

EVOLTREE EXTERNAL NEWSLETTER

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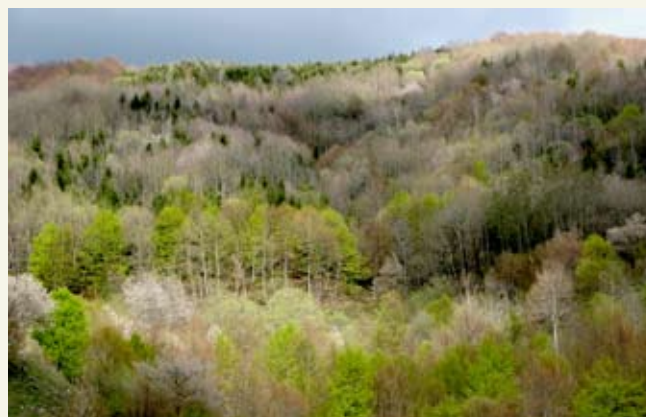
A. INTRODUCTION

*by Antoine Kremer (INRA, France)
EVOLTREE coordinator*

At the time this newsletter will be distributed, EVOLTREE will enter its third year. It took some time to get the Network on its tracks, to get used to the functioning of a Network of Excellence. Over the past few months significant achievements were made and partners will now benefit from the resources and facilities that were developed during the past two years.

Partial DNA sequences of genes were obtained for oaks, pines, beech, Norway spruce, insects, and mycorrhizal fungi in the form of more than 200,000 EST sequences. Single point mutations were explored in 65 candidate genes of adaptive traits belonging to 6 tree species.

The repository of genomic resources is now installed and operational. Research projects in the field of ecosystem genomics have started in the seven Intensive Study Sites that were installed across Europe. Major efforts were also made to disseminate the



Mixed forest on the Appenines, Central Italy (photo: Barbara Vinceti, Bioversity International)

results and achievements in different fora and media. A meeting between stakeholders and scientists was organised as a follow up of the annual meeting of the network, where practical applications of the Network's achievements were highlighted. This newsletter makes a detailed review of the progress made by the Network.

While the scientific goals of the Network are clearly long term and pan-european, the financial support is short term. EVOLTREE will be faced with the challenge to find ways for extending its activities beyond the financial support of the European Commission. This is a critical step for the Network and the solution depends on concerted actions of scientists, stakeholders and politicians.

There is no alternative choice or plan B for research on ecological genetics and genomics. We have to get organized at the European scale for the benefit of European forests!!



Beech forest on the Appenines, Central Italy (photo: Barbara Vinceti, Bioversity International)

B. PROGRESS IN INTEGRATION ACTIVITIES

Establishment of common research infrastructures

EVOLTREE is making progress in setting the foundations for durable integration in forest ecosystem genomics in Europe through the establishment of common research infrastructures. A centralized DNA repository center has been purchased and installed at the Austrian Research Centers GmbH – ARC, located in Seibersdorf, Vienna.

The repository centre is being fed with resources coming from different partners in the EVOLTREE Network of Excellence. The agreement on access rules is still under finalization and detailed information on these aspects is going to be made available online at this address: (http://www.evoltree.eu/index.php?option=com_content&task=category§ionid=8&id=50&Itemid=150).

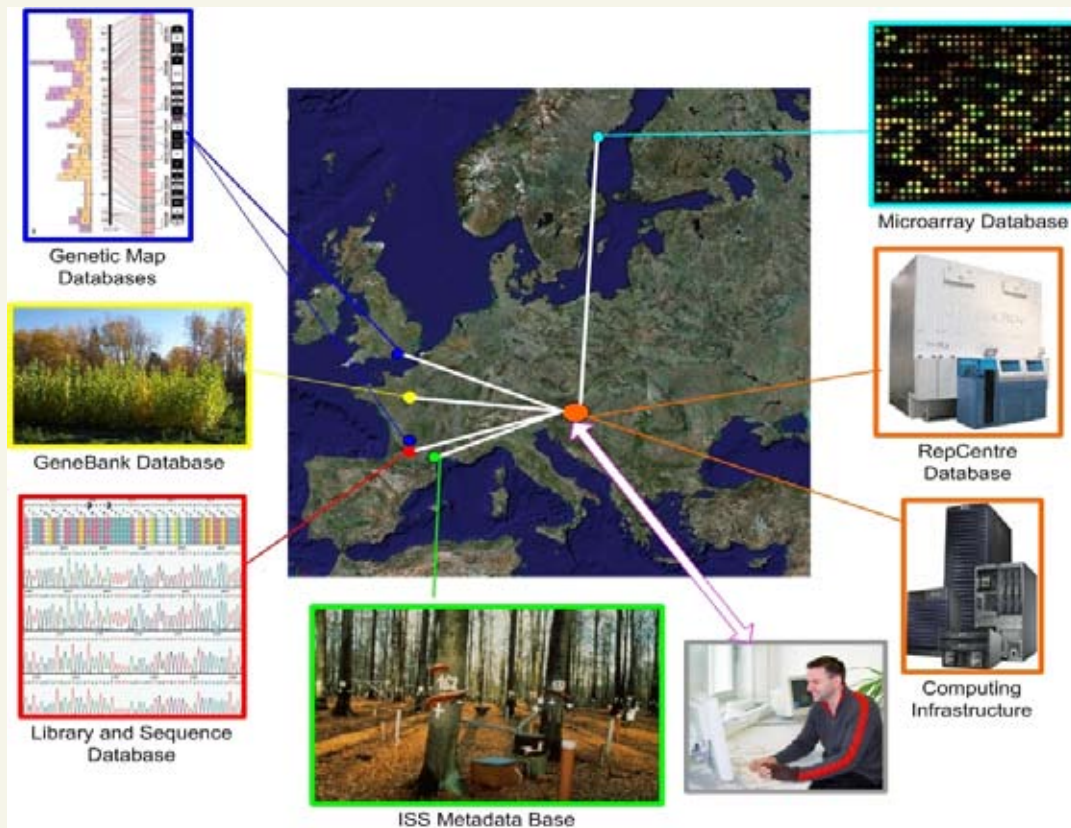


Installing EVOLTREE repository center at Austrian Research Centers GmbH – ARC, Seibersdorf, Vienna
(photos: Dieter Kopecky, Austrian Research Centers GmbH – ARC)

The repository center contains different types of plant gene resources: methylfiltration libraries, cDNA Expressed Sequence Tags (EST), mitochondrial library, Bacterial Artificial Chromosomes (BACs), genomic DNA. The materials stored as of January 2008 are listed below:

| Library | Provider | Clones | Status |
|--|--------------------------------|--------|-----------------------------|
| Pinus pinaster, cDNA | INRA Bordeaux, France | 9,034 | Material and data available |
| Quercus petraea, DiffSSH | INRA Bordeaux, France | 1,344 | Material and data available |
| Quercus robur/petraea, SSH | INRA Bordeaux, France | 4,032 | Material and data available |
| Quercus robur/petraea, cDNA | INRA Bordeaux, France | 49,920 | Material available |
| Pinus pinaster, SSH | INRA Bordeaux, France | 7,680 | Material in preparation |
| Pinus sylvestris, cDNA | Technical University of Munich | 4,992 | Material in preparation |
| Quercus petraea, cDNA | INRA Bordeaux, France | 15,360 | Material in preparation |
| Fagus sylvatica, cDNA | Technical University of Munich | 15,360 | Received |
| Lymantria dispar, cDNA | Max-Planck-Institute, Germany | 13,056 | Received |
| Lymantria monacha, cDNA | Max-Planck-Institute, Germany | 11,520 | Received |
| Picea abies, Gene enriched Genomic Library | Uppsala University, Sweden | 3,072 | Received |
| Pinus pinaster, Chloroplast Genome Library | CNR, Italy | 1,536 | Received |
| Pinus pinaster, Genomic Library | CNR, Italy | 4,992 | Received |
| Pinus sylvestris, cDNA | Alterra, The Netherlands | 9,216 | Received |
| Quercus petraea, cDNA | INRA Bordeaux, France | 4,992 | Received |
| Quercus petraea, SSH | INRA Bordeaux, France | 2,304 | Received |
| Quercus robur, cDNA | INRA Bordeaux, France | 19,968 | Received |
| Quercus robur, Chloroplast Genome Library | CNR, Italy | 1,536 | Received |
| Quercus robur, Gene enriched Genomic Library | Uppsala University, Sweden | 4,608 | Received |
| Quercus robur, Genomic Library | CNR, Italy | 4,992 | Received |
| Quercus robur, SSH | INRA Bordeaux, France | 4,992 | Received |
| BACs – Quercus robur, amount of clones: 15,000 | | | |

An e-Lab has been set up to link various databases at the different labs of the participating partners. The image below shows what the final architecture of the e-Lab would look like and the type of databases expected to be linked together and made accessible through the web portal established.



Architecture of EVOLTREE e-Lab

A centralized search engine has been created and it allows queries to be made against the whole set of databases. It searches the latest information available on a certain topic at any time during the project. The current version implemented by the Austrian Research Centers GmbH – ARC is a prototype created to test the platform and show what the e-Lab would look like.

Based on the results of the test, the search interface and the available search functions will be further improved before adoption and continuously refined in the course of the implementation process. Currently, the database of the repository centre (PICME) is integrated with the e-Lab.

In addition, the CBIB (Centre de Bioinformatique de Bordeaux) has made available new libraries fully sequenced and/or available for annotation through the SAM interface, which is also part of the e-Lab and accessible through the EVOLTREE portal.

The e-Lab framework also includes other datasets: the GeneBank database and the Intensive Study Sites (ISS) Metadata Base. The GeneBank database contains

all general information on those genetic resources managed by various EVOLTREE partner institutions, such as mapping pedigrees and association populations which are available in the form of collections, field trials, etc. Currently it contains information on mapping pedigrees and association populations of Fagaceae, Pinaceae and Salicaceae for a total of 28 mapping populations (9,500 genotypes) and 9 pedigrees + association populations. See the full list below:

- Fagaceae :
 - 4 Quercus
 - 1 Fagus
 - 1 Castanea
- Pinaceae:
 - 5 Pinus pinaster
 - 2 Pinus sylvestris
 - 5 Picea abies
 - 2 Larix
 - 1 Cedrus
- Salicaceae:
 - 6 Populus
 - 2 Salix

The development of the ISS Metadata Base is in progress. Currently, the database shows a description of the datasets available at each ISS, by aggregating the information in metadata, currently online (<http://www.evoltree.eu/geonetwork>) for a first test of the system. The ISS data are very heterogeneous and available in different types of formats (files, maps, databases, etc.), and therefore harmonization requires considerable efforts. The software adopted, GeoNetwork opensource, allows easy sharing of geographically referenced thematic information between different organizations.

The ultimate goals of this effort are the enhancement of data integration and exploitation and the maintenance of the wealth of information generated by past research initiatives in the different ISSs, adding value to the existing body of data produced.



The Intensive Study Site of Valais (Switzerland)
(photo: Arouna Woukeu)

A number of additional database applications are being developed to curate and share various resources between EVOLTREE partners. These applications are currently being populated and tested:

- **CMap database** application developed in Southampton: it allows users to curate map data and view comparisons of genetic and physical maps. It contains genetic, QTL/eQTL data, and physical/sequence maps.
- **QuercusMap database** developed in Bordeaux: a raw data management system for molecular, phenotypic and pedigree data. Initially developed for and populated with oak data, the database is to be made multi-species.

- **SSR database** in Southampton: it is currently under development.
- **Microarray database** in Umeå: a database for analysis and storage of Populus DNA microarray data, accessible through BASE, a comprehensive free web-based database produced to handle massive amounts of data generated by microarray analyses.

The Networks of Excellence and the challenge of durable integration

Networks of Excellence are instruments designed to strengthen Europe's scientific impact in different research fields, in particular by reducing the fragmentation of research efforts and by spreading excellence within and beyond the NoE. They were launched within the Sixth Framework Programme for research and technological development. One of the main purposes of NoEs is to create a framework that will allow a long-term integration of common infrastructures and other shared resources among the members of the NoE as a way of ensuring the future competitiveness of European research and technology. However, many NoEs are confronted with a variety of problems when trying to achieve this objective, ranging from financial and institutional obstacles to more fundamental legal constraints.



Participants to the First EVOLTREE Governing Board Meeting, October 2007, Rome (Italy) (photo: Bioversity International)

The EVOLTREE First Governing Board convened to discuss ways to ensure the long-term future and sustainability of the NoE, once EC support ends in March 2010, in a meeting which took place in Rome,

Italy, on 24 October 2007, at Bioversity International headquarters, one of the 25 main partners in EVOLTREE.

Despite uncertainties, the EVOLTREE partners expressed their willingness to extend their activities beyond the duration of EVOLTREE and the meeting offered an opportunity to explore different legal and financial frameworks to maintain a permanent collaboration among the partners. The meeting was well attended but the participation of executive directors of partner institutions was quite limited and preliminary formal agreements could not be reached (an audio interview of Antoine Kremer, coordinator of EVOLTREE, is available at: <http://news.bioversityinternational.org/index.php?itemid=1997&catid=2>).

The future of European NoEs was also discussed at another meeting which took place in Brussels in November 2007. On this occasion the EC met with a group of coordinators of NoEs to debate on this issue. A position paper to the EC entitled "Creating an Integrated European Research Area - The

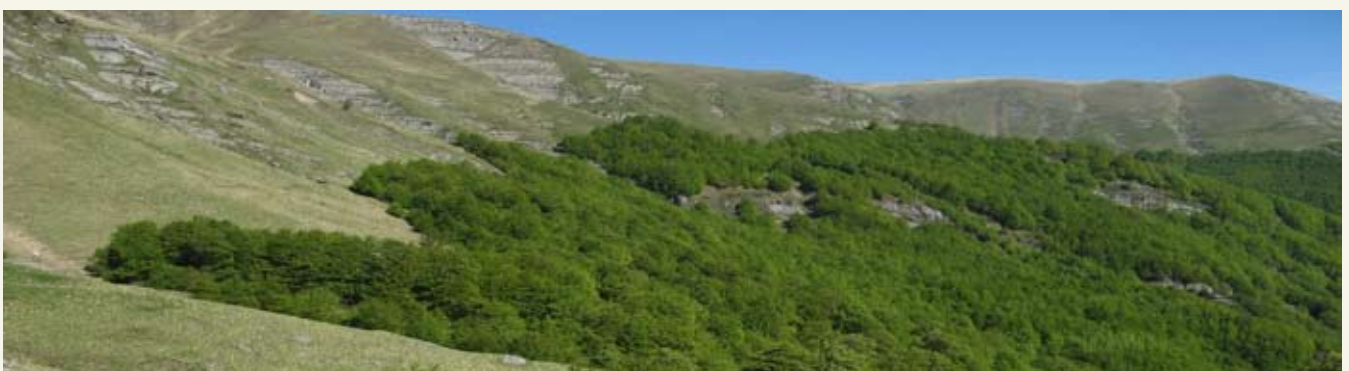
Future of the Networks of Excellence" (http://www.supportresearchnoes.eu/files/Opinion_Paper_2007-10-05_3.pdf), and describing the current status of the debate, was developed by the coordinators of 60 networks, including more than 15,000 researchers. The position paper asks the Commission to take actions to ensure long term sustainability by reconfirming its commitments to the Network of Excellence and providing the possibility for existing NoEs to access additional funding via a competitive process.

The selection should promote those networks that can prove real achievements in integration and have a convincing case that funding for a transition period could make the difference in reaching the highest level of integration and sustainability. Antoine Kremer also participated to the last scientific advisory board meeting of the European Forestry Institute (EFI) in Barcelona (5 March, 2008) and, on that occasion, he made a presentation on EVOLTREE and preliminarily explored the possibilities for a role of EFI in supporting the maintenance of the initiative after the funding period by the EU.

C. RESEARCH HIGHLIGHTS

The novelty of EVOLTREE resides in the combined approach of genomics and ecology to increase understanding of the mechanisms that contribute to the evolution of biodiversity in terrestrial ecosystems. These mechanisms are dissected both at the intra-specific and inter-specific level by analyzing interactions between trees and other organisms. Furthermore, the combined genomic-ecological approach is adopted in an evolutionary perspective, looking at past successions of glacial and interglacial periods in Europe that have resulted in either the extinction of species or the genetic diversification of the remaining species. The main research topics covered by EVOLTREE jointly executed research activities (JERAs) are:

- | | |
|---|---------|
| (1) identification of gene of adaptive significance | (JERA1) |
| (2) estimate of their diversity in natural populations | (JERA2) |
| (3) evaluation of their impact on the interaction between species and on the composition of communities | (JERA3) |
| (4) evaluation of their contribution to evolution | (JERA4) |



Beech forest on the Apennines, Central Italy (photo: Barbara Vinceti, Bioversity International)

Some new research projects have started within JERA3 and JERA4, and involve different combinations of partners. These projects are briefly described here:

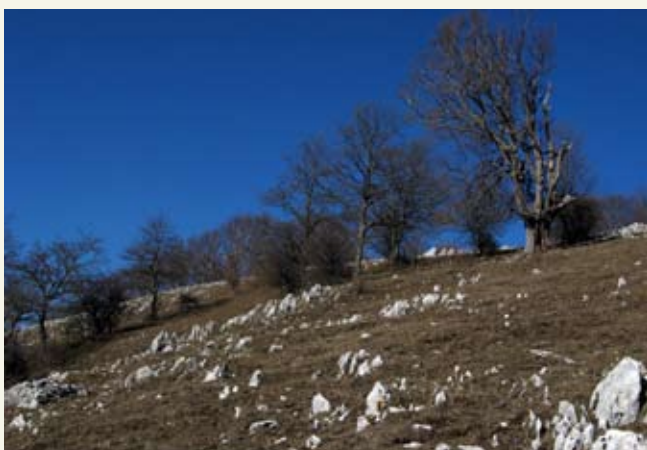
BEECH - Community structure and dynamics within beech stands (JERA3)

This project is focusing on: a) patterns of gene flow in beech (*Fagus sylvestris*) forests, b) the assessment of the variation of reproductive success of individual trees, c) the relation between the different reproductive success and phenotypic characters of individuals, d) the comparison of geneflow and structure in stands with different species composition: pure beech stands vs. beech mixed stands with Norway spruce (*Picea abies*) / silver fir (*Abies alba*). Differences and similarities of the reproductive system among various populations are examined using the ISSs recently established.

COMMUNI-TREE - Tree community genetics. Understanding diversity of associated mycorrhiza and insects (JERA3)

Interactions between species can be very complex. Recent investigations have shown that trees, as keystone species of ecosystems, can support large numbers of organisms, and some traits of trees were shown to have major influence on insect communities. Studying the genetic diversity of tree populations and effects of specific tree traits (genes) on associated communities is therefore an approach to understand ecosystem diversity. This knowledge may significantly influence our insight in optimal designs for reforestation and forest restoration.

This project is trying to develop a systematic inventory of the effects of poplar and oak trees on associated organisms (insects and mycorrhiza communities).



Beech in Central Italy (photo: Barbara Vinceti, Bioversity International)

Oak seedlings of known offspring with varying genetic diversity are being studied. This will enable to determine to what extent the intraspecific diversity of such keystone species affects communities in the process of tree establishment, and what are the causal relationships between genetic diversity of foundation species and community diversity of associated organisms.

In addition, well-characterized and clonally replicated poplar genotypes are being used to compare the effect of certain genotypes on the surrounding community.

INSECTS - Candidate genes and expression profiling in tree-insect interactions (JERA3)

Interactions between trees and their symbionts and/or pathogens/parasites are a driving factor in the evolutionary processes that characterize forest ecosystems. Genetic analyses of both trees and insects can provide insights into such processes. In particular, this project focuses on interactions between oaks and insect species, addressing the following questions:

- Why do some trees suffer less from defoliation than others?
- Are these trees genetically different from those which are more sensitive?
- Does genetic diversity of insects correlate with tree infection levels?

Observations in the European oak forests revealed that in years with high insect population densities, the extent of the defoliation varies between oak individuals. During the growing season, very fit individuals (defined as 'tolerant') can be found growing in proximity to other trees which are very susceptible to insects and are highly damaged by defoliation (defined as 'sensitive'). This project seeks to contribute to understand what 'defence' mechanisms determine varying degrees of defoliation as a consequence of insect attacks.

Meta-analyses of within species diversity in Mediterranean forest ecosystems (JERA3)

Meta-analyses are a powerful tool to monitor and test the importance of either large scale processes or common biological features in ecology, evolution and conservation. A meta-analysis performed on the genetic diversity of four Mediterranean conifer genera (*Abies*, *Cedrus*, *Cupressus*, *Pinus*) showed that

there is a marked east-west trend of diversity (mostly within population) that could be explained by climatic factors associated with the latest glacial cycle. This explanation, which is mostly correlative, can only hold true if similar patterns are found in other organisms associated to the same ecosystems and/or other forest ecosystems (e.g. deciduous forests).

This project is performing a meta-analysis on genetic diversity parameters within and among populations in order to understand the main ecological processes responsible for identified patterns of variation in intra-specific diversity in Mediterranean forest ecosystems.

Target organisms are key stone tree species, as well as associated plants and animals found in the same forests. Using all available datasets, this project is trying to find relationships between patterns of genetic diversity and climate data derived from published paleo-ecological and paleo-climatological studies.

The expectation is that major trends will be explained by some critical climatic factors, which are of relevance for the management and conservation of forests in the face of climate change.

Genetic variation and gene flow in the *Laccaria* spp. and their host trees (JERA3)

The ability of individuals within an ectomycorrhizal species to adapt to different environments and interact with different host genotypes resides in their genetic diversity. This diversity, most commonly manifested as simple nucleotide polymorphisms (SNPs), can provide clues to the adaptive strategies and population histories that have played roles in species' evolution. In addition, natural DNA polymorphisms form the basis for the intraspecific variation that is of great relevance to breeders.

A resource database of SNPs in *Laccaria bicolor*, *L. amethystina* and *Lactarius quietus* would provide researchers and breeders with a tool for answering questions concerning population structure or adaptation.

Laccaria is emerging as a model for fungal and tree biology, but in spite of its environmental and economic importance, little is known about genetic variation within this genus. *Laccaria bicolor*, the species whose genome has been sequenced, has a natural range that spans most European forest ecosystems.

As a first step towards analysing genetic variation in this species and its sister species *L. amethystina*, a reference collection of *Laccaria* DNA is being established within the framework of EVOLTREE. This collection will include samples from dozens of different populations that exhibit great phenotypic and molecular variations. This investigation will then be extended during the second half of EVOLTREE to non-targeted species, such as *Lactarius quietus*.

This project has the objectives to contribute to:

- a better understanding of genetic variability and structures in *Laccaria* populations at the micro- and macro-geographical scales;
- detecting the effects of genetic diversity of host trees on the diversity of *Laccaria* associates and the accompanying ectomycorrhizal community;
- monitoring the sequence polymorphism in symbiosis-regulated genes involved in the development of mycorrhiza and their functioning;
- detecting genetic associations between *Laccaria* symbionts and their host trees;
- extending these investigations to *Lactarius quietus*, an oak-specific species.



Different clones of poplar (photo: EUFORGEN)

Poplar community genomics. Understanding diversity of mycorrhiza and insects (JERA3)

This integrated project with plants, insects and mycorrhiza-specialised groups, is studying the following 'community traits' of poplar (*Populus* spp.) trees: a) diversity in the insect community and b) composition of mycorrhizal species. The controlled genetic material consists of three types of defined tree genotypes:

- *Populus nigra* cultivar *Italica* (one clone replicated in 100,000's of copies across Europe and the US)
- Clonal collections (arboreta in Poland, Hungary, Belgium, France, Netherlands, Italy, UK, ...) containing a number of common clones (species and hybrids) replicated across sites within and among countries
- Parents of segregating populations from the project Popyomics (to be replicated on a number of sites).

Different experimental set ups allow to link tree genotypes to difference in associated organisms and understand the role played by environmental factors (e.g., latitude and altitude, soil type, and surrounding vegetation, level of soil pollution).

The second phase of this project will focus on genomics, looking at the parents of existing segregating populations (e.g. from Popyomics). All differences in genotype-community interactions found between parents of segregating populations, can be used to 'phenotype' the segregating population, map the 'community' trait, and identify candidate genes using the genome sequence of poplar. Candidate genes may then, as a first step, be tested for differences in expression between parents.



New leaves of beech with the Apuan Alps in the background, Pisa, Italy (photo: Barbara Vinceti, Bioversity International)

WATER - Influence of genetic variation within Scots pine (*Pinus sylvestris*) and site water regime on the genetic and functional diversities of its ectomycorrhizal fungal associate *Cenococcum geophilum* (JERA3)

This project combines the four main disciplines in EVOLTREE (genomics, genetics, ecology and evolution) to examine interactions between Scots pine and its ectomycorrhizal associate *Cenococcum geophilum*.

Due to climate change, drought is becoming a pressing environmental condition; therefore the enhanced drought resistance of host trees provided by mycorrhizal symbiosis is a key area to be investigated. This project is trying to find out whether the genetic variation in the model tree species *Pinus sylvestris* is determining a structure in the genetic and functional diversity of the associated target ectomycorrhizal species, *Cenococcum geophilum*. To address this question, natural populations at different ISSs and field trials with different clones or families of Scots pine are being studied.

Another aspect analyzed is the possible impact of the site water regime on the genetic and functional diversity of *Cenococcum geophilum*, associated to *Pinus sylvestris*. This aspect is examined by studying natural populations within ISS or ISP sites with emphasis on a drought gradient and by a field experiment with irrigation, which is present in the ISS Valais. To study functional aspects of the symbiosis and the impact of the site water regime the following approaches and methods are adopted: transcriptomic approaches to measure gene expression in both, host tree and the mycorrhizal partner; a test to check the resistance of ectomycorrhizal roots to desiccation, and enzyme activity profiling on ectomycorrhizal root tips.

Diversity of water use efficiency and associated candidate genes in mixed natural stands of *Q. petraea* and *Q. robur* (JERA4)

Quercus robur and *Q. petraea* are two interfertile white oak species that cohabit throughout their natural distribution across temperate Europe. A large body of previous results obtained during the past 15 years has shown a clear species divergence at morphological (e.g. leaf morphology) and ecological traits (e.g. resistance to drought and water logging, difference in water use efficiency - WUE) in mixed forest stands despite a weak neutral molecular

differentiation. This is currently interpreted as resulting from divergent selection for phenotypes adapted to different soil types, ranging from deep well-drained soils (preferred by *Q. petraea*) to hydromorphic conditions (*Q. robur*).

Along these ecological gradients, mixed populations of the two species with a higher hypothetical percentage of hybrids can be found between the two extremes of the gradient where essentially monospecific stands occur. Five such topographic clines have been selected in Lorraine old growth forests (Eastern France) to increase understanding of the observed patterns in diversity and degree of adaptation to different conditions. A preliminary analysis showed a consistent difference of 13% in WUE between the two species, as estimated by carbon isotope discrimination, an important trait that might be linked to the differential adaptation.

This study will lead to an assessment of the phenotypic variability (among and within populations / species) of WUE and carbon isotope composition in the common garden experiment. In addition, the proportion of hybrids will be estimated, using a combination of Simple Sequence Repeats (SSRs) nuclear markers. To link water use efficiency to its underlying molecular basis, nucleotide diversity patterns at candidate genes potentially involved in WUE in oak species will be analysed. An exploratory association study will be performed by testing the relationship between variation at SNPs from candidate genes among progenies and variability in WUEs.

Evolution of genes involved in adaptive traits under different demographic and environmental scenarios driven by environmental changes (JERA4)

The aim of this project is to study the evolution of genetic diversity for complex traits, and the genes underlying these traits, in scenarios that present environmental changes. The objective is to develop models that are more realistic than those previously developed (e.g. METAPOPOP or CAPSIS). Four approaches are being adopted to achieve this result:

- account in the modelling for changes in environmental conditions over time in different scenarios of selection within and between populations, by allowing a variation of the optimum of phenotypic traits for fitness;

- compare different modelling of the relation between genotype and phenotype, including the possibility of pleiotropy (involvement of a given gene in several traits), and modelling of consanguinity effects.

- model explicitly the relation between phenotype and demography, i.e. linking the value of a phenotypic trait to the probability that an individual expressing this trait will survive, reproduce or disperse.

- integrate seed and pollen dispersal processes using realistic dispersal curves.

The dynamics of genetic diversity will thus be analyzed at both a local scale (spatially-explicit population) using CAPSIS, and at a larger scale with METAPOPOP (metapopulations or species-wide geographic scale with larger gradient of environmental changes).

Modelling of genetic impact of climate change on trees at different spatial scales (JERA4)

This project is focusing on modelling the genetic impact of climate change on trees at two spatial scales and the assessment of adaptation and dynamics of intra- and inter-specific genetic diversity. Modelling is carried out at a small, single species scale: a) to assess the adaptive response of phenotypic traits of the life cycle to climate change scenarios, thus to determine which traits are most important for the fitness of trees in response to climate change, b) to evaluate the consequence of climate change on genetic diversity of these traits, c) to estimate the demographic consequences of selection on adaptive traits.



Start of the vegetative season near the lake of Vico, Viterbo, Central Italy (photo: Barbara Vinceti, Bioversity International)

Modelling is also applied at a large, multi-species scale to estimate the impact of changes in species composition and species abundance caused by climate change on intra- and inter-specific genetic diversity. Finally, the two scales are linked through a comparison of, and data exchange between, the two genetic models adopted; the ForGEM that operates at a stand level, and the Eco-Genie that operates at a regional level.

Past dynamics of diversity (JERA4)

The over-arching aim of this research topic is to analyze European tree distribution dynamics during the last 10,000 years. The investigation is focusing on the drivers of these dynamics and on their interactions and relates this research to present day genetic variation. Three sub-projects are in progress to meet these aims:

- **Ancient DNA.** The aim is to develop reliable techniques for aDNA and use analyses to investigate changes in haplotype distributions during the Holocene with a focus on *Fagus* and *Picea*. The first aDNA analyses have yielded positive results. Plant macrofossils from *Fagus*, *Populus*, *Tilia* and *Quercus* up to 6,000 years old from Denmark and Germany were analysed in the ancient DNA laboratory at Copenhagen University. The plan is to continue and expand the work with *Fagus* to other sites and time periods.
- **Modelling climate-vegetation relationships and tree spreading during the Holocene.** Understanding and predicting regional transient terrestrial vegetation responses and feedbacks to climate change are challenges that require development of both models and datasets. The plan is to use state-of-the-art dynamic vegetation models and palaeovegetation data in order to study past climate-vegetation interactions to identify regions and time periods where vegetation has changed rapidly in the past with likely genetic consequences.
- **European Pollen Database (EPD).** This sub-project is focusing on the development of the palaeoecological database. This work is strategic to be able to undertake comparisons between vegetation history and current continental genetic structure. Enlargement of the pollen database with a focus on periods of past rapid climate change will support data-model comparisons of the modelling activity described above. The EPD is being re-organised and augmented with new sites. A large workshop has been held and further working-group meetings are anticipated.



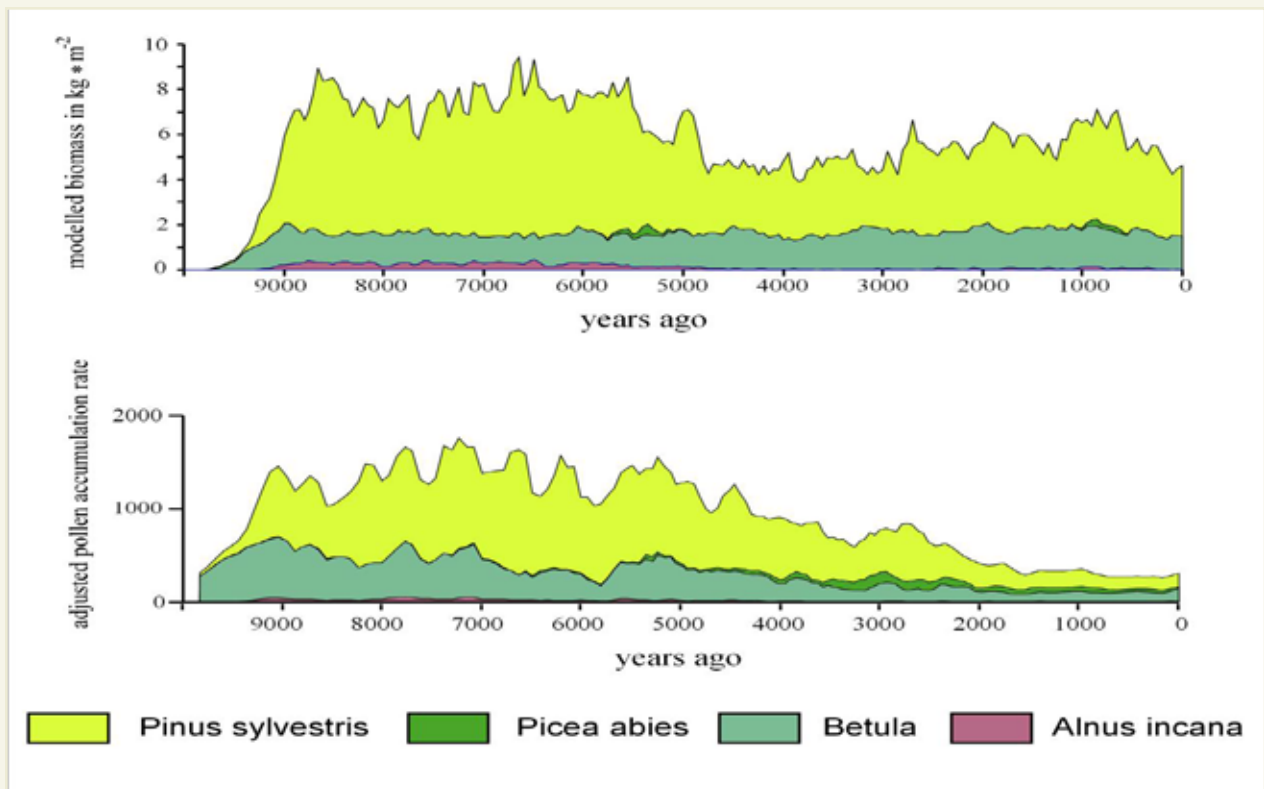
Mountain landscape from the Apuan Alps, Pisa, Italy (photo: Barbara Vinceti, Bioversity International)

Trees and climate changes

The effects of changing climate upon trees are of concern to scientists and forest managers and one way to investigate these effects is to study the past.

A group of EVOLTREE researchers is working with the palaeoecological archives of tree population dynamics that are held in the European Pollen Database. We ask the question "to what extent are European tree distributions and population dynamics controlled by climate?" This question is of fundamental importance for both the genetic structure of European trees and in managerial preparation for the forecasted period of rapid climatic change that we now enter.

Pinus and *Betula* dominated the vegetation at lake Tsuolbmajavri throughout the last 10,000 years, though *Alnus* was also more abundant prior to 4,000 years ago as compared to the present day. These patterns are in general agreement with the vegetation reconstructed using the PAR data. At present, the lake lies 30 km north of the *Pinus*-dominated forest, and *Alnus* is only present in very low numbers. Individual comparisons of adjusted PAR and biomass for *Pinus* and *Alnus* show that the model largely captures the observed trends, with a rise before 9,000 years ago, maximum between 8,000 and 6,000 years ago and



Adjusted pollen accumulation rate (PAR) (left column), and modelled biomass (right column), for each species, at lake Tsuolbmajavri, in Northern Finland

subsequent decline. These trends are chiefly driven by summer temperatures. Disturbance, fire and drought sensitivity experiments were found to have little effect on the overall modelled vegetation trends on millennial timescales. However, sensitivity experiments that altered interannual variability of summer and winter temperatures did influence the biomass proportion, year of establishment and even the very presence of a species near its bioclimatic limits. Comparison of quantitative palaeoecological data with results from the model shows that a combination of different abiotic and biotic factors is necessary to explain past forest dynamics.

Changes in interannual variability may be as important as millennial scale trends, and different climate variables may have become limiting at different times during the past. The combined use of palaeoecological data and dynamic vegetation models helps in understanding past vegetation changes which, in turn, will enable us to evaluate the impacts of future climate change on vegetation.

(contribution provided by Richard Bradshaw, University of Liverpool, UK)

EVOLTREE contribution to the challenge of sequencing conifers

Pines have a major ecological role, in particular in extreme environments such as the Mediterranean, where they are important for watershed and soil protection and they support a rich community of associated species. Pine species also play an especially important role in modern plantation forestry worldwide and now form a large part of both the annual wood harvest and the immature plantation forests that will provide wood in the future.

Pines are popular because they count a large number of species, suitable for different site and environmental conditions. Their wood is easily processed and utilized for a wide variety of end uses and various other forest products come from pines (e.g. resins, extracts from bark, nuts, etc.).

The complete sequencing and assembly of the *Arabidopsis*, poplar and rice genomes have afforded considerable insight into the evolution of other plants including pines. Some tree species, such as *Populus*, have very small genomes, about four times the size of the *Arabidopsis* genome, but conifers have genomes

more than 100 times the size of the *Arabidopsis* genome. The nearly full *Populus* sequence provides access to all areas of the genome. Some recent studies have shown that gymnosperms and angiosperms possess highly similar gene complements.

However, angiosperms and gymnosperms diverged from a common ancestor more than 300 million years ago, and consequently the utility of angiosperm sequences in the study of pine and other gymnosperms will be limited. Since the first loblolly pine (*Pinus taeda*) cDNA sequences were published, extensive expressed sequence tag (EST) resources have also become available for many other conifer species, including Norway spruce. Other genomic resources are rapidly improving.

Ultimately, the best means of advancing pine and conifer genomics is complete sequencing of a conifer genome. However, while it is now theoretically feasible to sequence the genome of any organism, the large, repetitive nature of conifer genomes will likely prevent them from being targets of full-scale genome sequencing for at least a few years. Nevertheless, the likelihood that the pine genome will be sequenced is high based upon past and present investments made by the US National Science Foundation (NSF) and other granting agencies and growing worldwide interest in pine as a biofuel/carbon sequestration crop.

EVOLTREE is contributing to this challenge by making available increasing genomic resources (BACs and ESTs sequencing) and collaborative sequencing efforts based on wide-range sampling across multiple populations and species to allow a much better understanding of genome-wide patterns that would reveal the signatures of natural selection.

Very importantly, in many cases the sequencing undertaken as part of EVOLTREE activities involved the full-length of the gene, including important gene parts of the regulatory region, which allowed to cover all variation found in a particular gene. Research on sequence variation, combined with work on natural phenotypic variation, allows obtaining significant contributions to dissecting the genetics of adaptations of tree populations.

To achieve this goal, EVOLTREE is promoting the development of association studies that will effectively connect genotypes with phenotypes for a wide range of genes and traits, with both ecological and economic

interest. In addition, transferring information between closely related conifer species is facilitated by high sequence similarity. In EVOLTREE, progress is being made in the identification, qualification and mapping of candidate genes regulating growth phenology (bud set and bud burst), targeting traits considered of importance in studying adaptation to climate change, in Scots pine, Norway spruce, poplar and oaks. In most of these species, candidate genes for drought-tolerance response are also being sequenced (such as several members of the dehydrin gene family) and in the near future these candidate genes will be tested for genotype-phenotype associations.

Collaborative efforts are being established in order to develop new statistical tools dealing with common problems in association studies, such as population structure or cline variation. Furthermore, collaborations are being established with partners outside the EVOLTREE network, in particular with the US NSF, for the exchange of genomic resources of Fagaceae, and with the University of California for a large scale re-sequencing of genes in conifers.

(source: Plomion et al., 2007. *Pines* (pp. 29-92), in *Genome Mapping & Molecular Breeding. Vol. 7: Forest Trees*, C.R. Kole, editor. Springer-Verlag, with inputs from Santiago C. González-Martínez, INIA, Spain)



Canary Island Pine (*Pinus canariensis*), Canary Islands (photo: Barbara Vinceti, Bioversity International)

Towards understanding relationships with the host: advances in sequencing mycorrhizal fungi

Mycorrhizae are critical elements of the terrestrial ecosystems, since approximately 85 percent of all plant species, including trees, are dependent on such interactions to thrive. Mycorrhizae significantly improve photosynthetic carbon assimilation by plants and underlie trees ability to generate large amounts of biomass or store carbon. These interactions between trees and soil microbes, known as fungi, helps trees in getting necessary, but scarce, nutrients such as phosphate and nitrogen.

When mycorrhizal fungi establish a partnership with plant roots a mycorrhizal root is created. The fungus within the root is protected from competition with other soil microbes and gains preferential access to carbohydrates within the plant.

Individual symbionts vary in their potential range of host-species, ability to colonize different genotypes of host-plant, ability to promote plant growth, and adaptation to abiotic factors, such as soil pH. The genetic mechanism of this symbiosis, which contributes to the delicate ecological balance in healthy forests, also provides insights into plant health that may enable more efficient carbon sequestration and enhanced phytoremediation—using plants to clean-up environmental contaminants.



Fruiting body of *Laccaria bicolor* (photo: Francis Martin, INRA-Nancy, France)

The genome of the ectomycorrhizal basidiomycete *Laccaria bicolor* has been fully sequenced through a collaboration between the U.S. Department of Energy Joint Genome Institute (DOE JGI) and European research institutions, including an EVOLTREE partner, Francis Martin from INRA, the National Institute for Agricultural Research in Nancy, France. This

international team effort also involved contributions from 16 institutions, including Ghent University, Belgium; Lund University, Sweden; Göttingen University, Germany; CNRS-Aix-Marseille University; Nancy University, France; and University of Alabama, Huntsville. The results have been published in the journal *Nature* on 6 March, 2008.

Laccaria bicolor occurs frequently in the birch, fir and pine forests of North America and is a common symbiont of poplar. The analysis of its 65-million-base genome, the largest fungus sequenced to date, yielded 20,000 predicted protein-encoding genes. In sifting through these data, researchers have discovered many unexpected features, including an arsenal of small secreted proteins (SSP), several of which are only expressed in tissues associated with symbiosis.

The most prominent SSP accumulates in the expending hyphae, the tips of the fungus that colonize the roots of the host plant. The proteins specific to this host-fungus interface seem to play a decisive role in the establishment of symbiosis.

This genome exploration led to the unexpected observation that the genome of *Laccaria* lacks the enzymes involved in degradation of the carbohydrate polymers of plant cell walls, but maintains the ability to degrade non-plant cell walls, which may account for *Laccaria's* protective capacity. These observations point towards the dual life that mycorrhizal fungi like *Laccaria* possess, that is, the ability to grow in soil fending off pathogens and using decaying organic matter, while serving as a custodian of living plant roots.

The team also discovered new classes of genes that may be candidates for the complex communication that must occur between the players in the host-plant subsoil arena during fungal development. They report that fungi play a critical role in plant nutrient use efficiency by translocating nutrients and water captured in soil pores inaccessible to roots of the host plant.

The *Laccaria* genome sequence, its analysis, associated genomics and bioinformatics tools provide an unprecedented opportunity to identify the key components of organism-environment interactions that modulate ecosystem responses to global change and increased nutrient input needed for faster growth. By examining and manipulating patterns of

gene expression, it is possible to identify the genetic control points that regulate plant growth and plant-mutualist response in an effort to better understand how these interactions control ecosystem function.

(contribution provided by Francis Martin, INRA-Nancy, France)

D. OUTPUTS OF MEETINGS

Annual Meeting, 4-7 February 2008, Mandelieu-Nice (France)

The members of EVOLTREE gathered for the Second Annual Meeting of the Network of Excellence in Mandelieu-Nice (France), from 4 to 7 February 2008. The event brought together more than 100 scientists and some invited speakers from outside the consortium. The Annual Meeting was an occasion to discuss progress in implementing various activities and to develop new work plans for the third year of the network.

Annual First Stakeholder Group Meeting, 7-8 February 2008, Mandelieu-Nice (France)

In addition, back to back to the Annual Meeting, the first meeting of the EVOLTREE Stakeholder Group was organized. The event was an opportunity to continue the dialogue between EVOLTREE scientists and policy-makers on issues of common interest. Several invited scientists from EVOLTREE presented research overviews of their specific areas of work. The objective was to illustrate the current level of knowledge acquired in different scientific areas related to forest tree genetics and genomics, highlighting the practical applications of possible interest to the Stakeholders.

The discussion covered different topics: from the availability of molecular markers to verify the origin of timber and forest reproductive material, to the benefits brought by the establishment of common research infrastructures (e.g., common DNA repository center); from the use of genomic approaches for bioenergy, looking at the case of poplar, to the need to integrate climate change adaptation into forest management.

There is a plan to summarize the results of the discussion into short briefs which could be then translated into different languages and widely distributed. The Stakeholders recommended that participation to

the next EVOLTREE Stakeholder Group meeting should be enlarged to include participants representing more organizations. It was also recommended that EVOLTREE should continue operating in close association with EUFORGEN and other relevant networks and projects that generate and disseminate knowledge on forest genetic resources in Europe.

Finally, the stakeholders also recommended that EVOLTREE should take note of the global initiatives on forest genetic resources, such as the FAO plan to prepare a report on the State of the World's Forest Genetic Resources, and the CBD review of its Extended Programme of Work on Forest Biodiversity.

A full report of the event and copies of the presentation are downloadable from the EVOLTREE portal in the Dissemination section.



First Stakeholder Group Meeting, Mandelieu-Nice (France), February 2008 (photo: INRA Transfert)



EVOLTREE participants to the First Stakeholder Group Meeting, Mandelieu-Nice (France), February 2008 (photo: Lennart Ackzell, Swedish Forest Agency, Sweden)

E. FORTHCOMING EVENTS AND ANNOUNCEMENTS

Forthcoming events in EVOLTREE

- **Workshop on Tuber Genome Annotation**

21-23 May, 2008. Location: CNS Genoscope in Paris-Evry and at INRA-Nancy (France). The goal of this workshop is to train members of the Tuber Genome Consortium and EVOLTREE networks on how to use the basic functions of the Genoscope and INRA Genome Portal for genome analysis and manual curation of predicted genes and functions. Attendees will learn how to navigate through the genome, analyze gene families and pathways, search for genes of interest, evaluate gene structures using available evidence and, if necessary, change them and assign gene names and functions. They will also use bioinformatics pipelines for SNP detection. This is a hands-on tutorial using laptop computers; please bring your own laptop. Contact: Francis Martin (Phone: +33 383 39 40 80, fmartin@nancy.inra.fr)

- **Workshop on Glomus Genome Annotation**

The preliminary date of the workshop is mid-September 2008 but the exact date has not been finalized yet.

The goal of this workshop is to train members of the Glomus Genome Consortium and EVOLTREE networks on how to use the basic functions of the JGI and INRA Genome portals for genome analysis and manual curation of predicted genes and functions. The workshop is structured as the one above on Tuber genome. It is a hands-on tutorial and participants should bring their own laptop.

Contact: Francis Martin (Phone: +33 383 39 40 80, fmartin@nancy.inra.fr)

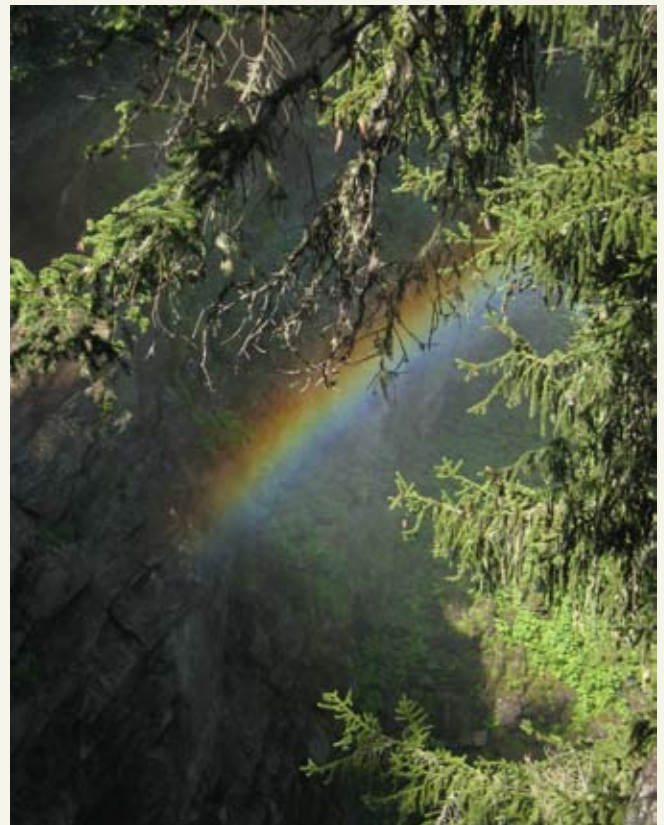
- **Workshop: Training course in meta-analysis**

1-4 July, 2008, Location: ETH or University, Zurich (Switzerland). This workshop is designed to provide participants with hands-on experience in conducting ecological meta-analysis. Participants will become familiar with what meta-analysis is, where it comes from, some examples of how it has been used in ecology, and its major strengths, weaknesses, advantages and limitations as a tool for the quantitative summary of research results. They will become familiar with using MetaWin 2.0 software to do the calculations involved in typical ecological meta-analyses, and learn how to interpret the output. They will be introduced to issues and methods for gathering data from the scientific literature to use in ecological meta-analysis, learn how to organize and input

those data into MetaWin. They will conduct a preliminary meta-analysis on their own data or on other ecological data. Finally, they will learn how to evaluate and critique the results. Participation is open to students and researchers with interest in data analysis methods across single experiments or data sets - active participation, at best with own data set. The Software (MetaWin) can be provided beforehand for data preparation and import.

- **Summer School: Functions of Microbial Communities in Soils**

8-19 September, 2008. Location: Nancy (France). Following the last edition held in 2006 in Munich, a new edition of the French-German Summer School devoted to the Functions of Microbial Communities in Soils will be held from September 8th to 19th in Nancy (France). We invite you to participate and/or to distribute the circular to your colleagues and collaborators. Please find information and the application form on the EVOLTREE portal.



Norway spruce (*Picea abies*) from the Western Alps, Italy (photo: Barbara Vinceti, Bioversity International)

Forthcoming events outside EVOLTREE

- **International Course on Molecular Evolution**

12-16 May, 2008. Location: Valencia (Spain). The third edition of the international course on: "Molecular Evolution, Phylogenetics and Phylogenomics" aims to provide the necessary background to understand the basic concepts of evolutionary and comparative biology that are commonly used in molecular biology and bioinformatics. It is organized in 5 full days and includes theoretical lectures and hands-on practicals. http://bioinfo.cipf.es/courses/mol_evol_phylo_3ed/

- **Workshop: Int. Course on Conservation Units**

9-13 June, 2008. Location: Cartagena de Indias (Colombia). This international course on Conservation units: "Management of in situ conservation units of forest species in South America" is sponsored by INIA (Madrid, Spain) and the Spanish Agency of Cooperation. Director of the course: Santiago C. González-Martínez (santiago@inia.es).



Beech tree growing in extreme environmental conditions, Central Italy (photo: Barbara Vinceti, Bioverity International)

- **4th EPSO Conference: "Plants for Life"**

22-26 June, 2008. Location: near Toulon (France). The fourth EPSO Conference will explore the theme 'Plants for Life'. The conference will address many of the challenges faced by the plant research community in an evolving world: climate change, preservation of the environment and of natural biodiversity, as well as the food and feed demands of a growing world population. The fourth EPSO Conference will bring together international scientists and experts who will provide insights into the most recent breakthroughs in the fields of genome structure and evolution, evolutionary biology, developmental biology, ecophysiology, system biology, economics, plant breeding and the challenges facing developing countries. <http://www.epsoweb.org/catalog/conf2008.htm>

- **International workshop on "Population, Quantitative and Comparative Genomics of Adaptation in Forest Trees"**

3-5 August, 2008. Location: Centro di Ecologia Alpina, Monte Bondone, Trento, Italy. Organized by: Centro di Ecologia Alpina, Fondazione Edmund Mach, in collaboration with the University of California, Davis (Department of Plant Sciences). <http://www.cealp.it>, e-mail - info@cealp.it

- **International conference on "Adaptation of Forests and Forest Management to Changing Climate with Emphasis on Forest Health: A Review of Science, Policies, and Practices"**

25-28 August, 2008. Location: Umeå (Sweden). The conference will focus on the current state of knowledge of ongoing changes in climatic conditions in different regions of the world, and the implications of these changes for forest management and conservation. Presentations and discussions will emphasise research, policies and practices that are needed to enable us to plan for and manage healthy, productive forests to meet future societal needs for forest products and the full range of forest goods and services. Ongoing research in various fields of forest and forest related sciences will be presented in parallel sessions of the conference. <http://www.forestadaptation2008.net/home/en/>

- **Summer Course on Computational Phyloinformatics**

24 July - 4 August 2008, location: Durham, North Carolina (USA). Computational Phyloinformatics is a 10-day summer course sponsored by and held at the National Evolutionary Synthesis Center (NESCent). The aim is to give students practical knowledge and hands-on skills in phyloinformatics. Apply through the course website. You will be asked to provide a resume, two references, a brief description of your computational and phylogenetic background, and your reasons for taking the course. Applications are due by April 15th, 2008.

Course Director: William Piel (piel@treebase.org)

Course Administrator: Jory Weintraub (jory@nescent.org)

- **European Plant Biology Congress FESPB 2008**

17-22 August, 2008. Location: Tampere (Finland). A large number of registrations has been received before the early registration deadline and there are already over 900 registered participants for the congress. Further information can be found on the web page: www.fespb2008.org

- **IUFRO Conference on “Population, Ecological and Conservation genetics”**

24-29 August, 2008. Location: University Laval, Québec City (Canada). The event is a joint conference of IUFRO Working Groups 2.04.01 (Population, ecological and conservation genetics) and 2.04.10 (Genomics), along with the Canadian Tree Improvement Association (CTIA) including satellites activities and workshops. It will be hosted by University Laval and its partners. <http://www.iufro-ctia2008.ca/index.php?id=40&L=0>

- **Summer school on Computational and Mathematical Modeling for Plant Systems Biology**

1-5 September, 2008. Location: VIB Department of Plant Systems Biology and Ghent University, Ghent, Belgium. This summer school will bring together a wide range of computational systems biologists, working on problems at different organizational levels, relevant to plant biologists. The course will start with phenomena occurring at the subcellular and cellular scale, including photosynthesis, cell cycle regulation and the organization of the cytoskeleton. Then it will gradually “scale up” to the tissue, organ, and whole plant levels. It will conclude with pattern formation in tissues, the mechanics of growth, and whole plant development and evolution. Organiser: Roeland Merks (roeland.merks@psb.ugent.be) Further information: www.psb.ugent.be/plantmodels



Canary Island Pine (*Pinus canariensis*), Canary Islands (photo: Barbara Vinceti, Bioversity International)

Announcements

Two new projects have received funding from the FP7, NovelTree and EnergyPoplar, and they will start their activities in spring 2008. Several EVOLTREE members contributed to the development of the successful research proposals and the projects are coordinated by EVOLTREE partners, both from NRA, France: Catherine Bastien is coordinator of NovelTree and Francis Martin is coordinator of EnergyPoplar.

NovelTree

NovelTree is a large collaborative project on novel forest tree breeding strategies coordinated by INRA, Orleans. It includes 14 partners (8 are also EVOLTREE partners) from Belgium, Finland, France, Italy, Spain, Sweden and United Kingdom.

NovelTree is designed to enable significant genetic improvement of tree characteristics and forest products properties to satisfy the needs (quality, quantity, sustainability, vulnerability) of the forest-based sector and consumers. The challenges facing forest geneticists and tree breeders include recognition of changing demands on forests for a wider range of high value forest products and sustainability of forest ecosystems under climate change.

NovelTree will provide a list of morphological and physiological traits relevant as selection criteria for pest tolerance, sustainable biomass production, wood properties for present and future use and plastic response to climate change.

Efforts will be put on identification of functional allelic polymorphisms for a suite of traits of interest thanks to a post-genomics approach. Concomitantly, the project will participate in the development of high throughput phenotyping and genotyping tools in collaboration with EVOLTREE NoE.

These new tools will allow earlier genetic evaluation, higher selection intensity, increased accuracy in genetic prediction and better monitoring of genetic diversity along generations. Novel and improved breeding strategies integrating phenotypic and genotypic information will be proposed. Demonstration of their efficiency will focus on model tree species of high economic importance in different European regions: Maritime Pine, Scots Pine, Spruce, and Poplar. Support decision tools will be made accessible to tree breeders

and forest owners for optimal deployment of improved genetic stocks in both prevailing and future climate, and under risk of pest and disease attacks.

NovelTree project will also provide training in emerging technologies in connection with on-going European projects, disseminate the results to different audiences and transfer technology to the Forest-based sector.

EnergyPoplar

EnergyPoplar is a small collaborative project focused on enhancing poplar traits for energy applications.

Crops which are grown specifically for the production of renewable energy offer new opportunities for sustainable forestry and agricultural systems. Where this involves marginal land, new economic potential can be realized. The current knowledge of dedicated energy crops is limited, both in relation to the biological processes involved in the synthesis of substances acting as raw material for biofuel production, as well as in relation to the discovery, domestication and/or development of new energy crops.

Realizing the potential of this area will necessitate the application of genetic and genomic technologies to facilitate gene discovery and fast-track breeding. It will also entail developing greater knowledge of supply chain issues including life cycle analysis and environmental impact. The expected output of this project are market driven, hardy, viable and profitable energy crops with enhanced traits derived from conventional and biotechnological breeding techniques which exploit the post genomic knowledge base.

The overall objective of EnergyPoplar is to develop domesticated energy poplars having both desirable cell-wall traits and high biomass yield under sustainable low-input conditions to be used as a source of lignocellulosic feedstock for bioethanol.

To achieve this goal, EnergyPoplar will integrate an ambitious multidisciplinary approach (molecular, cellular, organismal, and community) to i) optimize the amount, composition, and structure of walls (reducing lignin content and changing wall organisation and composition) for biofuel production and ii) domesticate and develop poplars with enhanced traits.

Much is yet to be discovered on the control of lignin and cellulose formation in *Populus*. EnergyPoplar will lead

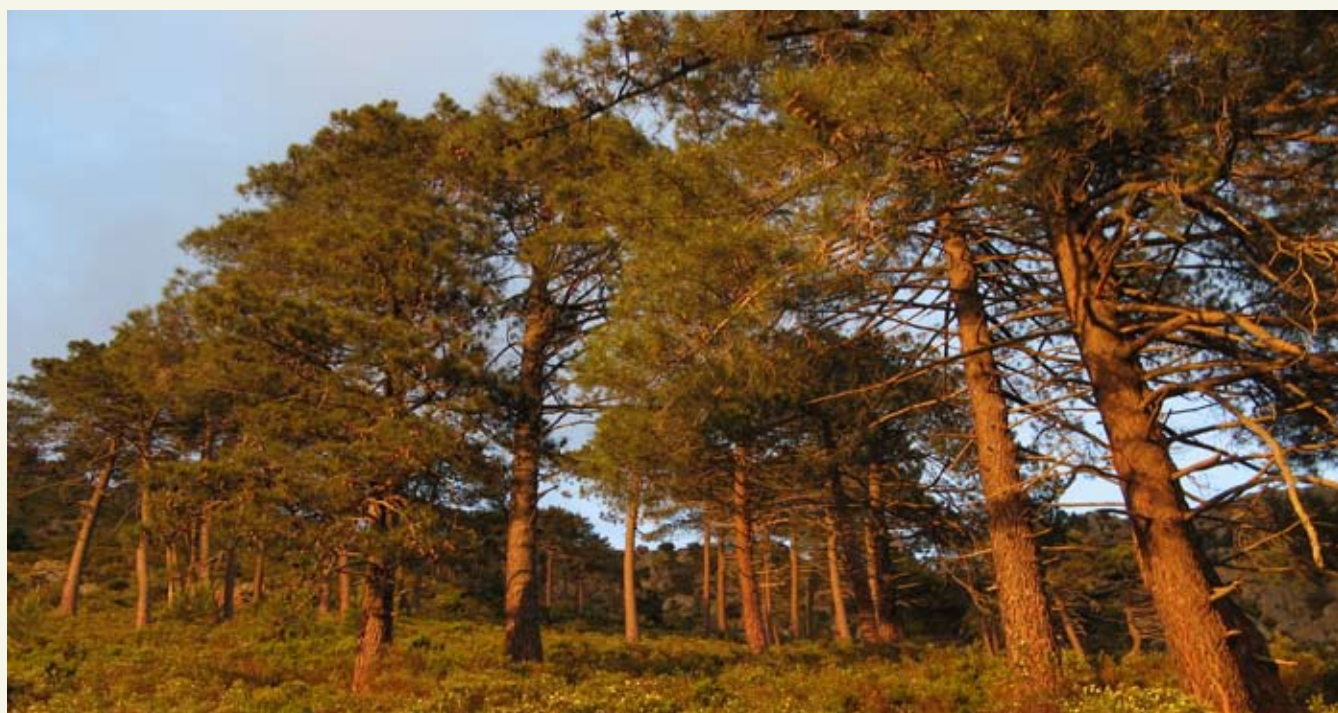
to an improved understanding of cell wall assembly and through marker-assisted and biotechnological routes, the development of 'low lignin/high cellulose' trees with increased nutrient use efficiency. It will use several novel approaches to dissect on the control of lignin and cellulose formation in *Populus*: better understanding of the formation of tension wood, a natural 'high cellulosic' resource; the use of fast growing 'triploid' *Populus*, also known to be natural 'high cellulosic' trees and in capturing natural variation in both segregating and wide population of *Populus*.

Beyond the life of this project it is hoped to capture further commercial benefits and to deploy the high-throughput genomics platform on a commercial scale with appropriate commercialization of the research.

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Corsican Pine (*Pinus nigra* subsp. *laricio*) (photo: Barbara Vinceti, Bioersivity International)

evoltree PARTNERS

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

- French National Institute for Agricultural Research, France
- Alterra - Wageningen University and Research, the Netherlands
- National Research Council, Italy
- Flanders Interuniversity Institute for Biotechnology, Belgium
- Georg-August Universität Göttingen, Germany
- INRA Transfert, France
- Bioersity International, Italy
- Natural Environment Research Council - CEH, United Kingdom
- Phillips University of Marburg, Germany
- Swiss Federal Research Institute WSL, Switzerland
- Technical University in Zvolen, Slovak Republic
- Technical University of Munich, Germany
- National Institute for Agriculture and Food Research and Technology, Spain
- University of Udine, Italy
- National Research Centre of Scientific Research, France
- Umeå Plant Science Centre, Sweden
- University of Bydgoszcz, Poland
- University of Oulu, Finland
- University of Southampton, United Kingdom
- University of West Hungary, Hungary
- Uppsala University, Sweden
- Max Planck Institute, Germany
- Austrian Research Centers GmbH - ARC, Austria
- University of Liverpool, United Kingdom
- Johann Heinrich von Thünen Institut, Germany

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



Bioersity International is associated with EVOLTREE and responsible for its dissemination activities. Contact: Dr. Barbara Vinceti, Bioersity International, Rome, Italy.
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