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**EVENTS**

## GenTree project kicks off

The GenTree project funded under the EU Horizon2020 scheme started in March 2016 and officially kicked off at a meeting held at INRA, Domaine Saint-Paul, Avignon, France from 20 to 22 April 2016. It gathered 52 participants from 22 partner institutions. The meeting enabled partners to revisit the project's goals and objectives, and to get organized to implement the activities planned.

One of the main challenges that emerged is how to organize the sampling for DNA analyses in a way that will be meaningful to tackle the key scientific questions the project is addressing:

Are selection processes shaping local adaptation at individual, local, landscape or regional scales?

How is selection shaping the evolution of phenotypes at small and large spatial scales, across the lifespan of a tree?

Providing a statistically sound experimental design with replicates to test these hypotheses is far from trivial. The task is further complicated by the fact that the project is investigating as many as [12 tree species](#), both conifers and broadleaves, of which seven are analyzed more in depth with regard to selection processes affecting genomic diversity. These seven main

species will be sampled across a variety of sites along environmental gradients, across several countries. Sampling will extend beyond collecting for genetic analyses and will include a set of additional parameters that will further characterize the sites and the tree individuals sampled. In particular, sampling will include phenotyping of key fitness-related functional traits at different stages of tree development (adults, juveniles and seedlings). The definition of a minimum set of phenotypic traits to be consistently sampled across sites was largely discussed. Despite the complexity of the project, partners are successfully producing an ecologically and evolutionarily meaningful sampling design and strategy that will be finalized just before the summer when sampling will begin.

The extensive field work to be carried out within a relatively short window of time across several countries, adds complexity to the coordination of the large sampling effort. GenTree has the objective of contributing to the characterization of the European *in-situ* conservation network of forest genetic resources, using genomic markers, phenotypic traits and demographic parameters, particularly focusing on range and ecological margins of species distribution, and on underexplored regions. Therefore, some sampling sites need to coincide with gene conservation units identified in Europe ([see definition](#)), introducing additional constraints to the sampling design.

At the administrative level, another challenge is posed by the need to comply with the Nagoya protocol for the movement across countries of samples from which DNA will be extracted. The Nagoya protocol on access to genetic resources and fair and equitable sharing of benefits arising from their utilization is a supplementary agreement to the Convention on Biological Diversity. The protocol requires Parties to implement appropriate administrative measures to allow access to their genetic resources. Accessing and utilizing genetic resources means conducting research and development on the genetic and/or biochemical composition of genetic resources, including through the application of biotechnology. Material transfer agreements will have to be developed between the origin country and recipient country where the laboratory analyses will be conducted.

The involvement of stakeholders is a very prominent activity in GenTree. Though the themes investigated by the project are difficult to communicate to a non-technical audience and to the general public, the project will contribute to raising awareness of the relevance of forest genetic resources in sustaining forests and the forestry sector in Europe. The project will generate innovative forest management and tree breeding options and it will seek engagement of stakeholders by soliciting their inputs early in the project through the organization of consultations, such surveys and workshops, and by transferring knowledge through training sessions and conferences.

#### **Related links**

[Genetic conservation units across Europe](#)

[The Nagoya Protocol on Access and Benefit-sharing](#)

## Achieving impact through strong stakeholders' engagement

Gentree is highly committed to achieving impact through the involvement of Stakeholders in the definition of the research questions and the identification of targets and objectives to be reached. The project partners are directing efforts towards creating opportunities for consultation with different actors in the forest sector.

The first Gentree stakeholders' event took place in November 2016 in Madrid, and focused on establishing a dialogue between associations of forest owners, forest nurseries, officers of certification schemes, policy-makers and researchers around a critical theme, that is, the management of forest reproductive material in light of environmental changes, addressed by Gentree's research.

New and improved strategies and decision support tools are needed for the exchange and use of forest reproductive material (FRM) under changing and uncertain environmental conditions. These could include using novel fitness-related traits and phenotypic plasticity in selection programmes, finding a balance between genetic diversity and genetic gain or optimizing the use of yet untapped or underused wild resources in well-known commercial species.

Understanding the perspective and demands of critical players in production and use of forest reproductive material, such as nurseries and forest owners and managers, is crucial to ensure that research products can respond to practical needs.

More than 40 participants representing different institutions from 21 European countries attended the event which resulted in concrete recommendations for Gentree research direction and for further uptake by the European Programme on Forest Genetic Resources (EUFORGEN).

[Download the full report](#)

## ACTIVITIES

# Survey on conservation and sustainable use of forest resources

The GenTree project carried out an international survey open to various stakeholders in the forest sector, such as forest managers, forest owners, policymakers, tree breeders, representatives of nurseries, seed harvesting or processing companies and the industry, available in seven languages.

The objective was to collect and analyse the knowledge of different stakeholders on aspects related to conservation and sustainable use of forest resources, in particular their genetic (intraspecific) diversity.

Knowledge on sustainable forest management held by managers and policy makers is often difficult to collect for research and, conversely, research results are not always efficiently conveyed to stakeholders. We propose to bridge this gap.

Answers to the survey will help create realistic scenarios for adapting forests and forest management to a changing climate and evolving socio-economic concerns about natural products. Results from the survey will be compiled by project partners (European Forest Institute, Bioversity International) and made available to all respondents who indicated interest in the final report and provided their emails.

Research results from scenario analyses will be posted on this website and shared with all those who contributed.

THE SURVEY IS NOW CLOSED.

## Mont Ventoux forest – a natural laboratory

Mont Ventoux, near Avignon in southern France, is an outpost of the Alps that lie to the northeast. Today forests cover its slopes, but these trees are a relatively recent phenomenon. And they are threatened by climate change. [In this new film](#), Dr Bruno Fady, Research Director at INRA, the French Research Institute for Agriculture, Food and the Environment, tells the story of the forests of Mont Ventoux and their uncertain future.



Dr Fady explains how a Roman, visiting the area 2000 years ago, would have found the mountain covered with trees, and it was the Romans who first started to clear the trees for timber and fuel. Over the following centuries, visitors would have seen either bare slopes, in period of high exploitation of forest resources for mining or grazing, or forested land, as was probably the case during the plague outbreaks of the Middle Ages, when the reduced demographic pressure enabled the

forest to recover, up until the 18th century when the forest was gone again. Today, thanks to reforestation by the state, “the landscape is really much different from what it used to be 150 years ago,” Dr Fady says. Mont Ventoux once again looks like the landscape the Romans would have known.

Human perception about forests is very biased. What looks old and natural can be recent and the result of human activity. Science can provide tools to unveil the past history of the forest and can also provide solutions to preserve it in the long run. For Dr Fady and GenTree, the crucial element for future survival is forest genetic diversity, which is essential to allow adaptation to changing environmental conditions.

On Mont Ventoux, many trees died as a result of the Europe-wide summer heatwave in 2003. We can clearly see these individuals today as dead, bare trees sticking out of the green canopy that covers the mountain. Why did these particular trees succumb to the heatwave? What does their death imply for the future of the forest?

The first task of the GenTree project is to decipher the role of genetic diversity and environmental variability in shaping adaptive traits in trees. One of the tools is to decode the genetic sequence of traits that matter for survival, for example size, number of seeds or when the tree comes into leaf in the spring. Another important line of investigation is to ask how demographic processes, such as the survival of some germinated seeds and not others, contribute to the genetic diversity we see today.

GenTree will generate the knowledge to provide insights on how and at what spatial scale tree species adapted to environmental changes in the past; the lessons learned can then be used as part of solutions for today’s challenges. Both history and natural selection shape genetic diversity; some events are natural, such as forest fires, while others, like selective removal of some species, are the result of human activity.

The results of the various components of work will inform current conservation priorities and will help refine breeding approaches and foster the establishment of resilient and climate-fit forests.

In the end, information provided by GenTree will help develop scenarios showing how different forest management strategies can influence the ways in which forests might adapt to climate change.

#### Different climatic zones on Mont Ventoux



Mont Ventoux is a steep mountain, so the local climatic conditions change rapidly as elevation increases. It has also been the site of human activities for centuries. For this reason, the site is particularly suited to scientific studies that look at the effects of both human and natural history on the genetic composition of tree species and at local adaptation of tree species to a changing climate.

The environmental and societal values of Mont Ventoux have been appreciated by UNESCO which listed it as a [Man and Biosphere Reserve](#).

## Sampling thousands of trees across Europe

GenTree uses a multi-scale tree sampling scheme to study gene flow and the role of genetic diversity and environmental variability in shaping adaptive traits in trees - traits that enhance the fitness and survival of individuals and have evolved by means of selection.

For each of seven species investigated in the project, trees are sampled in ten sites across Europe, from as far south as Spain and as far northeast as Lithuania. In each site, a pair of populations is selected, located at the two opposite ends of a specific ecological gradient. The two populations in a pair consist of 25 trees each and grow under contrasting ecological conditions but are connected by gene flow. On top of that, 10 plots of 25 trees (usually inside genetic conservation units) are investigated for other five species.

Simple maths highlights the impressive scale of this experiment: 120 sampling sites, 190 populations and a total of 4750 trees! That requires a lot of coordination among research teams. They first choose the sites and describe their ecology in detail. Then they collect leaves and needles from the higher parts of the canopy either by climbing the tree or by using other devices and core the trunks to extract wood samples. Finally, they send the collected material to three central laboratories for analyses: Italy for DNA analyses, Spain for ecophysiological analyses and Switzerland for wood analyses.

To harmonize sampling procedures across sites and to ensure the practices adopted were well aligned with international legislation, a protocol was developed. It has been used to guide

field teams in how to select the most appropriate site, what characteristics of the site to record and what traits of the individual trees and of the wood and leaf samples to measure. The protocol describes how to prepare the collected material so that it can be properly processed: leaves have to be fresh and intact for DNA sequencing and wood cylinders should be stored in particular containers that help preserve the sample until it is fully analyzed.

The sampling has progressed steadily since June 2016, but not without challenges and adventures. Lars Opgenoorth from the University of Marburg (Germany) shared the hardships of coring black poplar in August, with some notes from the field:

“It is a great pleasure given all the mosquitos, and the sheer size of the trees (and sheer size of my arms as a result of mosquito bites!...).

I had difficulties never experienced with other species that I cored before. Many cores broke after ca. 1-2 cm. I varied the duration of the pressure put on the core via the borer - between a couple of turns and up to 20 turns. This did not seem to produce any result.

Many of the poplars are extremely wet inside - in the sense that they really spill water - sometimes like a faucet - when the core is extracted. Apart from the smell and the somewhat sticky mess it creates, the real issue is that the cores expand and become extremely fragile, so it is sometimes hard to put them into their tubes in one piece.

The site located in a meadow is largely affected by a complex hydrological dynamics. Thus, trees do not grow straight; this is also caused by the fact that often a stump has more than 1 large stem, each looking for light and space. As a consequence, the choice of what individual to sample is not straightforward.”

To avoid being squirted by poplars, some teams postponed coring until the growing season is over. The lessons learnt on the ground contributed to the constant refinement of the protocol, which is now in its 87th version, soon to be published.

*A field workshop to test one of the intermediary versions of the sampling protocol took place on 10 June 2016 on Mont Ventoux (France), one of the GenTree project sampling sites. The following project partners participated in the field visit: Aristotle University of Thessaloniki (AUTH), Greece; Agencia Estatal Consejo Superior de Investigaciones Científicas (CSIC), Spain; the Institut National de la Recherche Agronomique (INRA), France; the Philipps-Universität Marburg (PUM), Germany; and the Swiss Federal Institute for Forest, Snow and Landscape Research (WSL), Switzerland.*

## 20,000 km across Italy to collect tree samples

At the beginning of the field sampling period, we were quite unaware of what was ahead of us!

Whilst we had imagined sampling leaves was straightforward, we were concerned about assessing complex plant traits (phenotyping) and tree coring (collecting historical information from living trees). These activities were quite new for us, and required using unknown tools. However, undeterred and thanks to the help of GenTree colleagues and the tutorials they suggested, we were eventually ready to undertake all field activities in June 2016!

Our first field trip was a 5-day sampling foray in the North-Eastern part of the Alps, 600 km north of Florence. Our goal was to collect needles and cores from a Swiss pine (*Pinus cembra*) population and individuals of Norway spruce (*Picea abies*) along an altitudinal transect (75 individuals in total). We were confident of having enough time to carry out all the planned activities, but we had not considered the volatile weather at high altitudes. Heavy rain during the first days of our field work made it very clear that the sampling season would be anything but easy. However, we definitely learnt how to plan future expeditions.

In the following seven months, we spent more than 60 days in the field, travelling for 20,000 kilometres from the Alpine arc in the north, to the Southern end of the Italian peninsula. We visited seven national parks and several protected areas, interacting with local forest managers and attracting their interest in the GenTree project. As a result, the project is now showcased on the websites of most of the natural areas we visited.

During sampling, we faced many difficulties: 40 m tall trees requiring numerous attempts to reach the higher part of the canopy, horsefly swarms attacking our car, having to scale steep slopes using mountaineering equipment, ticks crawling up our legs, wild boar always keeping a close watch on us and even a Marsican bear feeding close to the birch (*Betula pendula*) plot we were sampling. Hard days, however, were always rewarded by tasting the local delicacies along the 1,100 km food-and-wine transect of Italy!

Overall, we collected leaves and needles from 725 trees of [all twelve species studied in the project](#). We also succeeded in phenotyping and coring seven conifer species: black pine (*Pinus nigra*), scots pine (*Pinus sylvestris*), Swiss pine (*Pinus cembra*), Maritime pine (*Pinus pinaster*), Norway spruce (*Picea abies*), Silver fir (*Abies alba*), English yew (*Taxus baccata*) and one broadleaf species - European black poplar (*Populus nigra*), acquiring new skills and strong muscles (especially using the increment borer to extract carrots of wood from the trunk).

We have successfully achieved the most important goal of the first year of the project: collect enough material to start DNA analyses and characterize population genetic diversity across Europe. Our team leads the work on DNA extraction for English yew (*Taxus baccata*), so we are analysing more than 300 samples of this species, collected by other project partners' field teams across Europe. Their samples were all shipped to our laboratory in Florence (Italy).

*The Italian Team of the National Research Council, Florence: Camilla Avanzi, Francesca Bagnoli, Mariaceleste Labriola, Andrea Piotti, Ilaria Spanu, and Beppe Vendramin*



## **Two projects on forest genetic monitoring pool their resources**

Part of the research carried out within the GenTree project is addressing the challenging task of forest genetic monitoring for a large number of tree species across Europe. A similar objective is guiding the scientists within the LIFE GENMON project, an EU environmental fund implementation project.

The expected outputs of LIFE GENMON include the preparation of i) guidelines for forest genetic monitoring, ii) a manual and a decision support system for decision makers on establishing the forest genetic monitoring system, and iii) preparation of documents for possible future legislative developments, which all support better forest management.

Genetic monitoring as seen by LIFE GENMON shall lead to methods and tools for optimising the management of forest genetic resources (FGR) also in conservation units, one of the goals of GenTree. LIFE GENMON has a smaller geographic focus than GenTree and covers a transect spanning from Bavaria to Mt. Olympus in Greece. Actual experimental monitoring plots were established and studied in three European countries (Germany, Slovenia, Greece), while in the other parts of the transect, several monitoring parameters and policy prospects are being evaluated based on published data and opinions of experts. LIFE GENMON, a six-year project, will make two assessments in the same plots: one has already been done and the other is due in 2019/2020.

GenTree can offer to test the method that is being developed by LIFE GENMON over a much broader pan-European scale and envision what may facilitate, slow down or impede the implementation of genetic monitoring at political and management levels.

To facilitate exchange of knowledge and information between the projects, some of the GenTree partners were invited to attend the LIFE GENMON 3rd Advisory board meeting in Ljubljana at the Slovenian Forestry Institute in Sep 2016.

As a result of the discussions that took place in Ljubljana, it was agreed that the two projects would pool their resources and organize a stakeholders' event together showcasing what their outcomes imply for forest management, with particular focus on genetic resources management.

More information about the meeting [at the LIFE GENMON website](#)

# Summer school on ‘Integrated methods to detect polygenic adaptation from genomic data’

28 Aug – 30 Aug 2017, Zurich, Switzerland

Together with the [Graduate Campus of University of Zürich](#), the [EVOLTREE network](#) and WSL, GenTree is co-sponsoring a three-day summer school at the [Swiss Federal Institute for Forest, Snow and Landscape Research](#) (WSL), in Birmensdorf (close to Zürich, Switzerland) to learn about methodologies to detect polygenic adaptation from genomic data. These approaches can be applied to [tree species investigated in GenTree](#) and offer new tools to decipher the role of genetic diversity and environmental variability in shaping adaptive traits in trees.

## Why this event?

Over the last decade, the genomic revolution has offered the possibility to generate tremendous amounts of data that contain valuable information on the genetic basis of phenotypic traits, such as those linked to human diseases or those involved in species' adaptation to changing environments.

Most ecologically and economically relevant traits are controlled by a large number of genes with small individual effects on trait variation, but that are connected with one another through complex developmental, metabolic, and biochemical networks. As a result, it has recently been suggested that most adaptation events in natural populations are reached via correlated changes at multiple genes at a time, for which the name polygenic adaptation has been coined.

Detecting polygenic signals of adaptation in genomes is challenging and current genomic approaches often reveal only a small proportion of the genetic determinants of trait variation. We will explore what relevant information needs to be extracted from genomic data to detect signals of polygenic selection and eventually predict phenotypic evolution.

## Course objectives

This Summer School will offer the opportunity to learn new approaches to analyze genomic data to detect the signature of selection on polygenic traits, such as integrating functional data from gene interaction networks, or use information about genetic co-variation among genomic polymorphisms. Training in computational modeling will also be offered to learn how to generate genetic data and test the accuracy of proposed methods to detect signals of selection.

### Who is it for?

The course is aiming at PhD students, post-docs, and researchers that are using genomic data to study local adaptation, the genetic basis of phenotypic traits, and epistasis. Hands-on exercises will be mainly in R, but there will no introductory lesson to R. Therefore, basic knowledge of R is highly recommended.

### Registrations

Registrations are now closed. Please [visit the project website](#) for more information.

The summer school will be followed by [a symposium on the same topic](#) (31 Aug - 1 Sept, ETH Zürich, Switzerland) - abstract submission for oral or poster presentations is open until 15 May 2017.

## PUBLICATIONS

# How genomic research can help preserve world's forests

Forests face great challenges from climate change, including incidence of pests and diseases. Foresters and others want to understand how tree populations will respond. Will they adapt? Or will they vanish? Reforestation is no longer simple either, because climate change is also upsetting the - notion that “local is best” as a source of forest reproductive material. If not locally, though, where should seeds for planting come from?

While there are no simple answers to any of these vitally important questions, it is clear that genomic studies have the potential to lead to greater understanding and flourishing forests.

Last year, [a conference on Genomics and Forest Tree Genetics](#), organised by IUFRO, brought researchers together to discuss the state of forest tree genomics, how that informs the current understanding of evolutionary processes, and to consider how recent research can enhance conservation and sustainable use. [A recently published paper by some of the conference participants](#) summarized the presentations.

### Genomics

Sequencing tree genomes got off to a slow start but is now accelerating, with many economically and ecologically important tree species in the pipeline. One emerging aspect of interest is that even quite unrelated species often share the order of their genes on the chromosomes. This phenomenon, known as **synteny**, is also well known in crop plants; if anything, trees manifest synteny more strongly than crops, which hints that in trees there may

be more active selection to preserve the underlying organisation of the genome (although not the sequence itself) than in herbaceous annuals.

One of the most important uses of genetic data is to investigate the history of tree evolution and to find out how different species are related. This is important because it can offer insights into the processes that result in speciation. For example, one study of the Asian genus *Castanopsis* dates major speciation to the late Miocene era and links it to the uplift of the Himalayas.

### Adaptation

Looking closely at how past climate is related to both the distribution and the genetic variation of different species is beginning to shed light on how present tree populations might be affected by climatic change. Two different studies, one of mountain hemlock (*Tsuga mertensiana*) and one of Sitka spruce (*Picea sitchensis*), showed that recently-established populations contain high levels of genetic variation. This would not be expected if a new population was established by a few founders and then genetically isolated. For the two species, the landscape allows populations to connect; long distance dispersal of pollen and seed provides the genetic diversity that is an essential raw material as populations adapt to new environments.

Adaptation generally reflects many different kinds of environmental variation, for example in physical parameters such as photoperiod, water availability, temperature regimes and soil type as well as biological factors such as pests and diseases. Earlier studies have suggested that the importance of adapting to photoperiod and temperature across a wide range of latitudes and altitudes – so that the tree maximizes growth while minimising the risk of frost damage – might constrain the ability to adapt to novel climates. However, the meeting heard about a study of sessile oak (*Quercus petraea*) that showed very little correlation between adaptation to photoperiod and adaptation to temperature. This suggests that adaptability to future climate change might be less constrained than previously believed.

Pests and diseases that expand into new areas and new hosts under climate change present a different kind of problem, which may in some cases be easier to solve. For example, a single gene enables white spruce (*Picea glauca*) to resist spruce budworm (*Choristoneura spp.*). It ought thus to be possible to screen forest reproductive material to ensure that it is carrying the resistance gene.

### Conservation

The conference organisers were well aware of the practical importance of genetic information. The authors of the summary paper write: “Genomics has the potential to inform both forest conservation and tree breeding by providing greater knowledge of fine scale adaptation, allelic effects, and demographic processes.” That said, however, they also acknowledge that “building strategies that consider both genetic conservation and sustainable use remain largely anecdotal. The conference was a unique occasion to discover this little travelled road.”

As yet there is little concrete to show, but several promising possibilities. For example, ash trees (*Fraxinus spp.*) are threatened by ash die back (*Hymenoscyphus fraxineus*) in the UK and the emerald ash borer (*Agrilus planipennis*) in North America. Resistance to both seems to occur simultaneously in different branches of the ash evolutionary tree. A deeper understanding might help breeders to identify genes that could, through selective breeding, allow ash to continue to embellish our forests.

### Looking forward

One of the primary aims of the conference was to share widely the current state of research on forest tree genomics; its success in that regard will be manifest in the future research results. But there is also a very practical side to the work. As Santiago. C. González-Martínez at INRA in France, one of the conference organisers, explained, knowledge of tree genomes offers society two clear benefits:

“On one side, identifying genetic variation – that is, specific alleles – that could be relevant for local adaptation and, thus, for forest survival and health. And on the other side, to accelerate breeding, allowing increased productivity and access to new forest products.”

### NEWS FROM OUTSIDE THE PROJECT

## IUCN on track to give protected status to forest genetic conservation units

The World Conservation Congress, held in Hawai‘i in early September, adopted [a motion](#) calling for forest conservation units to be recognised with a new protection status, known in the motion as Protected Area Type IV. The motion, promoted by the French National Conservation Congress, will now be considered by national authorities and NGOs and is expected to help forest geneticists to work with conservationists to secure the long-term conservation of forest tree diversity essential for climate change adaptation.

The genetic conservation units listed in [EUFGIS](#), the European information system on forest genetic resources, are likely to be among the first beneficiaries of this new status.

Alexis Ducouso, president of the Forest Group of [the French IUCN conservation committee](#) spent two years working with colleagues from [the French Commission on Forest Genetic Resources \(CRGF\)](#) to get the motion adopted.

"You had protected species and protected ecosystems," he said, "but nothing to protect genetic processes."

The IUCN motion is based on the fact that "dynamic conservation of genetic diversity

favours the adaptive capacities and evolution of forests in the face of environmental changes." Its preamble includes several important statements. It recognises, for example, that "genetic diversity is not sufficiently taken into account in forest conservation programmes" and regrets that many countries conserve FGR only of "species of economic interest".

Ducouso organised meetings in France to bring conservationists and forest geneticists together to understand the importance of forest genetic resources in the long-term sustainability of ecosystems. As a result, the French IUCN conservation committee accepted the motion and put it forward for consideration by the World Conservation Congress.

Now, Ducouso says, "you have good connections between conservation at the ecosystem level and people involved in gene conservation". He hopes that the French example will encourage other European countries to build similar links between the two communities.

Countries still have to consider how to bring the motion's recommendations into their national regulations, which will involve discussions with departments of agriculture, environment and the like. In Europe, Ducouso said, the new protected area status will potentially apply to genetic conservation units as defined and registered in EUFGIS.

When the new motion finds its way into national regulations, that will add an extra layer of protection to forest conservation units and increase their visibility in the national and international biodiversity conservation programmes. Furthermore, opening the possibility to designate IUCN protected areas for the conservation of forest genetic resources will provide new opportunities to identify particular tree populations of interest in those networks that already fulfill the minimum requirements for dynamic conservation. Such links already existed with nature reserves and other protected areas in the French network of dynamic conservation units.

"Protected status will help to conserve these sources of genetic diversity," Ducouso says.

Having established the principle of conserving genetic diversity as such, rather than only species and ecosystems, might IUCN apply the same thinking outside forests? Ducouso says that political considerations originally restricted it to forests. However, he hopes that in due course the idea of genetic conservation will spread to all species.

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**For more news and information on the project, please visit our website <http://www.gentree-h2020.eu/> or follow us on twitter @GentreeProject**



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