



evoltree

EUROPEAN PROJECT ON
FOREST BIODIVERSITY

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evoltree EXTERNAL NEWSLETTER

evoltree is an interdisciplinary network of scientists in Europe. This Network involves 25 research groups from 15 European countries that are working together to identify and study genes of adaptive significance in order to evaluate the contribution they make to the evolution of tree species and tree communities. Research will also be carried out on organisms that interact with trees such as insects and mycorrhizal fungi.

www.evoltree.eu



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A. INTRODUCTION

Message of the coordinator

by *Antoine Kremer*, *evoltree* coordinator



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Evoltree is entering its last year and the dissemination of the results produced will be a major task of the partners within the Network of Excellence (NoE). While scientists are usually hesitant in disseminating their findings outside the scientific community, outreach is a major component of a network of excellence. The series of external newsletters produced by *evoltree* contributes to demonstrate that dissemination is not an impossible task. Dissemination is needed to support the dialogue between society and scientists at a time when science is at the forefront of major global issues. I will briefly recall some of the major dissemination initiatives that will take place during the last year of *evoltree*, which will end in September 2010.

The most significant scientific results of the network will be presented at the *evoltree* final international conference on 'Forest ecosystem genomics and adaptation', organized in June 2010, in Spain (San Lorenzo de El Escorial). Top ranking invited speakers from different regions of the world will present their perspectives on adaptation of trees to climate changes. Several review papers on the achievements of the NoE are currently being prepared and will be submitted to international journals.



Boreal forest in winter (Photo by B. Vinceti).

Evoltree has participated to major international meetings and conferences (for example, the World Forestry Congress held in Buenos Aires, Argentina, in October 2009) and in the course of 2010 will continue to actively contribute to major international scientific events: the IUFRO conference on 'Forests in the genomics era' to be held in March 2010 in Kuala Lumpur (Malaysia) and the IUFRO World Congress that will take place in August 2010 in Seoul (Korea).

For what concerns dissemination of scientific information to stakeholders, a special session will be organized at the international scientific conference mentioned above, to be held in San Lorenzo de El Escorial (Spain) in June 2010. This is in line with the efforts so far undertaken by *evoltree* aimed at ensuring that research findings influence policies and contribute to the sustainable use of forests and their biodiversity. During the stakeholders' event, the potential practical implications of the expanding research area of forest ecosystem genomics will be illustrated to stakeholders. The scientific outputs produced within *evoltree* and other research initiatives will be discussed in relation to the challenge of integrating climate change adaptation into forest management practices. I strongly encourage scientists and stakeholders to participate actively to these dissemination events.

The future of *evoltree*

The identification of a collaborative instrument that would ensure the continuation of *evoltree* after the end of the EU financial support, in September 2010, is an important step for the NoE. The consultations so far held on this subject have led to the identification of a set of activities currently carried out by the Network of Excellence which should be continued in future and some common infrastructures set up by *evoltree* which should be maintained. Collaborative research activities would be implemented only if external financial resources were made available (through ERA NETs, or FP7 or FP8 projects). In absence of external funding, at least the maintenance of the infrastructures and some collaborative activities should be continued with resources coming from the contributing organizations.

A small set of activities, which could ensure a 'minimum metabolism' of the network, would consist of the following tasks: (1) maintenance and upgrade of the *evoltree* portal and eLab, (2) access to and use of the common DNA repository centre, of the Intensive Study Sites, and of the high throughput genotyping and sequencing facility, (3) organization of training (summer schools) mobility and dissemination, (4) coordination

of activities. Funding mechanisms to maintain these activities are currently being explored within each country. In addition, the different legal systems that **evoltree** will adopt are also being investigated. The final decision on what solutions should be adopted to continue **evoltree** beyond September 2010 will be taken by the Network Governing Board which is formed by the heads of the different research organizations involved.

B. PROGRESS IN INTEGRATION ACTIVITIES

Recent development in the **evoltree** eLab

by *Johanna Schmidt, Dieter Kopecky and Sivia Fluch*



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JOHANNA SCHMIDT is a software developer at the Austrian Research Centers, Seibersdorf (web applications and design). She is administering the EVOLTREE Portal and develops the e-lab application.

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Very large amounts of data, knowledge and other heterogeneous information are generated by **evoltree** research partners. The eLab has been implemented to integrate all these distributed resources and to make them available from a single web platform. The internet portal allows integrated searches across all thematic databases. As discussed in the Newsletter 2008/2, the eLab has already been brought into routine work one year ago. Since then the interface has been further developed and additional databases have been integrated into the system. The databases currently connected are: (a) CBiB Library and Sequence Database, (b) INRA CMap, (c) INRA Quercusmap, (d) INRA (GD)², (e) INRA TreePop,

(f) SOTON CMap, (g) PICME Material Database and (h) UPSC Microarray Experiment Database. Further database integration steps are currently underway.

The eLab user interface has been revised and new elements have been added to improve data characterization and presentation. Additional information fields are now displayed and allow a more user-friendly browsing through the data sets. Furthermore, information on the owner of each data item is displayed together with a link to the partner's homepage and an email address (if available).

The eLab BLAST service, that allows users to search homologues for a particular DNA sequence, has been extended. In addition to all the sequences from Evoltree cDNA libraries, sequences and unigene sets from NCBI for Evoltree related species have been included. So, the search allows not only to select the species of interest, but also to select the source of the search, i.e., whether the BLAST query should be made against the whole set of sequences or just against the sequences coming from NCBI or from **evoltree** respectively.

When launched in 2008 the eLab was only accessible to members of the **evoltree** project but soon the eLab will be made accessible to all visitors of the **evoltree** portal, enabling scientists from outside the project to get an overview of the research work of the network and the resulting genomic resources assembled in the eLab.

In future, it will be possible to access portions of the original datasets but the regime that should regulate access, and the different types of permissions to be granted to different users, are currently being discussed within the **evoltree** consortium. The access regime that is being defined will therefore determine what data should be visible only to **evoltree** members, and what data could be viewed also by other users. The data visualization will be dynamically adapted to the user's access rights in order to ensure that intellectual property rights are respected. After a final test and the formal acceptance of the **evoltree** partners involved in feeding the databases, the eLab will go online with a much wider data accessibility, extended to a larger scientific community.

For further information please refer to the web side: (<http://www.evoltree.eu/index.php/e-resources>).

The image associated to this article shows a screenshot of the *Quercus robur* dataset, accessible through the eLab.

eLab Search :: Details

Details of Crossing:

Name	Ef03 x SI03
Species	Quercus robur
Type	F1
Size	579

Data comes from:

- INRA TreePop Database
- INRA QuercusMap Database

Reiner Finkeldey
Georg-August-University
Göttingen (PG)

[Website](#) [Email](#)

Application Properties

You are logged in as:
Johanna Schmidt

Current Page:
Ef03 x SI03
(Crossing)

Previous Page:
Result
[\[go back\]](#)

[New Search](#)

Genotypes | Family Members | Phenotypic Traits | Genotypic Traits | Assigned Maps

579 Organisms Page 1 / 29

ID	Species	Genus	Family
1	Pinus sylvestris	Pinus	Pinus
10	Quercus petraea	Quercus	Quercus
100	Quercus petraea	Quercus	Quercus
101	Quercus petraea	Quercus	Quercus
102	Quercus robur	Quercus	Quercus
103	Pinus sylvestris	Pinus	Pinus

Screenshot of the *Quercus robur* data set in the Elab (<http://www.evoltree.eu/index.php/elab-start>)

C. RESEARCH HIGHLIGHTS

CRIEC – A resequencing initiative for European conifers

by Santiago Gonzalez-Martinez and Giovanni Vendramin



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Single Nucleotide Polymorphisms (SNPs) are becoming markers of choice for population and evolutionary genetic studies because they are very abundant in the genome, have the potential to reflect adaptive variation and are easy to genotype using high-throughput platforms. A first necessary step, however, is to discover SNP locations by either resequencing or through a bioinformatic analysis of EST libraries. CRIEC (Conifer Resequencing Initiative for European Conifers) has been developed as a collaborative initiative to develop such

resources in several non-model (mostly European) conifer species, with funding support from CNR (Consiglio Nazionale delle Ricerche) in Italy, INIA (Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria) in Spain and [evoltree](#), and the contributions of several research groups within [evoltree](#) (INIA-Madrid, CNR-Firenze, INRA-Avignon, UMARBURG-Marburg, WSL-Birmensdorf, INRA-Bordeaux & UOULU-Oulu) and outside the NoE (BFW-Vienna, UARISTOTLE-Thassaloniki, METU-Ankara & INTA-Bariloche).

Within CRIEC, a total of 300 candidate genes that were successfully transferred from loblolly pine (*Pinus taeda* L.), a New World conifer, to maritime pine (*P. pinaster* Ait.), a conifer from southwestern Europe, in the framework of CRSP project at UC Davis (PI: David B. Neale; see <http://dendrome.ucdavis.edu/NealeLab/crsp>) were tested for transference to 18 conifer species, as shown in figure on the next page. The species panel has been collectively chosen to include all conifers that are supported by European research linked to [evoltree](#).

Transference of candidate gene information from model to non-model species is especially challenging in conifers due to nearly-identical paralogs and big gene families, a consequence of their large genomes. Nevertheless, based on the current dataset of 176 candidate genes (the sequencing of the remaining genes to get to 300 is ongoing) transference rates were relatively high, 80% within the *Pinus* genus and 40% for species less closely related to loblolly pine. The original 300 candidate genes

	1	2	3	4	5	6	7	8	9	10	11	12
A	<i>Abies pinsapo</i>	<i>Abies pinsapo</i>	<i>Abies pinsapo</i>	<i>Juniperus thurifera</i>	<i>P. leucodermis</i>	<i>P. leucodermis</i>	<i>P. leucodermis</i>	<i>P. leucodermis</i>	<i>P. leucodermis</i>	<i>P. leucodermis</i>	<i>P. leucodermis</i>	blank
B	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>	<i>P. brutia</i>
C	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>
D	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>
E	<i>Cupressus sempervirens</i>	<i>Cupressus sempervirens</i>	<i>Juniperus communis</i>	<i>Juniperus communis</i>	<i>Juniperus communis</i>	<i>Austrocedrus chilensis</i>	<i>Austrocedrus chilensis</i>	<i>Austrocedrus chilensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>
F	<i>Cedrus atlantica</i>	<i>Cedrus atlantica</i>	<i>Cedrus atlantica</i>	<i>Cedrus atlantica</i>	<i>Cedrus libani</i>	<i>Cedrus libani</i>	<i>Cedrus libani</i>	<i>Cedrus libani</i>	<i>Cedrus brevifolia</i>	<i>Cedrus brevifolia</i>	<i>Cedrus brevifolia</i>	<i>Cedrus brevifolia</i>
G	<i>P. palustris</i>	<i>P. palustris</i>	<i>P. palustris</i>	<i>P. palustris</i>	<i>P. palustris</i>	<i>P. palustris</i>	<i>P. palustris</i>	<i>P. palustris</i>	<i>P. echinata</i>	<i>P. echinata</i>	<i>P. echinata</i>	<i>P. echinata</i>
H	<i>P. echinata</i>	<i>P. echinata</i>	<i>P. echinata</i>	<i>P. echinata</i>	<i>P. echinata</i>	<i>P. echinata</i>	<i>Pinus elliotti</i>	<i>Pinus elliotti</i>	<i>Pinus elliotti</i>	<i>P. palustris</i>	<i>P. echinata</i>	<i>P. echinata</i>

	1	2	3	4	5	6	7	8	9	10	11	12
A	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. canariensis</i>	<i>P. canariensis</i>	<i>P. nigra</i>	<i>P. pinea</i>	<i>P. pinea</i>
B	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. canariensis</i>	<i>P. canariensis</i>	<i>P. nigra</i>	<i>P. pinea</i>	<i>P. pinea</i>
C	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. canariensis</i>	<i>P. canariensis</i>	<i>P. nigra</i>	<i>P. pinea</i>	<i>P. pinea</i>
D	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. canariensis</i>	<i>P. canariensis</i>	<i>P. nigra</i>	<i>P. pinea</i>	<i>P. pinea</i>
E	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. canariensis</i>	<i>P. nigra</i>	<i>P. nigra</i>	<i>P. pinea</i>	<i>Taxus baccata</i>
F	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. canariensis</i>	<i>P. nigra</i>	<i>P. nigra</i>	<i>P. pinea</i>	<i>Taxus baccata</i>
G	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. canariensis</i>	<i>P. nigra</i>	<i>P. nigra</i>	<i>P. pinea</i>	<i>Taxus baccata</i>
H	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. pinaster</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. halepensis</i>	<i>P. canariensis</i>	<i>P. nigra</i>	<i>P. nigra</i>	<i>P. pinea</i>	blank

CRIEC sequencing panel. A larger sequencing panel for maritime pine (*Pinus pinaster*) is being generated in the framework of the EU project NovelTree.

sequenced in *P. taeda* were all expressional candidates for abiotic stress response, disease resistance and wood formation.

Successfully transferred genes include, for instance, a glutathione S-transferase that is induced under cold temperatures or different peroxidases (that are involved in the response to oxidative stress after desiccation).

Once the full CRIEC dataset is gathered, sequences will be processed by automatic pipelines (PineSAP, UC Davis; SeqQual, INRA-Bordeaux), a sample of polymorphisms will be visually validated (to ensure correct automatic pipeline performance) and all sequence and SNP data will be made available through public databases, such as GenBank or EvoTree eLab databases.

Apart from SNP discovery in non-model conifer species, CRIEC will make available a large candidate gene set across several conifer species with contrasting life- and evolutionary- histories, opening the opportunity for extensive comparative studies at the DNA sequence level.

D. SPREADING OF EXCELLENCE ACTIVITIES

Use of DNA-fingerprints to control the origin of forest reproductive material for oak stands

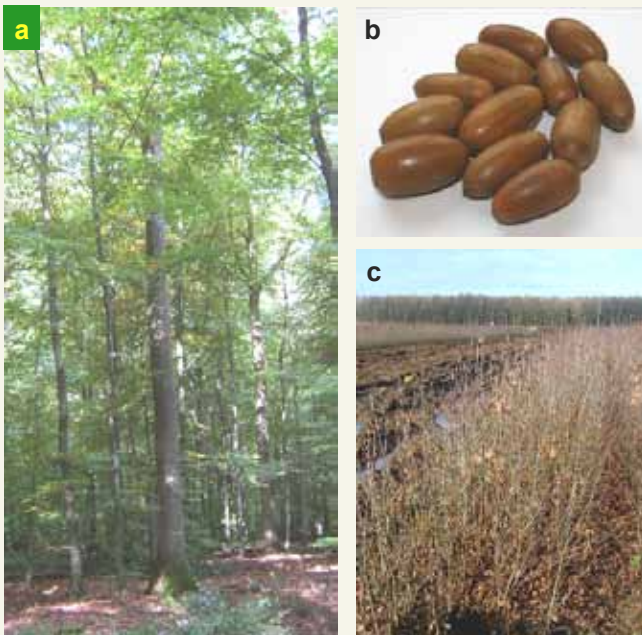
by Bernd Degen and Aki Höltken



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AKI HÖLTKEN is forest scientist with focus on molecular genetics of forest trees (reproductive material, tropical timber tracking, genetic barcoding). He is managing the company 'Plant Genetic Diagnostics' at the Johann Heinrich von Thünen Institute (vTI), Germany.



Efficient tools to control the origin of forest reproductive material all along the chain-of-custody are important; a. registered pedunculate oak seed stand in Germany, b. collected seeds, and c. oak saplings in the nursery (Photo: by Johann-Heinrich von Thünen Institute)

Well-adapted, high quality reproductive material is key to the success of forest plantations. Thus, the collection and trade of forest reproductive material is regulated in many countries by certification to promote the use of reproductive material of known origin and genetic quality for consumer protection, and the use of material appropriate to a given region.

More economic and efficient tools for the identification of the origin of reproductive material are needed to comply with these regulations. These regulations include, among others, the Organisation for Economic Co-operation and Development's (OECD) Scheme for the Certification of Forest Reproductive Material at the international level, and the Council Directive 1999/105/EC for the European Union. Certification schemes already established in Germany use genetic inventories to compare reference samples collected at different steps of the chain of custody.

In the frame of the work-package SEA 3 "Technology Transfer" we successfully conducted a feasibility study for a new approach using DNA-fingerprints that efficiently controls the origin of seed sources without these reference samples. Only a sample of adult trees within the seed stand is needed. The control is directly made for each suspicious plant or a group of suspicious plants by use of multilocus genotype assignment.

In co-operation with the Forest Service of the state North-Rhine-Westphalia (NRW) we made a field test with

samples of adults and seedlings from 5 registered seed stands of *Quercus robur* in Western Germany. A total of 8 highly variable nuclear microsatellites were used to genotype each individual. In 4 out of 5 cases the group of seedlings were assigned with a score > 0.95 . In all these cases the seedlings were assigned to the correct adult population. Furthermore, we used simulations to create a baseline population of *Quercus petraea* in a 50km x 50 km landscape. The objectives of the simulations were to analyse the impact of (a) number of sampled individuals, (b) number of gene loci, (c) extent of missing or incomplete data and (f) the influence of errors in genotyping on the accuracy of assignment of individuals and groups of individuals to the correct adult population.

The group-wise assignment was robust against low sample sizes, missing data, and errors in genotyping. When group samples included at least 4 individuals and 8 loci, the proportion of correctly assigned groups was greater than 93%.

The conclusion of the field study and the simulations is that a large scale application of this new approach to control the origin of forest reproductive material is feasible. As a visible output of the "Technology Transfer" work-package, the company "Plant Genetic Diagnostics" of Aki Höltnen was created as a research spin-off of the von Thünen Institute (vTI) in Grosshansdorf. Now the company is working on expanding the adoption of the new control system to registered oak stands in NRW.

The **evoltree** mobility program

The mobility program is one of the **evoltree** projects with little visibility but potentially strong impact on the future of the forest ecology scientific community in Europe. In the framework of this program each member of the NoE had a chance to apply for a mobility grant that would fund visits to other **evoltree** partners. Over the last 3 years more than 60 scientists visited an **evoltree** partner for a period between 1 week and 6 months. The incentives ranged from training PhD students, to setting up new research strategies and programs, to implementing actual experiments jointly.

Interview with Jennifer DeGoody

To highlight the positive aspects of this program we interviewed Jennifer DeGoody, a successful applicant to the mobility grant. Jennifer DeWoody is a PhD student in the Plants and Environment Lab at Southampton University, headed by Prof. Gail Taylor. Her **evoltree** mobility grant helped her fund a 4 week stay at the INRA lab in Bordeaux.

NewsletterTeam: *Jennifer, what is the subject of your PhD project?*



JENNIFER DEGOODY is a PhD student in the Plants and Environment Lab at Southampton University. She works on the evolution of leaf size as an indicator for water use efficiency.

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DeWoody: I am currently working on my PhD with Professor Gail Taylor, studying the evolution of leaf size in *Populus nigra* (black poplar) as a trait indicative of water use efficiency and drought tolerance. To this end I will be looking at sequence differences between genes involved in cell and leaf development, as well as putatively neutral markers to assess the evolutionary history of the populations. By comparing the historic population dynamics, current environmental conditions, phenotypic differences, and genetic variation, I hope to elucidate the mechanisms underlying leaf traits in this variable and valuable forest species.

NewsletterTeam: *What were the objectives of your 4 weeks at INRA Bordeaux?*

DeWoody: The primary objective of the mobility proposal was to understand how genetic differentiation at neutral markers and QTL underlying adaptive traits will vary in response to changing selective optima (e.g. a changing climate), in particular for *Populus* species. The program Metapop, developed and maintained by INRA, is used to simulate the genetic structure and adaptive response of populations of forest trees, allowing different scenarios (parameter sets representing different evolutionary pressures) to be tested.

NewsletterTeam: *How did your visit go?*

DeWoody: First, before building models to simulate the demographic patterns observed in *Populus*, I worked on simple scenarios in order to learn how to use the Metapop program and build appropriate parameter sets. This initial training was necessary to insure I understood the numerous parameters available in this program. Second, as the version of the Metapop I used was recently created by merging two different simulation programs, I tested the new program for simple scenarios versus analytical predictions. This work closely mirrored the scenarios I used to learn the program, but also provided an opportunity for the developers of this program (F. Raspail and P. Garnier-Géré) to better test some example files for initial users in response to the requests of this project.

Finally, I tried to find a parameter set (scenario) for the Metapop program that will simulate a dioecious plant or animal species, if possible. As the program was designed for forest trees which typically have perfect flowers or are monoecious, the program is not strictly appropriate for modelling dioecious species. The program allows users to define a number of demographic parameters (male and female fecundity, age classes, survival, etc), and this flexibility may enable a dioecy-like scenario to be developed, and the effects of dioecy on population structure, compared to monoecious forest species, explored. In addition, the ability to simulate dioecy will increase the number of questions and model systems available for analysis.

Newsletter Team: *How does that relate to your work on *Populus nigra*?*

DeWoody: These test scenarios will serve as the basis for future work building more complex models, with the ultimate goal of simulating the genetic and phenotypic differentiation in *Populus nigra*.

Newsletter Team: *Was your experience useful?*

DeWoody: Indeed! Learning how to test the basic functioning of a simulation program, build a complex model using available biological information (e.g. generation times and QTL characteristics), and interpreting the results represent the major gains I obtained from the mobility scheme.

Newsletter Team: *Do you think that the hosting group profited as well from your stay?*

DeWoody: I was able to provide some recommendations for the improvement of the user documentation to the software Metapop. This software and the documentation are available via the [evoltree](#) management platform website (IA1.4).

The [evoltree](#) Stakeholder Group visit the common DNA Repository Centre

by Barbara Vinceti



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A Second Stakeholder Group meeting of the [evoltree](#) Network of Excellence has taken place in Eisenstadt, Austria on 16-17 September 2009. The meeting was well

attended and was aimed at continuing the involvement of **evoltree** stakeholders in the activities of the Network, to ensure that research findings influence policies and contribute to sustainable use of forests and their biodiversity.

The workshop illustrated to non-specialists the most recent scientific findings related to how forest ecosystems respond to major environmental changes. The presentations stimulated a discussion with the Stakeholders on possible actions to support sustainable use and conservation of forest resources based on the most advanced scientific understanding.

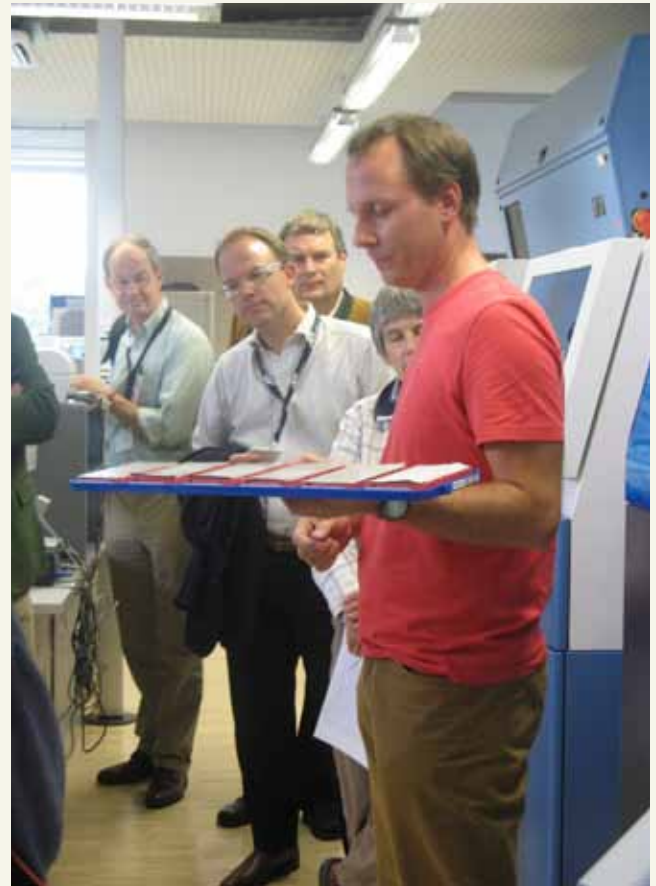
The various ongoing European research frameworks and initiatives related to different aspects of intraspecific diversity of trees were presented to illustrate their different focus and complementarities. In particular, speakers representing the following European projects and initiatives were invited to deliver presentations: TREEBREEDEX, NovelTree, EUFORGEN, EUFGIS, COST Action E52 on the "Evaluation of Beech Genetic Resources for Sustainable Forestry".

Furthermore, a visit was organized to the common DNA repository centre, established within the **evoltree** framework at the Austrian Institute of Technology (AIT) in Seibersdorf, as a common infrastructure of the Network. Silvia Fluch, AIT staff and **evoltree** partner, welcomed the visitors and gave a presentation on the hosting research center and on the common DNA repository.

This was followed by an illustration by Dieter Kopecky of the e-Lab, another joint effort and permanent common infrastructure set up within the framework of **evoltree**.

The e-Lab (<http://www.evoltree.org/index.php/elab>) is a virtual laboratory through which a series of distributed databases, maintained by **evoltree** partners, are accessible and can be queried. In this way, the e-Lab allows to perform a simultaneous search inside all the databases currently shared by partner institutions within the **evoltree** project. Access to the e-Lab is currently restricted to **evoltree** partners, but should be soon opened to the larger scientific community.

Moreover, invited scientists from **evoltree** presented a series of 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 topics covered were: the movement of forest reproductive material: a strategy to cope with climate change (by Reiner Finkeldey, University of Göttingen,



Stakeholders visit the common DNA repository center in Seibersdorf (Austria) (Photo by B.Vinceti)

Germany); examples of practical applications of tree genetic and genomic research: incorporating genomic insight into forest management, screening for drought resistance (by Bruno Fady, INRA, France); molecular tools for certification of plant material (by Giovanni Giuseppe Vendramin, CNR, Italy); and application of modelling approaches to anticipate future scenarios with regard to European forests (speaker: Koen Kramer, Alterra, The Netherlands).

Two points in particular were presented to the attention of the Stakeholders to seek their feedback: i) the preparation of policy briefs or information notes on scientific findings of relevance to the Stakeholders, derived from **evoltree** and associated initiatives; and ii) the organization of the last Stakeholder Group meeting in occasion of the final **evoltree** scientific conference, to be held in San Lorenzo del Escorial, near Madrid, on 9-11 June 2010. Participants agreed that more policy-makers should be involved in the process of discussion with scientists, but that this is a challenging tasks. It was also observed that the Stakeholders whom **evoltree** is trying to reach belong to distinct groups (policy-makers and forest practitioners) and the messages should be diversified to meet different needs or action should be



Staff of the Austrian Institute of Technology (AIT) explain to the Stakeholders the functioning of the common DNA repository centre. (Photo: by B. Vinceti)

taken to address primarily policy-makers, who would themselves influence other categories of stakeholders.

It was also noted that final recipients of the policy briefs should not be overwhelmed by information and a common agreement was reached on a series of simple messages to be communicated to policy-makers with regard to forest genetic and genomic resources. The topics proposed for the policy briefs were reviewed in light of a strategic approach.

The messages to be disseminated should focus on highlighting the consequences of unadapted management practices (in terms of job losses, economic value lost), and on communicating a sense of what the chances of success will be in fostering adaptation by looking at tree genetics and genomics. However, also simple, basic concepts should be flagged to the attention of a wide audience, such as the idea that genetic diversity is fundamental for adaptation to environmental changes.

Finally, the Stakeholders provided some preliminary ideas on how to organize the final Stakeholders' event to be held in conjunction with the [evoltree](#) final scientific conference.

E. OUTPUTS OF MEETINGS AND TRAINING

Training course on DNA sequence analysis and association genetics, Valsaín (Spain) 13-17th July, 2009

Santiago C. González-Martínez & Ricardo Alía (CIFOR-INIA).

In July 2009, a workshop on DNA sequence analysis and genetic association took place in Valsaín, Segovia. The course was attended by 30 participants from Poland, Germany, Turkey, France, Italy, Switzerland, Finland,

Austria, Spain and Argentina. The venue was situated in the facilities of the Spanish Ministry of Environment that are located within one of the best known national forests of Spain: the Valsaín forest. This is a notable example of a forest with multiple functions, from hosting some of the very scarce endangered Iberian eagles (*Aquila adalberti*) to the production of one of the best-quality Spanish saw wood (from Scots pine). Valsaín is also close to the historical town of Segovia, a few kilometers away from La Granja palace, used as a summer residence by the Kings of Spain.

The course was organized in three modules and counted lecturers from CIFOR-INIA, INRA-Bordeaux & Univ. Zaragoza. The first module (given by Dr. Santiago C. González-Martínez and Dra. Delphine Grivet) was devoted to candidate gene analyses, including nucleotide diversity estimates, linkage disequilibrium, recombination, demographical model fitting (based on coalescence simulations and summary statistics) and neutrality tests (including new-generation ones, such as the compound tests). The second module (given by Dra. Pauline Garnier-Géré) was related to population genomics approaches, in particular to methods for outlier loci detection that are becoming popular in forest trees.

Finally, the third module (given by Dr. Ricardo Alía and Dr. Santiago C. González-Martínez) focused on quantitative genetics, including lectures on analysis of common garden experiments (experimental design, BLUPs) and association genetics. With respect to the latter, all of us enjoyed a very educative invited lecture on the use of Bayesian approaches for association genetics by Dr. Luis Varona, Prof. of Animal Breeding at the University of Zaragoza.

Most interesting of all, however, was that participants contributed to the workshop by presenting their research projects and goals, which raised discussions and valuable insights.



An image of the Valsaín forest (Photo: by H. Lalagüe)

But not all was science in this meeting, we had also a (very large) sample of local (and meaty, to the despair of the vegetarian participants) food that culminated with a traditional roasted pigling banquet at Segovia, a UNESCO World Heritage town and a worldwide recognized source of high cholesterol. We had also time for interaction and discussions between participants and teachers and among participants themselves, early morning jogging and a nice walk in the forest (where the organization got everybody lost but not too badly) and, as it could not be otherwise in summer in Spanish mountains, we suffered heat during the first days of the course and froze during the last ones. All in all a very enjoyable event!



Traditional farewell dinner in Segovia. (Photo: by S. Gonzalez-Martinez)

Evoltree at XIII World World Forest Congress, Buenos Aires, Argentina, 18-23 October 2009

by Barbara Vinceti

During the XIII World Forestry Congress held in Buenos Aires, Argentina, 18-23 October 2009, within a congress session that covered tree genetic diversity, Antoine Kremer gave a presentation on the [evoltree](#) Network of Excellence.

The first World Forestry Congress was held in Rome in 1926 and has generally taken place every six years since then. These events constitute an opportunity for governments, universities, civil society and the private sector to exchange views and experiences and to formulate recommendations for implementation at national, regional and global levels. The last edition of the Congress was very well attended, with more than 7,000 participants from 160 countries.

In the final declaration of the World Forestry Congress (http://foris.fao.org/meetings/download/_2009/xiii_th_world_forestry_congress/misc_documents/wfc_declaration.pdf), considerable emphasis was placed on the threats posed by climate change on forests, on the goods and services they provide, as well as the potential



Antoine Kremer, [evoltree](#) coordinator, at the World Forestry Congress, held in Argentina, in October 2009 (Photo: by B.Vinceti)

of forests in climate change adaptation and mitigation. However, the role of genetic resources was not mentioned in this official statement although their importance is self-evident.

Genetic diversity is the foundation for adaptation of natural forests to climate change and is also the resource basis for the selection of adapted forest reproductive material to establish planted forests and agroforestry systems. Despite this, intra-specific diversity of tree species is a dimension of forest biodiversity that is often neglected and there seems to be a lot of work to be invested in trying to raise awareness.

E. FORTHCOMING EVENTS AND ANNOUNCEMENTS

Evoltree Forest ecosystem genomics and adaptation, 9-11 June 2010, Spain

Preparations are underway for the final scientific conference of the [evoltree](#) Network of Excellence. The event will focus on forest ecosystem genomics and adaptation and will take place on 9-11 June 2010, in San Lorenzo de El Escorial (Madrid), Spain.

The conference will present the main research findings generated by [evoltree](#), but the event is also open to the scientific community outside the Network of Excellence. In addition, a Stakeholders' event is planned during the conference, aimed at engaging policy makers, practitioners and scientists in a discussion on how to incorporate the research findings into sustainable forest

management. The programme of the conference is structured around the following main scientific themes:

- o Phenomics under climate change;
- o Population genomics of adaptive traits;
- o Evolutionary responses to environmental change;
- o Community responses to environmental change;
- o Migration under climate change;
- o Eco-regional trends in adaptation;
- o New technologies in ecosystem genomics;
- o Climate change mitigation options.



The Royal Monastery of San Lorenzo de El Escorial (Madrid), Spain.
(Photo: by B. Vinceti)

A

series of high profile speakers from *evoltree*, as well as from outside the Network of Excellence, have confirmed their contribution:

- o **Prof. Robert Watson** - Defra Chief Scientific Adviser (United Kingdom);
- o **Prof. Graham Bell** – McGill University, Montreal (Canada);
- o **Prof. Christopher G. Eckert** – Department of Biology, Queen's University, Kingston, Ontario (Canada);
- o **Dr. Jessica J. Hellmann** - Assistant Professor of Biological Sciences, University of Notre Dame, Indiana (USA);
- o **Dr. Olivier Jaillon** - Genoscope, Evry (France);
- o **Prof. Stefan Jansson** – Umeå Plant Science Centre, University of Umeå (Sweden);
- o **Dr. Konstantin Krutovsky** - Associate Professor, Department of Ecosystem Science & Management, Texas A&M University, Texas (USA);
- o **Dr. Magnus Nordborg** - Scientific Director, Gregor Mendel Institute (GMI) of molecular plant biology (GMI in Vienna, Austria, and the University of Southern California, Los Angeles, USA);
- o **Dr. Thomas G. Whitham** - Executive Director, Merriam-Powell Center for Environmental Research, Northern Arizona University and (USA).

For more information, please refer to the conference website: www.ecosystemgenomics2010.fgua.es

Submission of abstracts: 15.02.2010,
Early registration - conference (only): 15.03.2010,
Joint registration (evoltree annual meeting and conference): 15.03.2010,
Closing of registrations: 10.05.2010

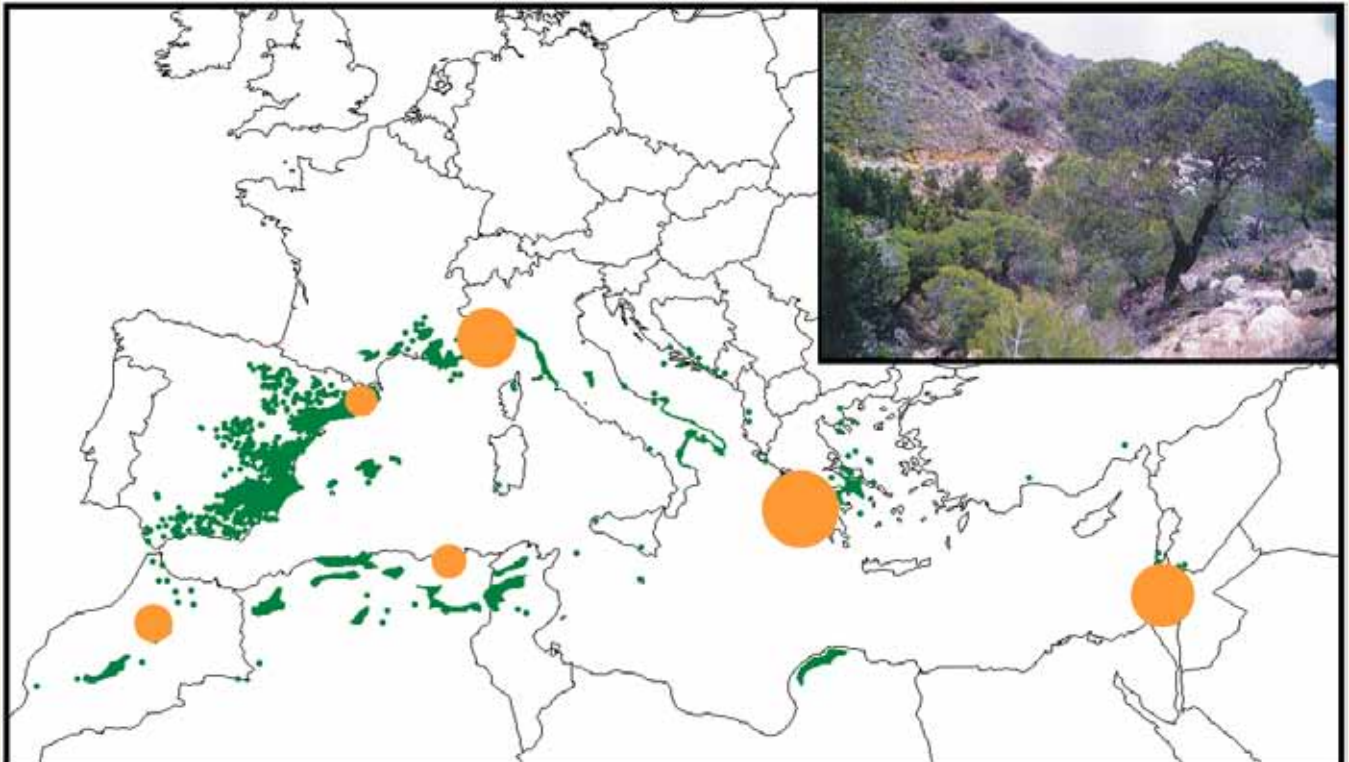
E. PUBLICATIONS AND OTHER PRODUCTS

Grivet D., Sebastiani F., González-Martínez S.C., Vendramin G.G. (2009): Patterns of polymorphism resulting from long-range colonization in the Mediterranean conifer Aleppo pine. *New Phytologist*, in press.

ABSTRACT: Aleppo pine (*Pinus halepensis*) is a species with scattered distribution across the Mediterranean Basin, which populations can grow and survive a broad set of climatic conditions (see map in the next page). One central evolutionary question is: how has this species adapted to such environmental constraints and more especially to drought? Aleppo pine is well adapted to drought but this factor can constitute an important threat to individual growth and survival at all life stages. In the present study we examine, in six populations covering the species range, the variation of four neutral markers and ten candidate genes associated with traits related to stress tolerance, with two main objectives: i) infer the demographic history of this species, and ii) look for signatures of selection in candidate genes related to drought tolerance. Our results show that during the Last Glacial Maximum (25,000-18,000 yr BP) Aleppo pine populations went through intense bottlenecks that reduced the level of genetic diversity of populations away from eastern refugia, and that natural selection most likely acted on some genes linked to drought tolerance within populations confronted to new environments following long-range colonization. This knowledge is of crucial importance for the conservation and management of forests in the face of climate change in the Mediterranean Basin.

Heuertz M., Teufel J., González-Martínez, S.J., Soto A. Fady B., Alía R., Vendramin G.G. (2009): Geography determines genetic relationships between species of mountain pine (*Pinus mugo* complex) in western Europe

ABSTRACT: This paper uses chloroplast DNA microsatellites to examine the genetic structure of the *Pinus mugo* complex in western Europe. It concerns *Pinus uncinata* from the Pyrenees, the western Alps, and from marginal Iberian populations, *P. mugo* from the Alps, and bog-affected populations classified as *P. rotundata* or *P. x pseudopumilio* from the Vosges, Jura



Distribution map of *Pinus halepensis* (source: EUFORGEN, Bioversity International) along with the average nucleotide diversity of candidate genes (the size of the circles is proportional to the level of diversity).

and Black Forest. The main determinant of genetic structure in the complex is geography, not taxonomy. Different gene pools were found in the Pyrenees and in the Alps, and in particular, *P. uncinata* from the Alps are genetically closer to *P. mugo* than to *P. uncinata* from the Pyrenees. This pattern is probably due to postglacial colonisation of each mountain chain from a separate series of glacial refugia. It suggests that different growth forms (single stemmed *P. uncinata*, multistemmed *P. mugo*) and probably ecological adaptations evolved in different parts of the distribution range of the complex and were maintained despite the existence of extensive gene flow. Global warming represents a serious threat to marginal *P. uncinata* populations: sufficient elevations for upslope migration are not available in low Iberian mountains. Those populations represent distinct gene pools, so that their loss may reduce the adaptive potential of the species. Bog-affected populations of the complex are strongly differentiated from one another and have very different levels of diversity, suggesting that they were colonised from multiple glacial refugia located north of the Pyrenees and Alps, and that some of them experienced low population sizes.

Buée M., Reich M., Murat C., Morin E., Nilssen R.H., Uroz S., Martin M. (2009): 454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. *New Phytologist* 184: 449-456.

ABSTRACT: Soil fungi play a major role in ecological and biogeochemical processes in forests. Little is known, however, about the structure and richness of different fungal communities and the distribution of functional ecological groups (pathogens,

saprobies and symbionts).

Here, we assessed the fungal diversity in six different forest soils using tagencoded 454 pyrosequencing of the nuclear ribosomal internal transcribed spacer-1 (ITS-1). No less than 166 350 ITS reads were obtained from all samples. In each forest soil sample (4 g), approximately 30 000 reads were recovered, corresponding to around 1000 molecular operational taxonomic units. Most operational taxonomic units (81%) belonged to the Dikarya subkingdom (Ascomycota and Basidiomycota). Richness, abundance and taxonomic analyses identified the Agaricomycetes as the dominant fungal class. The ITS-1 sequences (73%) analysed corresponded to only 26 taxa. The most abundant operational taxonomic units showed the highest sequence similarity to *Ceratobasidium* sp., *Cryptococcus podzolicus*, *Lactarius* sp. and *Scleroderma* sp. This study validates the effectiveness of high-throughput 454 sequencing technology for the survey of soil fungal diversity. The large proportion of unidentified sequences, however, calls for curated sequence databases. The use of pyrosequencing on soil samples will accelerate the study of the spatiotemporal dynamics of fungal communities in forest ecosystems.

Jump A.S., Matyas C., Penuelas J. (2009) The altitude-for-latitude disparity in the range retractions of woody species. *Trends in Ecology and Evolution* 24 (12): 697-701.

ABSTRACT: Increasing temperatures are driving rapid upward range shifts of species in mountains. An altitudinal range retreat of 10 m is predicted to translate into a 10-km latitudinal retreat based on the rate at which temperatures decline with

increasing altitude and latitude, yet reports of latitudinal range retractions are sparse. Here, we examine potential climatic, biological, anthropogenic and methodological explanations for this disparity. We argue that the lack of reported latitudinal range retractions stems more from a lack of research effort, compounded by methodological difficulties, rather than from their absence. Given the predicted negative impacts of increasing temperatures on wide areas of the latitudinal distributions of species, the investigation of range retractions should become a priority in biogeographical research.

Ramirez-Valiente J. A., Lorenzo Z., Soto A., Valladares F., Gil L., Aranda I. (2009) Elucidating the role of genetic drift and natural selection in cork oak differentiation regarding drought tolerance. *Molecular Ecology* 18 (18): 3803-3815.

ABSTRACT: Drought is the main selection agent in Mediterranean ecosystems and it has been suggested as an important evolutionary force responsible for population diversification in these types of environments. However, population divergence in quantitative traits can be driven by either natural selection, genetic drift or both. To investigate the roles of these forces on among-population divergence in ecophysiological traits related to drought tolerance (carbon isotope discrimination, specific leaf area, leaf size and leaf nitrogen content), we compared molecular and quantitative genetic differentiation in a common garden experiment including thirteen cork oak (*Quercus suber* L.) populations across a gradient of rainfall and temperature. Population differentiation for height, specific leaf area, leaf size and nitrogen leaf content measured during a dry year far exceeded the molecular differentiation measured

by six nuclear microsatellites. Populations from dry-cool sites showed the lowest nitrogen leaf content and the smallest and thickest leaves contrasting with those from humid-warm sites. These results suggest (i) these traits are subjected to divergence selection and (ii) the genetic differences among populations are partly due to climate adaptation. By contrast, the low among-population divergence found in basal diameter, annual growth and carbon isotopic discrimination (a surrogate for water use efficiency) suggests low or no divergence selection for these traits. Among-population differentiation for neutral markers was not a good predictor for differentiation regarding the quantitative traits studied here, except for leaf size. The correlation observed between the genetic differentiation for leaf size and that for molecular markers was exclusively due to the association between leaf size and the microsatellite QpZAG46, which suggests a possible linkage between QpZAG46 and genes encoding for leaf size.

Chen J., Källman T., Gyllenstrand N., Lascoux M. (2009): New insights on the speciation history and nucleotide diversity of three boreal spruce species and a Tertiary relict. *Heredity*: In press.

ABSTRACT: In all, 10 nuclear loci were re-sequenced in four spruce species. Three of the species are boreal species with very large natural ranges: *Picea mariana* and *P. glauca* are North American, and *P. abies*, is Eurasian. The fourth species, *P. breweriana*, is a Tertiary relict from Northern California, with a very small natural range. Although the boreal species population sizes have fluctuated through the Ice Ages, *P. breweriana* is believed to have had a rather stable population size through the Quaternary. Indeed, the average Tajima's D was close to zero in this species and negative in the three boreal ones. Reflecting differences in current population sizes, nucleotide diversity was an order of magnitude lower in *P. breweriana* than in the boreal species. This is in contrast to the similar and high levels of heterozygosity observed in previous studies at allozyme loci across species. As the species have very different histories and effective population sizes, selection at allozyme loci rather than demography appears to be a better explanation for this discrepancy. Parameters of Isolation-with-Migration (IM) models were also estimated for pairs of species. Shared polymorphisms were extensive and fixed polymorphisms few. Divergence times were much shorter than those previously reported. There was also evidence of historical gene flow between *P. abies* and *P. glauca*. The latter was more closely related to *P. abies* than to its sympatric relative *P. mariana*. This last result suggests that North American and Eurasian species might have been geographically much closer in the recent past than they are today.



Picea abies on the Rachel Mountain in Bavaria Forest National Park. (Photo: by L. Opgenoorth)

evoltree

GLOSSARY

candidate genes: A candidate gene is a gene, located in a chromosome region suspected of being involved in the expression of a trait such as a disease, whose protein product suggests that it could be the gene in question. A candidate gene can also be identified by association with the phenotype and by linkage analysis to a region of the genome.

cDNA: Complementary DNA: DNA synthesized from a => mRNA template in a reaction catalyzed by the enzyme => reverse transcriptase. cDNA therefore comprises functional DNA regions (eukaryotes: exons and introns, prokaryotes: exons) which are expressed at a special physiological state. Continuous cDNA fragments are called => ESTs

chloroplast: A major component of a plastid in green plants and eukaryotic algae of any colour. It is involved in photosynthesis. Prokaryotic photosynthetic organisms do not have chloroplasts. Due to prokaryotic ancestors (=> endosymbiotic theory), chloroplasts exhibit their own DNA material, which is used for population genetics.

conifers: Cone bearing trees. This is a class of the Gymnospermae which includes needle-leaved trees such as pines and cypresses. Their flowers are in cones, and male and female cones are separate. The oldest (bristlecone pine) and the largest (sequoia) extant organisms belong to this Class. Their unique feature is the inheritance of cytoplasmic DNA (chloroplasts) via pollens.

cpDNA: chloroplast DNA, see => Chloroplast

demography: The statistical study of populations with respect to size, density, and distribution.

DNA sequence: DNA sequencing is the process of determining the nucleotide order of a given DNA fragment.

gene flow: The movement of genes within a population or among populations following genetic admixture. Gene flow creates new combinations of genes or alleles in individuals that can be tested against the environment. This way it is one of the sources of variation in the process of natural selection.

genetic diversity: Genetic diversity is a level of biodiversity that refers to the total number of genetic characteristics in the genetic makeup of a species.

genotype: The genetic characteristic of an organism that can not be seen (<-> phenotype).

genotyping: The process of determining the Genotype of an organism/Individual.

heterozygote: A diploid organism showing different alleles at one locus.

holocene: The geological epoch from 11,700 yrs until today.

homozygote: A diploid organism showing two identical alleles at one locus.

hybridization: Hybridization is the process of combining different varieties or species of organisms to create a hybrid.

ITS: Internal transcribed spacer. Ribosomal DNA spacer region, frequently used for molecular species identification.

ISS: Intensive Study Sites. Large scale ecosystem plots, where trees and selected associated species are mapped, genotyped and phenotyped

JERA: Jointly executed research activities

JSP: Joint Scientific Project

microsatellite markers: Microsatellites, or => Simple Sequence Repeats (SSRs), are polymorphic loci present in nuclear and organellar DNA that consist of repeating units of 1-6 base pairs in length. They are typically neutral, co-dominant and are used as molecular markers which have wide-ranging genetic applications (e.g. population genetics).

mitochondria: A cell organelle in eukaryotic cells, supplying cellular energy, therefore involved in signalling, cellular differentiation and growth, cell cycle and cell death. Due to prokaryotic ancestors (=> endosymbiotic theory), mitochondria exhibit their own DNA material, which is used for population genetics.

Palaeoecology: a scientific branch of ecology focussing on

ancient environments, plants and animals.

phenotype: The visible or measurable (i.e., expressed) characteristics of an organism (see => genotype).

phenotyping: The process of determining the Phenotype of an organism/Individual.

physiology: A discipline of science which studies mechanical, physical, and biochemical functions of living organisms.

pyrosequencing: A new technique used to sequence DNA using chemiluminescent enzymatic reactions. Here, DNA strands are sequenced and then synthesized enzymatically (the complementary strand).

quantitative traits: ecological characters of species (or other taxa) that can be quantified, e.g. number of seeds, spores or biomass.

RNA: Ribonucleic acid. A molecule with a long chain of nucleotides. Similar to DNA but with the base uracil rather than thymine. RNA is central to the synthesis of proteins.

sequencing: DNA sequencing is the process of determining the nucleotide order of a given DNA fragment.

SNP: Single nucleotide polymorphism: DNA sequence variation occurring when a single nucleotide (A, T, C or G) of a shared sequence differs between individuals (of one or different species).

SSR: Simple Sequence Repeat, see => Microsatellite marker

sympatric: When two different plant or animal species occur in the same region, they are sympatric <-> allopatric.

evoltree PARTNERS

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
- Bioversity 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 Paul Cézanne - Aix-Marseille III, France
- Forest Research Institute (IBL), Poland
- Institute of Dendrology (IDPAN), Poland
- The Finnish Forest Research Institute (METLA), Finland
- Forest Research Institute (ERTI), Hungary

EVOLTREE ACTIVITIES

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



Bioversity International is associated with **evoltree** and responsible for its dissemination activities. Contact: Dr. Barbara Vinceti, Bioversity International, Rome, Italy.
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