Some research approaches in forest genetics resulting from the EVOLTREE network (NoE)

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EVOlution of TREEs as drivers of terrestrial biodiversity

EVOLtRREE

Area III: Biodiversity and ecosystems
Topic III.1: Assessing and forecasting changes in biodiversity, structure, function and dynamics of ecosystems and their services with emphasis on marine ecosystems functioning
Sub-topic III.1.2: Genomics for terrestrial biodiversity and ecosystem research
Call identifier: FP6-2002-Global-3
Type of instrument: Network of Excellence
Co-ordinator organisation: Institut national de la recherche agronomique (INRA)
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EVOLTREE: linking disciplines

Response and adaptation to global change

Dynamics of biodiversity

Genomics  Evolution

Ecology  Genetics

Management and conservation of populations

Ecosystems processes
EVOLTREE: major objectives

• Contribute to understanding adaptive diversity in trees and associated organisms (mycorrhizal fungi and insects)

• Assemble and integrate the complementary disciplines in the field of ecological genetics and genomics (ecosystem genomics)

• Establish and implement a European research platform in this field in the form of “laboratory without walls”

• Install common infrastructures (repository centre), field experimental sites, data management systems

• Spread a high level excellence to the scientific community, end-users and to the public
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Activities

IA 1 - Laboratory without Walls for Ecosystem Genomics
IA 2 - Common infrastructures
IA 3 - Network harmonisation, consolidation, and perpetuation
IA 4 - Human resource exchange
JERA 1 - Ecological genomics
JERA 2 - Genomic diversity in natural populations
JERA 3 - Community structure and dynamics
JERA 4 - Dynamics of biodiversity and evolution of populations
MA 1 - Network strategy
MA 2 - Programme monitoring
MA 3 - Consortium management
SEA 1 - Training and Education
SEA 2 - Dissemination
SEA 3 - Technology transfer
SEA 4 - International cooperation / cross-linking
Integrating activities

**IA1:** Establishment of the Evoltree’s **Laboratory without Walls for Ecosystem Genomics** which mission is to assemble genomics know-how and toolkits, integrate bioinformatics resources and tools, develop common genomic resources and create an informative modelling platform.

**IA2:** Installation of **common infrastructures** (repository centres, intensive study sites, gene banks, experimental infrastructures).

**IA3:** **Harmonisation** of the partners’ research programmes in order to avoid overlaps and address uncovered issues and **durability of the Network** trough search of alternative funding sources and set up of legal status for the Network.

**IA4:** **Human exchange** within the network by providing information, practical assistance, and financial means, to candidates to mobility within the Network.
Jointly executed research activities

JERA1 – Ecological Genomics, which will identify in trees and associated species (insects and mycorrhizal fungi) the genes that are involved in their response to biotic and/or abiotic selective pressures caused by global change.

JERA2 – Genomic diversity in natural populations is to assess the level and geographic distribution of genomic diversity in the genes identified in JERA1, in all three groups of species (trees, insects and mycorrhizal fungi).

JERA3 – Community structure dynamics has as main objective to elucidate the relationships between the genetic diversity of trees and the biodiversity of associated organisms across space and time and ultimately its effect on ecosystem processes.

JERA4 – In Dynamics of biodiversity and evolution of populations, Evoltree will evaluate the effects of far-reaching environmental change on the future dynamics and adaptability of tree populations starting from evaluation of the role they had in the past on evolutionary processes and patterns of genetic variation.
Management activities

The overall objective of the management activities is to provide the suited framework needed for the optimum achievement of activities.

MA1 – Network strategy is designed to maintain the relevance of the Network’s programme of activities as knowledge increases, techniques evolve and socio-economic environment changes.

MA2 – Project monitoring is aimed at ensuring the progress of the Network’s programme in conformity with what has been planned in terms of results, agenda as well as spent resources by designing, developing, and implementing tools such as the indicators of performance, the balanced scorecards, the quality plan, the risk management plan, the use and exploitation plan, the collaborative working platform, etc.

MA3 – Consortium coordination is dedicated to all logistic, administrative, and financial tasks needed to ensure optimum exchange within the consortium and between the consortium and the EC, and appropriate fulfilment of the EC Contract and the Consortium Agreement from the legal and financial points of view.
Spreading excellence activities

**SEA1 – Training and education**, is aimed on the one hand at providing the Network of excellence with necessary skilled personnel to carry out the jointly executed research activities, on the other hand at training future researchers and experts in ecosystem genomics.

**SEA2 – Dissemination** is dedicated to communication with the scientific community, relevant stakeholders and the general public, and includes organization of the Evoltree biannual conference on ecosystem genomics, etc.

**SEA3 – Technology transfer** is dedicated to the protection of knowledge resulting from the project, the identification of opportunities of exploitation, pre-marketing development if any, and commercialization.

**SEA4 – International cooperation** aimed at cross-linking with other EU programs, collaboration with international initiatives in tree genomics and population genetics and with INCO target countries.
Activities 2006:


Genetic variation patterns and sustainable management of genetic resources of Eurasian conifers (poster).

European Forest-Based Sector Technology Platform (FTP) 3rd Conference: Speed up innovation in the Forest Based Sector. Lahti, Finland, November 22-23, 2006
Genetic variation patterns and sustainable management of genetic resources of Eurasian conifers

**Project Coordinator (Europe):** Dr. Giovanni Vendramin, Plant Genetics Institute, National Research Council, Florence, Italy

**Project Co-Coordinator (Russia):** Dr. Dmitri V. Politov, Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia, Email: dvp@vigg.ru

**RESEARCH CONSORTIUM:**
- **European Union:**
  - Plant Genetics Institute, National Research Council, Florence, Italy (Dr. Giovanni Vendramin)
  - Swiss Federal Research Institute WSL, Birmensdorf, Switzerland (Dr. Felix Guggeri)
  - Institute of Forest Genetics and Forest Tree Breeding, Georg-August University of Göttingen, Germany (Dr. Rainer Finkoldey)
  - INRA, Bordeaux, France (Dr. Remy Petit)
  - Faculty of Forestry, Technical University, Zvolen, Slovakia (Prof. Ladislav Paule)

- **Russia:**
  - Vavilov Institute of General Genetics, Moscow, Russia (Dr. Dmitri V. Politov)
  - Institute for Monitoring of Climatic and Ecological Systems, Russian Academy of Sciences, Siberian Branch, Tomsk (Dr. Sergey N. Goroshkevich)
  - Department of Genetics, Biological Faculty, Moscow State University (Prof. Sergey V. Shushakov)
  - Institute of Biological and Soil Science, Russian Academy of Sciences, Far Eastern Branch, Vladivostok (Dr. Vladimir V. Potapko)
  - Institute of Forest, Russian Academy of Sciences, Siberian Branch, Krasnoyarsk (Dr. Natalia Oreshkova)
  - Institute of Plant and Animal Ecology, Russian Academy of Sciences, Ural Branch, Ekaterinburg (Dr. V. L. Semenkov)
  - Institute of Forest, Russian Academy of Sciences, Khabarovsk Science Center, Petropavlovsk (Dr. Boris R. Raevsky)
  - Siberian Institute of Plant Physiology and Biochemistry, Russian Academy of Sciences, Siberian Branch, Irkutsk (Dr. Yuri M. Krashantsev)
  - Evrogen Joint Stock Company (Dr. Sergey Lukianov)

- **Ukraine:**
  - All-Ukraine Institute of Civil Defense of Population and Territory from Technogenic and Natural Emergencies (Mykola D. Kuchma)

- **Associated Partners:**
  - Dep. of Forestry and Horticulture, Texas A&M University, College Station, Texas, USA (Dr. Konstantin V. Krulovsky)

**Related Strategic Objective**

4. Meeting the multifunctional demands on forest resources and their sustainable management

**Related SRA - Research Areas**

4-1: Forests for multiple needs
4-2: Advancing knowledge on forest ecosystems
4-3: Adapting forestry to climate change
Comparison of spatial genetic structure of species like these is aimed to understanding of main factors driving adaptation processes and related dynamics of gene pools. As a result, the comprehensive strategy for the conservation and the sustainable management of genetic resources of both species will be developed. Similar distribution pattern in Russia and EU countries are found in Norway and Siberian spruces and other socio-economically important conifer species providing by this broad spectrum of subjects in the proposed research area.
Goal:
Development of a comprehensive strategy for the conservation and the sustainable management of genetic resources of selected conifers based on range-wide inventories of genetic variation patterns by using molecular genetic markers

Objectives:
• to develop a comprehensive set of MGMs as indicators and verifiers of genetic diversity for use in genetic monitoring and gene conservation programs for selected pines (Pinus spp.) and spruces (Picea spp.)
• to characterize gene pools of conifer species having a broad distribution in Europe and Northern Asia (Trans-Eurasian Conifers, TECs) by means of putatively neutral (SSRs) and potentially adaptive (ESTs; SNPs in candidate genes) MGMs
Objectives:

• to create databases for variation in adaptive traits and combined variation of phenotypic (morphology, growth rate, phenology, cold resistance) and genetic (MGMs, candidate genes) traits in economically important conifers for use in gene conservation and breeding

• to develop markers for the identification of pure species and hybrids in TECs, and to assess the genetic basis of heterotic effects, viability, and fitness in conifer hybrids as potential for their use in forestry (Swiss, Siberian, Korean and Japanese stone pines, spruces)

• to develop molecular tools to identify, trace and certify the origin of wood from Eurasian conifers for application in conservation
General Objectives:

- Development of operational tools to control the origin of reproductive material and wood based on MGMs
- Development of genomic resources including DNA sequences for multiple use in breeding programs
- Strategy for the exploration and the use of heterosis and increased fitness in intra- and interspecific hybrids of TECs (stone pines, spruces) in production forests and for maintenance of genetic diversity in threatened species (five-needle pines)
OUTCOME

• Recommendations for the application of different types of molecular genetic markers (MGMs) in selected conifer species and genera for the sustainable management of their genetic resources including conservation and breeding

• Development of criteria for the establishment and maintenance of genetic reserves and gene banks for the *in situ* and *ex situ* conservation and use of germplasm in trans-Eurasian conifers (TECs) of high economic and ecological value

• Development of principles for the application of of MGMs in breeding and propagation populations (including seed orchards), managed, and unmanaged forests in Eurasian pines and spruces

• **Databases** for polymorphism and variability at MGMs and at economically important and adaptive traits for economically important trans-Eurasian conifers