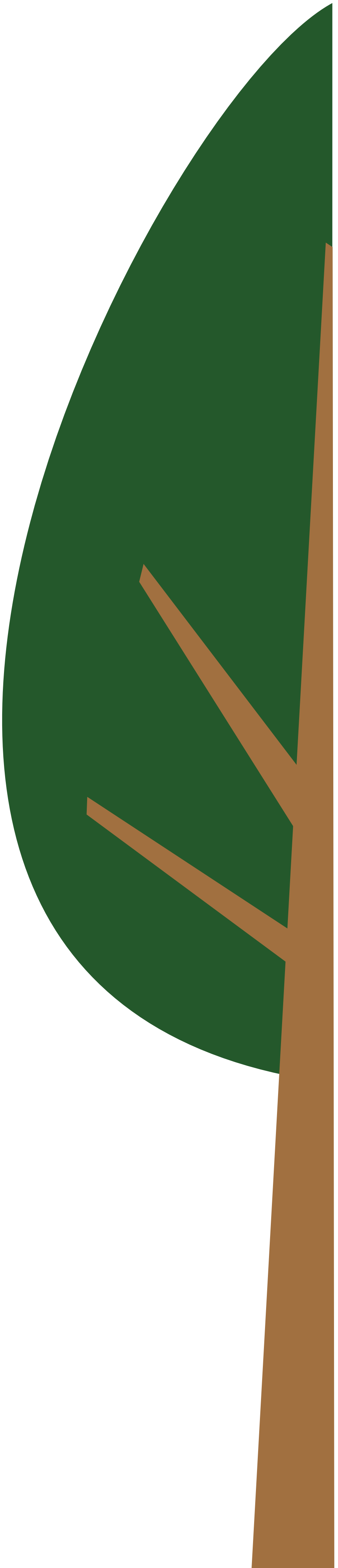

LIFE GEN MON
LIFE FOR EUROPEAN FOREST GENETIC MONITORING SYSTEM

LIFEGENMON
final conference

FOREST SCIENCE FOR FUTURE FORESTS:

Forest genetic monitoring and biodiversity in changing environments

From 21st of September till
25th of September 2020

Ljubljana, Slovenia

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CONFERENCE SCHEDULE

MONDAY, 21.09.2020

Opening of the LIFEGENMON conference/Start of the LIFEGENMON videoconference

Session 1: Genetic diversity and climate change

14:30	**15:00**	***Keynote speaker***	**Santiago C. Gonzalez-Martinez**	**Using genomic data to improve adaptive-trait prediction at large geographical scales**
15:00	**15:30**	***Keynote speaker***	**Silvio Schueler**	**Utilizing the adaptive potential of trees for assisted gene flow and climate smart forestry**
15:30	15:45	*Oral pr.*	Evangelia Avramidou	Epigenetics & Genetics: unrevealing the secrets beyond genes empire; a holistic way to cope with climatic changes
15:45	16:00	*Oral pr.*	Rok Damjanić	Temporal variation in effective reproductive success and non-random dispersal in forest trees
Coffee Break				
16:30	16:50	*Oral pr.*	Azucena Jiménez	Measuring recent gene flow among large tree populations: a case study with *Pinus sylvestris* populations in different edaphic environments
16:50	17:10	*Oral pr.*	Marjana Westergren	Evolutionary potential in a natural beech population
17:10	17:30	*Oral pr.*	Gaye Kandemir	Identification of genetic diversity by molecular markers in natural *Pistacia lentiscus* populations and mastic clone park
17:30	*17:50*	*Oral pr.*	Heino Konrad	Population differentiation in *Acer platanoides* at the regional scale – laying the basis for conserving its genetic resources in Austria
17:50	*18:10*	*Oral pr.*	Giovanbattista de Dato	Genetic Analysis of Silver Birch (*Betula pendula* Roth) Populations in Their Southern European Distribution Range
18:10	*18:15*	*Poster pr.*	Devrim Semizer - Cuming	Adapted relict oaks (*Quercus* spp.) for climate resilient forests
18:15	*18:20*	*Poster pr.*	Lazar Kesić	Variability of leaf anatomical properties in pedunculate oak genotype (*Quercus robur* L.) in natural population
18:20	*18:25*	*Poster pr.*	Josef Frýdl	Conservation and reproduction of genetic resources of resistant variants of Norway spruce in Ore Mountains to mitigate effects of drought and ongoing environmental changes and to support stability of mountain forest ecosystems
18:25	*18:30*	*Poster pr.*	Mirzeta Memišević Hodžić	Frost damages of common beech in the international provenance test in Bosnia and Herzegovina compared to spring phenology in 2019
Welcome mixer at LIFEGENMON Conference Room Foyer				

TUESDAY, 22.09.2020

Session 2: Forest genetic monitoring – LIFEGENMON

9:00	**9:30**	***Keynote speaker***	**Hojka Kraigher**	**Forest genetic monitoring - where from and where to**
9:30	**10:00**	***Keynote speaker***	**FA (Phil) Aravanopoulos**	**The utility of gene-linked SNPs as a marker of choice for forest genetic monitoring**
10:00	10:15	*Oral pr.*	Philip Brailey-Jones	Introducing a web-based population genetics analysis platform for use in the LIFEGENMON project and beyond
10:15	10:30	*Oral pr.*	FA (Phil) Aravanopoulos	What constitutes a biologically significant difference in the frame of forest genetic monitoring temporal assessments?
Coffee Break				
11:00	**11:30**	***Keynote speaker***	**Paraskevi Alizoti**	**Monitoring tree phenology: a simple early warning system on climate change impacts in forest ecosystems**
11:30	**12:00**	***Keynote speaker***	**Barbara Fussi & Darius Kavaliauskas**	**The indicator “gene flow / mating system” to monitor genetic changes over time in European beech and Silver fir**
12:00	12:15	*Oral pr.*	Ermioni Malliarou	Genetic monitoring in beech populations with genetic and epigenetic markers
12:15	*12:30*	*Oral pr.*	Nikolaos Tourvas	Genetic monitoring in the hybridogenous fir (*Abies borisii-regis*): Interpretation of the first temporal and intergenerational comparison using SSR genetic markers
Lunch at LIFEGENMON Conference Room Foyer				
14:00	*14:15*	*Oral pr.*	Marko Bajc	Lifegenmon Forest Genetic Monitoring Manual
14:15	***14:45***	***Keynote speaker***	**Darius Kavaliauskas & Gregor Božič**	**Guidelines for conducting forest genetic monitoring of the seven tree species – *Abies alba/Abies borisii-regis* complex, *Fagus sylvatica*, *Fraxinus excelsior*, *Pinus nigra*, *Populus nigra*, *Prunus avium*, *Quercus petraea/Quercus robur* complex**
14:45	*14:50*	*Poster pr.*	Marjana Westergren	Guidelines for conducting genetic monitoring in the field: *Fagus sylvatica* L.
14:50	*14:55*	*Poster pr.*	Darius Kavaliauskas	Guidelines for conducting genetic monitoring in the field: *Abies alba/Abies borisii-regis*
14:55	*15:00*	*Poster pr.*	Gregor Bozič	Guidelines for conducting genetic monitoring in the field: *Populus nigra* L.
15:00	*15:05*	*Poster pr.*	Marjana Westergren	Guidelines for conducting genetic monitoring in the field: *Fraxinus excelsior* L.
15:05	*15:10*	*Poster pr.*	Paraskevi Alizoti	Technical Guidelines for the genetic monitoring of *Pinus nigra* Arn.
15:10	*15:15*	*Poster pr.*	Darius Kavaliauskas	Guidelines for conducting genetic monitoring in the field: Wild cherry (*Prunus avium* L.)
15:15	*15:20*	*Poster pr.*	Kristina Sever	Guidelines for conducting genetic monitoring in the field – *Quercus robur* L. and *Quercus petraea* (Matt.) Liebl.
15:20	***15:50***	***Keynote speaker***	**Marko Bajc**	**“What’s the damage?” The assessment of cost of forest genetic monitoring based on the Lifegenmon project activities**
Coffee Break				

16:20	*16:25*	*Poster pr.*	FA (Phil) Aravanopoulos	Delineation of regions for forest genetic monitoring on a transect from Bavaria to Greece
16:25	*16:30*	*Poster pr.*	Natalija Dovč	Development of the sampling design within the LIFEGENMON project
16:30	*16:35*	*Poster pr.*	Rok Damjanić	The implementation of a database system for forest genetic monitoring (FGM) within the LIFEGENMON project
16:35	*16:40*	*Poster pr.*	Natalija Dovč	Phenological observations within the LIFEGENMON project in Slovenia
16:40	*16:15*	*Poster pr.*	Paraskevi Alizoti	Monitoring phenology to assess the response and adaptive potential of a Hellenic *Abies borisii-regis* population to inter-annual climate variability
16:45	*16:50*	*Poster pr.*	Paraskevi Alizoti	Assessing the response of a Hellenic *Fagus sylvatica* population to interannual climate variability via monitoring the phenology of various biological traits
16:50	*16:55*	*Poster pr.*	Maria Cristina Monteverdi	Traditional monitoring of foliar phenology concerns in situ observations on single trees
16:55	*17:00*	*Poster pr.*	Marko Bajc	Interlaboratory comparison of microsatellite data. An approach used in the Lifegenmon project
17:00	*17:05*	*Poster pr.*	Nikolaos Tourvas	Minimum Requirements for Genetic Monitoring: A Proposed Workflow
17:05	*17:10*	*Poster pr.*	Domen Finžgar	Genetic monitoring of the products of the British Sitka spruce (*Picea sitchensis (Bong.*) Carr) breeding programme
17:10	*17:15*	*Poster pr.*	Barbara Fussi - German project Genmon	The joint research project GENMON: Implementation of long-term genetic monitoring in beech and spruce stands in Germany
			Coffee Break	

Session 3: Forest resilience, conservation and management of forest genetic resources

17:45	**18:15**	***Keynote speaker***	**Ivan Scotti**	**Conservation of forest genetic resources, adaptation, and resilience: what do we know and what do we still need to know?**
18:15	**18:45**	***Keynote speaker***	**Cristina Vettori**	**Genetic and genomic landscape approach for adaptative forestry in climate change**
18:45	19:00	*Oral pr.*	Kristina Sever	Forest tending of the seed stands with the I+ Trainer virtual tool
19:00	19:15	*Oral pr.*	Laura Guillardin	Genetic effects of applying Continuous Cover Forestry in non-native conifer UK populations

THURSDAY, 24.09.2020

Session 3: Forest resilience, conservation and management of forest genetic resources

9:00	9:15	*Oral pr.*	Bruno Fady	Contribution of the H2020 GenTree project to selecting meaningful proxies for gene conservation and genetic monitoring
9:15	9:30	*Oral pr.*	Fotios Kiourtsis	Integration of forest genetic monitoring in forest management plans
9:30	9:45	*Oral pr.*	Boris Rantaša	From Science to Practice: the Implementation of Forest Genetic Monitoring in Policy, Regulation and Forestry Practice
9:45	10:00	*Oral pr.*	Hojka Kraigher	Policy and practice in conservation of FGR in selected LIFEGENMON transect countries
10:00	*10:05*	*Poster pr.*	Janez Kermavnar	Microclimate in Dinaric fir-beech forests is controlled by the interaction effect between management intensity and topography
10:05	*10:10*	*Poster pr.*	Andreja Gregorič	Protocol for handling of forest tree seedlings and Protocol for obtaining seed material, parts of plants and seedlings
10:10	*10:15*	*Poster pr.*	Kristina Sever	Proposed guidelines on forest genetic conservation for integration in forest management plans in Slovenia
10:15	*10:20*	*Poster pr.*	Lado Kutnar	Changes of forest understory vegetation are driven by disturbances: Intensive Monitoring of Slovenian forests
10:20	10:35	*Oral pr.*	Luka Krajnc	A comparison of radial wood increment and wood density of six different beech provenances
10:35	10:50	*Oral pr.*	Peter Prislan	Xylogenesis in European beech under climate change
10:50	*10:55*	*Poster pr.*	Darius Kavaliauskas	Development of DNA marker-based traceability system for forest reproductive material in Lithuania
10:55	*11:00*	*Poster pr.*	Vladislava Galović	Biochemical and transcriptomic approach: the selection tools for afforestation of halomorphic environment
				Coffee Break

Session 4: Forest dynamics, interactions and biodiversity at different scales

11:30	**12:00**	***Keynote speaker***	**Douglas Godbold**	**Taxonomic and functional diversity of ectomycorrhizas in European forest- size matters**
12:00	**12:30**	***Keynote speaker***	**Magda Bou Dagher Kharrat**	**Forest ecosystem restoration success factors and the role of animals in seed dispersal inferred from DNA metabarcoding**
12:30	*12:35*	*Poster pr.*	Felicita Urzi	Population genetic structure of red fox in Slovenia
12:35	*12:40*	*Poster pr.*	Urška Gerič	Does the genetic component has an influence on fitness parameters (body mass and reproductive ability) in roe deer
12:40	*12:45*	*Poster pr.*	Aja Bončina	Genetic variability, relatedness and reproductive spatial behaviour in two highly abundant ungulate species
12:45	*12:50*	*Poster pr.*	Sandra Potušek	First insight into MHC genes (class II) variation in European roe deer in Slovenia
				Lunch at LIFEGENMON Conference Room Foyer
14:30	**15:00**	***Keynote speaker***	**Petr Baldrian**	**Seasonal dynamics of microbial communities and their activity at the root-soil interface of a coniferous forest soil**
15:00	*15:05*	*Poster pr.*	Tine Grebenc	Drivers of ectomycorrhizal fungi diversity and their contribution to a global soil biodiversity and ecosystem functions
15:05	*15:10*	*Poster pr.*	Tanja Mrak	Ectomycorrhizal fungi of *Quercus pubescens* suffering from drought and wildfire

15:10	*15:15*	*Poster pr.*	Tijana Martinović	Describing succession of decomposer fungi on coarse woody debris in virgin forest Rajhenavski Rog in Slovenia
15:15	*15:20*	*Poster pr.*	Tijana Martinović	Bacterial community response to forest clearcutting
15:20	*15:25*	*Poster pr.*	Erna Vaštag	Assessing the negative effects of severe powdery mildew infection on chlorophyll a fluorescence and stomatal characteristics of *Quercus robur* L.
15:25	*15:30*	*Poster pr.*	Ilaria Fracasso	Turning well-known climatic archives into biological archives: an environmental metabarcoding approach
15:30	*15:35*	*Poster pr.*	Luka Duniš	Isolation of exogenous fungal DNA from non-invasive samples

Coffee Break

Session 5: The science – policy interface

16:05	**16:35**	***Keynote speaker***	Michele Bozzano	Genetic aspects in production and use of forest reproductive material – coordination and dialogue
16:35	*17:05*	***Keynote speaker***	Ewa Hermanowicz	Storytelling for science communication and media engagement
17:05	*17:35*	***Keynote speaker***	Katja Sonnenschein	LIFEGENMON communication and dissemination activities
17:35	*17:50*	*Oral pr.*	Urša Vilhar	General public dissemination of the LIFEGENMON project: a story of success
17:50	*17:55*	*Poster pr.*	Chryse Sarvanl	Spreading the word about the LIFEGENMON project - Greek dissemination approach
17:55	*18:00*	*Poster pr.*	Mark Walter	Spreading the word about the LIFEGENMON project - German dissemination approach
18:00	*18:05*	*Poster pr.*	Mark Walter	The Seedhunter App
18:05	*18:10*	*Poster pr.*	Boris Rantaša	LIFEGENMON communication: a 360 degree approach
18:10	*18:15*	*Poster pr.*	Evangelia Avramidou	Monitoring climate change adaptation plans for Urban Green Areas using indicators: LIFEGRIN project, a case study in Greece
18:15	*18:20*	*Poster pr.*	Alexandra Solomou	Utilization of green infrastructures for more resilient cities in Greece

FRIDAY, 25.09.2020

Session 3: Forest resilience, conservation and management of forest genetic resources

9:00	**10:00**	***Final Keynote***	**Robert Mavsar**	**The past, the present, the future**
10:00	*11:00*	Round table		
11:00	*12:00*	Press conference and Closure of the LIFEGENMON conference & videoconference		
12:00	*12:30*	Presentation of COST actions & The movie on LIFEGENMON		

Lunch at LIFEGENMON Conference Room Foyer

14:00	*18:00*	LIFEGENMON project AB meeting

LIFEGENMON working dinner (for AB meeting members only)

KEYNOTE PRESENTATIONS

EVI ALIZOTI

Evi Alizoti obtained her B.Sc. in Forestry, the M.Sc. in Plant Genetics and Breeding and her Ph.D. in Quantitative Genetics and Tree Breeding from the Aristotle University of Thessaloniki, Greece. In the course of her studies she has been awarded several times scholarships for exceptional performance and for conducting her M.Sc. research. She was also a one year Post-Doc fellow in the Faculty of Forestry of North Carolina State University, USA.
She began his professional career as a researcher on quantitative genetics and tree breeding at the Aristotle University of Thessaloniki. She then became a Lecturer, an Assistant Professor and since 2019 an Associate Professor at the School of Forestry and Natural Environment – Aristotle University of Thessaloniki. She is instructing sixteen undergraduate and postgraduate courses on the fields of forest genetics, tree improvement, conservation of genetic resources, quantitative genetics, molecular breeding and clonal forestry/biomass production. She is the Head of the Forest Production, Forest Protection and Natural Environment Department, Administrative Council member, and ERASMUS+ Coordinator at the School of Forestry and Natural Environment of the Aristotle University of Thessaloniki. She is Coordinating the IUFRO Working Unit 2.02.13 'Breeding and Genetic Resources of Mediterranean Conifers' and she is co-leading the IUFRO Task Force 'Strengthening Mediterranean Nursery Systems for Forest Reproductive Material Procurement to Adapt to the Effects of Climate Change'. She is National Focal Point of Greece in the EUFORGEN and EUFGIS Programs. She participated in numerous competitive national and European research projects, as well as EU COST Actions, via active participation and via leading or co-leading working groups. She is acting as reviewer in numerous peer review scientific journals and she is Task Editor for the 'Forests' scientific journal. She is a member of numerous scientific societies and she served as member of their boards for several terms. She has authored and co-authored numerous publications, book chapters and invited papers.

FILIPPOS A. ARAVANOPOULOS

Dr. Filippos (Phil) A. Aravanopoulos, is Professor of Forest Genetics & Tree Breeding at the Aristotle University of Thessaloniki and a Full Member of the Hellenic Agricultural Academy holding the Chair of Forest Science. His background couples Forest & Environmental Science (B.Sc.) & Tree Genetics (Ph.D., postdoctoral research) & has studied in Greece, Canada & Sweden. His research has been funded by International Organizations (European Commission, International Energy Agency) and National Organizations of Canada, Greece & Sweden. He is has served as the Chairman of the Scientific Council of the National Agricultural Foundation of Greece, overseeing scientific research, research staff recruitment & promotions for 30 research institutes that focus on agriculture, forestry, fisheries & veterinary science. Prof. Aravanopoulos has also served as Leader of the Genetic Monitoring Working Group of EUFORGEN, as a member of the FAO Expert Group on the State of the World Forest Genetic Resources and as the Chair of the Hellenic Scientific Society for Plant Genetics & Breeding. He is the Deputy Coordinator, of the Population, Ecological & Conservation Genetics Unit of IUFRO. He serves as reviewer for more than 40 international journals & as an editorial member in four (among them Associate Editor in PLoS One). He has given over 30 invited presentation in Universities & Conferences in Europe, Canada, China, Cyprus, Germany, Greece, Serbia, Slovenia, Spain, Sweden & Turkey. He has published about 200 research papers, of which 95 in international peer-reviewed journals & 38 in refereed books & international proceedings.

PETR BALDRIAN

- Graduated in Microbiology from the Charles University in Prague, Czech Republic
- Since 2006, Head of the Laboratory of Environmental Microbiology, Institute of Microbiology, Prague
- Focus on microbial processes in natural ecosystems and the roles of fungi and bacteria
- Forest soils, their properties and dynamics are the main study subject
- Teacher at Charles University in Prague (Microbial Ecology, Bioinformatics)

MICHELE BOZZANO

Michele Bozzano is the coordinator of the European Forest Genetic Resources Programme (EUFORGEN), an international cooperation programme promoting the conservation and sustainable use of forest genetic resources in Europe as an integral part of sustainable forest management. EUFORGEN has developed a series of strategies and guidelines on the role and potential of forest genetic resources in adaptation of forests to climate change.

DARIUS KAVALIAUSKAS

BSc in ecology and environmental sciences; MSc in ecology and environmental sciences (specialization – forest ecology); PhD in forestry (specialization – forest genetics).
In 2015 I have defended my PhD thesis in the field of forest population genetics (Topic: “Genetic structure and genetic diversity of Scots pine (Pinus sylvestris L.) populations in Lithuania”). In this thesis I have addressed the problem of detecting the genetic structure and geographical variation of genetic diversity among natural Scots pine populations in Lithuania. Therefore, I have focused on the neutral part of genome, where the genetic structure is strongly affected by the post-glacial migration, demography, mutations, genetic drift and gene flow. These effects and genetic population structure were examined based on mtDNA cpDNA and nDNA markers. Since 2015 I am working as researcher in the project LIFEGENMON at the Bavarian Office for Forest Genetics (Germany). Project aims to develop and implement forest genetic monitoring concept and to define optimal indicators and verifiers for monitoring of genetic diversity change in time across for two selected model forest tree species – Silver fir and European beech.
My research interests are forestry, forest genetics, population genetics, ecology, conservation of forest genetic resources, applied forest genetic research e.g. traceability of forest reproductive material, provenance research, etc.

EWA HERMANOWICZ

Ewa Hermanowicz is a science communicator with special interest in digital storytelling. Before joining the European Forest Genetic Resources Programme at the European Forest Institute where she leads the communication activities related to forest genetics, she was part of the capacity building and science communication team at Bioversity International, focusing on topics of agrobiodiversity, food security and gender. Her work includes websites, blogs, campaigns and short films such as ‘Afforesting Iceland’ featured by National Geographic.

BARBARA FUSSI

Dr. Barbara Fussi, PhD Botany, is a scientific researcher and Head of Unit Applied Forest Genetics Research at the Bavarian Office for Forest Genetics (AWG) in Teisendorf, Germany. Her main interests are in population genetics and applied forest genetic research, including conservation of forest genetic resources and studying adaptation-relevant markers. Within the LIFEGENMON project, she is the beneficiary leader of AWG.

DOUGLAS L. GODBOLD

Douglas L. Godbold is the Professor of Forest Ecology at the Universität für Bodenkultur (BOKU), Vienna and since 2015 he is also a senior Scientist of the Czech Academy of Sciences. Until 2011 he was Professor of Forest Sciences at Bangor University, UK. He obtained a PhD from the University of Liverpool in 1983 and moved to the University of Göttingen in 1984 and after his Habilitation in 1991 became Apl. Professor in 1995. In 1995-1996 he was a Charles Bullard Fellow at Harvard University USA. His research interests have mainly been on belowground process in forest ecosystems including fine roots and mycorrhizas. His more recent work has focused on biodiversity ecosystem function relationships in forest trees and mycorrhizas.

HOJKA KRAIGHER

Prof. Dr. Hojka Kraigher is the Head of Department for Forest Physiology and Genetics and of the Research Program Forest Biology, Ecology and Technology at the Slovenian Forestry Institute, and an associated member of the Slovenian Academy of Sciences and Arts. Her expertise is in physiology and ecology of forest trees and their symbionts, and in conservation of forest genetic resources. She is the authorized person for approval of basic material and reporting to FOREMATIS, and for certification of the forest reproductive material. She has been the national coordinator EUFORGEN since 1995. Currently she is coordinating the LIFE+ project on development of a system for forest genetic monitoring “LIFEGENMON” and participating as partner and working group leader in LIFE SySTEMiC and the H2020 project GenRes Bridge.

MAGDA BOU DAGHER KHARRAT

Prof. Magda BOU DAGHER KHARRAT, head of laboratory Biodiversity and Functional Genomics at the Faculty of Science in Saint-Joseph University (USJ) Beirut.

Prof. Kharrat is a Plant Geneticist with special interests in endemic species conservation and in conifer genetics. She employs genomic tools to investigate plant and animal populations in order to understand their phylogeny, phylogeography and their historical evolutionary processes.

The results of her research have allowed her to define conservation policies and forest ecosystem restoration strategies that are optimizing the survival of tree populations in the face of climate change. She is the co-founder and President of “Jouzour Loubnan”, an NGO dealing with reforestation in Lebanon since 2008.

Her work on restoration and rehabilitation of degraded mountain ecosystems and genetic investigation and in-situ and ex-situ conservation of the Lebanese flora is recognized at national and international levels.

She was awarded in 2008 by UNESCO-L’Oréal for “Women in Science” for her work on valorization and conservation of native Lebanese flora and for launching its first online data base. In 2012 she was nominated by the Program of U.S. Embassies and Consulates in the Middle East and North Africa (MENA) as “Outstanding Woman Scientist”. In 2020, she was nominated as one of the 80 International Faces of Exchange of the USA International Visitors Leadership Program.

ROBERT MAVSAR

Robert Mavsar (PhD) is the Deputy Director of the European Forest Institute (EFI), being responsible for the overall operational management and the development of research activities of the institute. He holds a PhD in economics and a MSc degree in forestry. His main areas of expertise are in the field of forest bioeconomy. In this field he has also been coordinating European research projects and acting as a member of various advisory groups for the European Commission (e.g., member of the European Commission Expert Group on the Review of the EU Bioeconomy Strategy).
Before joining the EFI, Dr Mavsar worked for the Forest Science and Technology Centre of Catalonia (Spain), Slovenian Forestry Institute and the Ministry for Agriculture, Food and Forestry of the Republic of Slovenia.
The European Forest Institute (EFI) is an international organisation established by European States. EFI conducts research and provides policy support on forest-related issues.

SANTIAGO C. GONZÁLEZ-MARTÍNEZ

Dr. Santiago C. González-Martínez hold a PhD in Forest Science (UPM, Madrid, 2001) and is currently Research Director at INRA (UMR1202 BIOGECO: Biodiversity, Genes & Communities), in Bordeaux (France) and associate researcher to CREAF (Barcelona, Spain). Previously, he was postdoctoral researcher at the Institute of Evolutionary Sciences of Montpellier (ISEM-UM2, France), Fulbright Scholar at the University of California (UCDavis, USA) and Senior Marie Curie Fellow at the Department of Ecology and Evolution of the University of Lausanne (DEE-UNIL, Switzerland), and worked for several years at the Forest Research Centre (CIFOR-INIA) in Madrid, first as 'Ramón y Cajal' Fellow and afterwards as Tenured Scientist.He has been conducting research in several topics in the general field of Evolutionary Biology, with a focus on evolutionary processes explaining the distribution of genetic diversity in forest trees, from gene flow and fine-scale spatial genetic structure studies to research on candidate genes for adaptive responses, in particular related to climate adaptation, following both classical and new-generation population genetic and genomic approaches. Currently, he develops a broad research line on ecological genetics and genomics of local adaptation, which relies both on genome-wide genotyping/sequencing and evolutionary quantitative genetics. He has published over 130 research papers with more than 7,000 accumulated citations and he is currently Associate Editor for GENETICS and Reviews Editor for TREE GENETICS AND GENOMES, as well as Coordinator of IUFRO's Division 2 (Physiology & Genetics) and the EVOLTREE European Research Group (www.evoltree.eu).

SILVIO SCHUELER

Silvio Schueler is head of the Department for Forest Growth and Silviculture at the Austrian Research Centre for Forests (BFW) in Vienna since 2017. He and his team are responsible for developing strategies for sustainable forest management in Austria with regard to climate change and growing wood demand and by considering forests' natural resources and biodiversity. Dr. Schüler has a degree in biology of the University of Jena and has thereafter worked at the Thünen Institute in Hamburg. He joined the BFW in 2005 as Head of the Unit for Provenance Research and Breeding. His projects are strongly devoted to develop strategies for adapted forest management in climate change and to transfer and apply scientific knowledge in forest practice. Examples of his projects are the online recommendation platform www.herkunftsberatung.at, a tool to find the best seed provenances for forest stands in Austria. Furthermore, he established a large oak provenance trial series in Austria and reevaluated large provenance trial datasets to estimate the requirements for assisted migration and gene flow for native and non-native trees. Further projects include the modeling of forest development und connected ecosystem services under different adaptation strategies.

IVAN SCOTTI

I am a population biologist interested in the mechanisms underlying local adaptation, and in particular microgeographic adaptation, that is, adaptation to environmental variations occurring within populations. Such processes are theoretically related to the maintenance of diversity within populations and to a selection-dispersal balance, and can occur when the environment is patchy or changes abruptly over short distances. I contend that such conditions are encountered frequently by plant populations, e. g. in soil composition and fertility, light and water availability, competition, occurrence of predators.

I like to work cooperatively with people from other fields, in a truly multidisciplinary approach to tackle the question of microgeographic adaptation. I collaborate (mostly) with ecologists, ecophysiologists and statisticians, locally and in other research centres, to build a comprehensive view of adaptation, covering all of its aspects (Darwinian selection, demography, plasticity, …).

My biological models are forest trees. I consider trees an excellent study system to investigate microgeographic adaptation, thanks to their large, perennial populations, high fecundity and genetic diversity. I am a lover of trees and forests, and I consider it very important to contribute to the study of adaptation in the prospect of climate change, as this may help preserving forests worldwide from the threats associated to global warming.

I am also active in science popularisation. I am involved in the presentation of evolutionary theory and ideas to the general public of all ages, and I do not hesitate to argue for proven scientific facts of evolution when they come under attack by anti-science groups. I am in favour of public, independent research and I favour a publication system that values quality of science above publisher industrial goals.

CRISTINA VETTORI

Dr. Cristina Vettori, in May 1998 get the PhD in “Crop and Forest Genetics” at the University of Florence (Italy) in relation to Microbial Ecology and Genetics.

From June 1998 to 26 December 2001 post doc fellow at the IMGPF-CNR.

From 27 December 2001 is researcher of National Research Council of Italy (CNR), actually at the Institute of Biosciences and Bioresources (IBBR), and Responsible of the Florence Division of IBBR from January 2019.

Cristina Vettori has over 20 years’ experience in forest genetics and molecular genetics with particular research interest in phylogeography and phylogenesis of Fagaceae, genome analysis, biosafety research in transgenic trees, ancient DNA analysis, and recently in adaptative silviculture.

She has participated to several EU projects of the FP6 and FP7.

She has been Coordinator of LIFE08 NAT/IT/000342 (Development of a quick monitoring index as a tool to assess environmental impacts of transgenic crops) and Chair of the COST Action FP0905 (Biosafety of forest transgenic trees: improving the scientific basis for safe tree development and implementation of EU policy directives), and actually is Project Manager of the LIFE SySTEMiC (Close-to-nature forest sustainable management practices under climate changes) project.

The publication list contains more than 40 reviewed publications in scientific International and National journals, and outstanding papers have been published in Nature Biotechnology, Heredity, BMC Evolutionary Biology, and Nature Plants.

GREGOR BOŽIČ

Dr Gregor Božič is a senior researcher at the Slovenian Forestry Institute. He has more than 25 years of experience in forest genetics related to conservation of forest genetic resources (*in-situ, ex-situ*) and characterization of forest tree species by biochemical markers, provenance research, and clonal tests in link to applications with practical forestry. He has experiences in exploring the potential of poplars and willows to maintain biodiversity in riparian forests, and identification of plant material with boarder adaptive properties for timber, biomass, and ecosystem services. He has been a Slovenian representative in pan-European conservation efforts for *Populus nigra* (L.) and Conifers forest tree species (EUFORGEN Networks), he has participated in EUFORGEN WG for Forest Genetic Monitoring. Currently he is the representative of the National Poplar Commission of Slovenia in the FAO - International Poplar Commission governance body and a member of Scientific Board of the Slovenian Forestry Institute.

KATJA KAVČIČ SONNENSCHEIN

Katja Kavčič Sonnenschein, MSc in Economics and MSc in Environmental Management & Policy, has many years of experience with EU projects, as a leading partner (Alpine Space, Life) or as a county expert (studies for DGENV, Green Budget Europe). She has worked on projects that deal with environmental taxation and budgetary reform, best practices in CO_2 reduction, energy systems and distributed economies. She currently works at the Slovenian Forestry Institute in the Department of Forest Physiology and Genetics as a communication and dissemination manager for the LIFEGENMON project. She also works on other EU projects that emphasise the importance of forest genetic diversity in times of climate change.

Monitoring Forest Tree Phenology: a simple early warning system on climate change impacts in forest ecosystems

Paraskevi Alizoti

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Phenology – the annually recurring sequence of plant life-cycle events - is of great importance for plant functioning and forest ecosystem services, and a leading indicator for tracking climate change impacts. Phenology of plant traits (i.e. bud break, leaf senescence, flowering, fructification) is influenced by the local climate and responds to its interannual changes, via the expressed plasticity of forest trees. Phenology though is also controlled by genetic factors. Genes responsible for the timing of phenophases of several phenological traits have been identified up to now both for angiosperms and conifers. Phenology determines the development and senescence of the tree foliage and the physiological activity of the canopy, that includes the photosynthesis and CO2 fluxes, the evapotranspiration and H2O fluxes, energy fluxes and VOC emissions, which affect the atmospheric structure and composition and thus the weather and climatic conditions. Thus, phenology is affected by climate but affects climate as well. Phenology determines also the initiation, duration and termination of female and male flowering, and consequently the flowering synchronization, which is a basic requirement of panmixia. Continuous discrepancy of flowering synchronization due to climate change is expected to result in seed crops with reduced genetic variation; fact that may put at risk the natural regeneration and sustainability of forest ecosystems. For all the above reasons monitoring of phenology is considered to be of vital importance, as it can serve as an early warning system for the impacts of climate change on forest tree populations and species and a necessary tool for the application of adaptive to climate change forest management strategies.

Keywords: genetic control of phenology, flowering asynchrony, genetic variation of seed crop, adaptive forest management.

The utility of gene-linked SNPs as a marker of choice for forest genetic monitoring

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Quantifying temporal alterations (at ≥10 year intervals for genetic markers) in genetic diversity and structure (forest genetic monitoring, FGM), brings prognosis before irreparable harm befalls. As the FGM implementation widens, one looming question is which marker system to invest on. Until recently, microsatellites have been the de-facto choice for population genetics, because of their relatively low-cost and high information content. However, various uniplex and multiplex SNP genotyping platforms have emerged, promising more representative genome scans with a cost competitive to microsatellite analysis. In this work, three *Abies alba* and three *Fagus sylvatica* stands (from Germany, Greece and Slovenia (note *A. borisii-regis* from Greece), were analyzed using 270 SNPs for Abies and 170 SNPs from Fagus, derived from the KASP uniplex genotyping technique. From each stand two temporally separated cohorts were sampled (adult trees and natural regeneration). The results are compared with SSR data from the same individuals to identify marker-specific biases. Moreover, the role of gene region linked FST outlier SNPs, to explain adaptive diversity is explored. The application of FGM in the temporarily separated cohorts is also evaluated in light of the markers used.

Keywords: FGM, SNP, FST-outlier, *Abies alba, Abies borisii-regis, Fagus sylvatica*

“What’s the damage?” The assessment of cost of forest genetic monitoring based on the Lifegenmon project activities

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The establishment of forest genetic monitoring (FGM) will, among other factors, depend on securing the long-term funding of such an endeavour. Seeking funding for FGM will, inevitably, require presenting policy makers and potential financers with concrete numbers for the cost of FGM.

In the Lifegenmon project all the costs associated with FGM were logged throughout the duration of the project. The presented cost assessment was therefore based on analysis of actual costs of FGM activities carried out in the Lifegenmon project. Costs were calculated for a 10-year monitoring interval per species, country and monitoring level.

Besides overall cost of FGM, contributions of different activities (Plot selection, Plot establishment, Field observations/measurements, Sampling, Laboratory analyses) and cost types (Cost of materials, Cost of labour, Cost of travelling) to the total cost were evaluated.

In terms of activities, “Field observations and measurements” were identified as the major contributor to the overall cost of the FGM, representing 59% to 91% of the total cost of FGM, depending on the monitoring level, species and country; “Cost of labour” was identified as the major contributing cost type overall, representing 38% to 76% of the total cost. Additionally, “Cost of travelling” can contribute significantly to the cost of FGM with a 15% to 53% share of total cost for a 100km travelling distance to the plot.

Keywords: Forest genetic monitoring, cost assessment

Seasonal dynamics of microbial communities and their activity at the root-soil interface of a coniferous forest soil

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Forest soils are of global importance since they represent an important sink of carbon (C). In forest soils, bacteria and fungi are important drivers of soil processes, mediating both decomposition and nutrient transfer from and to trees, the main primary producers. It was demonstrated recently, that microbial activity varies among seasons. Here we have explored the contribution of bacteria and fungi to soil processes in a temperate coniferous forest in the context of the seasonal differences among metabolomes. The combination of metabolomics, metagenomics, metatranscriptomics and metaproteomics as well as microbial community sequencing was used to assess the seasonality of nutrient availability at the root/soil interface and its effects on the composition of the microbiomes and their contribution to C and N cycling in early and late vegetation season and early and late winter. Profound differences in metabolome profiles were found between periods of tree activity during the vegetation season and in summer. While the communities of bacteria and fungi were similar across all seasons, their activity and growth rates differed seasonally. The rhizosphere and root compartments were the most dynamic, but roots, comprising ectomycorrhizal symbionts of tree roots showed higher activity of fungi, especially in summer. The C-cycle processes were dominated by bacteria in soil and rhizosphere and by fungi in litter and roots. Profound seasonality was also detected in the expression of N-cycling genes. Interestingly, protein pools appeared to be less seasonally variable than microbial transcription. Our results show that the understanding of soil microbiome functioning is impossible without considering the activity of forest trees, demonstrated by the seasonality of metabolomes of soil microhabitats. Forest soils represent highly complex systems where bacteria and fungi locally dominate and contribute together to the C and N cycling in the ecosystem.

Keywords: forest soil; microbial ecology; plant-microbe interactions; seasonality; nutrient cycling

Genetic aspects in production and use of forest reproductive material – coordination and dialogue

Michele Bozzano

European Forest Institute (EFI) / EUFORGEN

The genetic makeup of Forest Reproductive Material is directly affected by the decisions made by the various actors involved in its production chain. These decisions, which often ignore the genetic perspective, will have a major impact on the survival of future forests.

Coordination and dialogue are crucial for the long-term success of actors across the whole production chain: from forest managers through nurseries to policy makers at different scales (local, regional, national, European).

The presentation, which builds on a recent report developed by the EUFORGEN programme, will highlight its most relevant recommendations and provide arguments and examples for the need to coordinate actions between actors and communicate effectively.

This work is the result of an international collaboration that EUFORGEN has pursued for more than two decades. It rests on the firm belief that genetic aspect is decisive for the creation of a resilient forest capable of surviving threats and adapting to changes, thus enabling evolution of ecosystems and conservation of the productive landscape.

Using genomic data to improve adaptive-trait prediction at large geographical scales

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The development of models to predict adaptive-trait variation across species ranges is essential to assess the potential of populations to survive under future environmental conditions. In forest trees, large forest inventories and common gardens have long been used to predict population responses to climate change. In the last decade, the come-of-age of high-throughput sequencing and genotyping in forest trees have provided large genomic datasets. In this talk, we will review current use of genomic data in predictive models of natural population responses to environment and will develop a case study in maritime pine (*Pinus pinaster* Aiton). For this species, and using a clonal common garden consisting of 34 provenances of maritime pine planted in five sites under contrasted environments (33,121 observations), we compared twelve hierarchical models to: (i) separate the genetic and plastic components of height growth, a key adaptive trait in forest trees, (ii) identify the relative importance of factors underlying height variation across individuals and populations (i.e. adaptation to climate, demographic history, and genomic background, as evaluated by the number of Positive-Effect Alleles, PEAs), and (iii) improve height-growth prediction of unknown observations and provenances (an observation being a height measurement in a given year on one individual). Overall, models combining genomic and climatic information explained as much variance as models using height data measured in the common gardens. These models also explained substantially more variance when predicting new provenances, particularly in harsh environments. Thus current modelling efforts would benefit from further integrating ecological and genomic information.

Keywords: climate change, local adaptation, SNPs, polygenic scores, predictive models

Taxonomic and functional diversity of ectomycorrhizas in European forest - size matters

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Scale is a fundamental factor in assessing biodiversity, giving rise to the concepts of alpha, beta and gamma diversity measures. In forests, above and belowground ecological functions operate at different scales. For example, carbon sequestration in soils is only meaningful measured at a large stand or landscape scale, whereas soil nutrient mobilization can be a small scale process within mm of soil at the root surface. Ectomycorrhizal fungi are pivotal drivers of ecosystem functioning in temperate and boreal forests. Ectomycorrhizas constitute an important pathway of plant-derived carbon into the soil and facilitate nitrogen and phosphorus acquisition. Ectomycorrhizal diversity and abundance can be determined through measurement of ectomycorrhizal root tips, and diversity through metagenomics of soils. In this presentation we will discuss how scaling influences estimates of ectomycorrhizal taxonomic and functional diversity, and how and why different estimation methods may led to contrasting estimates. Much of the work presented originates from a meta-analysis for a total of forest 98 sites. We investigated structural and functional traits of ectomycorrhizal communities of three important tree species in European forests, namely *Fagus sylvatica, Picea abies* and *Pinus sylvestris.* A common pattern in the ectomycorrhizal community structure emerged, with a small number of high abundance taxa and a large number of low abundance taxa. However, the species identity of the high or low abundance taxa depends upon which structural part of ectomycorrhizas is used in the estimate, and the estimation method used.

Storytelling for science communication and media engagement

Ewa Hermanowicz

European Forest Institute

Storytelling is one of the most effective and natural mechanisms to supply new knowledge to the human brain. Using a storytelling approach in communications enables audiences of different professional and social backgrounds to learn about forest research projects. It also increases the likelihood of engaging media, thus increasing the visibility of the work. The session will focus on digital storytelling and filmmaking, which can be used effectively in a broad range of projects to drive change.I will outline the building blocks of an effective story and explain how these translate into film production. An essential building block is a character to whom viewers can relate, who conveys the key messages through an authentic voice. The session will include a screening of a film ‘The past and future of a unique pine population’ to illustrate the proposed ideas and analyze the steps for a successful production.

Keywords: storytelling, communication, filmmaking

Guidelines for conducting forest genetic monitoring of the seven tree species – *Abies alba/Abies borisii-regis* complex, *Fagus sylvatica, Fraxinus excelsior, Pinus nigra, Populus nigra, Prunus avium, Quercus petraea/robur* complex

Darius Kavaliauskas[1], Barbara Fussi[1], Marjana Westergren[2], Paraskevi Alizoti[3], Gregor Božič[2], Andrej Breznikar[4], Marko Bajc[2], Dalibor Ballian[5], Evangelos Barbas[3], Rok Damjanić[2], Natalija Dovč[2], Domen Finžgar[2], Ermioni Malliarou[3], Katja Kavčič Sonnenschein[2], Nikos Tourvas[3], Filippos Aravanopoulos[3], Hojka Kraigher[2]

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Genetic monitoring guidelines for seven target tree species (*Abies alba/Abies borisii-regis* complex, *Fagus sylvatica, Fraxinus excelsior, Pinus nigra, Populus nigra, Prunus avium, Quercus petraea/robur* complex) were developed within the LIFEGENMON project in order to facilitate the implementation of their genetic monitoring at the European level. They provide concise guidance on how to select and establish genetic monitoring plots and on recording all field level verifiers and background information for different "model" species by taking into account their differences in mating systems, distribution, ecology, etc. The emphasis was put on the peculiarities of genetic monitoring for each tree species. Genetic monitoring guidelines for each one of the seven species took into account the biology of the species (e.g. pollination system), distribution (scattered or continuous) and the economic and ecological value of the species. The guidelines for *Fagus sylvatica* and *Abies alba/Abies borisii-regis* were prepared based on results from actual test sites, monitored in the frame of the LifeGenMon Project, in the transect from the south of Germany to the north of Greece. The above test sites will remain available for future genetic monitoring and research. The FGM guidelines of the seven selected species are expected to contribute to the establishment of a network of genetic monitoring plots across Europe for the early assessment of climate change impacts on the genetic variation of forest tree populations, so that their adaptive management can be implemented efficiently and effectively.

Keywords: LIFEGENMON, genetic monitoring plots, verifiers, indicators, monitoring plots network

The indicator “gene flow / mating system” to monitor genetic changes over time in European beech and Silver fir

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Gene flow (Nm) is among the most important factors shaping the genetic diversity and structure of forest tree populations and can be determined by the mating system that intervenes the recombination and variety of genes between generations and determines the level to which genes are exchanged between individuals and populations. Therefore, variation in the mating success of both males and females disrupts the assumption that populations/trees are mating randomly. Plant mating systems are usually defined by the mixed mating model, where one part of seeds/plants are derived from selfing (self-fertilization) and the rest are derived from outcrossing at random. In particular outcrossing, promotes gene flow, homogenizes populations, increases heterozygosity, and favors gametic linkage equilibrium.

However, climate change can affect gene flow and mating system patterns e.g. trough irregular reproductive cycles, asynchrony in flowering time and changes in gene flow. Therefore, reproduction success and genetic variation of seed crop/upcoming generation can decrease drastically in different forest populations. In order to understand how gene flow and mating patterns impacts genetic diversity forest genetic monitoring (FGM) should be used as an early warning system.

Six FGM plots, three for *Fagus sylvatica* and three for *Abies alba/Abies borisii-regis*, were established in a transect (Fig. 1) from south of Germany to Greece. In total 400 seed (20 seeds per 20 mother tree) and 250 adults were genotyped from each plot at 11 microsatellite loci. Results regarding gene flow and mating system analysis will be presented.

Keywords: outcrossing, inbreeding rate, FGM, *Fagus sylvatica, Abies alba, Abies borisii-regis*, SSR

Forest ecosystem restoration success factors and the role of animals in seed dispersal inferred from DNA metabarcoding

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Forest ecosystems restoration is a growing field to palliate to biodiversity loss and desertification and to tackle climate change issues. However, many reforestation projects are limited to planting trees very often of the same species, disregarding their genetic diversity and their function in the future forests as well as their resilience. Taking into consideration the plant species diversity, the plants genetic diversity; animals and microbiological components are key factors to insure the success of the ecological restoration action.

In my presentation I'll be addressing forest ecosystem restoration in the Eastern Mediterranean Region (EMR) which includes high diversity of tree species at the hinge of three continental fringes. In this region, climate and geological events played a key role in determining the spread of these species and the persistence in their natural habitats. These events left genetic imprints that we were able to unravel using genetics tools. Recently, humans have had a local impact on the EMR forest ecosystems that made it fragmented and degraded, where some of these tree species have been intensively exploited and /or overgrazed, especially the ones sited at timber lines at high altitude. Besides, while exploring different restoration practices related to plantation techniques and genetic resources used, we tackled an important ecological process which is seed dispersal by different frugivorous guilds animals. An innovative approache has been used based on the identification of consumed plant species by characterization of animal DNA collected using DNA metabarcoding following a non-invasive sampling technique. This is important for the conservation of habitats, because it can palliate the effects of fragmentation by connecting natural remnants. Furthermore, by combining ecological and genetic tools, we have been able to discern different complex ecological interactions that may drive forest ecosystem restoration to success.

Answering these questions allows us to gain a holistic view on the forest ecosystem and include in the management plans tangible steps to address success factors.

Forest genetic monitoring – where from and where to?

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The existence of different 'landraces' of forest trees have been reported already in the 18th century, first provenance trials were established in early 19th century, and large disasters from using inappropriate origin of forest reproductive material lead to the establishment of the corresponding IUFRO session in 1910 (Nanson 2004). Consequently the role of genetic diversity of forest trees has become aparent through the acitivies of the Department for Forest Genetic Resources at FAO (since1968), and the establishment of a programme on forest genetic resources was proposed at MCPFE (Forest Europe) conferences (Strassbourg 1990, Helsinki 1994).

Since 1995 EUFORGEN, through its 6 phases, has been developing the basis for the establishment of a dynamic gene conservation units network, the principles for forest genetic monitoring (FGM), as well as a number of reports and reccommendations for forestry professionals and policy makers.

EUFORGEN has been supported not only by national agreements, but also by a few international projects. Among these, LIFEGENMON is the first European-wide implementation project aiming at developing a system for FGM, starting from selecting and testing the methods of aquisition, importance and costs of FGM indicators and verifiers, to presenting and implementing the system in forestry practice and national legislation, as well as through promotion of forests and forestry to different audiences.

In 2020 the 6,5 years project is fully preparing the Manual for FGM Application in Europe and the Decision support system supporting the AFTER LIFE plan for conservation of the adaptive potential of future forests under changing environment.

Forests - The past, present and the future

Robert MAVSAR

European Forest Institute

Forests has always been an important element of our societies. Even during the past decades, when fossil fuels had been the main "engine" of the economic development and prosperity, forest have maintained their role, and even further strengthened it by an increasing importance of ecosystem services. With the current climate crisis and the urgent need to re-think our economic model, making it sustainable within the boundaries of our planet, forests are again at the center of attention. For example, the European Green deal, which highlights the circular bioeconomy concept, aiming at decoupling the economic growth from the environmental degradation, is stronger relying on renewable and "locally" produced resources, like wood. However, at the same time forests are also consider as key for the conservation of biodiversity.

This brings an enormous responsibility to forest owners, managers, policy makers and experts to design policies and management practices and tools, that will help fostering the resilience of forests to adapt to- and mitigate impacts of clime change, while at the same time provide the society with the demanded goods and services in a sustainable way. It will require innovative approaches to all aspects of forest management. For example, in terms of forest regeneration and restoration it will require to substantially improve the characterization of seed sources, and science based tools should be developed and made available to support end-users to identify forest reproductive material that is genetically fitted for a specific sites. There is also the need to create a better link between conservation and targeted use of forest reproductive material. But it will also require adjusting current policies to allow forest management practices to better respond to the increased expectations from forests and the forest based sector.

Utilizing the adaptive potential of trees for assisted gene flow and climate smart forestry

Silvio Schueler

Department for Forest Growth and Silviculture, Austrian Research Centre for Forests, Austria

Developing and implementing management strategies to mitigate the negative consequences of climate change and to adapt forest ecosystems have become a priority within the last decade. Among a variety of measures, afforestation programs have become the mostly claimed nature-based solution to remove carbon from the atmosphere and to store them in natural forests and wood products even if their extent and side effects are discussed controversially. Moreover, forest transformation and reforestation programs including new tree species mixtures, non-native tree species and new regeneration stocks are supported to maintain the provision of ecosystem services also in the future. Both, afforestation and reforestation activities require the selection of appropriate forest reproductive material (FRM) to become effective. Therefore, forest genetic knowledge and its applications in forest and landscape management are expected to play a pivotal role at this turning point of our human society. Our future work will need to be based on past challenges and experiences, as for example the understanding of patterns of genetic diversity, the monitoring of genetic resources and their conservation across species ranges. Newly appearing challenges include for example a better utilization of genetic resources in reforestation and afforestation schemes without limiting transfer to national boundaries and a stronger connection between forest genetics to adjoining disciplines such as silviculture or forest protection in order to transfer knowledge into forest practice. In my presentation, I will introduce and discuss these challenges and provide insights into past and ongoing research activities aiming to tackle them.

Conservation of forest genetic resources, adaptation, and resilience: what do we know and what do we still need to know?

Ivan Scotti

Ecologie des Forêts Méditerranéennes, French National Institute for Agriculture, Food, and Environment (INRAE)

The conservation of forest genetic resources needs to take adaptive potential and resilience into account. Over the course of the last decades, knowledge has accumulated about functional molecular variation and the variability of adaptive traits, but this does not automatically mean that we hold the key of the understanding of adaptive mechanisms and their potential utility in defining conservation programs.

We need to be both optimistic and realistic in the evaluation of the kind of information we possess and the disclosures we may obtain within the next decade. It is likely that we will need to integrate multiple areas of research and heavily rely on modelling if we wish to really take advantage of adaptively significant variation in conservation programs. In this talk, I will review the state of the art and suggest some matters for discussion about where to go next.

Keywords: adaptability, climate change, forest dynamics, population genetics

LIFE for European Forest Genetic Monitoring System (LIFEGENMON) communication and dissemination activities

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A large share of the LIFEGENMON project was dedicated to communication and dissemination activities. The aims and results of the project with regards to the LIFE+ requirements were communicated and disseminated to the general public and to specific target groups with different approaches. The general public was informed about the importance of forests' ability to adopt to the changing climate and the role of FGM through films, festivals, events, fairs, the most common social media (facebook, twitter & linkedin) and even a smartphone app called Seedhunter. In all these activities scientific information was explained in a simple language. The aquired knowledge enables the public to make better informed everyday decisions and exercise pressure on policy makers if needed. A special focus of the communication activities was put on children. Children books, workshops and events were aimed at creating a respectful attitude towards forests from the early age. In contrast, the scientific community, forestry professionals and policy makers were addressed mainly through workshops, publications and presentations. All project communication and dissemination activities informed about genetic diversity as a key factor in maintaining the vitality of forests to cope with different environmental conditions, pests and diseases. Communication and dissemination supported the project objective to develop measures for adaptive forest management based on genetic forest protection. They encouraged knowledge exchange within and between project partner countries (Slovenia, Germany and Greece).

Keywords: communication, dissemination, media, events, wokshops, policy makers

Genetic and genomic landscape approach for adaptative forestry in climate change

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The functioning of ecosystems depends on the adaptation of living organisms to their environment. Forests will need to respond within a few generations to more frequent extreme climate events, modified average climate parameters and other related changes. Consequently, forest services will depend on the intensity and speed of the evolution of tree populations response to climate change. Genetic adaptation, the genetic change of a population in response to natural selection, can be rapid and contribute to the ecological success of species facing climate change. The European Environment Agency stated that “genetic variety in regionally adapted forests is essential for adapting to new environmental conditions such as climate change”. The State of the World’s Forest Genetic Resources reported that roughly half of the forest species were threatened or subject to genetic erosion. The adaptability of forest tree populations is enormous but not unlimited. It is extremely important to provide a sustainable forest management approach to local and rural community for sustainable use of forest products while preserving forest genetic resources. The potential of using a genetic (neutral markers) and genomic (adaptive markers) landscape approach to study the adaptation of trees to the environment and the potential of local populations to cope with climate change appears to be the most suitable tool to address silvicultural practices for better adaptive forestry. Therefore, LIFE SySTEMiC’s principal aim is to apply the landscape genetic and genomic approach for examining best close-to-nature forest management regarding FGR in different European Forest Types for diverse forest management systems.

Keywords: adaptative genetics, landscape, climate change, silviculture

VOLUNTARY ORAL PRESENTATIONS

What constitutes a biologically significant difference in the frame of forest genetic monitoring temporal assessments?

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A major challenge of forest genetic monitoring (FGM) is the absence of established protocols for comparing genetic monitoring indicators. FGM may operate on the statistical significance and/or critical difference of temporal reference points. Three levels of critical difference are identified: statistically significant differences (SSD), differences that in addition to the above exceed by ≥ 25% the previous value, and differences that, besides being SSD, exceed by ≥ 50% the previous value. For the verifiers of indicator “selection” (mortality, survival, natural regeneration abundance, number of reproducing trees, flowering, fructification), of indicator “genetic variation” (latent genetic potential, inbreeding coefficient, allelic richness, interspecific hybridization) and indicator “mating system” (gene flow, multilocus outcrossing rate, actual inbreeding rate), an ANOVA approach (e.g. a t-test) can be used to assess for SSD among the values obtained over temporal assessments, or alternatively a non-parametric test can be used (e.g. a Kruskal-Wallis test). For verifier “allele frequencies” that belongs to indicator “genetic variation” the Fisher’s exact test for contingency tables can be employed. Verifier “effective population size” is an exception to the rule of using comparative reference points, as a minimum threshold value of Ne ≥ 500 is suggested. The level of response by scientists and managers given the level of differences detected in the temporal assessments and the actions to be followed are presented. This is dependent on the number of verifiers that show a negative trend over the total number of verifiers, and the simultaneous provision that some specific verifiers are included among those showing the negative trend. Examples on the application of this scheme are shown.

Keywords: forest genetic monitoring (FGM), indicator, verifier

Epigenetics & Genetics: unrevealing the secrets beyond genes empire; a holistic way to cope with climatic changes

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Forest species already facing a variety of biotic and abiotic threats acting singly and in combinations, which are triggered by climatic changes. Trees cannot avoid unfavorable situations by moving over long distances to more suitable environments. Ensuring future survival of forest species became a priority for the European countries, by establishing reservoirs of genetic variation (eg Natura 2000 protected areas), but is this enough for their conservation? As scientific results raise, new insights about Lamarck’s theory, which stated that the environment might affect phenotype and this new character can be inherited are being scientifically proved through epigenetics. Epigenetics is defined as the study of heritable changes that do not alter DNA sequence. Methylation of DNA, modification of histones, structural changes in chromatins and non-coding RNA are mechanisms of epigenetics. The current study will focus on five axes: genetics and relation with epigenetics; epigenetics and speciation; epigenetics and conservation; epigenetics and heritability and monitoring epigenetics. A holistic approach that encourages the study of genetic and epigenetic variation may be the missing data that science has to discover to ensure sustainability, conservation, and adaptation for forest species under changing environmental conditions.

Measuring recent gene flow among large tree populations: a case study with *Pinus sylvestris* populations in different edaphic environments

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INIA

The estimation of recent gene flow rates among vast and often weakly genetically differentiated tree population remains a great challenge, even if it would provide necessary empirical information about the poorly understood interaction between gene flow and local adaptation in forests. The objective is to estimate recent gene flow rates among two big native Scots pine (*Pinus sylvestris*) populations in central Iberian Peninsula, growing on contrasting edaphic conditions six kilometers apart from each other, using a Bayesian approach, based on uniparentally inherited markers. We found substantial and asymmetric gene flow rates (8 and 21%) among the two populations and even greater recent gene inmigration (42-64%) from nearby plantations. Overall, we believe that a combination of hypothesis might explain the apparent joint presence of gene flow and strong adaptive genetic differentiation: divergent selection, decreasing migrant fitness with age and environmental maternal effects.

Keywords: Pollen dispersal, Bayesian inference

Lifegenmon Forest Genetic Monitoring Manual

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In the light of negative impacts of climate change and other human disturbances on forest ecosystems, genetic monitoring has been identified as a tool that can help preserve genetic diversity and serve as an early warning system for negative changes in forest ecosystems. The scope of Lifegenmon project was the implementation of forest genetic monitoring system for European beech (*Fagus sylvatica* L.) and Silver fir / King Boris' fir (*Abies alba* Mill. / *Abies borisii-regis* Mafft.) in Germany, Greece and Slovenia.

Forest genetic monitoring manual represents the culmination and the pivotal deliverable of the implementation of forest genetic monitoring system in the Lifegenmon project. Instructions and recommendations for carrying out all stages of genetic monitoring ¬– from selection of monitoring plots to analysis and interpretation of data – are described within it, based on hands-on experience and findings accumulated during the project by the participating partners. The manual is intended as a go-to document for any organisation wishing to establish a forest genetic monitoring system in their country. The focus of the presentation is the organisation and contents of the manual.

Keywords: forest genetic monitoring, guidelines, protocols, manual

Introducing a web-based population genetics analysis platform for use in the LIFEGENMON project and beyond

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We have developed an open-source, web-based Shiny application designed to facilitate the analysis and interpretation of results from population genetics studies principally within the R environment. There are both many stand-alone programs (e.g. GenAlEx) and R packages available in CRAN and other repositories which can be used for this purpose, but a comprehensive analysis pipeline requires switching between programs, or finding the correct R package to perform the required function. We have aggregated a number of available packages to create a novel analysis pipeline which simplifies and streamlines data analysis while ensuring transparency and reproducibility. Our application can filter data, assess population diversity and structure, and deliver publication quality ordinations and other figures to visualise data. This is both an integral part of data analysis and result dissemination within the LIFEGENMON project, and a stand-alone application to be used by others in the field.

Keywords: Population Genetics; Shiny; R; Bioinformatics

Temporal variation in effective reproductive success and non-random dispersal in forest trees

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The effective population size and population genetic diversity, two key evolutionary parameters shaping the adaptive potential of forests to climate change, are affected by the differential contribution of individual mother and father trees to the regeneration. Individual parent contributions coupled with post dispersal mortality, microsite heterogeneity, genotype-microsite interactions and Janzen-Connell effects will shape the diversity of natural regeneration which carries the potential gene pool to withstand the impact of climate change.

To gain insight into the patterns of recruitment of European beech (*Fagus sylvatica*) and silver/King Boris fir (*Abies alba/Abies borisii-regis*), the seedling and seed dispersal kernels coupled with temporal variation in the effective reproductive success were studied. Per species 250 adult trees, 200 seedlings from two reproduction events and 400 seeds from 20 half-sib families were sampled in Greece, Germany and Slovenia. Parentage was reconstructed with 11 SSR loci using a Mixed Effects Mating Model, which estimates the pollen and seed dispersal function and the variance in fecundity on the basis of spatial and genetic information.

The first results (Slovenia) for the first sampling show highly skewed effective reproductive success in both species. This is because the age of natural regeneration in the first sampling greatly varied, representing multiple cohorts that have already undergone a certain level of natural selection, whereas in the second sampling all saplings were approximately the same age. The models based on seeds showed a different dispersal kernel than those based on seedlings, suggesting post-dispersal mortality in seedlings that was not random.

Keywords: adaptive potential, parentage reconstruction

Genetic Analysis of Silver Birch (*Betula pendula* Roth) Populations in Their Southern European Distribution Range

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In the main distribution area, the genetic pattern of silver birch is dominated by two haplotypes: haplotype A located in the western and north-western Europe, and haplotype C in eastern and southeastern Europe, characterized by high levels of neutral genetic variability within populations, and low differentiation among populations. Information about the amount and structure of genetic variation in the southern marginal areas, representing rear populations left during the expansion of this species from southern glacial refugia, are lacking.

The study aimed to investigate the patterns of genetic organization, variation and gene flow in two European silver birch (Betula pendula) refugia, on the Italian Apennines and Greek Southern Rhodope, and compare them with populations of the southern part of the main distribution range on the Alps and Balkans.

Genetic analysis was performed using nuclear microsatellites loci on 311 trees sampled from 14 populations.

We observed a lower genetic diversity and higher differentiation in the peripheral Apennines populations compared to the core populations, with evident genetic barrier detected around these sites. On the contrary, in the Greek populations, neither a change in diversity nor in differentiation from the core area was observed. The Greek populations also showed evident gene flow with the Alpine and Balkan areas. Our study has shown that it is not the peripherality or the ecological marginality that may shape the genetic diversity and structure of marginal and peripheral populations, but primarily their position as part of the continuous range or as disjunct populations. This outcome suggests different considerations on how to manage their gene pools and the role that these rear populations can play in maintaining the biodiversity of this species.

Keywords: marginal populations, population structure analysis, gene flow

Contribution of the H2020 GenTree project to selecting meaningful proxies for gene conservation and genetic monitoring

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Through its consortium and its strong stakeholder engagement, GenTree was able to disseminate ideas, increase knowledge and raise awareness of the importance of genetic diversity as a resource for safeguarding healthy forests in an era of climate change and evolving societal demands, thus strengthening the European programme EUFORGEN.

The 12 forest tree species studied by the GenTree consortium can be considered as models for all forest tree species listed in Directive 1999/105/EC, which regulates their trade in the EU. This is because these 12 species cover a wide range of bioclimates and forestry use, but also because the scientific analysis approaches used in GenTree relied strongly on integrated sampling strategies, transferable genomic methods and process-based modelling. When fully exploited, the data provided by GenTree (open access and re-usable) will have considerably increased our understanding of the where and how of local adaptation.

Other long-term expected impacts include providing evidence of the role of policy change concerning FGR on the forest nursery sector, demonstrating the role of FGR conservation in managing protected areas, contributing to nature-based solutions and helping sustainably manage forests at a time when environmental conditions are drastically changing.

In total, 4700+ trees from 12 species and 210 sites were sampled across Europe. Trees in populations were characterized for traits useful for adaptation and response to global change, from both a conservation and a breeding perspective, and their leaves sampled for DNA extraction and functional trait measurements. The ecological and climate conditions of the sites were fully described. I will discuss which traits seem useful for genetic monitoring.

Genetic effects of applying Continuous Cover Forestry in non-native conifer UK populations

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Even-aged plantations of non-native conifer species and clear-cutting silvicultural practices are widely used in UK forestry to maximize timber harvest yield. However, increasing concern for the future adaptability of forests and current policy promoting forests that support a full range of ecosystem services are leading to changes in forestry management. Continuous Cover Forestry (CCF) is an approach to forest management based on the development of diverse stand structures composed of a mixture of species, managing the ecosystem rather than the trees and encouraging natural regeneration. While the transition to this type of woodland is a well-defined silvicultural approach, there is a current paucity of studies on how the transmission of the gene pool from canopy trees to the next generation may affect the genetic diversity (GD) of future forest stands. The GD of non-native plantations may be lower compared to native woodlands. Moreover, the offspring of a population already lacking genetic diversity may be maladapted. The purpose of this project is to assess the genetic effects of applying CCF approach in non-native conifer UK populations composed by *Pseudotsuga menziesii*, *Thuja plicata* and *Tsuga heterophylla*. Therefore, we will compare genetic diversity parameters between canopy trees and natural regeneration by testing populations from natural distributions in North America and non-native populations in the UK exhibiting different stages of CCF. The genetic diversity will be measured using a SNPs genotyping approach developed in a high-throughput microfluidic PCR system. The integration of these results will be used to develop recommendations for natural regeneration management in CCF populations.

Keywords: Forest Management, Continuous Cover Forestry (CCF), Natural Regeneration, Genetic Diversity, Single Nucleotide Polymorphism (SNP)

Identification of genetic diversity by molecular markers in natural *Pistacia lentiscus* populations and mastic clone park

Gaye Kandemir, Yasemin Tayanç, Burcu Çengel, Selim Kaplan, Hikmet Öztürk

Mastic tree (*Pistacia lentiscus*) is one of the inportant shrubs in Mediterranean scrub. In Turkey there are two taxons of mastic trees as Pistacia lentiscus and Pistacia lentiscus var. chia. Although, there is secretion of gum from both taxons by the injury of phloem channels of trees, mastic production has been get only from P. lentiscus var. chia. Which are very important economically and ecologically therefore the conservation of this species are essential for the sustainability of future populations. In addition, for the effective protection of species, there is the need of genetic knowledge.

Aim of this study is to examine the genetic diversity of natural populations and selected clones which are used for the construction of clone park. In the line of this goal the relationship of 90 clones in clone park was determined by SSR primers. It has been found that 5 clones have the same band structure and 2 clones have a very similar structure. Using the same primers, genetic diversity information of 3 natural populations (from İzmir- Çeşme, Muğla- Fethiye and Muğla-Köyceğiz) was obtained by using scattered distributed 40 individuals (20 female and 20 male) from each populations. Population differentiation were found to be quite low (Gst = 0.0618). However, the variance between wild populations and Clone Park is 16%. The highest variation among the populations was found in the Çeşme male (Ho = 0.467) population. The lowest variation was found in the clone park (Ho = 5.75).

Keywords: *Pistacio lentiscus, Pistacio lentiscus* var. *Chia*, mastic tree, microsatellite SSR

Forest genetic monitoring Integration to forest management plans

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The European Commission has adopted the new E.U Biodiversity Strategy for 2030 as a core part of the European Green Deal. Also F.A.O during 2020 reports have upgrade the impact of genetic resources to the forest management and to the effectiveness of policies of conservation and sustainable development outcomes.

Forests serve both human and environmental needs and have major role in climate change. This role can be reached under sustainable forest management where biodiversity conservation is the end point. The variation of forest management and common objectives across Europe follows the diversity of sites condition while the history of management and land use effects the current status of forests and its genetic diversity. Genetic monitoring focus on the systematic observation of genetic processes within a population on a long-term scale and to conclude throughout the ages for the gene flow stability and the plants phenology.

Our selected purpose through this paper is to compile the necessary protocols and specifications of selected parameters and indicators of forest genetic monitoring for species that were selected as important for EU forestlands as common objective of forest management plans. Also to propose to integrate the existing management plans protocols, in accordance with current legislation, the environmental economy and the selected objectives.

Keywords: forest genetic monitoring, forest management plans, climating change, LIFEGENMON

Population differentiation in *Acer platanoides* at the regional scale – laying the basis for conserving its genetic resources in Austria

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Norway maple (*Acer platanoides* L.) is a widespread forest tree species in Central and Northern Europe but with a scattered distribution. On the other hand it is widespread as an ornamental tree and is naturalizing in waste places in urban areas. In the debate on climate change driven changes in species selection in the forest, Norway maple has recently received raised interest because of its comparatively high drought resistance (higher than in sycamore maple). Therefore it is an interesting species for sites high in carbonates and where other trees species have become demolished by pathogens (e.g. elm, ash). In Austria also the demand on saplings has risen, while there is only very little domestic reproductive material available (on average more than 95% of saplings are imported from neighboring countries). This study was undertaken to identify genetic diversity and population structure of Norway maple in Austria to lay the foundation for the establishment of respective seed orchards.

Keywords: Population Genetics; Shiny; R; Bioinformatics

Policy and practice in conservation of FGR in selected LIFEGENMON transect countries

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Forest genetic resources (FGR) grow accross national borders. To support the adaptation potencial of forests to the changing environments, enrichment planting with provenances adapted to possible future conditions, and a highly diverse forest reproductive material (FRM), should be supported when used for reafforestation.

The performance of FRM in certain environments can only be tested through long-term provenance trials. Provenance trials can in practice be replaced by a series of well designed and documented regular enrichment planting in different forest management regimes. For this, selected provenances from SE regions with respect to the destination site of planting would preferably be chosen, if the legislative basis of trading and use of FRM allows.

During a series of workshops the LIFEGENMON team has collaborated closely with experts from each 'transect' country between Slovenia & Greece, acting as the National Focal points (NFPs). NFPs have provided detailed knowledge of the performance of each of their provenances of forest trees in different environments, as well as contacted responsible ministries and other important stakeholders at the national level. During the workshops, the national legislation has been checked up for BiH (two entities), Bulgaria, Croatia, North Macedonia and Serbia. Two of the mentioned transect countries are part of the EU, 2 are part of OECD Forest Seed and Plant Scheme, while for others the legislations and control procedures yet need to be harmonized efficiently in order to allow a limited quantity of FRM to be used (and tested) in the future provenance trials within the EU.

A comparison of radial wood increment and wood density of six different beech provenances

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Slovenian Forest Institute

Tree-ring widths and wood density were examined in 21-year-old beech (*Fagus sylvatica* L.) trees from the international beech provenance trial set on Kamenski vrh, Novo mesto, Slovenia in 2019. Six different provenances were selected for sampling, three originating from Slovenia (Postojna Mašun, Idrija-II/2 and Postojna Javorniki) and three originating from elsewhere in Europe (Soignes from Belgium, Val di Sella from Italy, and Nizbor from the Czech Republic). Wood density was measured in 30 standing trees using resistance drilling and increment cores were taken from a smaller subsample of 11 beech trees. The cores were then dried, glued into holders, sanded and tree-ring widths measured. Diameters at breast height of the selected trees were similar between the sampled provenances. Although the Idrija provenance from Slovenia had the highest mean wood density, the values of mean density were relatively similar across the six provenances. Larger differences between provenances were found between maximum and minimum wood densities than between mean values. When comparing tree-ring widths of the six provenances, there are notable differences between them. For example, in the year 2014 with above average precipitation, the highest radial increment can be found in the Soignes provenance (5 mm) and the lowest in trees originating from Val di Sella (3 mm), which is a 40 % difference. In year 2017 with below average precipitation, all provenances were similarly affected, and the largest difference was 0.5 mm, between Soignes and Idrija. A more thorough analysis of the obtained density values is required to make any definite conclusions.

Keywords: tree-ring width, wood density, beech, provenances

Genetic monitoring in beech populations with genetic and epigenetic markers

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Genetic monitoring is a tool of study and research with prognostic value which ensures the protection of processes that maintain genetic variation in natural populations. Genetic monitoring was applied in three different stages of a natural population of *Fagus sylvatica* (adult trees, regeneration and seeds). Two experimental plots with diversifying characteristics were chosen in the Neochori region, in Chalkidiki. Sample collection took place at a temporal scale, in two different time points over a 5-year period. To estimate the levels of genetic diversity, 16 f-SSR markers in three combinations in 1971 samples of Fagus sylvatica taken from both plots were used and 16 loci with an average of 7.17 alleles per locus were found. Percent polymorphic loci for both plots was 98.96%. Moreover, the potentially adaptive genetic variation in terms of single-nucleotide polymorphisms was studied, using 144 SNPs derived from 58 genes that are implicated in mechanisms related to drought tolerance, in 219 beech trees from the low altitude stand. The total number of bi-alleles that was observed in the adult population was 269 and in the regeneration population 263. Eight combinations of f-MSAP markers were used in 503 samples from both plots. They yielded 1811 epigenetic loci. The percent of polymorphic epigenetic loci for both stands was 33.33%. The results showed that the studied populations overall maintain their genetic diversity and their adaptive evolutionary potential, however the process of genetic monitoring must continue, as an evolving process and within the framework dictated by the current theory.

Keywords: SSR markers, MSAP markers, *Fagus*, SNP, gene flow, genetic diversity

Xylogenesis in European beech under climate change

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Climate scenarios for Slovenia suggest an increase in the mean annual temperature by 2°C over the next six decades, associated with changes in the seasonal distribution of precipitation. It is important to understand the influence of changing environmental conditions xylem productivity and phenology of wood formation in European beech, which is among the most widespread species in Europe. We hypothesised that the ongoing warming and reduction in precipitation during the growing season would shorten the period of xylem development, thus limiting beech growth in the next decades.

Xylem formation was monitored weekly between 2008-2016 at two sites in Slovenia. Onset and cessation of cell enlargement and secondary wall formation, as well as xylem growth, were used to evaluate climate-growth relationships by means of partial least squares regression and to predict xylem formation phenology and annual xylem increments under climate change scenarios.

A positive correlation of spring phenological phases with March–May temperatures was found. In contrast, autumn phenological phases showed a negative correlation with August and September temperature, while high temperature at the beginning of the year delay growth cessation. According to the selected climate change scenarios, phenological phases may advance by 2 days decade-1 in spring and delay by 1.5 days decade-1 in autumn. The duration of the growing season may increase by 20 days over the next six decades, resulting in 38% to 83% wider xylem increments. The growth of beech is expected to increase under a warming climate in the sites characterised by abundant water availability.

Keywords: climate change, cambial productivity, phenology, PLS regression, wood formation, *Fagus sylvatica*

From Science to Practice: the Implementation of Forest Genetic Monitoring in Policy, Regulation and Forestry Practice

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LIFEGENMON (LIFE for European Forest Genetic Monitoring System) is a project for the development and implementation of a forest genetic monitoring (FGM) system. In order to implement its results in forestry practice and forestry and environmental regulations, policy and legislation in different European countries, a multitude of activities have been planned and carried out.

The LIFEGENMON project team has organised and participated in several international and global workshops for different expert stakeholders. This culminated in the LIFEGENMON and GenTree Common Stakeholders Event (Thessaloniki, 2017), which gathered relevant experts, stakeholders, practitioners and scientists from Europe and promoted and facilitated the understanding of forest genetic monitoring for different levels of stakeholder groups.

National workshops have been organised in Slovenia, Germany, Greece and other European countries, with the aim of knowledge transfer and stakeholder dialogue in different countries and regions and on all levels of discussion - from academics to the general public. Expert workshops for forestry professionals formed the backbone of the targeted project dissemination and raised awareness of project aims and results within expert communities.

Materials for different stakeholders have been published via printed and e-publications, web portals, videos, children's books and materials for teachers, guidelines, presentations etc. A special emphasis was placed on working with the media in order to reach wider audiences and build political support for the implementation of the FGM system.

The final results of the undertaken work will become visible after the project's conclusion, however, the early adoption of parts of FGM system has already begun.

Keywords: Forest Genetic Monitoring, Workshops, Policy, Legislation, Practice, Implementation, Dissemination, LIFEGENMON

Forest tending of the seed stands with the I+ Trainer virtual tool

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A Lifegenmon workshop on forest tending of seed stands was intended for the forestry experts with the main focus on planning and implementing measures of forest tending in the seed stands.

Beech seed stand Pri Studencu, located in Dvor pri Žužemberku, Slovenia is a plot for forest genetic monitoring of European beech (*Fagus sylvatica*). To show principles of forest tending in seed stands, the I+ Trainer virtual tool was used. With this tool, we made a virtual tree selection. The most important criteria that influenced the decision to select trees for felling were the morphological signs of the tree, the provision of their seed and the structure of the forest stand. The focus was primarily on keeping the highe quality trees in the stand and removing the trees with negative morphological signs (eg. twin stem, curvature of the trunk, asymmetry of the crown, etc.).

I+ Trainer is used together with Marteloscopes, that are 1 ha big plots, a training areas for the selection of trees for felling. On these plots all trees are numbered, tree locations and all parameters (dbh, height, microhabitats or different phenotypic signs in our case) are defined. All trees on the plot are displayed in the I + Trainer application that is installed on tablet computers. With this application, the participants select trees that should be harvest and at the end of the workshop results of different groups can be reviewed and compared with each other.

Keywords: I+ trainer, virtual tool, seed stand, workshop, Marteloscope

Genetic monitoring in the hybridogenous fir (*Abies borisii-regis*): Interpretation of the first temporal and intergenerational comparison using SSR genetic markers

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Abies borisii-regis Mattfeld, is an interspecific hybrid resulting from the introgression between silver fir (*Abies alba* Miller) and the endemic Greek fir (*Abies cephalonica* Loudon). Hybridogenous populations of the species include hybrids and backcross generations and are expected to respond to climate change more efficiently by exploiting their unique gene pool originating from two species occupying different ecological niches. Forest genetic monitoring (FGM) has the potential to elucidate the effects of environmental stress imposed by climatic change to this hybridogenus fir in terms of demography, diversity and differential genome dynamics. A FGM plot of *Abies borisii-regis* has been established in Mt. Olympus - Greece, within the framework of the EU LifeGenMon project. In 2015, 250 adult trees, 200 saplings from the natural regeneration, and 400 seeds were sampled and genotyped at 11 microsatellite loci. Furthermore, in 2019 the genetic diversity of a second sample of 200 seedlings from the same plot was also assessed. In this work, the results of these analyses are evaluated by comparisons between: (a) the three life-stage cohorts, (b) the two temporal samples, as well as by (c) assessing differences with the published literature for proximal populations of the same taxon.

Keywords: conservation genetics, EU LifeGenMon project, FGM, genetic diversity

General public dissemination of Lifegenmon project: a story of success

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The dissemination strategy of the LIFEGENMON project focused on the promotion of forestry, forest management, forest genetics and the effects of climate change on forests. The aim was to address the general public as well as various stakeholders and policy makers. In order to achieve an efficient transfer of knowledge, the dissemination activities were divided into main target groups, taking into account differences in age, interests and level of knowledge. Particular attention was paid to dissemination activities for kindergarten children and pupils in primary and secondary schools. The dissemination activities for this target group brought knowledge not only through listening and watching, but also through touching, smelling and personal experiences in the forest. The challenge that arose was: How can children and pupils be reached most effectively? The answer of the LIFEGENMON project was: through activities and teaching materials for kindergartens, schools and families. Five different approaches were used:

1. children's books and cartoons about forests, forestry, forest genetic resources with augmented reality animations,

2. workshops and public open days for kindergartens and schools, aimed at children, their teachers and educators,

3. training courses and teaching materials for teachers and educators,

4. a smartphone app for children, their teachers, educators and parents,

5. events for families.

Through the activities and materials, more than 56,600 children, parents, teachers and educators were reached and got to know the LIFEGENMON project and its results, some of them through more than one approach, which allowed a synergistic effect of the dissemination activities.

Evolutionary potential in a natural beech population

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Local survival of natural populations of forest trees relies on standing genetic variation and their capacity for adaptation to changing environments. Selection gradients, heritability, evolvability and selection response was studied in a natural population of European beech (*Fagus sylvatica*) in Slovenia. Adult trees (250), saplings (200), from two different reproduction events, and 400 seeds obtained from 20 mother trees, were genotyped with 15 nuSSRs. Adaptive traits related to growth, reproduction and spring and autumn phenology were assessed for all adult trees. Effective reproductive success, a fitness proxy, was estimated via parentage analysis. Log-linear models were used to compute selection gradients correlating adaptive traits with fitness. Heritability was estimated using mixed models based on pedigrees reconstructed using nuSSRs. The study revealed skewed effective reproductive success and significant selection gradients. Heritability was low to moderate and significant for all traits. Low phenotypic variance for phenological traits in combination with moderate selection gradients resulted in low responses to selection. However, evolvability reached up to 20% for certain traits, suggesting that the population has potential to adapt locally to novel conditions.

Keywords: *Fagus sylvatica* L., selection gradients, effective reproductive success, growth, phenology

POSTER PRESENTATIONS

Technical Guidelines for the genetic monitoring of *Pinus nigra* Arn.

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European black pine (*Pinus nigra* Arn.) is a wind-pollinated, monoecious, mainly outcrossing, high elevation, circum-Mediterranean conifer, that also grows in Austria, Crimea, and the Black Sea. Due to the species extensive distribution in a broad spectrum of environments, that led to its morphological and genetic differentiation, five interfertile sub-species can be recognized across its natural distribution. Moreover, numerous populations of the species can be considered as geographically or ecologically marginal and are thus of great interest for genetic monitoring in the face of climate change. Black pine is a valuable key-stone species of high economic and ecological importance, producing wood of high quality and natural durability. It is characterized by its tolerance to abiotic stresses, such as poor and salty soils, frosts, ice weight, strong winds, and drought. For all the reasons above the species is extremely suitable for genetic monitoring. The technical guidelines provide all the detailed information needed for its genetic monitoring, and specifically on the topics of species ecology, reproduction, threats, genetic monitoring plot establishment and maintenance, as well as detailed protocols for recording genetic monitoring verifiers and indicators at the basic, standard, and advanced monitoring levels. Goal of the guidelines is to facilitate the across Europe establishment of a genetic monitoring plots network that could yield detailed information on the species genetic response, adaptive potential and limitations to climate change.

Keywords: monitoring plots, monitoring verifiers, levels of genetic monitoring, genetic response

Monitoring phenology to assess the response and adaptive potential of a Hellenic *Abies borisii-regis* population to inter-annual climate variability

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Monitoring phenological traits may provide information of vital importance on the ability of individuals, populations, or species to adjust to climatic variations, by shifting the initiation and duration of biological events. Phenology could thus serve as an indicator of forest genetic material vulnerability in the face of climate change. The timing of phenological events, such as bud-break, flowering, etc. is dictated by environmental, physiological and genetic factors. Phases of phenological traits though, such as initiation of bud-burst or flowering has been proved to be under strong genetic control. In the present work the phenological trends of bud-break related to interannual climatic variability will be presented for two generations of a Hellenic *Abies borisii-regis* population, based on the assessment performed on 40 adult fir trees and 200 individuals of natural regeneration, growing in a LifeGenMon monitoring plot. The performance of natural regeneration individuals when compared to that of the adult trees may shed light on the adaptive potential of the genetic material to climate change. Additionally, results on flowering and its synchronization are presented for those years that flowering took place, testing whether the panmixia requirement has been satisfied, fact that indicates the expected genetic variation level in the produced seed crop.

Keywords: EU LifeGenMon project, monitoring plot, flowering, bud break, adults vs natural regeneration

Assessing the response of a Hellenic *Fagus sylvatica* population to interannual climate variability via monitoring the phenology of various biological traits

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Monitoring of phenology is the tool to assess the shifts of phenophases of biological phenomena due to interannual climate variability. Phenology is affected by environmental, physiological, as well as genetic factors. Phenological monitoring is thus essential to understand how the genetic material, (species, populations or even individuals) responds to changing environmental cues and to identify the potential limits of this response. Especially the phenology of flowering and its synchronization determines the levels of genetic variation present in the produced seed crop. Consequently, prolonged flowering discrepancies, due to climatic changes, may lead to reduced genetic variation of the produced seed and consequently the natural regeneration. For all the above reasons, and within the framework of the EU LifeGenMon project, the phenology of different biological phenomena (i.e. bud-break, leaf senescence, female and male flowering) has been monitored in a Hellenic *Fagus sylvatica* monitoring plot, located in the region of Chalkidiki peninsula. In the present work the phenological trends of bud-break, leaf senescence, female and male flowering will be presented, following their monitoring for four consecutive years. The results, based on the monitoring of the same 40 adult trees, growing in the monitoring plot, for all the studied traits, are discussed in conjuction to the interannual climate variation recorded in the site. The response of the genetic material to climatic factors, as determined by the phenology of initiation and termination of its growth period, and the initiation, duration and termination of its male and female flowering is discussed, together with the consequences that may occur from phenological discrepancies of the above biological phenomena.

Keywords: EU LifeGenMon project, monitoring plot, flowering, bud break, leaf senescense

Delineation of regions for forest genetic monitoring on a transect from Bavaria to Greece

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Conservation and management of forest genetic resources for sustainable use is a crucial, but not an easy task and special tools, such as forest genetic monitoring are needed to recognize the state and changes in their composition in a timely manner. Because resources are limited, one of the elementary requirements needed for implementation of forest genetic monitoring is delineation of monitoring regions, i.e. regions where genetic monitoring should be conducted to have maximum effect. Within the project, this has been done for seven tree species or species complexes differing in their biology and distribution (*Fagus sylvatica, Abies alba / A. borisii-regis* complex, *Fraxinus excelsior*, *Populus nigra, Pinus nigra, Prunus avium, Quercus robur / Q. petraea* complex). Criteria for selecting and delineating monitoring regions were: (i) equal coverage of environmental zones, (ii) coverage of distinguished races or ecotypes as well as inclusion of marginal and peripheral populations at the (latitudinal and altitudinal) leading and rear edge of the species distribution range, (iii) each region should preferably include already defined dynamic gene conservation units (EUFGIS), (iv) known levels of standing genetic variation, (v) equal coverage of standing genetic structure and recolonisation routes, (vi) local expert knowledge regarding forest types, vitality and value (biodiversity, economic) of populations. Six to nine monitoring regions per species / species complex were recognized.

Monitoring climate change adaptation plans for Urban Green Areas using indicators: LIFEGRIN project, a case study in Greece

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Temperatures are already rising in cities around the world due to both climate change and the urban heat island effect. Understanding the impact of climate change on the urban environment will become even more important, with increasing urbanization. Cities already face harsh climate, due to obvious anthropogenic impacts, responsible for the alteration of both natural surface and atmospheric conditions. These impacts range from microscale (e.g. replacing trees with a parking lot) to macroscale (e.g. carbon dioxide effects on global climate by fossil fuel combustion and emissions). In Greece, 49% of the population lives in cities of different sizes. Urbanization has severe environmental, social and economic impacts on cities, since buildings contribute considerably to energy consumption and CO_2 emissions. Adapting a strategic management plan for monitoring Urban Green Areas (UGAs) in relation to climatic changes includes the monitoring of indicators which may track adaptation in a microscale and a macroscale time framework. During the pandemic crisis of COVID 19, UGAs was the only solution for cities residents for outdoor activities. In the current case study, LIFEGriN project which is being implemented in Greece, in two municipalities, will be presented. Specifically, the indicators which are being used for monitoring UGAs adaptation to climatic changes will be presented. The significance of monitoring and evaluating mitigation, adaptation and resilience management plans for UGAs and cities is highlighted in order to ensure a sustainable living of residents of cities.

Interlaboratory comparison of microsatellite data. An approach used in the Lifegenmon project

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The LIFEGENMON project is a combined effort of Slovenia, Germany and Greece to implement a microsatellite marker-based (SSR) forest genetic monitoring (FGM) system for European beech (*Fagus sylvatica* L.) and Silver fir / King Boris' fir (*Abies alba* Mill. / *Abies borisii-regis* Mafft.).

Fluorophore dyes, DNA polymerase and PCR cycling conditions, separation polymers and electrophoretic buffers, detection platforms and human factor can all affect the observed allele size in fragment analysis of microsatellite markers. If studies using microsatellite markers were to be replicated, directly compared or run in parallel between different laboratories, adjustment of raw data must be performed in advance. For that purpose, institutions participating in the LIFEGENMON project established and accomplished a robust inter-laboratory comparison test. In this presentation, the methodology used and findings of inter-laboratory comparison of microsatellite data in LIFEGENMON is detailed and discussed.

Although inter-laboratory comparison is not necessary for the establishment of an FGM system, it is required if SSR-based genetic monitoring is to be applied across spatial scales or across the species natural range by different laboratories, rendering this formal exercise of paramount importance for a proper and reliable genetic analysis.

Keywords: microsatellites, inter-laboratory comparison, forest genetic monitoring

Genetic variability, relatedness and reproductive spatial behaviour in two highly abundant ungulate speciest

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European roe deer (*Capreolus capreolus* L.) and wild boar (*Sus scrofa* L.) are the two most widespread ungulates in Europe and Slovenia. Population size of both species is increasing across the European continent due to their high reproductive and survival rate, accompanied by their great plasticity that enables them to colonise also (semi)urban environment. Both species have polygynous matting strategy, male-biased dispersal of sub-adults, distinct reproductive movements (e.g. mating excursions of roe deer females), and stronger social bonds in female-based groups. We used microsatellites (13 for roe deer and 14 for wild boar) to study their fine scale genetic structure, relatedness and reproductive spatial behaviour in a 2,600 ha large hunting ground (Oljka, Šmartno ob Paki; Savinjsko-Kozjansko hunting management district) in central Slovenia. We analysed 61 roe deer and 30 wild boar (of both sexes and all age classes) harvested during regular hunting seasons from 2017 to 2019. We investigated the genetic variability of the two species and tested kinship using Cervus 3.0 programme to investigate the spatial behaviour of individuals (e.g. seasonal dispersion), and to determine the potential impact of spatial barriers on gene flow. By knowing exact locations (coordinates) of the harvest of any single animal obtained from the hunting informational system combined with relatedness data we got insight in the ecological and behavioural features of both species (e.g. seasonal dispersions and social grouping). The potential of molecular markers to clarify the relatedness among individuals may have great implication for population management as well as for understanding and forecasting comprehensive ecological effects of management decisions such as mitigation measures for controlling disease spreading.

Keywords: Ungulates, genetic variability, microsattelites, population manegament

Guidelines for conducting genetic monitoring in the field: *Populus nigra* L.

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European black poplar is an ecologically important fast growing and short-lived deciduous forest tree species of mixed riparian forests with physiological adaptation to colonize open areas after disturbances and survive in changes associated with its dynamic river system. It naturally forms metapopulation of inter-linked local populations rather than isolated populations. To ensure representative sampling across the metapopulation is important to design a genetic monitoring system with randomly selected monitoring plots of adult trees in local populations and their natural regeneration centers along the river system. Genetic identification of Populus nigra (L.) trees must be performed by use of species diagnostic DNA markers. The FGM plot should include 50 mature (reproducing) genetically different *Populus nigra* (L.) trees in sex ratio 1:1 of male and female. The monitoring plot in each local population should include at least 20 adult trees in maximum distance of 5 km. Sampling design of natural regeneration follows the metapopulation concept of multiple regeneration centers (subplots) to capture the whole genetic diversity of European black poplar and assess the risk of gene introgression and hybridization from exotic poplar species, and Lombardy poplar sources in the given area. The possible subplots of natural regenerations should be frequently monitored from April to June and where are occurring the newly seedling should be sampled immediately. The main obstacle of FGM in the case of European black poplar is to find habitats where the mating system can develop in a natural way, and offspring can find regular, suitable mid- to long-term conditions.

Keywords: European black poplar, *Populus nigra* L., forest genetic monitoring, metapopulation

First insight into MHC genes (class II) variation in European roe deer in Slovenia

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Major histocompatibility (MHC) genes are an important genetic marker for studying the processes of adaptive evolution in different species. The high degree of polymorphism observed in these genes may be result of increased need of organisms to recognise different pathogens that co-evolve with the host to evade immune recognition; moreover, in some species it may also have a potential role in higher mating success (or in avoiding inbreeding). The goal of our study was to examine spatial distribution of allelic diversity at exon 2 of MHC class II DRB locus of the European roe deer (*Capreolus capreolus*), the most widespread and abundant large mammal in Slovenia, using next generation sequencing approach (Ion Torrent S5, Thermo Fisher).

We identified 14 alleles in 93 analysed individuals, harvested in the period 2013–2019. Two of those alleles had already been previously found in roe deer in Europe, while the remaining 12 alleles were newly identified. The number of variable nucleotide sites in detected alleles was 28 (11.0%), and the number of variable amino-acid positions in translated sequences was 17 (20.4%). The most frequent allele, Caca0301 allele exon 2, was identified in 51.6% of individuals; 6 alleles were present only in a single individual each. Our results provide evidence of multiple co-amplifying copies, showing that MHC class II DRB is a complex multilocus system with a high level of polymorphism in roe deer.

Keywords: roe deer, genes, major histocompatibility complex, next-generation sequencing, allelic diversity

Methods of leaf phenological monitoring to support management of resilient beech forest: networking activity between Life AForClimate and LIFEGENMON project.

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Traditional monitoring of foliar phenology concerns in situ observations on single trees, while remote sensing techniques allow to analyse inter-annual variations in vegetation on a geographical wider scale. Traditional methods provide timely monitoring, but they require continuous inspections during the growing season. Remote monitoring is less expensive, nonetheless, even in case of high temporal resolution satellites, the possible presence of clouds could compromise the data acquisition.

The Life AForClimate project provides for the monitoring of leaf phenology in two beech stands in central Apennines and compares in situ and remote methods in different sectors. Additionally, within the networking activity with the LIFEGENMON project, where foliar phenology is a part of forest genetic monitoring, another beech stand from Slovenia was included. Main aims are to improve the efficiency of the survey and to evaluate the possible environmental and management effects.

Leaf phenology has been monitored, with weekly in-situ observations during spring on 80 dominant trees per site in AForClimate and on 250 or 500 per site in 2018 and 2019 in the LIFEGENMON project. Synthetic phenological scale, with 5 scores for the bud flush has been adopted. Moreover, leaf phenology has been monitored using the SAR (Synthetic Aperture Radar) remote sensing system.

Results showed a significant different length of the vegetative spring period, spanning from dormant buds, up to leaves completely unfolded, among sites. Through SAR estimation, this study demonstrates that leaf-out can be monitored with an extreme accuracy (RMSE < of 4 days) with a geometric resolution of 10 m.

Keywords: leaf phenology; SAR, remote sensing; climate change; *Fagus sylvatica*

The implementation of a database system for forest genetic monitoring (FGM) within the LIFEGENMON project

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Databases are sets of data that are arranged in tables and rows, similar to Microsoft Excel or other alike programs, but interconnected in relationships. Tables have their own predefined structure that ensures the right data format and data order. The user enters data into the database in a systematic and orderly manner via forms. Database tables compared to Microsoft Excel normally have very strict rules or series of integrity constraints defining what data and how it can be inserted. This is very important to exclude user input errors and to follow predefined protocols. These are not the only errors which we can avoid using a database, for example Ziemann et al., 2016 showed with a programmatic scan of leading genomics journals that approximately one-fifth of papers with supplementary Excel gene lists contained erroneous gene name conversions.

In FGM we are dealing with many different data types, e.g. genetic, phenological, meteorological data and other field data. To ensure data integrity with so many data types and different protocols, a database system is needed. There are many possibilities regarding database selection. In LIFEGENMON two database management systems have been tested: Open Foris and a standalone PostgreSQL database. The organization and the underlying database schema will be presented.

Ziemann, M., Eren, Y. & El-Osta, A. Gene name errors are widespread in the scientific literature. Genome Biol 17, 177 (2016). https://doi.org/10.1186/s13059-016-1044-7

Development of the sampling design within the LIFEGENMON project

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In the LIFEGENMON project a system for forest genetic monitoring (FGM) is being developed. A FGM plot is the basic unit where genetic monitoring is conducted; it is the base for all the following work. Therefore, it is paramount that the experimental plot is well designed and is able to give the most relevant results with managable amount of effort. During the project, the sampling design changed considerably. At the beginning of the project, an experimental plot was established following a protocol, where 250 trees were randomly selected within the intensive section of 100 x 100 m. If the tree density was too low to reach the number of 250 trees, the remaining trees were included in the extensive section of 200 x 200 m. During the first assessment of the beech monitoring plot questions about the appropriateness of the described design arose, since it lacks some of the statistical concepts of sampling and therefore calls representativeness into question. In order to assess genetic diversity and its changes over time as objectively as possible an alternative sampling design was devised that meets the statistical criteria of replications, independence, randomness and interspersion. The alternative sampling design consists of 5 plots with 50 adult trees in each, randomly distributed within the entire stand. Subsequently, due to the decision to reduce the sample size to 50 trees, it was decided to use the alternative sampling approach with one FGM plot, within which 50 adult trees and 50 natural regeneration trees are randomly selected.

Phenological observations within the LIFEGENMON project in Slovenia

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Phenological observations are an important part of the LIFEGENMON project. Phenology is a highly important adaptive trait, which determines the growing season and the reproductive period of plant species. Climate change, the associated increasing temperature and late spring frost damage are the main reasons why phenology is changing over years. Due to its importance, phenophases flowering and fructification were included among verifiers within the indicator selection, while bud break and senescence serve as background information, which help to interpret other verifiers. Monitoring of phenological phases has been carried out since 2016 on two Forest genetic monitoring (FGM) plots, one plot for common beech (*Fagus sylvatica* L.) and one for silver fir (*Abies alba* L.). It includes annual monitoring of bud break, flowering and fructification for both species and additionally senescence for common beech. At the beginning of the project, phenological observations were carried out on 40 trees on both FGM plots, and from 2017 onwards phenology monitoring was extended to 250 trees on the beech FGM plot. In 2019, an alternative sampling design for FGM was established and tested in the beech stand, from which additional 50 trees were added to the observations. The number of silver fir trees remained 40 throughout the entire period of phenology monitoring. The collected data of phenological observations from Slovenian FGM plots will be presented. Because phenology variables are sensitive to climate conditions, they will be shown along with meteorological parameters in order to see how they affect phenological development and its inter-annual variability.

Keywords: phenology, monitoring, LIFEGENMON, Slovenia

Isolation of exogenous fungal dna from non-invasive samples

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Mycorrhizal fungi are symbionts of a large majority of terrestrial plants. The symbiotic relationship allows the exchange of nutrients along with other benefits of mycorrhization to the plants. Large mammals with their processes (i.e. nutrition and excretion, zoohory) are important vectors for the transfer and distribution of fungi within and between different environments. We tested efficiency of two different isolation kits (Qiagen QIAamp Fast DNA Stool Mini Kit, and Qiagen DNeasy PowerSoil Kit) for fungal DNA extraction from roe deer (*Capreolus capreolus*) and red deer (*Cervus elaphus)* feces. We estimated kits efficiency by measuring the concentration of isolated DNA and by the amplification success using arbuscular mycorrhizal specific NS31 and AM1 primers for the 18S region of the ribosomal RNA. Amplicons of 550 bp mycorrhizal DNA were isolated and amplified, and we optimized the annealing temperatures of the PCR by using qPCR. In terms of better PCR amplification, our results showed that the Qiagen DNeasy PowerSoil Kit is performing better than the Qiagen QIAamp Fast DNA Stool Mini Kit. By analyzing the lengths of amplicons we revealed that feces of wild ungulates can be a useful tool in environmental genetics, for example as a source of fungal DNA allowing studying of potential animal dispersal of mycorrhizal fungi and other ecological interactions (e.g. nutrition preferences and consumption of fungi, reasons of wild boar rooting, transmission of fungi by zoohory) in terrestrial ecosystems.

Keywords: arbuscular mycorrhiza, fungi, wild ungulates, deer, DNA isolation, 18S, PCR

Genetic monitoring of the products of the British Sitka spruce (*Picea sitchensis* (Bong.) Carr) breeding programme

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Every forest tree domestication programme results in a hierarchical stepwise fragmentation of genetic diversity, proceeding from undomesticated, large natural populations with high genetic diversity to a genetically improved population, characterised by a restricted number of parents and potentially lower effective population size and genetic diversity. A project is underway to assess genetic diversity at several levels within the British Sitka spruce breeding programme. To achieve this, we are sampling natural populations on Haida Gwaii island (Canada), and unimproved populations in the Farigaig 1974 IUFRO provenance trial (Scotland). We will then assess loss of genetic diversity during production of forest reproductive material (FRM) in an open-pollinated seed orchard (Delamere, England), and during the nursery production and field establishment of vegetatively propagated (VP) FRM. In the seed orchard, a set of 14 microsatellite markers will be used to assess mating patterns and the genetic diversity of the seed crop. Results will be compared against non-molecular proxies for estimating genetic diversity that make use of phenological observations, germination trials and master certificate records. The effect of standard vegetative propagation and planting procedures on genetic diversity of VP FRM will also be studied. Sitka spruce is a non-native species in the UK where reforestation generally involves clearfelling and replanting with improved material. Pollen flow from outside the UK is unlikely. This unique UK situation presents a rare opportunity to observe the effects of a real-life improvement programme performed under near laboratory conditions. Here we present the project overview and progress after two years.

Keywords: Genetic diversity, molecular and non-molecular methods, microsatellite markers

Turning well-known climatic archives into biological archives: an environmental metabarcoding approach

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Climate change is leading dramatic changes within communities. Identifying the link between climatic, environmental and communities' changes is of fundamental importance for determining the future of an ecosystem. The aim of our study is to determine this connection by exploiting peatlands as climatic and biological archives, using the eDNA metabarcoding approach on plants and animals. A peat core (10x10x100cm) was extracted from the Lupicino peatbog (Nova Ponente

– BZ), divided into 3 cm layers, and subjected to radiometric dating and total DNA extraction. Plants and animals were characterized through the use of two different metabarcodes: the plastidial marker trnL (194-310 bp) and the mitochondrial marker CO1 (157-159 bp), respectively. The radiometric dating revealed the presence of a hiatus to the depth of 50 cm (800 BP), which caused a chronological shift, while the deepest sample resulted to correspond to 1500 BP. Through the trnL we have identified 18 plant taxa (7 at the species level), while with the CO1 we have identified 6 taxa of arthropods (5 at the species level) and 3 of rotifers. In both cases, the largest number of reads was identified as belonging to organisms supposedly alive nowadays. This has resulted in a reduction in the abundance of the species living in the past, or even a failure to detect them. Despite these limitations, this study demonstrated the usefulness of eDNA metabarcoding on peat bogs; the results are encouraging and can be immediately used for new tests designed to improve the taxonomic resolution of this approach.

List of abbreviations:

eDNA: environmental DNA

trnL: chloroplast trnL (UAA) intron

COI: Cytochrome c oxidase I

Keywords: environmental DNA, metabarcoding, paleoenvironmental archives, biodiversity.

Conservation and reproduction of genetic resources of resistant variants of Norway spruce in Ore Mountains to mitigate effects of drought and ongoing environmental changes and to support stability of mountain forest ecosystems

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The relative resistance of some Norway spruce individuals, which for a long time survived during several periods of imission load in the recent past in the Czech Republic in Ore Mountains, this is basis for another practical utilization of this phenomenon in the forestry practice. Previous research activities in mentioned area were aimed to preservation and reproduction of resistant variants of the local Norway spruce ecotype, incl. use of DNA analyses. Implementation of indicated rescue programs requires, among others, the use of proven vegetative propagation technology of surviving spruce individuals, resp. of their ex situ conserved clonal variants, for their repatriation back to original area of their occurrence. Those sub-populations of resistant spruce have proven their adaptability and vitality in the past period of air pollution, so it is possible to also suppose their vitality and resistance to adverse effects of current deteriorated environment on mountain forests ecosystems.

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Keywords: Norwy spruce; genetic resources

The joint research project GENMON: Implementation of long-term genetic monitoring in beech and spruce stands in Germany

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Genetic diversity represents the basis for adaptability and survival of tree species in changing environmental conditions. Global warming will cause extreme weather events in the future. To gain information about the long-term development of the genetic systems of forest tree populations there is an urgent need to establish a monitoring system for forest genetic resources. After testing a concept, developed on behalf of the Federal-State-Working Group for Forest Genetic Resources in Germany in a pilot study, the experiences were used to implement the joint project „GenMon". A system comprising 14 monitoring plots in *Fagus sylvatica* L. and 10 plots in *Picea abies* [L.] Karst. in Germany has been established according to a defined plot design. Neutral microsatellite markers were used to analyze the genetic structures at the population level. Phenological observations of bud flushing, flowering, fructification and vitality are performed every year. Data of all plots are stored in a database, which in this initial step is used to calculate genetic diversity in adult stands and their progenies to describe and to compare the current genetic state of the populations. Furthermore, the selection of individuals suitable for the development of adaptation-relevant markers was facilitated. In future, further analyses and data evaluation will allow the assessment of the intactness of the genetic mechanisms that ensure the conservation, production and transmission of genetic diversity to the next generation. This provides the basis for a monitoring system to estimate and evaluate the factors as well as the direction and intensity of their influence on adaptability of tree populations.

Keywords: *Fagus sylvatica, Picea abies*, environmental changes, genetic system, DNA-marker, phenology, monitoring, adaptation

Biochemical and transcriptomic approach: the selection tools for afforestation of halomorphic environment

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Halomorphic soils cover the significant area in Vojvodina region and represents economical challenge in forestry sector. Therefore, the aim of the study was to investigate the salt tolerance mechanisms of four economically important Serbian poplar clones to select the most tolerant one that could be used in afforestation of halomorphic soils. Seven candidate genes, two putative poplar homologues of GRAS family TFs (GRAS17 and GRAS16), DREB2 from ABA-independent pathway DREB family TFs and four abiotic stress inducible genes (RD29B, RD17, P5SC1, SOS1) were examined for their expression profiles. Furthermore, several biochemical parameters such as different radical scavenger capacities (estimated by DPPH and ABTS assays) and accumulation of total phenolic content and flavonoids as well as accumulation of two osmolytes, glycine betaine and proline, were quantified. Three perspective clones of *Populus deltoides* (B229, 182/81 and Pe19/66) and one of hybrid genetic background (*P. nigra* x *P.deltoides*) e.g. *P.x euramericana* (clone M1) were subjected to NaCl induced salt stress in concentration range from 150mM to 450mM hydroponically and the plant responses were tracked at different time points at the leaf level.

Keywords: poplar, salt stress, transcriptomics, scavenger capacity, osmolytes

Does the genetic component has an influence on fitness parameters (body mass and reproductive ability) in roe deer

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Roe deer (*Capreolus capreolus*) is an income breeder, which means that seasonal effect has only moderate influence on body mass variability within the year, and that the reproductive success is not dependent on food intake and energetic reserves accumulated outside the short reproductive period in mid-summer. For this reason, body mass of roe deer can serve as a good proxy of individual condition and quality, and it has a crucial importance in determining the reproductive success of the species, particularly females, however, there is a lack of data on the influence of intrinsic (i.e., genetic) factors on body mass variability and consequently also on fitness parameters at individual level. To overcome this gap in knowledge, we analysed neutral genetic variation and its possible effect on body mass and reproductive ability in large sample set of yearling roe deer does collected throughout the whole gradient of the species presence in Slovenia. Genetic analysis was performed on 11 microsatellites for 213 individuals. We analysed only yearlings due to the following reasons: (i) to standardize sample set according to the precisely known age; (ii) this age category has much larger variability in ovulation/fertility rates in comparison to adult females, therefore effects of different influential factors are much more expected in yearlings. The results revealed existence of three independent genetic clusters correlated with spatial distribution of roe deer in the country. Moreover, results show a positive relationship between mean microsatellite heterozygosity, seasonally standardized body mass and reproductive ability (potential litter size) of primiparous does. This suggests that genetic diversity has an important influence on fitness and increment rates in roe deer.

Keywords: roe deer, microsatellites, population structure, body mass, reproductive ability

Drivers of ectomycorrhizal fungi diversity and their contribution to a global soil biodiversity and ecosystem functions

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Soils are a significant reservoir of the global biodiversity and functions that contribute to many crucial ecosystem functions. From this point it is crucial to know general patterns related to the distribution and functioning of soil organisms, to support their conservation efforts and to pinpoint their consideration by governance and potential uses. A literature-based study, that we performed, revealed that there is a large discrepancy between available information in all reviewed taxonomic group including ectomycorrhizae, namely spatial, environmental, taxonomic, and functional gaps (Guerra et al. 2020). To overcome that, both a large-scale guild, the ectomycorrhizal fungi, across forests at a spatial scale was done to explore key biotic and abiotic predictors of ectomycorrhizal diversity and to identify dominant responses and thresholds for change across complex environmental gradients (van der Linde et al. 2018). Further, there is a need for more functional/ecological studies such as effects of tree phenology on ectomycorrhiza diversity (Unuk et al. 2019) of ectomycorrhiza community changes after planting (Železnik et al., unpublished) to fill lack of knowledge on the importance of ectomycorrhizal biodiversity and their ecosystem functions at local and global scale.

Guerra, C.A. et al. (2020). Blind spots in global soil biodiversity and ecosystem function research. Nature Communications 11, 3870.

Unuk et al. (2019). Root-associated fungal communities from two phenologically contrasting Silver Fir (*Abies alba* Mill.) groups of trees. Frontiers in plant science 10, article 214

van der Linde et al. (2018) Environment and host as large-scale controls of ectomycorrhizal fungi. Nature 558, 243–248

Keywords: ectomycorrhiza, diversity, distribution

Protocol for handling of forest tree seedlings and Protocol for obtaining seed material, parts of plants and seedlings

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The two presented protocols purpose is to provide simple yet important guidelines for foresters and forest owners in Slovenia on procedures for production of forest reproductive material and handling of forest tree seedlings till planting.

The Protocol for handling of forest tree seedlings from the excavation in the nursery to their planting in the forest aims to ensure the proper organization of work at all stages of reforestation by planting. Following the protocols shall allow to achieve best success in reforestation. It includes: Handling and responsibilities in individual phases of production and handling of forest tree seedlings; What does successful restoration with planting depends on; How to procure the seedlings; Why is the origin of seedlings important and the Importance of genetic diversity in forests.

The Protocol for production of forest reproductive material for reforestation by planting provides an overview of all procedures and stages in seed collection. The uniform procedure will ensure quality of the forest reproductive material and assists users with professional support. It includes: How to obtain forest reproductive material; Steps needed to obtain a certificate for forest reproductive material; Basics of the legislation on forest reproductive material; The control system.

The importance of conservation of forest genetic diversity and forest genetic monitoring was highlighted in both protocols

Keywords: protocol, forest, seedlings, seed, reproductive material

Guidelines for conducting genetic monitoring in the field: *Abies alba/Abies borisii-regis*

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Silver fir (*Abies alba* Mill.) and King Boris fir (*Abies borisii-regis* Mattf.) are wind-pollinated, monoecious, generally outcrossing conifer tree species, which belong to the Abies genus. Silver fir is one of the most important forest tree species from an economic and ecological point of view in several European countries. King Boris fir is an important natural hybrid between *Abies alba* and *Abies cephalonica* growing mainly in Greece. Both species are facing many threats and challenges due to climate changes and therefore they are both considered for forest genetic monitoring.

The guidelines shortly describe Silver fir and King Boris fir, their reproduction system, environmental requirements and threats. They provide guidance on how to establish and maintain a forest genetic monitoring plot and on recording all field level verifiers and phenotypic data at the basic, standard, and advanced monitoring levels. The emphasis is given to the particularities of genetic monitoring of Silver fir and King Boris fir compared to other conifer (e.g. *Pinus nigra*) species.

Guidelines for conducting genetic monitoring in the field: Wild cherry (*Prunus avium* L.)

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Wild cherry (*Prunus avium* L.), is a medium sized, fast growing and rather short-lived deciduous tree, with wide natural distribution range, which includes western Eurasia and the northern part of Africa. The species is a pioneer one that grows in a wide range of habitats; however, the species is extremely scattered throughout its distribution as it is highly light demanding and a weak competitor. The species natural populations are characterized by their small size and occur in small groups or are comprised of single trees growing at the edges and in the gaps of forest stands. Wild cherry is an important forest tree species from an ecological (it is vital as a food source for many bird and insect species) and economic point of view (wood of wild cherry is of valuable as it is of high-quality and easy working, therefore is often used for veneer and furniture production, cabinetry, etc.).

The guidelines shortly describe the Wild cherry, its reproduction, niche requirements and threats. They provide guidance on establishing and maintain a genetic monitoring plot and on recording all field level verifiers at the basic, standard, and advanced monitoring levels. The emphasis will be given to the particularities of genetic monitoring of Wild cherry compared to other species.

Development of DNA marker-based traceability system for forest reproductive material in Lithuania

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Scots pine, Norway spruce, Pedunculate oak and European beech are among the economically and ecologically most important forest trees species in Lithuania. According to the Regulation of Forest Planting and Restoration of Lithuania (2018) and the Regulations on Forest Reproductive Material (FRM) (2017) forests must be planted and replanted with the target tree species, using high quality seeds and seedlings from a given provenance. EU Council Directive (1999/105/EC) indicates that EU Member States are responsible for the regulation, requirements and implementation of FRM quality and traceability system. The existing FRM control system in Lithuania is based on the control actions of the supporting documents regarding the origin of FRM. However, this FRM traceability system is limited and in some cases cannot ensure that FRM used for reforestation/afforestation originates from the declared place of origin or belongs to a certain seed or plant lot. We seek to build a two level DNA marker based FRM traceability control system on (1) reference seed lot samples from each seed collection from seed stands and (2) DNA “fingerprints” of seed orchard clones.

Existing forest genetic research infrastructure in Lithuania and Good Practice Examples in Europe (e.g. Germany and Slovenia) provide opportunities to implement FRM traceability system based on DNA markers. The aim of the project is to perform a pilot FRM traceability study based on microsatellite markers and to prepare a methodology for FRM traceability system implementation in Lithuania. The project and its implementation plan will be presented.

This work is supported by the Project. No. 09.3.3-LMT-K-712-19-0007.

Keywords: FRM, traceability system, DNA, Scots pine, (*Pinus sylvestris* L.), Norway spruce (*Picea abies* (L.) H.Karst.), Pedunculate oak (*Quercus robur* L.), European beech (*Fagus sylvatica* L.)

Microclimate in Dinaric fir-beech forests is controlled by the interaction effect between management intensity and topography

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Forest microclimate is affected by topography and management activities, as these directly alter overstory structure. In turn, microclimatic conditions act as strong determinant for post-disturbance tree regeneration. We analysed the dependence of microclimatic conditions on topographic and management-related factors in managed fir-beech forests in the Dinaric Mountains, Slovenia. These forest ecosystems are characterized by rugged karst terrain with numerous sinkholes. Cutting treatments were experimentally applied in an area of 0.4 ha: uncut controls (CON), 50% cut of stand growing stock (intermediate management intensity – IMI) and 100% cut (high management intensity – HMI). Effects of slope exposition on microclimate (air temperature – T, relative humidity – RH, vapour pressure deficit – VPD) were assessed by comparing central, south-facing and north-facing within-sinkhole positions. Daily Tmax and VPDmax in HMI treatment were up to 5.9 °C (on average 3.5 °C) and up to 1.4 kPa (0.6 kPa) higher compared to CON treatment, respectively, whereas daily RHmin was up to 22.7 (13.0) percentage points lower. South-facing positions in the HMI treatment exhibited the most extreme conditions, i.e. the highest Tmax and lowest RHmin. Differences in microclimate between treatments were strongly modulated by canopy cover. The results also suggest that overstory removal increases the dependence of microclimate on local topographic factors. Topographically induced variation of microclimate has important implications for management planning and biodiversity protection. Microsites within canopy gaps with adverse microclimate can create stressful conditions (high VPD) for regeneration layer of two key late-successional tree species in studies forests, European beech (*Fagus sylvatica*) and silver fir (*Abies alba*).

Keywords: tree cutting, air temperature, relative humidity, karst topography, canopy cover

Variability of leaf anatomical properties in pedunculate oak genotype (*Quercus robur* L.) in natural population

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Leaf anatomy depends on genetic information and environmental condition. Furthermore, leaf anatomy has an important impact on leaf gas exchange, especially on photosynthesis. Hence, leaves structures are important from the aspect of biomass production. The objective of this study was to determine the genotypic variability of leaf anatomical properties originating from a natural population. For the purposes of this research, seven parameters were estimated: abaxial epidermis thickness, main vein diameter, spongy parenchyma thickness, palisade parenchyma thickness, adaxial epidermis thickness, lamina thickness, and sclerenchyma thickness. Leaves were sampled from ten genotypes from the natural pedunculate oak forest in Morović. The highest variability was estimated for the main vein diameter (6.69%), while the lowest variability was observed for the sclerenchyma thickness (2.83%). The contribution of adaxial and abaxial epidermis thickness in leaf lamina ranged from 11.39 to 17.51 %, and 9.92% to 15.30%. The contribution of palisade and spongy parenchyma thickness ranged from 31.56% to 41.70% and 31.06% to 38.92%, respectively. The lowest values for palisade parenchyma thickness (68.96 µm) and spongy parenchyma thickness (63.68 µm) were found in genotype 3, resulting in the thickest leaf lamina (165.36 µm). The highest values for main vein diameter and sclerenchyma thickness were found in genotype 10, while. These quantitative differences between studied parameters are the consequence of interaction genotypes and common environmental conditions.

Keywords: leaf anatomy, Quercus robur, pedunculate oak, genotypic variability

Changes of forest understory vegetation are driven by disturbances: Intensive Monitoring of Slovenian forests

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In this study, we quantified changes in the diversity and composition of the forest understory layer in the Slovenian Intensive Monitoring (Level II) sites between 2004/05 and 2014/15. In total, 60 plots were placed across 10 different managed forest types, ranging from lowland deciduous and mid-altitude mesic mixed forests to mountain conifer forests. To examine how disturbance influenced understory dynamics, we estimated the disturbance impacts considering both natural and/or anthropogenic disturbances that cause significant damage to trees and to ground-surface layers, including ground-vegetation layers and upper-soil layers. The mean value of disturbance estimates per site increased from 0.8% in 2004/05 to 16.3% in 2014/15, which corresponded to a reduction in total vegetation cover, including tree-layer cover. Species richness across 10 sites (gamma diversity) significantly decreased during the study period, while mean species richness per site did not significantly change. The mean value of site level Shannon diversity indices and evenness significantly increased. The cover of most common plant species increased during the monitoring period. More disturbed sites showed larger temporal changes in species composition compared to less disturbed sites, suggesting that forest disturbances caused understory compositional shifts during the study period. Rather than observing an increase in plant diversity due to disturbance, our results suggest a short-term decrease in species number, likely driven by replacement of more specialized species with common species.

Keywords: vegetation dynamics; vascular-plant diversity; understory layer; disturbance; monitoring; Slovenia

Describing succession of decomposer fungi on coarse woody debris in virgin forest Rajhenavski Rog in Slovenia

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Species composition and interspecies interactions of decomposer fungi are continuously changing throughout the sequential decomposition of wood. The succession is not unidimensional - after a specific decomposing species peaks, it is not always replaced by the determined species. Instead, succession follows different decomposition paths.

The aim of this study was to describe the fungal succession in the decomposing wood within the virgin forest Rajehnavski Rog in Slovenia. Following the 6 class description of decomposition stages (Kraigher et al., 2002) samples from coarse woody debris (CWD) from the first five stages were collected. The wood dust was obtained ex-situ, and used for DNA extraction. Fungal ITS2 region was used for amplicon sequencing on Ilumina MiSeq.

Early decomposition stages were characterized by higher relative abundance of *Basidiomycota* compared to *Ascomycota* (average 62% in the first decomposition stage), while *Ascomycota* were dominant in the later stages (average 93% in the latest stage). While genera *Aureobasidium* and *Purpureocillium* (*Ascomycota*), both common soil fungi, were present in all the decomposition stages, genus *Bjerkandera* (*Basidiomycota*), comprising of mainly white-rot species, was among the more dominant genera in the first decomposition stage. Higher relative abundance of genus *Fomes* (*Basidiomycota*), also wood-decomposing fungi, was observed in the second and third decomposition stage.

As Rajhenavski Rog continues to be one of the most researched forests in Slovenia in terms of fungal decomposition, our results complement previous records, and offer a great insight in both understanding the succession of fungal communities in decomposing wood, and limits of different methods.

Keywords: coarse woody debris, fungi, decomposition, succession

Bacterial community response to forest clearcutting

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The lack of flow of photosynthates to the belowground due to forest management practices, such as clearcut harvesting, leads to a complex ecosystem response. While root litter represents a decomposition hotspot for fungi following clearcutting, less is known about the response of bacteria to such forest management practice.

In this study, we aimed to assess the changes in bacterial community structure in response to forest clearcutting.

Roots, rhizosphere soil and bulk soil samples were collected from a *Picea abies* stand during a period of two years after clearcutting, and the results of the 16S rRNA sequencing were compared to the data before the tree harvesting.

While there was no clear distinction of the community structure between the rhizosphere and bulk soil in the first months after the clearcutting, the bacterial communities associated with roots were distinct and underwent more profound changes over time. The early stages of root decomposition were characterized by the presence of the *Actinobacteria* while the relative abundance of *Proteobacteria* (mainly *Burkholderia)* increased in the later stages. Moreover, bacterial communities on decomposing roots differed significantly from those on live roots before clearcutting.

Our results indicate that the termination of tree root activity was followed by the changes in root bacterial communities, as well as soil bacterial communities in the later stages of the post-harvest sampling.

Clearcutting can cause both changes in microbial community structure and the decrease in microbial biomass, where the effects seem to be pronounced in both fungi and bacteria.

Frost damages of common beech in the international provenance test in bosnia and Herzegovina compared to spring phenology in 2019

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Common beech (*Fagus sylvatica* L.) is one of the most ecologically and economically important species. The research aims to determine the dates of beginning and end of leafing phases of common beech provenances, to identify damages of plant canopies by frost, and to check if there is a correlation between dates of leafing phases and vulnerability by frost.

Researchers observed common beech plants in the international provenance test in Bosnia and Herzegovina. The test contains provenances from different altitudes, eight from Bosnia and Herzegovina, four from Germany, three from Serbia, two each from Croatia, Romania, and Switzerland, and one from Hungary. Six leafing phases were observed from 31.3. to 18.5.2019.: A - sleeping bud; B - buds swelling; C - buds opening; D - folded leaves appearing; E - leaves unwound; F - leaves fully developed. Canopy damages by frost that occurred on the 8th of May were observed in three categories: partial, medium, and complete damage.

There were no significant differences in the start and end of the leafing phases. Most provenances entered phase B at 14.4. The highest percent of completely damaged plants had provenances BW Wildbad. Germany (68%), Sihlwald Switzerland (64%), Alba Iulia Romania (60%), and the lowest Konjuh Bosnia and Herzegovina (3%).

Since there were no significant differences concerning dates of occurrence of leafing phases, the extent of frost damage cannot be explained by it. The research should be continued to include different seasonal climatic conditions affecting the leafing phases and frosts occurring earlier in the spring.

Keywords: frost damages, leafing phenophases, common beech, international provenance test

Ectomycorrhizal fungi of *Quercus pubescens* suffering from drought and wildfire

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Slovenian Forestry Institute

Due to global climate change, the probability of heatwaves, droughts and fires is expected to rise, affecting forest productivity and the distribution of tree species. Due to their role in the supply of water and nutrients ectomycorrhizal (ECM) fungi are crucial for tree survival during stress conditions, but knowledge from the field is still limited. Our study was investigated the vitality and community composition of *Quercus pubescens* Willd. ectomycorrhizal fungi over two consecutive years in a stress-prone Submediterranean area. Over the investigated period, two summer droughts and a superficial wildfire occurred in the area. The vitality of ECM fungi was strongly reduced due to stress events, while community composition was mainly affected by the plot. Different water-holding capacity of soils on the plots did not affect overall ECM community composition, but affected the abundance of a stress resistant ECM fungus *Cenococcum* sp. The most abundant ECM lineages were *Tomentella* and other *Thelephoraceae*, *Sebacina* and *Cenococcum*. *Cenococcum* sp. significantly increased in abundance after wildfire and *Sebacinales* significantly decreased. The short distance exploration type was the most abundant ECM exploration type which occurred with significantly higher abundance at the limestone plot most affected by the wildfire. The presented results indicate a complex interplay of abiotic stress factors, soil type, tree vitality and ECM fungi that needs further investigation.

Keywords: pubescent oak, abiotic stress, Submediterranean, ECM fungi community composition, exploration types

LIFEGENMON Communications, A 360° Approach: Communicating Forest Genetic Resources to Different Target Audiences

Rantaša Boris, Breznikar Andrej, Gregorič Andreja, Sever Kristina, Vilhar Urša, Železnik Peter, Sonnenschein Katja, Westergren Marjana, Baloh Tjaša, Finžgar Domen, Kraigher Hojka

Abstract: Effective communication of complex biological phenomena such as forest genetic resources, forest genetic diversity and forest genetic monitoring requires innovative and adaptive approaches when addressing different, especially general, audiences. Within the LIFE LIFEGENMON project, we have the opportunity to communicate extensively and gather valuable experience about these topics. The contribution shall present general guidelines on communicating these topics and several practical examples.

General guidelines for communicating forest genetic resources include: 1. Providing context / helping your audience to see the big picture (by answering questions such as: What is genetics? What is DNA? What is biodiversity? Why are forest genetic resources important?) Make sure your audience understands the basics before deepening the discussion. When this is not possible (due to time constraints or similar), briefly explain that forest genetic diversity is essential for the survival and adaptability of forests. 2. Highlighting the importance of forest genetic resources and forest genetic diversity for the future of forests. 3. Using comparisons to familiar topics, i.e explain forest genetic diversity in a way that relates to the genetics of human or (edible) plant populations. 4. Using communication tools, suited to target audiences (brochures, films and video, comics, children's books and cartoons, toys, etc.) 5. Engaging target audiences in a continuous dialogue. Practical examples/guidelines comprise of: 1. Communicating forest genetic diversity to children. 2. Communicating forest genetic resources to teachers. 3. Communicating forest genetic monitoring to foresters.

Keywords: communication, forest, genetic, diversity

Spreading the word about the LIFEGENMON project – the Greek teams' dissemination approach

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Science dissemination is a planned process of providing new scientific information, ideas, initiatives, findings, and results to the public at large. It is duty of the scientist to make sure that their work is heard by the public and to assist in creating a society that thinks for itself, filters all information and isn't gullible and naive. The dissemination activities of the project LIFEGENMON provide a tool for communicating the project, its outcomes, the profiles of the participants, and creating synergies with other stakeholders and initiatives. Thus, they contribute to informing the general public and important policy makers who can apply its outcomes and improve future management.

People have the need to know where and how their taxes are spent and to feel that they also contribute to the greater good. Throughout the six years of the LIFEGENMON project, we have shared our knowledge, experiences and results through oral presentations, workshops and publications. These actions enticed the attendees and readers to seek further and more detailed information about the project. Our goal, to reach the general public and specified target groups in order to increase their awareness concerning the importance of forests and forest genetic resources, their necessity and need for continual conservation has largely been met.

Keywords: Dissemination, LIFEGENMON, forest genetic resources

Adapted relict oaks (*Quercus* spp.) for climate resilient forests

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Relict oaks (*Quercus* spp.) on extremely dry and unproductive sites in Central Europe often show poor growth characteristics, making them undesirable for practical forestry. However, such oaks are most probably autochthonous, have long-term habitat continuity and might have reached the climax community in the early Holocene and stayed more or less unchanged since then. This means that they might have adapted to regular water shortage over many generations and thus harbour valuable genetic resources for adaptation to future climates. Here, we apply a multifaceted approach to (1) identify the site conditions of the oak stands on putatively relict sites in southern Germany and Alsace and confirm the relict status by identifying indicator floral and faunal species, (2) characterize the refugial origin of the oaks in these stands via nuclear and chloroplast DNA markers and compare the results with the existing data on managed oak forests, (3) investigate adaptive genetic variation using a targeted sequence capture method and examine associations between genotypes and environmental and physiological stress variables, (4) study mature trees and their progenies in terms of their stress physiology to gain insights into drought resistance, and (5) provide a basis for the establishment of a progeny trial to test genetically determined growth characteristics in the stands. Preliminary results are in agreement with our hypothesis of autochthony. The project outcomes are expected to help assessing the use of reproductive material from these stands for establishing climate resilient oak forests.

Keywords: adaptation, climate change, drought, relict oaks, resilience

Guidelines for conducting genetic monitoring in the field – *Quercus robur* L. and *Quercus petraea* (Matt.) Liebl.

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Among the 13 European white oak species, pedunculate (*Quercus robur*) and sessile (*Quercus petraea*) oaks are economically and ecologically the most important deciduous forest tree species. Both oaks are widely distributed in Europe and closely related; they can mix, compete and naturally hybridize with one another and with other oaks. These light-demanding tree species are found as a main component in temperate deciduous mixed forest. In valleys and flood plains pedunculate oak can form stands with sycamore, plane, maple, ash and elm. With its high ecological importance and strong wood, this species is a good candidate for genetic monitoring. The guidelines shortly describe both oak species, their reproduction, environment and threats. They provide guidance on establishing a genetic monitoring plot and on recording all field level verifiers. The emphasis will be given to the particularities of genetic monitoring of oaks compared to other species.

Keywords: oak, pedunculate, sessile, guidelines, genetic monitoring

Proposed guidelines on forest genetic conservation for integration in forest management plans in Slovenia

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Two proposed guidelines were written in the frame of Lifegenmon project: Guidelines for providing forest reproductive material and Guidelines for monitoring and conservation of genetic diversity. Their purpose is the implementation of their content in forest management plans in Slovenia, since the conservation of forest genetic monitoring is of great importance for future forests.

Forest genetic diversity helps to maintain the adaptive potential of forests to future environmental conditions. Therefore, measures for forest genetic conservation are all aimed at preserving and increasing the genetic diversity of the future forest. In the Guidelines for monitoring and conservation of genetic diversity measures, that help protect genetic diversity, are described.

Guidelines for providing forest reproductive material give some general information on forest reproductive material and further describe guidelines for forest tending and maintenance of seed stands, production and use of forest reproductive material, tending of forest genetic reserves and give guidelines for main tree species (*Fagus sylvatica*, *Abies alba*, *Picea abies*, *Quercus* sp., *Prunus avium*, *Fraxinus* sp., *Acer* sp. and *Larix decidua*) and tree special that are potentially suitable to grow in our environment (*Pseudotsuga menziesii, Juglans nigra* and *Robinia pseudoacacia*).

Keywords: guidelines, forest management plans, genetic monitoring, genetic conservation, forest reproductive material

Utilization of green infrastructures for more resilient cities in greece

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Green infrastructure includes any punctual urban green area and element as well as the ecological intervention adopted by city authorities which are crucial to provide multiple benefits in order to support a green economy, improve quality of life, protect biodiversity and enhance the ability of ecosystems to deliver services such as disaster risk reduction, water purification, air quality, space for recreation and climate change mitigation and adaption. The LIFE GrIn project aims to incorporate the climate change adaptation and mitigation perspectives with green infrastructure management and conservation in local governance in cities, through the establishment of an integrated policy framework focusing on Urban Green Areas (UGAs). LIFE GrIn will utilize all available tools and indicators at European level to assist in strategic planning and management of UGAs in the context of climate change adaptation and mitigation. The LIFE program started at 2018 and has a 3.5 year - duration. Six different partners are participating from Greece. Scientific Coordinator for the project implementation is the Institute of Mediterranean & Forest Ecosystems-HAO DEMETER and other partners are the Environmental Management Company - Homeotech Co, the Central Union of Hellenic Municipalities, the Greek Municipalities of Amarousion and Heraklion and the Hellenic Ministry of Environment and Energy.

Keywords: Urban green areas, Indicators, Cities, Resilient, Management of UGAs

Population genetic structure of red fox in Slovenia

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Considering adaptation to urban environments, red fox (*Vulpes vulpes*) is one of the best studied species among European fauna. It is generalist and an opportunistic feeder, which explains its successful adaptation to (sub)urban areas. Urban ecosystems alter several abiotic and biotic factors, and consequently affect the evolutionary potential of species. Understanding the species metapopulation structure, behaviour, and the identification of population gene flow between peripheral suburban populations or from isolated sampling sites within urban and rural areas are important for conservation and management of (semi)urban populations. We investigated the genetic consequences of barriers within and between urban and rural areas on population structure of red fox, sampled throughout Slovenia, central Europe. We used 19 microsatellite loci to genotype 70 red foxes and performed basic population genetics analyses to study genetic structure and dispersal behaviour of this mobile mesocarnivore across the urban–rural landscape. We provided first insight into differences of genetic diversity and genetic structure among urban and rural foxes in Slovenia in regards to potential anthropogenic and/or natural barriers. Although red fox is very abundant species in Slovenia, different structures (e.g. natural and infrastructure barriers, settlements, urban environments) may affect and reduce its migration/dispersal patterns. Therefore, identification of gene flow enabling estimation of species dispersal potential and connectivity of populations may help to understand the nature of species subpopulation structure and possible limitations of its functionality. By defining differences we can better understand dispersal of other urban wildlife and also make a prediction how spatial behaviour can shape population genetic structure beyond physical barriers.

Keywords: red fox, population genetic structure, urban ecosystems, urban ecology, habitat fragmentation, metapopulation

Minimum Requirements for Genetic Monitoring: A Proposed Workflow

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A major challenge for the wider adoption of forest genetic monitoring (FGM) is to identify the minimum and optimum resources (number of sampled trees and / or loci) required to detect the effects of environmental change through temporal assessments in the genetic diversity of populations. Such a validation is especially important in the determination of the number of loci, when using microsatellites, given SSR marker heterogeneity. In this study, we propose a workflow to be implemented within genetic monitoring schemes in order to assess the feasibility of achieving comparable accuracy of estimates with fewer resources. We have constructed subsamples, employing different numbers of loci (starting from the most polymorphic locus and sequentially adding the rest), and using different sample sizes by sampling without replacement individuals from extensive empirical data sets (Abies alba / borisii-regis and Fagus sylvatica populations of n=200 up to n=400). We have then calculated genetic diversity parameters (allelic richness, expected/ observed heterozygosity, FST) and their variance, to evaluate the parameter estimates dynamics under different sample specifications. This analysis provides a valuable insight into optimizing sampling designs and contributes to the establishment of biomonitoring at the gene level as an economically viable protection strategy. Its importance also lies in the fact that it is using extensive real data sets and not simulations to derive to parameter estimates.

Keywords: genetic monitoring, sample size, SSR

Assessing the negative effects of severe powdery mildew infection on chlorophyll a fluorescence and stomatal characteristics of *Quercus robur* L.

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Oak powdery mildew (*Erysiphe alphitoides* (Griffon and Maubl.) U. Braun and S. Takam.)) has been addressed as the most common foliar pathogen of oaks, exploiting harmful effects, especially on young seedlings. To assess, evaluate and monitor these negative effects, an experiment in semi-controlled conditions was set up and constituted of 10 one-year-old disease-free seedlings of *Quercus robur* L., and the same number of seedlings with 50% and 75% of leaf coverage by epiphytic mycelia of oak powdery mildew. During the experiment, the infection progressed by its natural course, and in the end, the leaves of the first infected treatment group have reached a coverage of 75% with epiphytic mycelia, and the second infected group has progressed to 100% leaf infection coverage. All observed parameters of chlorophyll a fluorescence transient were shown to be highly effective in the evaluation and monitoring of severe biotic stress caused by oak powdery mildew. Moreover, the studied parameters of slow fluorescence kinetics were under the notable negative influence, with the coefficient of non-photochemical fluorescence quenching and Stem-Volmer type non-photochemical fluorescence quenching parameters exhibiting the fastest responses to observed biotic stress. Considering leaf stomatal traits, the reduction of stomata guard cell width in line with the increase of stomatal density was pointed out as the protective mechanism of *Q. robur* against the stressor. The overall results evidenced the adverse effects of powdery mildew infection on the photosynthetic apparatus of pedunculate oak seedlings, which progressed in time and depended on the severity of the infection.

Keywords: biotic stress, epiphytic mycelia, chlorophyll a fluorescence, Pedunculate oak, stomatal density

Tree faces: forest genetics at your fingertips - A selection of dissemination activities in Germany

Mark Walter, Barbara Fussi, Darius Kavaliauskas

As part of the project, the Bavarian Office for Forest Genetics (AWG) developed a communication concept to convey information on forests in general, forestry, climate change and forest genetics to specific target groups. One of the main challenge was to develop specific workshops for children under 10 years of age. In the programme “A forest has many faces” for example, the children received basic knowledge about the relationship between forest trees. Bavarian schools showed particular interest in the thematic focus “The forest in climate change”. Almost 250 school classes applied for one of the 40 planned events.

Furthermore, the AWG organised many events to raise general awareness on the importance on biodiversity, such as the „Forest experience day” for families, where more than 21 regional institutions were able to communicate their main topics on the subject of “Diversity in the forest“ or a symposium for wood carving students on the motto “Native animals in climate change – winners and losers“ with big oak trunks which fell in enormous summer storms.

Within special training courses the German Lifegenmon-Team explained the importance and procedures of forest genetic monitoring to forest students and foresters. Since scientific cooperation on an international level is indispensable in times of climate change, numerous researchers from abroad visited the project’s plots where the project’s scientists explained the best procedure for establishing a long-term forest genetic observation system. In addition, the AWG presented various results at national and international conferences, such as Interforst in Munich or IUFRO in Brazil.

The Seedhunter App

Mark Walter, Barbara Fussi, Darius Kavaliauskas, Peter Železnik, Xrysi Sarvani, Ermioni Malliarou, Katja Sonnenschein

With »Seedhunter« the Bavarian Office for Forest Genetics (AWG) developed a forest pedagogic app for Android that sends young people into the forest to hunt for tree seeds. The seeds are virtual objects which can be placed by the project partners and cooperating state forests in selected forests worth seeing. In order to collect a virtual seed, the player has to approach it with a smartphone and store it in the so called »Seed Safe« within the app. For each collected seed the player gets rewarded with points. Rare species are more difficult to find but give a higher score. A ranking list allows the player to compete with others and become the most successful »Seedhunter«.

In the »Seed Safe« interested people find further information about tree species and their seeds. The information is designed from simple to complex. In addition to general characteristics of the tree species, the user will also find information about the typical place of discovery and the cultivation of the real seed. Therefore the seed safe is interesting for forest novices as well as for experienced forest enthusiasts.

Seedhunter intends to draw the attention to forest diversity and rare tree species in a playful way. Besides the forest pedagogic aspects, a main aspect of the concept was that the gaming challenge of Seedhunter takes place outside, in nature's most precious forests and not at home on the couch. In order to win, the player has to visit as many forests as possible.

Guidelines for conducting genetic monitoring in the field: *Fagus sylvatica* L.

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European beech (Fagus sylvatica) is a monoecious, stand forming deciduous tree species present throughout most of Europe. This very competitive and shade tolerant tree species can naturally regenerate in continuous cover silvicultural systems and is able to conserve the productive capacity of the soil better than many other species. With its high ecological importance and strong wood, this species is a good candidate for genetic monitoring.

The guidelines shortly describe the European beech, its reproduction, environment and threats. They provide guidance on establishing a genetic monitoring plot and on recording all field level verifiers.

The emphasis will be given to the particularities of genetic monitoring of European beech compared to other species.

Keywords: European beech, genetic monitoring, field level verifiers

Guidelines for conducting genetic monitoring in the field: *Fraxinus excelsior*

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Common ash (*Fraxinus excelsior*) is a polygamous, scattered deciduous tree species present all throughout Europe except in the driest Mediterranean areas. It is closely related to narrow leaved ash with whom it hybridises. With its high ecological importance and utility in timber industry, this species strongly threatened by the ash dieback, is a prime candidate for genetic monitoring.

These guidelines shortly describe the common ash, its reproduction, environment and threats. They provide guidance on establishing a genetic monitoring plot and on recording all field level verifiers.

The emphasis will be given to the particularities of genetic monitoring of European beech compared to other species.

Keywords: Common ash, genetic monitoring, field level verifiers

Index of Authors