each other can be established by physical mapping.

### Phenology

It can be defined as the timing of natural living processes with weather events.

### Mapping population

It is a group of related organisms used in constructing a

genetic map.

**Pedigree**

A family tree diagram that shows how a particular genetic trait or disease has been inherited.

**Breeding population**

A set of trees within which crosses are made to generate material for the next cycle of selection.

**Test or field trial**

A research planting established in a scientific design to develop knowledge or information on the performance of genetic materials (species, provenances, seed sources or progeny) on traits or attributes (survival, growth, pest susceptibility, frost hardiness, wood quality, etc.) of interest.

**Nucleotide diversity**

A concept in molecular genetics which is used to measure the degree of polymorphism within a population. It is defined as “the average number of nucleotide differences per site between two randomly chosen DNA sequences” in a population. This variable is of considerable interest to conservationists, population geneticists, and evolutionists and its efficient assessment in natural populations is a research priority.

**Linkage disequilibrium**

A term used in the study of population genetics for the non-random association of alleles at two or more loci, not necessarily on the same chromosome. It describes a situation in which some combinations of alleles or genetic markers occur more or less frequently in a population than would be expected from a random formation of haplotypes (set of closely linked genetic markers present on one chromosome which tend to be inherited together) from alleles based on their frequencies. Non-random associations between polymorphisms at different loci are measured by the degree of linkage disequilibrium (LD).

**Phytophagous insects**

Insects feeding on plants.

**Mycorrhizal fungi**

They infect or invade plant roots to obtain necessary nutrients. In return, these fungi assist the roots in uptake of minerals, most importantly phosphorus, from the soil. This added nutrient uptake may help plants deal with environmental and site-related stresses. The two most common types of mycorrhizas are the ectomycorrhizas and the endomycorrhizas (more commonly known as arbuscular mycorrhizas). The two groups are differentiated by the fact that the hyphae of ectomycorrhizal fungi do

not penetrate the cell wall of the plant’s root cells, while the hyphae of arbuscular mycorrhizal fungi penetrate the cell wall.

**Phylogeographic studies**

They analyze the processes controlling the geographic distributions of lineages by constructing the genealogies of populations and genes.

**Genetic marker**

A gene or other identifiable portion of DNA whose inheritance can be followed. Markers can be expressed regions of DNA (genes) or some segment of DNA with no known coding function but whose pattern of inheritance can be determined. Chloroplast DNA is found chloroplasts, the organelles that carry out photosynthesis and starch grain formation in plants, instead of the cell nucleus where most genetic material is located. Mitochondrial DNA is the genetic material found in mitochondria, the organelles that generate energy.

**Microsatellite markers**

Segments of DNA characterized by a variable number of copies (typically 5-50) of a sequence of around 5 or fewer bases (called repeat units). At any one locus (genomic site), there are usually several different “alleles” in a population, each allele identifiable according to the number of repeat units. This existence of multiple alleles (high level of polymorphism) has enabled microsatellites to be developed as powerful markers in many different species. They are detected by the polymerase chain reaction.

**Single nucleotide polymorphism (SNP)**

DNA sequence variations that occur when a single nucleotide (A, T, C, or G) in the genome sequence is altered.

**Gene expression**

The process by which a gene’s coded information is converted into the structures present and operating in the cell. Expressed genes include those that are transcribed into mRNA and then translated into protein and those that are transcribed into RNA but not translated into protein (e.g., transfer and ribosomal RNAs).



# evoltree

## PARTNERS

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**EVOLTREE brings together 25 research groups from 15 European countries and a number of associated parties.**

- P1 French National Institute for Agricultural Research, France
- P2 Alterra - Wageningen University and Research, the Netherlands
- P4 Federal Research Centre for Forestry and Forest Products Hamburg, Germany
- P5 National Research Council, Italy
- P6 Flanders Interuniversity Institute for Biotechnology, Belgium
- P7 Geological Survey of Denmark and Greenland, Denmark
- P8 Georg-August Universität Göttingen, Germany
- P9 INRA Transfert, France
- P10 Bioersity International, Italy
- P11 Natural Environment Research Council - CEH, United Kingdom
- P12 Phillips University of Marburg, Germany
- P13 Swiss Federal Research Institute WSL, Switzerland
- P14 Technical University in Zvolen, Slovak Republic
- P15 Technical University of Munich, Germany
- P16 National Institute for Agriculture and Food Research and Technology, Spain
- P17 University of Udine, Italy
- P18 National Research Centre of Scientific Research, France
- P19 Umeå Plant Science Centre, Sweden
- P20 University of Bydgoszcz, Poland
- P21 University of Oulu, Finland
- P22 University of Southampton, United Kingdom
- P23 University of West Hungary, Hungary
- P24 Uppsala University, Sweden
- P25 Max Planck Institute, Germany
- P26 Austrian Research Centers GmbH - ARC, Austria

### Associated parties

- Université de Bordeaux I, France
- Université de Nancy I, France
- Université d'Evry, France
- CNRS, France
- Plant Research International, The Netherlands
- A&F, The Netherlands
- Universidad Politecnica de Madrid, Escuela Tecnica Superior de Ingenieros de Montes (ETSI), Spain
- Instituto Vasco de Investigacion y Desarrollo Agrario (NEIKER), Spain
- Université Paris-Sud - Paris XI, France
- AgroParisTech, France
- Université Victor Segualen - Bordeaux II, France
- Université Sciences et Technologies - Bordeaux I, France
- Université Paul Cézanne - Aix-Marseille 3, France
- Université Sciences et techniques du Languedoc - Montpellier II, France
- Forest Research Institute (IBL), Poland
- Institute of Dendrology (IDPAN), Poland
- The Finnish Forest Research Institute (METLA), Finland
- Forest Research Institute (ERTI), Hungary
- Agricultural Quality Control (OMMI), Hungary



## EVOLTREE ACTIVITIES

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**EVOLTREE WILL LINK FOUR MAJOR DISCIPLINES** (genomics, genetics, ecology and evolutionary studies) to improve understanding of forest ecosystems structures, dynamics and processes, by investigating their adaptive diversity, their role in structuring the diversity of associated species (insects and mycorrhizal fungi) and their evolution in response to environmental changes.

**THE NETWORK IS FOSTERING INTEGRATION** through interdisciplinary research. The genomic activities will be conducted within a 'laboratory without walls' where techniques will be integrated and applied to a wide range of trees and associated species, starting with model species. EVOLTREE will install and enhance the necessary integrated experimental infrastructures, information systems and bioinformatics resources for common use by the partners. Large data sets will be compiled and made accessible for the analysis of geographic and temporal distribution of genetic diversity.

**EVOLTREE WILL SPREAD ITS KNOWLEDGE** and expertise for the purpose of education, biodiversity monitoring, and conservation. The network will develop training capacities and facilitate mobility opportunities throughout Europe.

**SYNERGIES WILL BE ACHIEVED** through facilitating the implementation of large-scale genomic projects, by integrating different groups into multidisciplinary research teams, working in intensively studied plots.

[www.evoltree.eu](http://www.evoltree.eu)



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