B4EST

Adaptive BREEDING for productive, sustainable and resilient FORESTs under climate change

Deliverable D6.6

B4EST International Conference

Planned delivery date (as in DoA): M51

Actual submission date: 14/12/2022 - M56

Workpackage: WP6

Workpackage leader: EFI

Deliverable leader: IEFC

Version: 1.0

Project co-funded by the European Commission within the Horizon 2020 Programme (2014 - 2020)	
Dissemination Level	
PU Public	**PU**
CI Classified, as referred to Commission Decision 2001/844/EC	
CO Confidential, only for members of the consortium (including the Commission Services)	

Research and Innovation action: GA no. 773383

Start date of the project: May 1st, 2018

Table of Contents

1 Summary ... 3
2 Introduction ... 3
3 Preparation of the event ... 4
4 Report of the conference ... 6
4.1 Opening session ... 6
4.2 Session A – Rethinking breeding strategies for an uncertain future ... 7
4.3 Session B- Forest Genetic Resources and adaptation to climate change ... 9
4.4 Session C-Deployment of Forest Reproductive Material ... 11
4.5 Session D- Science policy interface for mitigation, adaptation and risk management in forestry ... 13
4.6 Conclusions and perspectives from these 2 days of conference ... 15
4.7 Session on B4EST tools presentation ... 16
4.8 Training courses ... 17
4.9 Field visit ... 17
4.10 IEFC open session ... 18
4.11 Working group sessions ... 18
5 Dissemination activities about the conference ... 18
6 Conclusions ... 19
7 Partners involved in the work ... 19
8 Annexes ... 20
8.1 Annex 1: Conference Timetable ... 20
8.2 Annex 2: Working group sessions timetable ... 21
8.3 Annex 3: Conference Program ... 22
8.4 Annex 4: International conference's participants list (20-21 June) ... 35
8.5 Annex 5: Training session's participants list (22-23 June) ... 37
8.6 Annex 6: Working group's participants list (22-23 June) ... 37

1 Summary

The B4EST International Conference, **Managing Forest Genetic Resources (FGR) for an Uncertain Future**, was held on 20-23 June 2022 in Lisbon, Portugal at the Instituto Superior de Agronomia. This document describes both the preparation of the event with the role of the different partners involved and the report from those 4 days of conference, training courses and discussions. Even if remote attendance was highly restricted in order to promote a good quality of exchanges with the people onsite, a replay of the sessions and access to presentations and a summary of the conference were made available on the B4EST website (to increase dissemination corresponding links on the website are provided in this deliverable).

Science-based innovations in forest management practices will only be widely adopted through intense information sharing and international collaboration among researchers, practitioners and policymakers. The present B4EST International Conference brought together various actors from the forestry sector and provided a broad overview of innovative scientific knowledge, methods and tools that could be or are already being implemented in forest tree breeding, and FRM deployment strategies. The conference was also an opportunity to present platforms such as EUFORGEN, which is specifically dedicated to promoting dialogue among the different actors, developing strategies and setting priorities for the conservation and sustainable use of FGR in Europe. We hope that it will stimulate future work and major improvements in the way forests are managed and conserved, which, given the pressing threats to Europe's forests, is urgently needed.

2 Introduction

The B4EST project international conference “Managing Forest Genetic Resources (FGR) for an uncertain future” was organized on 20 – 23 June 2022 in Lisbon, Portugal. The local organizer was IEFC with the help of the INRAE for the scientific program and with support from the Instituto Superior de Agronomia (ISA) for the local logistics. The main goal of the conference was to disseminate B4EST’s results to the scientific community and a large array of forestry stakeholders through plenary and side events. The event, only open in physical attendance would enable the participants to meet and have room for networking. Another aim of the meeting was to attract a lot of young researchers or PhD students both by giving an opportunity to expose their work but also to follow lectures needed in their doctoral process.

The event gathered 77 participants (listed in Annex 4) with 54% of project members but also a large audience of scientists and practitioners from other organisms of 11 European countries.

3 Preparation of the event

Once the localisation of the event has been set up in Lisbon by the B4EST executive committee, the IEFC was responsible of the onsite organisation. The IEFC booked the conference room and its audio facilities to host online guests and to record the meeting, but also classrooms for working group sessions in smaller groups. The IEFC was also in charge of finding service providers for the catering (lunch and coffee breaks), a restaurant for the social diner and a bus for the field trip.

A scientific committee composed of project members was tasked with the design of the content of the international conference and preparation of a summary of presentations and discussions in the different sessions. This scientific committee involved both young scientists (phD students, postdocs) and senior scientists: Juliette Archambeau (INRAE), Simone Bianchi (LUKE), Joukje Buiteveld (WUR), Marta Callejas-Díaz (INIA-CSIC), Stephen Cavers (UKCEH), Henrik Hallingbäck (SKOGFORSK), Chedly Kastally (Univ. Helsinki, Viiki plant science center) ,Marina de Miguel (INRAE), Sven Mutke (INIA-CSIC), Leopoldo Sánchez-Rodriguez (INRAE), Richard Whittet (FR), Santiago C. González-Martínez (INRAE) and Catherine Bastien (INRAE).

The coordinator wants to stress the high engagement of these young scientist before, during and after the conference and hopes that this experience will serve their professional trajectory. The two days of conference were divided into 4 thematic sessions, each time composed of a

keynote speaker, animated by two session chairs and with room for voluntary speakers identified through a call for abstracts. Sessions offered different intervention format:

- A 45 minutes talk from the keynote speaker
- Regular talks (20 min), short talks (10 min) and flash talks (5 min) followed by questions from the audience
- Roundtable with 4 panellists discussing on a common topic

The IEFC has set up the call for abstracts and its advertisement, open from the 25th of April to the 30th of May. The scientific committee has then taken over the selection of 25 speakers upon the 31 abstracts submitted.

In addition of those two days of international conference, the consortium has carried out a set of side events:

- A field visit organised in the nursery of a B4EST partner (Altri Florestal)
- A demonstration of tools developed in B4EST
- Two open training courses on genomic topics offering a state of the art and show cases
- The IEFC open discussion about planted forest & general assembly
- B4EST working group sessions only open to B4EST partners and aiming at clarifying the remaining work before the end of the project on a selection of deliverables and other collaborative productions.

Each side events were organized and managed by B4EST scientists in a role of teacher or animator. The calendar was managed to allow participants to attend different sessions and split restricted and non-restricted events. By offering several options, the participants would be able to choose and attend the side events they were interested in.

Finally, both IEFC and EFI worked to produce the practical information document, a graphical agenda, a detailed scientific program of the conference (Annex 1) and name badges. Those materials were shared on the B4EST website throughout the conference preparation but also printed and distributed at the beginning of the event.

4 Report of the conference

4.1 Opening session

Forests cover 35% of the European land area (i.e. 227 million hectares), of which 2.2% are untouched by human intervention, 3.9% are plantations and 75% are available for wood supply (Forest Europe 2020). Forests are reservoirs of biodiversity and provide multiple ecosystem services, in particular through their major role in water cycle, regulation of global (via carbon storage) and local (via evapotranspiration) climate, prevention of soil erosion and production of wood (e.g. timber) and non-wood products (e.g. food, cork, resin, oils). About 42% of timber volume is used for energy generation, 24% for sawmills, 17% for the paper industry and 12% for the panel industry (Forest Europe 2020). In addition, about half of the renewable energy consumed in Europe comes from wood and the forestry sector accounts for about 1% of European gross domestic product (Forest Europe 2020). Forests also hold an essential place in European culture, history and tourism, and contribute to the well-being of urban and rural communities.

Climate change triggers an increase in biotic and abiotic threats to European forests, including gradual climatic shifts, more frequent extreme climatic events (e.g. droughts or frosts), large-size fires (not restricted to the Mediterranean area any more), storms (mostly in western and central Europe) and insect outbreaks (Seidl et al. 2018; Forzieri et al. 2021; Obladen et al. 2021). How natural and managed forest tree populations will cope with these threats is highly uncertain. Indeed, although the range of tree species and populations are shifting northward and to higher elevations, these processes are unlikely to be fast enough to keep up with the current rate of climate change (Boisvert-Marsh Laura et al. 2014; Davis and Shaw 2001). Natural forest tree populations will thus have to persist in their current geographic area, by relying on their phenotypic plasticity (up to a certain threshold; Nicotra et al. 2010) and their adaptive capacity, which depends on the genetic variation of the populations and on the presence of beneficial alleles under future climates. In this context, predicting which populations will survive the forthcoming changes constitutes an active research area (Alberto et al. 2013). In managed forests, implementing effective strategies for the deployment of Forest Genetic Resources (FGR, the genetic variation in trees of present or potential benefit to humans; FAO 1989) and tree breeding programmes, including low-input ones, will be key to obtain forests adapted to the upcoming changes. In particular, conservation and management

strategies must take into account the uncertainty of future climate predictions by ensuring that sufficient levels of genetic variation are maintained within populations, i.e. that the adaptive potential is high enough to cope with new conditions.

In light of the challenges raised by climate change, new genomic technologies hold the potential for better anticipating the response of natural forest tree populations to climate change, better characterising FGR, and accelerating tree breeding. For instance, natural forest tree populations that are at risk of maladaptation under climate change may be identified based on the disruption of their gene-environment relationships (e.g. Fitzpatrick & Keller 2015). Large genomic datasets offer opportunities for improved characterization of FGRs, such as more precise delineation of gene pools, quantification of genetic diversity or identification of the adaptive genetic variation underlying disease resistance or drought tolerance. They have also proven highly useful for genomic selection (GS), in which all available genomic markers are used to predict the additive genetic value of individuals (Meuwissen et al. 2001), leading to tremendous progress in livestock improvement (García-Ruiz et al. 2016), and now increasingly used in tree breeding. In addition, the recent integration of multi-omics data into GS approaches may result in more accurate predictions of phenotypes.

Deploying the most effective and robust management and conservation strategies in the face of climate change involves sharing new scientific knowledge among experts, practitioners, and policymakers. It is therefore essential to make the most up-to-date research and tools easily accessible and to strengthen the links among the various actors in the forestry sector. With this in mind, B4EST, an European H2020 project conducted between 2018 and 2022 (www.b4est.eu), provided forest tree breeders, forest owners, managers, and policymakers with sound scientific knowledge to increase forest survival, health, resilience, and productivity in the face of climate change, while maintaining genetic diversity and key ecological functions, and promoting a competitive European bioeconomy. As a closing to the project, the B4EST International Conference, 'Managing Forest Genetic Resources (FGR) for an Uncertain Future' (https://b4est.eu/b4est-conference), was held on 20-23 June 2022 in Lisbon, Portugal, at the Instituto Superior de Agronomia. This conference brought together a wide range of stakeholders from both the public and private forestry sector, researchers, and policy authorities. It was organised into 4 sessions, which addressed current issues for the implementation of sustainable management and robust conservation of European forests: (1) How can new genomic technologies support the forest tree breeding sector in facing new challenges and an uncertain future? (2) How should Forest Reproductive Material (FRM) be deployed to build resilient forests to climate change? (3) What is the role of FGR and the potential of FRM deployment in different European countries and forest types in a context of climatic and societal change? (4) How is FRM deployment differently organised across national/subnational governance systems and what role do scientists play in it?

4.2 Session A – Rethinking breeding strategies for an uncertain future

Genomic innovations in the last decade have led to promising improvements in the way tree breeding is conducted. The development of new genotyping tools is a cornerstone of this progress. The 4TREE Axiom 50K SNP array was developed within the H2020 project B4EST for economically important species in Europe: poplar (*Populus* sp), ash (*Fraxinus* sp), maritime pine (*Pinus pinaster* Ait.) and stone pine (*Pinus pinea* L.). Based on *de novo* sequencing resources and existing genomic resources of loci of interest, it is primarily aimed at breeders

by providing low genotyping costs and fostering collaboration between breeding programs across Europe. Sanna Olsson (INIA-CSIC, Spain) presented some examples of the advantages of the 4TREE SNP array in stone pine: unprecedented resolution of the population structure and unambiguous clonal identification.

The availability of large sets of genomic markers has opened the door to the use of more powerful statistical tools to predict phenotypes of interest, in particular GS, which has already revolutionised animal breeding practices. Indeed, GS offers new prospects to accelerate genetic gain through the shortening of breeding cycles, to reduce phenotyping costs by defining more targeted phenotyping (replacing all or a portion of the phenotyping effort with genotyping), to improve predictive and explanatory analyses decrypting phenomena and to optimise the performance in progeny. As an example, Geoffrey Haristoy (CIRAD, France) showed how GS can be applied in the ALTRI's breeding program that manages close to 70,000 hectares of *Eucalyptus globulus* in Portugal. He used GS to correct pedigrees and showed that GS achieved enough accuracy for predicting height, diameter, and survival across generations, although the accuracy remained higher when individuals from the same generation were included in the training population.

However, implementing GS in recurrent breeding programs may accelerate genetic diversity erosion and long-term genetic gains may be compromised by higher inbreeding rates. New approaches are therefore being developed to achieve better long-term monitoring and management of genetic diversity in breeding and conservation programs, which is essential for an uncertain future. In this line, Laurence Moreau (INRAE, France) gave a keynote talk on how GS can be used at different stages of a breeding program to better manage genetic diversity over time. She illustrated with a case study in maize how GS models calibrated on collaborative diversity panels (i.e. panels combining primary genetic resources and recent elite materials) can identify sources of favourable alleles that could enrich a given breeding program (Allier et al. 2020a). She then presented an optimised breeding strategy in which GS and optimal cross selection (i.e. optimal selection of crosses under a constraint on genetic diversity in the progeny) are combined to improve genetic resources (i.e. pre-breeding), bridge the improved genetic resources with elite materials (i.e. bridging), and manage the introduction of donors into the elite breeding population (Allier et al. 2020b). Such strategies are highly promising as they broaden the available genetic resources for commercial breeding programs and have therefore the potential to increase long-term genetic gain with only a limited reduction of short-term commercial gain (Allier et al. 2019). It was also demonstrated by Matthieu Tiret (Uppsala University, Sweden), who implemented the concept of group selection in the breeding program of black poplar (*Populus nigra* L.) and showed that maintaining genetic diversity can both provide long- and short-term genetic gains (i.e. through intraspecific interactions).

Another challenge in genomic selection is to select for trees not only based on traits related to growth and wood quality but also traits related to disease or drought resistance. Victor Papin (INRAE, France) estimated breeding values that vary along environmental gradients (e.g. different levels of aridity) for a dendrophenotype (ring surface) in maritime pine and emphasised the importance of determining whether breeding programs should select genotypes that perform well in a wide range of environments or in specific environments. Giorgio Tumino (Wageningen University & Research, The Netherlands) estimated breeding values of two traits related to resistance to ash dieback disease in common ash (*Fraxinus excelsior* L.) based on the 4TREE SNP array and found that lesion length was more predictable

than the percentage of defoliation. Chiara Biselli (CREA, Italy) identified loci for resistance to the woolly poplar aphid (*Phloeomyzus passerinii* L.) in poplar and showed that molecular markers explained more than 50% of the total phenotypic variance for resistance. Since most cultivated poplar clones are susceptible to the disease, this study is a step towards building a collection of resistant clones that could enrich poplar breeding. Last, Ricardo Alia (INIA-CSIC, Spain) presented a review of the genetic variation in resistance and tolerance to abiotic/biotic stresses in forest trees, resulting from B4EST new research, in which he suggested that genetic correlations among traits will not constrain genetic improvements for most traits.

Recent developments in GS also include the integration of muti-omics data in phenotypic prediction. Leopoldo Sánchez-Rodriguez (INRAE, France) presented an approach that integrates transcriptomic and genomic data in phenotypic prediction by combining concatenation (data integration) with ridge regression (prediction). Using 21 phenotypes and 241 genotypes from two common gardens in black poplar, he showed that expression quantitative trait loci (eQTLs; loci explaining variation in gene expression levels) play a major role in the predictions and that the benefits of integrating transcriptomic data decrease with the redundancy of the predictors.

In summary, this session illustrated, through case studies, some of the methodological developments and proof-of-concept initiatives aimed at exploiting the full potential of genomic technologies so that they can maximally benefit forest tree breeding programs. The possibilities offered by these new approaches are highly promising, but further appreciation is needed regarding the impacts that these new developments could bring at the organisation level of the breeding programs

4.3 Session B- Forest Genetic Resources and adaptation to climate change

Predicting how natural and plantation forest tree populations will persist in their current location or respond to new environments (e.g. after translocations) is a difficult task, yet necessary for planning effective management and conservation strategies. Indeed, many aspects of population responses to changing conditions remain to be understood, e.g. the relative contribution and interaction between plasticity and adaptation, the limits of phenotypic plasticity, the rate of adaptive genetic change, the trade-offs among adaptive traits, the role of maternal effects, etc. Moreover, projections of future climates are still very uncertain, especially those related to future precipitation, hence requiring the development of methods to incorporate these uncertainties into predictions. Case studies and statistical approaches presented in this session aimed to provide predictions of the short-term responses of forest tree populations to new climatic conditions using a wide range of concepts and tools from population and quantitative genetics, spatial modelling or community-level modelling.

In his keynote talk, Tongli Wang (University of British Columbia, Canada) shared his perspective on recent method development for predicting forest tree population responses to climate change. Future population ranges were first predicted with climate niche models, which have the limitations of not considering intraspecific variation and of taking into account only the realised niche of the species instead of the fundamental niche. Transfer and response functions were then developed based on phenotypic data from multi-site common gardens to predict trait variation across the species range, and were called Universal Response Functions (URF) when both transfer and response functions were combined in a unique model (Wang et

al. 2010). The predictions from those functions rely on the association between trait variation and the climate-of-origin of the populations (i.e. genetic component) and the climatic conditions in the common gardens (i.e. plastic component). Those functions have been shown to provide less pessimistic predictions of population responses than climate niche models (Benito-Garzón et al. 2019). Since the generalisation of genomic tools, a new set of approaches have been developed to predict population responses to future climatic conditions based on genomic data. Tongli Wang showed as an example how landscape genomics methods can be used to define seed and breeding zones in lodgepole pine (*Pinus contorta*) (Yu et al. 2022).

The session speakers gave a complementary overview of different methods and traits studied to anticipate the responses of European forest trees to climate change. Katharina Liepe (Thuenen Institute of Forest Genetics, Germany) and Zhi-Qhiang Chen (Umeå Plant Science Centre, Sweden) used height data from 20 common gardens and 1,100 provenances in Norway spruce (*Picea abies* L.) and applied the URF framework to predict height patterns in the 1980s across the species range. Both studies found that most height variation was explained by phenotypic plasticity, although the two studies did not identify the same climatic drivers. Katharina Liepe showed that height models predicted a substantial contraction of the species range towards the core of the distribution, though these predictions were less alarming than those from occurrence-based species distribution models. She suggested that transferring optimal populations would only marginally avoid range contraction given the high phenotypic plasticity of Norway spruce, although it may help maintain growth in the remaining distribution. In this line, Zhi-Qhiang Chen showed that using the optimal populations in each common garden may enhance productivity by 51.1% and 30.7% over the productivity of the 2010s for temperature increases of 1°C and 2°C, respectively. Still on Norway spruce, Arne Steffenrem (NIBIO, Norway) investigated an understudied plastic response in forest trees: the effects of the maternal reproductive environment. His study suggests that temperatures during reproduction and seed maturation can have long-lasting and predictable effects on seedling phenology. Controlling such maternal effects in management and conservation programs may prove useful for maximising the performance of trees grown in nurseries. Transgenerational effects were also investigated by Marta Callejas-Díaz (INIA-CSIC, Spain) in a common garden experiment of maritime pine. She showed that seedling height and ontogeny were influenced by the interacting effects of seedling cohorts and mother genotype (Callejas-Díaz et al. 2021).

While most predictions of future population responses to climate change are based on growth traits (e.g. diameter at breast height, height) or traits related to wood properties (e.g. stiffness), a more complete picture of the adaptive and plastic responses of forest trees may be obtained by considering other types of traits. Āris Jansons (Silava, Latvia) presented a case study in Scots pine (*Pinus sylvestris* L.) in which the climatic sensitivity of radial growth was examined using rings of trees from seven southeastern Baltic provenances grown in five common gardens in Germany and Latvia. The highest heritabilities were found for the sensitivity of radial growth to the summer heat moisture regime and to a lesser extent to climatic conditions in winter and late summer of the preceding year.

Laura Guillardin (Oxford University, UK) highlighted needs to address the question of management of genetic diversity over generation when planted forests are converted in continuous cover forests, as genetic diversity is an important lever of adaptation capacity of forest ecosystems. She presented first steps of two study cases concerning Douglas fir and western red cedar plantations under conversion.

Annika Perry (UKCEH, Scotland) also argued for the relevance of considering other traits in phenotypic prediction, such as phenology-related traits that may affect survival and fitness (e.g. earlier bud burst associated with higher sensitivity to late frosts; Muffler et al. 2016). She presented an innovative study that combines a multispecies approach to identify SNPs associated with growth and phenology traits with single species genomic prediction models (Perry et al. 2022). Based on genomic data from a large new SNP array (Perry et al. 2020), 118 SNPs were found associated with the traits in three closely related pine species (*Pinus sylvestris, Pinus mugo* and *Pinus uncinata*). Genomic prediction models were trained and tested on phenotypic data from a glasshouse experiment of Scots pine and validated in two independent field trials. Their predictive ability was strongly limited by genotype-by-environment (GxE) interactions. However, using some of the height models as genomic selection tools would result in the selection of trees on average taller than the average for each site, thus highlighting the potential of the present approach for accelerating tree breeding. Last, Octávio S. Paulo (cE3c, Portugal) presented a case study in cork oak in which populations that may be at risk of potential maladaptation under climate change were identified using landscape genomics approaches, i.e. Gradient Forests (Vanhove et al. 2021) and RONA (Pina-Martins et al. 2019).

4.4 Session C-Deployment of Forest Reproductive Material

Planning forest conservation and management strategies requires consideration of the multiple ecosystem services and transition pathways to bioeconomy that we want our forests to provide. The ambition of this session was to present examples of how breeding programmes and FRM are being developed across European countries for an increasing number of species and how scientific knowledge and decision-support tools can be useful for practitioners.

The keynote talk of Conceição Silva (UNAC, Forest Owner Association, Portugal) deal with FRM regulation, certification and markets in Portugal for the five main forest tree species in the region, namely eucalypt (*Eucalyptus globulus* Labill.), cork oak (*Quercus suber* L.), holm oak (*Quercus rotundifolia* Lam.), maritime pine (*Pinus pinaster* Ait.) and Mediterranean stone pine (*Pinus pinea* L.). Although private landowners (87% of the forests are private in Portugal) consider climate change adaptation and mitigation as a priority need, the cork, wood and pulp industry sectors struggle with a lack of raw material adapted to the new climatic and biotic conditions. Indeed, breeding programs initially optimised genetic gain for traits related to growth and wood quality (e.g. in maritime pine and eucalypt) or the production of pulp (eucalypt), resin (maritime pine), cork (cork oak) or pinyons (stone pine). Recent breeding programs now aim to improve tree resistance to pathogens (e.g. resistance to the pine wilt disease caused by the pine wood nematode for maritime pine) and other traits.

Esteban Torres-Sánchez (Lourizán Forest Research Centre, Spain) introduced the Galician breeding program for maritime pine that started in the 1980s and initially focused on selection for growth, bark thickness, straightness and (low) ramification. He demonstrated that selecting for wood quality at an early stage is possible due to phenotypic correlations between juvenile and mature trees and will not result in growth loss (i.e. no trade-off between growth and wood quality). Toms Kondratovics (Silava, Latvia) presented results on the light requirements of hybrid aspen (*Populus tremula* L. x *P. tremuloides* Michx) seedlings to optimise propagation rates in growth chambers and thereby accelerate breeding.

Besides sharing scientific knowledge, cooperation between researchers and practitioners also requires the development of decision-support tools that are easy to access and use. In this line, Daniel Blanco-Ward (INIA-CSIC, Spain) presented the new version of the Forest Map of Spain (FMS) that updates the species distribution maps and provides information on FRM geographic origin. Pauls Zeltiņš (Silava, Latvia) showed that some height growth functions belonging to the generalised algebraic difference approach (GADA) have a good predictive ability in young stands of improved Scots pine (*Pinus sylvestris* L.) and silver birch (*Betula pendula* Roth), and could be easily implemented by foresters to predict height growth. The B4EST project also supported the development of a web-based decision-support tool called the Planter's Guide which provides recommendations for a given regeneration site of the best available Scots pine and Norway spruce seedlings from seed orchards in Sweden and Finland. These recommendations correspond to URF predictions for growth and survival based on tailored climate variables. Mats Berlin (Skogforsk, Sweden) presented the tool's new developments such as a new interface that handles many sites and seed orchards simultaneously for actors with large forest holdings (and often nurseries). This new interface also optimises the use of available seeds by maximising mean annual growth. The next developments include expanding to other countries (Norway for both species and Latvia, Lithuania and Estonia for Norway spruce), incorporating other scenarios of future climate (scenarios RCP2.6-8.5) and better accommodating the prediction uncertainty of future climates by providing 'uncertainty maps'.

The session ended with a round table discussion including Juha Hakkarainen (FINSILVA, Finland), Brigitte Musch (ONF, France), Felipe Pérez (MITECO, Spain) and Christophe Orazio (IEFC, France). The panellists have been asked to address the following questions: which ecosystem services will be paramount for European forests in the 2050s? Which role will have the use of improved forest material in this context? What are the experiences and lessons learned from your country? They first stressed that the main challenges for current management and conservation strategies are to maintain, in the context of climate change, healthy, resilient forests that will continue to provide ecosystem services critically important in 2050, such as provisioning food, timber and other products to the bioeconomy, regulating water retention, carbon sink, cooling effect in cities, erosion and desertification prevention and biodiversity, as well as contributing to human cultural and spiritual well-being. They argued that addressing these challenges will require a strong dialogue among researchers, policymakers and practitioners, the establishment of protocols and open access databases, the development of breeding programs for a wide range of species and provenance trials outside the species ranges, and the development of new statistical or decision-support tools. These actions will have more impact if they are implemented on a European scale, and supported by strong cooperation among actors, common legislation across countries and better traceability of genetic material. FRM will be a cornerstone of future forest management and will have to meet the challenge of providing trees resilient to new climates and resistant to diseases and pests, while maintaining sufficient genetic diversity. A good balance will also have to be found between forest production, social uses and conservation, and between forest management and naturalness. Felipe Pérez brought up the example of holm oak dieback in Spain to argue that sound conservation strategies of natural populations will have to rely also on improved material for biotic tolerance. Juha Hakkarainen underlined the key role of labels to protect natural populations and ensure sustainable forest management, taking as an example the whole forest area of FINSYLVA which has now received the double PEFC and FSC certification.

4.5 Session D- Science policy interface for mitigation, adaptation and risk management in forestry

Investing in FGR has the potential to improve economic gains in tree breeding and the success of ecological restorations (e.g. the introduction of diverse FGR in the Basque Country radiata pine breeding programme, which originally relied on a single provenance, Año Nuevo; Herrero et al 2021). However, the time return on investment in research and development can be very long and priorities may shift due to political changes. Therefore, scientists have a responsibility to communicate benefits and risks of new uses of FGR and FRM development, to be clear and honest about prediction uncertainties, but also to understand the needs of and learn from practitioners, who are often expert FGR stewards without realising it. The aim of this session was to provide examples of different systems of FGR management and FRM development and to outline the roles that scientists, end-users and policymakers should play in them.

Michele Bozzano (EUFORGEN, EFI, Spain) introduced in his keynote talk the Forest Genetic Resources Strategy for Europe, a coordinated and cooperative effort in the European Forest Genetic Resources Programme (EUFORGEN) which aims to improve the conservation and sustainable use of European FGR. This strategy extends and strengthens the existing pan-European Strategy for Genetic Conservation of Forest Trees by placing further emphasis on increasing the availability of and access to improved information about FGR (e.g. more accurate characterisation and classification of Genetic Conservation Units, GCUs) and by including genetic information to define conservation targets. It has three major objectives: (1) facilitate knowledge sharing and communicate with key stakeholders, (2) coordinate and monitor the conservation of FGR and (3) promote the appropriate use of FGR. This strategy also defines principles for better coordinating activities at policy level, in particular the roles of European countries and the EUFORGEN network, and also proposes actions and collaborations among organisations at the international level.

Anssi Ahtikoski (LUKE) presented case studies stemming from B4EST, evaluating the impacts of deploying improved FRM in four regions of Europe, with different growing conditions, forest structure, forest management procedures and expected risks of environmental change (climatic and biotic). The long-term benefits and risks of improved FRM were assessed by estimating biomass production, carbon sequestration, seed production resilience and biodiversity but also plywood production, biomass for bioenergy and phytoremediation in alluvial regions. This evaluation was performed on different species depending on the studied region (e.g Scots pine and Sitka spruce in Scottish woodlands, or maritime pine and stone pine in the Atlantic regions of southern Europe), under different scenarios of future climate and forest management.

Isabel Carrasquinho (INIAV, FAO, Portugal) presented how FGR are used in conservation and genetic improvement in Portugal. In 2020, five R&D projects were funded by the national operational program (PROGEN) to evaluate diversity trends and status in maritime pine, cork oak, stone pine, prickly juniper and white crowberry. These innovative projects moved from a classical gene conservation strategy to a dynamic conservation approach with three main objectives: (1) to create the conditions for future evolution, (2) to conserve specific adaptations in marginal populations, and (3) to save endangered populations. For that, they rely on two

types of *in situ* forest managed areas: GCUs and certified seed production units. Seven species also benefit from ongoing breeding programs aiming at improving diverse traits and supported either by public institutions or private actors, e.g. INIAV's breeding program on maritime pine selecting for resistance to pine wilt disease or higher resin production, or the two independent breeding programs of RAÍZ and ALTRI in eucalypt selecting for higher pulp production.

Richard Whittet (Forest Research, UK) discussed opportunities for reopening the Scots pine breeding program in Scotland, which arose from a B4EST case study. This program started in the 1950s with the selection of 1,065 plus trees tested in about 100 half-sibling progeny tests established on 17 different forest sites (Lee 2002). The program stopped in 2002 with the reselection of a breeding population of 226 parents for height and straightness and the best parents were archived in clone banks, but breeding work discontinued. As the East of Great Britain becomes drier under climate change, it may become unsuitable for growing quality timber from Sitka spruce, which is the main commercial species in the UK. Scots pine is considered more drought tolerant than Sitka spruce and improved FRM is in high demand, yet supplies are inadequate. Analysis of genetic trial data suggested that simultaneous improvement of growth and disease resistance (*Dothistroma septosporum*) is possible and was shown by a stakeholder survey to be in the public and private interest. Economic modelling also showed that the expected gains in growth and disease resistance for growers can cover their investment in reopening the Scots pine breeding program. The ideas incubated under the B4EST case study have been presented to the UK Government's Department for Environment, Food and Rural Affairs and funding has been secured for a three year project to reinitiate Scots pine breeding in Great Britain.

Catherine Bastien (INRAE, France) gave a summary of the transformative changes in tree breeding and FRM deployment investigated by the B4EST project to improve forest resilience to climate change and thus maintain forest ecosystem services and their contribution to the bioeconomy. These transformative changes rely on new knowledge and tools, many of which were presented at the conference. They also benefit from collaborative efforts, allowing for example access to other sources of information such as high quality phenotyping across different scales or high resolution real-time monitoring of European forests based on new numerical technologies.

A round table discussion concluded the session, bringing views from different international organisations represented by Bent Leonhard (EFNA), Barry Gardiner (IEFC), Chris Kettle (Bioversity International) and Jarkko Koskela (FAO). The panellists have been asked to address the following questions: How much evidence is enough for action given high levels of uncertainty? How should long-term investment in FGR be encouraged in a changing environment? What are a recent important lesson learnt for mitigation/adaptation to climate change?. A key role of experts outlined by all panellists is to provide scientific-based information to policymakers and practitioners. Increasing information sharing with practitioners will rely on providing easy-to-understand information based on sound scientific knowledge, including practical information such as the number of seeds to sow or the nursery to use, or information related to the risks and challenges specific to each forest tree species, geographical area, etc. Experts should also provide more input into certification policies, decision-making and regulatory bodies, potentially through the creation of intermediaries, and by clearly articulating short-term and long-term effects of compromises. Experts also have a role to play in ensuring that information is shared across borders and cultures and in involving

indigenous communities and traditional knowledge in the development of FRM. Barry Gardiner went further by arguing that given the urgency of the situation, experts have to be more visible and act as 'activists'.

4.6 Conclusions and perspectives from these 2 days of conference

Faced with accelerating climate change and environmental degradation, European countries have made strong commitments in recent years. The European Green Deal, approved in 2020, is the European growth strategy to transition towards a sustainable economy and with the overarching objective of becoming the first climate neutral continent by 2050. Within this framework, the EU Biodiversity Strategy for 2030 was adopted with the ambitious goal of ensuring that all of the ecosystems are restored, resilient, and adequately protected by 2050. As European forests are essential for continental biodiversity (Muys et al. 2022) and 25% of their total area is covered by the Natura 2000 network (Sotirov 2017), forest management and conservation will have a key role to reach biodiversity goals. In parallel, the New EU Forest Strategy for 2030 aims to propose concrete actions to improve the quantity and quality of European forests and to enhance their protection, restoration and resilience in the face of the high uncertainty brought about by climate change. Among the measures proposed in the strategy is a commitment to improve the size and biodiversity of forests by planting 3 billion new trees by 2030, additionally to current plantation efforts. Last, the EU Bioeconomy Strategy, updated in 2018, contains among its objectives the sustainable management of natural resources, and the limitation and adaptation to climate change.

Projects such as EU H2020 B4EST, which aim to strengthen the link among researchers, practitioners and policymakers, play a key role in meeting European commitments on forests. As outlined in the conference, B4EST has generated and consolidated high value scientific knowledge for the implementation of tree breeding programmes and the identification and deployment of FRM. Climate-based URF (Wang et al. 2010; Leites et al. 2012), and more recently landscape genomics approaches (Capblancq et al. 2020), have proven effective to

identify climate-adapted seed sources while GS approaches have been specifically developed to select elite material in breeding, e.g. trees whose progeny will perform best under future climates or be resistant to pathogens. Most of these approaches are still subject to improvement, e.g. through a better understanding of trade-offs among breeding targets, better control of plastic effects (including transgenerational effects), incorporation of the concept of group selection in GS, etc. Scientific knowledge is also essential to assess the risks and benefits of different forest tree management and breeding strategies. For example, scientists have warned about the decline in genetic diversity caused by the implementation of GS in tree breeding (Grattapaglia 2022), and have shown that counteracting this trend is in the interest of private stakeholders, as the long-term benefits of maintaining sufficient genetic diversity in cultivated forests largely outweigh the short-term costs.

Science-based innovations in forest management practices will only be widely adopted through intense information sharing and international collaboration among researchers, practitioners and policymakers. The present B4EST International Conference brought together various actors from the forestry sector and provided a broad overview of innovative scientific knowledge, methods and tools that could be or are already being implemented in forest tree breeding, and FRM deployment strategies. The conference was also an opportunity to present platforms such as EUFORGEN, which is specifically dedicated to promoting dialogue among the different actors, developing strategies and setting priorities for the conservation and sustainable use of FGR in Europe. We hope that it will stimulate future work and major improvements in the way forests are managed and conserved, which, given the pressing threats to Europe's forests, is urgently needed.

4.7 Session on B4EST tools presentation

The third conference day offered several options for the participants to choose and attend the side events they were interested in.

A major role of the B4EST project has also been the development or improvement of easy-to-use tools for both scientists and practitioners. An extra session of the conference was dedicated to the presentation of two climate tools developed within the framework of B4EST. Duncan Ray (Forest Research, UK) presented the Climate Matching Tool (https://climatematch.org.uk/), a web-based decision-support tool that can be used by practitioners to identify the geographic areas for which (1) the current climate matches the projected future climate at a location of interest, (2) the projected future climate matches the current climate at a location of interest. Maurizio Marchi (CNR, Italy) presented the Climate Downscaling Tool (Climate DT; https://www.ibbr.cnr.it/climate-dt/), a geo-web service on which scale-free climatic variables and indexes of current and future climates can be downloaded on a 1-km grid. Among other tools developed within the B4EST project, Luberon2 is a simulation tool using demo-genetic modelling to assess how silviculture may contribute to genetic improvement and conservation of genetic diversity in the short and long-term and test innovative uses of improved FRM. Last, the Planter's Guide tool (https://www.skogforsk.se/plantersguide) is probably the best example of how up-to-date scientific knowledge can be translated into very practical recommendations, in this case recommendations on the best Scots pine seedlings available in seed orchards in Sweden and Finland (Berlin et al. 2019).

4.8 Training courses

Another major aspect of advancing research around FGR and tree breeding is the need for scientists to have a solid and up-to-date knowledge of quantitative and population genetics. During the conference, two training courses were organised, with one of them also part of the EVOLTREE training program (www.evoltree.eu). The course on 'Polygenicity and population genetics' included lectures about (1) the omnigenic model and its implications, with a case study in maritime pine (Santiago C. González-Martínez, Marina de Miguel), (2) recent trait-based and landscape genomics approaches aimed at predicting short-term population responses to climate change (Juliette Archambeau), (3) the effects of local vs global adaptation and genotypic redundancy on genome architectures (Sam Yeaman), and (4) a newly developed approach inferring selection from genome-wide temporal change in allele frequencies and its application in oaks (Martin Lascoux). The second course, on 'Data integration for prediction and breeding – new tools for obtaining, processing and integrating phenomic and genomic data', dealt with: (1) latest genotyping and sequencing methodologies to obtain 'omics' databases (Patricia Faivre-Rampant and Véronique Jorge), (2) a case study on transcriptomic, metabolomic and phenomic data integration in *Eucalyptus* (Fabien Mounet), (3) simple ways of combining transcriptomics and genomic polymorphisms for phenotype prediction (Abdou Wade, Harold Duruflé and Leopoldo Sánchez-Rodriguez), and (4) a case study on genomic reaction norm construction in maritime pine (Victor Papin, Laurent Bouffier, Leopoldo Sanchez-Rodriguez), and was accompanied by a hands-on practical session.

4.9 Field visit

In the meantime, participants could get the chance to go in the Portuguese countryside for a field visit kindly hosted by ALTRIFORESTAL. After a meeting-room presentation of the company, we were able to discover their nursery activities, controlled crossings tests, forest stand management but also biodiversity hotspot preservation. This field tour gave the opportunity for the participant to have a concrete vision of the issues discussed during the conference session, exemplified with the Eucalyptus species.

4.10 IEFC open session

Finally, the participants did also get the chance to assist at the European Institute of Cultivated Forests (IEFC) General Assembly that took place all day in ISA. In the morning, an open session gave the opportunity to some researchers and PhD students to expose their work on various topics related to planted forests management in the light of the new EU Forest Strategy.

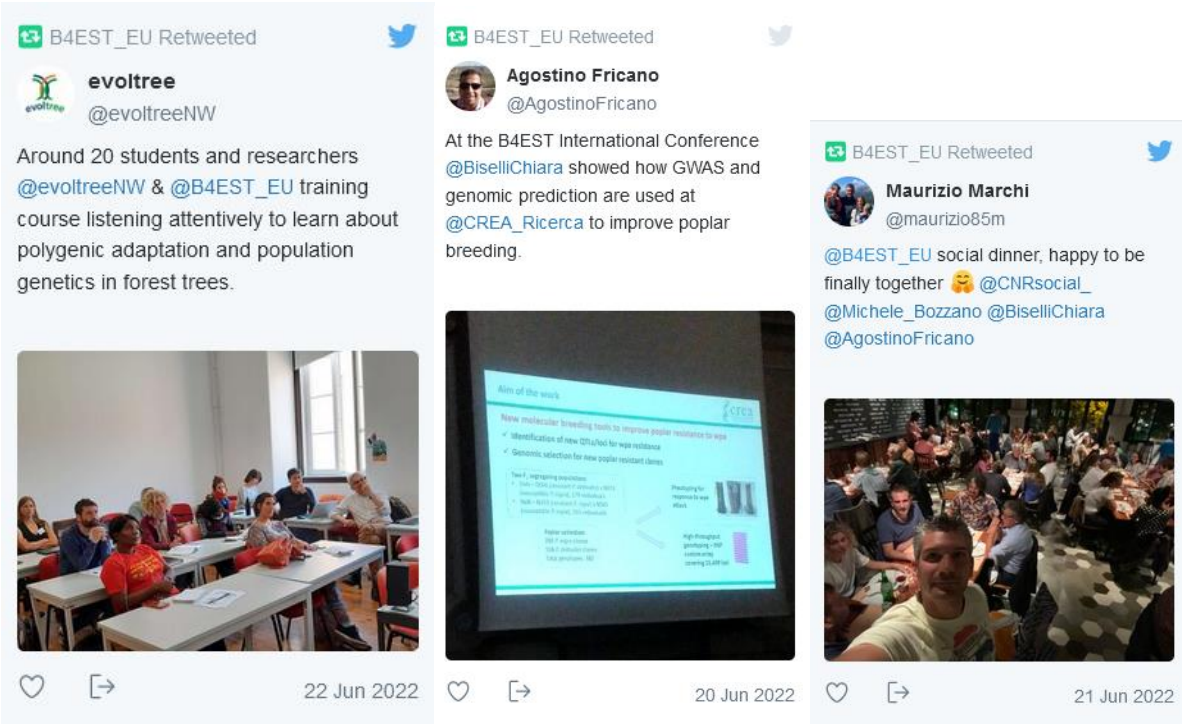
4.11 Working group sessions

This in person event was also a rare opportunity for B4EST partners to meet and discuss on the work achieved but especially the work yet to be achieved. Therefore, a dozen of working group session was organized for the B4EST partners to discuss of the last expected deliverables and WP tasks. The objective was to provide updates on the progress made and then to set the path for the last contribution and writing improvement before the end of the project. The objectives were also to discuss how to make value of these deliverables through dissemination activities (list of publications, operational guidelines, etc.).

5 Dissemination activities about the conference

The conference was promoted via internet, using mainly the project website and social media. The call for abstracts were also advertised on the EFI and IEFC website and on specialized networks EVOLTREE, EUFORGEN, EC Research events and EIP-AGRI.

The holding of the conference has resulted in a strong social network activity with publication on both the B4EST account but also by the partners and the invited speakers.



All session recording and conference presentations are uploaded on the B4EST website at this address: https://b4est.eu/b4est-conference/programme

6 Conclusions

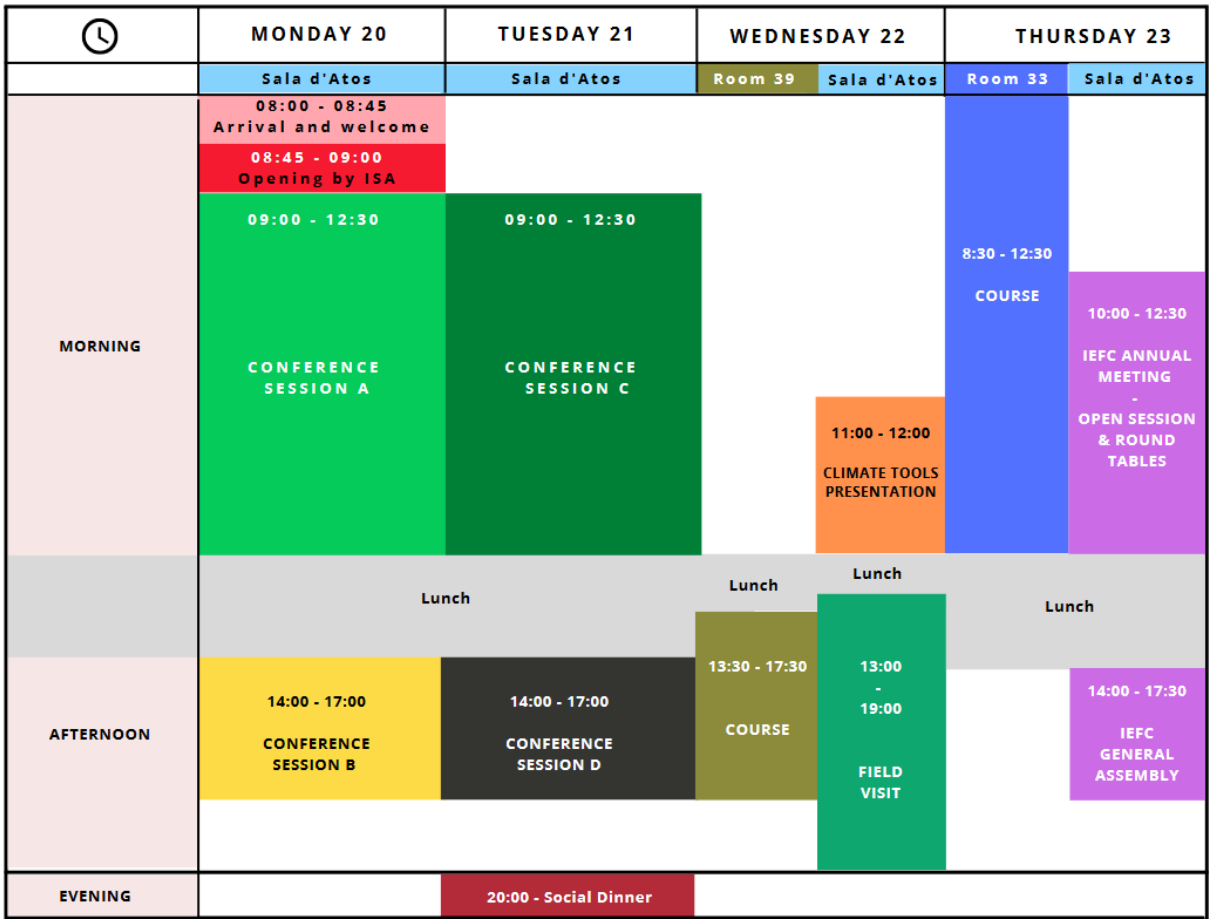
This event clearly suffered from the COVID pandemic, with physical meetings no longer being a popular format. The COVID situation in early 2022 induced some uncertainties concerning the on-site logistics and unfortunately prevented some participants to join us. The event was nevertheless very successful regarding to the objectives of gathering a large audience and sharing knowledge around the topic of tree breeding. This event was the last major event before the B4EST final meeting that was held remotely on September 21-22 2022.

7 Partners involved in the work

This work is a joint effort between IEFC, INRAE, INRAE Transfert and the members of the executive and scientific committee.

8 Annexes

8.1 Annex 1: Conference Timetable



8.2 Annex 2: Working group sessions timetable

	WEDNESDAY 22		THURSDAY 23
08:30 - 09:00	Discussion around the use of arrays and association studies	D4.9	
09:00 - 09:30			
09:30 - 10:00			
10:00 - 10:30	D1.5 (Part 1)	D5.8 & D5.9	
10:30 - 11:00			D2.1
11:00 - 11:30	WP6	D2.2 (Part 1)	
11:30 - 12:00			
12:00 - 12:30	LUNCH OFFERED		
12:30 - 13:00			LUNCH OFFERED
13:00 - 13:30			
13:30 - 14:00			
14:00 - 14:30			D1.5 (Part 2)
14:30 - 15:00			
15:00 - 15:30			
15:30 - 16:00			D2.2 (Part 2)
16:00 - 16:30			
16:30 - 17:00			

8.3 Annex 3: Conference Program

B4EST International Conference

Managing Forest Genetic Resources (FGR) for an uncertain future

Scientific program

Place: Instituto Superior de Agronomia, Lisbon, Portugal

Date: 20th-23rd June 2022

Organised by:

With support from:

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 773383

B4EST International Conference Monday, 20 June, 2022

Session A: Accelerating breeding to cope with new challenges and uncertain future

[Opening at 09.00]

Chairs: Leopoldo Sánchez-Rodríguez (INRAE, France), Chedly Kastally (University of Helsinki, Finland)

Keynote: **Laurence Moreau** (GQE-Le Moulon, INRAE; France)

Session description:

Genomic innovations in the last decade have led to **promising improvements** in the way **tree breeding** is conducted. Considerable benefits are expected from this new source of information: the shortening of breeding cycles, the rationalising of phenotyping in terms of costs, and the improved predictive and explanatory analyses decrypting phenomes, to name a few. At the same time, genomic data open up new possibilities for a better monitoring and **long-term management of genetic diversity in breeding** and conservation programs, which is essential for a challenging future. To leverage these new data to their full potential, **methodological developments and proof-of-concept initiatives** are required, not only for genome-wide predictions for which substantial advancements already exists in most domesticated species including some forest trees, but also by accounting for new ways of evaluating tree performance that are sensible to underlying interactions at genomic, environmental and conspecific levels. Last but not least, insights are needed on the impacts that these new developments could bring at the organisation level of the breeding programs. The aim of **this session** is to showcase methods harnessing new genomic technologies developed for forest tree breeding and illustrate using case studies the possibilities offered by these approaches, including their impacts to the breeding sector.

[09:05 – 09:45] Keynote talk:

Use of genomic selection to better manage and enrich genetic diversity in breeding programs. Application to maize.

Laurence Moreau[1]*, Antoine Allier[1,2,3], Stéphane Nicolas[1], Delphine Madur[1], Cyril Bauland[1], Christina Lehermeier[3], Simon Teyssèdre[3], Dimitri Sanchez[1], Brigitte Gouesnard[4], Alain Charcosset [1]

[1]Université Paris-Saclay, INRAE, CNRS, AgroParisTech, GQE – Le Moulon, Gif-sur-Yvette, France; [2]Syngenta, 31790 Saint-Sauveur, France; [3]RAGT, 12510 Druelle, France;[4] AGAP, CIRAD, INRAE, Institut Agro, Univ Montpellier, Montpellier, France

Genetic diversity is of key importance for the success of breeding programs and their potential to adapt to new challenges. Genomic selection (GS) offers new prospects to accelerate genetic gain and, in the case of maize, to revisit hybrid selection schemes but it may also accelerate genetic diversity erosion. I will introduce how GS can be combined with Optimal Cross Selection processes to control diversity over time in a closed breeding population (Allier et al., 2019). I will present how GS models calibrated on cooperative panels, ranging from primary genetic resources to recent elite materials, can be used to identify sources of favourable alleles not present yet in a given breeding program (Allier et al., 2020a). I will then present simulation work highlighting the benefit of bridging populations, obtained by crossing genetic resources and elite materials, to incorporate efficiently useful genetic diversity in elite breeding programs (Allier et al., 2020b). Finally, I will introduce how advances in high throughput genotyping of maize landraces should facilitate the identification of those which are original with respect to current breeding pools.

Keywords: Genetic Diversity, Genomic Prediction, Bridging, Maize

---

Regular talks:

Each presentation is made of a 20 minutes talk with 4 minutes for questions

Time schedule	Presenting author	Presentation title	Keywords
09:45 – 10:10	Victor Papin (INRAE)	**Reactions norms for maritime pine**	*Genomic reaction norms, maritime pine*
10:10 – 10.35	Mathieu Tiret (Uppsala University)	**Implementation of group selection in forest tree breeding**	*Genomic selection, group selection, breeding, populus nigra*
10.40 – 11.00	** BREAK **		
11.00 – 11.25	Haristoy Geoffrey (CIRAD, INRAE)	**Genomic prediction in a multi-generation Eucalyptus globulus breeding population**	*Eucalyptus globulus, genomic selection, progeny validation, pedigree error, breeding program*
11.25 – 11.50	Giorgio Tumino (WUR)	**In search for resistance to ash dieback disease in F. excelsior using GWAS and genomic prediction analyses**	*Fraxinus, dieback, GWAS, QTL, genomic prediction*

Flash talks:

Presentations last for 5 minutes and 15 minutes are allocated at the end for questions

Time schedule	Presenting author	Presentation title	Keywords
11.55 – 12.00	Ricardo Alia (INIA, CSIC)	**Genetic variation for resistance to abiotic and biotic stresses in breeding populations of European forest trees**	*Genetic variation, field tests, artificial inoculations tests, evaluation in breeding populations*
12.00 – 12.05	Sanna Olsson (INIA, CSIC)	**Utility of the 4TREE SNP array in clonal identification of Mediterranean stone pine (Pinus pinea L.)**	*Pines, pine nuts, clonal identification, breeding, SNP array*
12.05 – 12.10	Chiara Biselli (CREA-VE)	**Discovery of new sources of resistance against Woolly Poplar Aphid (Phloeomyzus passerinii L.) and integration of QTL mapping and genomic prediction to sustain poplar breeding**	*Poplar, Woolly Poplar Aphid, resistance, QTL mapping, genomic prediction*
12.10 – 12.15	Leopoldo Sánchez (INRAE)	**eQTLs are key players in the integration of genomic and transcriptomic data for phenotype prediction**	*Genomic Prediction, omics, Multi-omics integration, eQTL, Populus nigra*

[End of the session at 12.30]

B4EST International Conference Monday, 20 June, 2022

Session B: Forest genetic resources (FGR) and adaptation to climate change

[Opening at 14.00]

Chairs: Stephen Cavers (UKCEH, UK), Juliette Archambeau (INRAE, France)

Keynote: **Tongli Wang** (University of British Columbia; Canada)

Session description:

Climate change is already impacting forests through gradual climatic shifts and more frequent extreme climatic events, triggering changes in biotic (e.g. insects, diseases) and abiotic (e.g. floods, fires) disturbance. **Natural populations of forest trees can respond to these changes** by migrating to new sites or persisting in their current locations and relying on their dispersal ability, phenotypic plasticity and **ultimately genetic adaptation**, the only mechanism likely to ensure long-term persistence. In production forests, the use of the genetic variation within species (**forest genetic resources, FGR**) to adapt to new conditions may play a fundamental role in providing resilience and maintaining wood and non-wood product provision. **Assessing the vulnerability of forests to climate change** involves understanding the mechanisms that underlie responses to change and predicting how populations will respond over time. Such predictions will have to incorporate the uncertainty associated with the timing and magnitude of climate change, the interaction with other threats (e.g. land-use change) and the inherent stochasticity of population responses (e.g. stochastic demographic or evolutionary processes). In **this session**, we welcome population and quantitative genetic and modelling studies related to past and future forest tree adaptation to climate change and how to make use of FGR and their evolutionary potential to maintain forests (managed or unmanaged) in the face of the changes ahead.

Regular talks:

Each presentation is made of a 20 minutes talk with 4 minutes for questions

Time schedule	Presenting author	Presentation title	Keywords
14.05 – 14.30	Zhi-Qhiang Chen (Umeå Plant Science Centre)	**Effects of future climate change on Norway spruce adaptation and growth across Europe**	*Response function, tree growth, local adaptation, phenotypic plasticity*
14.30 – 14.55	Katharina Liepe (Thuenen	**High phenotypic plasticity, but low signals of local adaptation in a**	*Climate change, Picea abies, height growth, species distribution*

	Institute of Forest Genetics)	**large-scale provenance trial of Norway spruce**	*model, universal response function*
14.55 – 15.20	Octávio S. Paulo (cE3c)	**Predict climate response and adaptation in Cork Oak using gradient forest**	*Climate change, Gradient Forest, landscape genomics, local adaptation, Quercus suber L*
15.25 – 15.45	** BREAK **		
15.45 – 16.10	Arne Steffenrem (NIBIO)	**Estimation of phenotypic plasticity in Norway spruce (Picea abies L. Kars.) as maternal reproductive environment alter adaptive performance**	*Phenotypic plasticity, adaptation, phenology, picea abies*

Flash talks:

Presentations last for 5 minutes and 15 minutes are allocated at the end for questions

Time schedule	Presenting author	Presentation title	Keywords
16.15 – 16.20	Marta Callejas-Díaz (INIA-CSIC)	**Response to selection in an aerial conifer seed bank**	*Aerial seed bank, Heritability, Maternal effects, Pinus pinaster, Selection*
16.20 – 16.25	Laura Guillardin (University of Oxford)	**The genetics behind the Continuous Cover Forestry approach - do UK plantations hold enough genetic diversity to face environmental changes?**	*Climate Change, Genetic diversity, Single Nucleotide Polymorphism (SNP), Forest management, Continuous Cover Forestry (CCF)*
16.25 – 16.30	Āris Jansons (Silava)	**Heritable weather-growth relationships: case study of Scots pine provenances**	*Local adaptation, climate-smart forestry, climate sensitivity*
16.30 – 16.35	Annika Perry (CEH)	**Why we should consider phenology as well as growth traits when developing predictive models in forest trees**	*Marker-trait association, predictive model, quantitative trait, Scots pine, SNP array*

[16:50 – 17:30] Keynote talk:

Using forest genetic resources for climate change mitigation and adaptation

Tongli Wang (University of British Columbia; Canada)

Climate change is causing a mismatch between the climate that trees have adapted to in the past and the climate that the trees will face in the future. Natural migration and evolution may take too long to achieve new local adaptation. Using the available genetic resources created by nature and tree improvement programs will probably be the most effective way to mitigate and adapt to climate change. Nature has created a large number of tree species for different climate conditions and among-population variation along climate gradients within species for local adaptation. Improved genetic materials have been produced through breeding for various objectives, including fast growth and resistance to pests, diseases, and harsh environments. However, challenges remain in making effective use of these genetic resources to fight against climate change. My presentation will address some issues in the following aspects: 1) using climate niche models to assess the impact of climate change and to assist species in matching their suitable climate; 2) using transfer and response functions to understand the genetic and physiological responses of populations to climate change; and 3) the use of genomic information for delineation of seed and breeding zones.

[End of the session at 17.30]

B4EST International Conference Tuesday, 21 June, 2022

Session C: The forests we want: deployment of forest reproductive material (FRM) for forest-based solutions

[Opening at 09.00]

Chairs: Sven Mutke (CSIC, Spain), Marina de Miguel (INRAE, France)

Keynote: **Conceição Silva** (UNAC, Forest Owner Association; Portugal)

Brief description:

Forest and landscape restoration goals has significantly evolved from the first tree plantations for land reclamation, aiming to regulate and provide ecosystem services (erosion control, flood prevention, timber and biomass production), to the current prominence for **transition pathways to bioeconomy** and **multipurpose forest management** (including non-wood forest products and cultural ecosystem services). Recently, these issues are gaining increased relevance with the UN Decade on Ecosystem Restoration, aiming at preventing, halting and reversing the degradation of ecosystems worldwide, and new European policy (e.g. the EU Biodiversity Strategy for 2030). One key question is whether to rely on **forest reproductive material (FRM) from local seed sources**, often seen as reservoirs of adaptive genetic diversity, or rather on **genetic improved FRM** (or exotic seed sources) **that are the result of breeding programs** and allow for the use of the best available plant resources for a given site, climate conditions and forest management goals – already accounting for expected major changes in local climates over this century (i.e. assisted migration). The ambition of **this session** is to support foresters with scientific evidence and decision support tools. Thus, we aim to learn about the role and the potential of FRM deployment in different European countries and forest types in a context of climatic and societal change.

[09:05 – 09:45] Keynote talk:

FRM status in Portugal – What are the challenges for the main forestry sectors?

Conceição Silva

(UNAC, Forest Owner Association; Portugal)

In this presentation a brief overview will be made on the Forest Reproductive Materials regulation, certification and markets in Portugal considering the top 5 main forest species in the territory – Eucalyptus (Eucalyptus globulus), Cork oak (Quercus suber), Holm oak (Quercus rotundifolia), Maritime pine (Pinus pinaster) and Umbrella pine (Pinus pinea). Cork, wood and

pulp sectors struggle with lack of raw material, for different reasons, including vitality issues connected with climatic changes. Thoughts on how the Forest breeding programs that exist in Portugal connect to the real needs of these forestry sectors in order to address the future challenges.

Short talks:

Each presentation is made of a 10 minutes talk with 2 minutes for questions

Time schedule	Presenting author	Presentation title	Keywords
09.45 – 09.57	Daniel Blanco-Ward (CIFOR)	**Incorporation of origin and regions of provenance in the Forest Map of Spain (FME): a case study with Pinus pinaster and Taxus baccata**	*Origin of population, regions of provenance, forestry maps, Pinus pinaster, Taxus baccata*
09.57 – 10.10	Esteban Torres-Sánchez (Lourizán Forest Research Center)	**Is it possible to select according to wood quality and growth in Pinus pinaster? Galician breeding population case study**	*Maritime pine, modulus of elasticity, basic density, heritability, genetic gain*
10.10 – 10.22	Toms Kondratovics (Silava)	**Morphological and physiological responses of hybrid aspen (Populus tremula L. x P. tremuloides Michx.) in vitro cultures to different light intensities**	*Shade-avoidance, photomorphogenesis, photosynthesis, woody plants, LED luminaires*
10.22 – 10.35	Pauls Zeltiņš (Silava)	**Height growth models for young stands of genetically improved Scots pine and silver birch in Latvia**	*FRM; GADA models; genetic gains; growth modelling*
10.40 – 11.00	** BREAK **		

Regular talk:

A 20 minutes talk with 4 minutes for questions

Time schedule	Presenting author	Presentation title	Keywords
11.00 – 11.24	Mats Berlin (Skogforsk)	**Planter's guide: progress and future challenges**	*Assisted migration, genetically improved FRM, deployment, decision support, climate change*

[11:25 – 12:30] Round table:

A one hour round table discussion between the following panelists:

- **Juha Hakkarainen**, Managing Director of Finsilva (Finland)
- **Brigitte Musch**, Research & Development at the French National Forests Office (ONF, France)
- **Felipe Pérez**, Head of Genetic Material service at the Spanish Ministry of Ecological Transition and the Demographic Challenge (MITECO, Spain)
- **Christophe Orazio**, Director of the European Institute for Cultivated Forest (IEFC, France)

[End of the session at 12.30]

B4EST International Conference Tuesday, 21 June, 2022

Session D: Science policy interface for mitigation, adaptation and risk management in forestry

[Opening at 14.00]

Chairs: Richard Whittet (Forest Research, UK), Simone Bianchi (LUKE, Finland)

Keynote: **Michele Bozzano** (EUFORGEN, EFI; Barcelona, Spain)

Brief description:

Investment in forest genetic resources (FGR) tends to pay off very substantially in genetic gains delivered through breeding and better outcomes in ecological restoration. However the **rate of return on investment in research and development** is relatively long and priorities shift due to environmental and political change. Due to the generally necessary use of technical language, it often falls to scientists to **communicate benefits and risks of developing FGR** although for most purposes, no more than an intuitive understanding of genetics is truly required and many foresters are expert stewards of FGR without realising it. What role **do** and **should scientists, end-users and policy-makers play** in governance and coordination of FGR and over which timescales and within which geographical or administrative boundaries? For example, how do scientists retain and manage a blend of long- and short-term research infrastructure? How do end-users feed into policy and research agendas and where is the line between public good and private gain? How do policy makers handle uncertainty and how do their attitudes risk influence progress? The aim of **this session** is to demonstrate examples of regional or national/subnational systems of governance and coordination of FGR with a special focus on the role scientists play in them. Positive and negative examples are equally welcome in this session. Our intention is to learn from each other what works and why.

[14:05 – 14:45] Keynote talk:

The FGR Strategy For Europe: a policy document that provides the framework for enabling the transition to an effective FGR conservation and sustainable use in Europe

Michele Bozzano

(EUFORGEN, EFI; Barcelona, Spain)

The *Forest Genetic Resources Strategy for Europe* is a coordinated and cooperative effort in the *European Forest Genetic Resources Programme (EUFORGEN)* to improve the conservation and sustainable use of European forest genetic resources. The Strategy goes beyond the individual countries' efforts and encompasses not only conservation but also sustainable use of forest genetic resources. It introduces new key elements for more accurate

characterisation and classification of conserved FGR. It also highlights the need to expand scientific knowledge, defines principles for coordination activities at policy level and recommends future actions and collaborations among different entities and international organisations

In this presentation, after introducing the EUFORGEN programme and the *Forest Genetic Resources Strategy for Europe*, the presenter will give an overview of the innovative elements of the strategy and some relevant key commitments showing how European countries will cooperate in the next decade on FGR conservation and sustainable use.

Regular talks:

Each presentation is made of a 20 minutes talk with 4 minutes for questions

Time schedule	Presenting author	Presentation title	Keywords
14.45 – 15.10	Anssi Ahtikoski (LUKE)	**Case studies for the deployment of improved FRM in different regions of Europe: assessment of benefits, costs and risks**	*FRM deployment, adaptive breeding strategies, decision-support tools, policy recommendations*
15.10 – 15.35	Isabel Carrasquinho (INIAV, FAO)	**Forest genetic resources conservation and breeding activities in Portugal**	*Forest Genetic conservation; Forest genetic improvement, Maritime pine, Cork oak*
15.40 – 16.00	** BREAK **		
16.00 – 16.25	Richard Whittet (Forest Research)	**Opportunities to improve Scots pine in Scotland (and England) – B4EST Case Study**	*Forest reproductive material, forest history, stakeholder perspectives, Dothistroma septosporum, climate change, genetic gain, Scots pine*
16.25 – 16.50	Catherine Bastien (INRAE & B4EST project coordinator)		

[16:50 – 17:30] Round table:

A 40 minutes round table discussion between the following panelists:

- **Bent Leonhard**, Technical Secretary of the European Forest Nursery Association (EFNA, Denmark)
- **Barry Gardiner**, Senior Researcher at the European Institute for Cultivated Forest (IEFC, France)
- **Chris Kettle**, Senior Researcher in Ecology and Genetics at Bioversity International (Italy)
- **Jarkko Koskela**, Forestry Officer at the Food and Agriculture Organization of the United Nations (FAO, Italy)

[End of the session at 17.30]

8.4 Annex 4: International conference's participants list (20-21 June)

Last Name	First Name	Organisation	Country
Afanou	Suzanne	IEFC	France
Ahtikoski	Anssi	Natural Resources Institute Finland	Finland
Alia	Ricardo	CIFOR-INIA, CSIC	Spain
Almeida	Maria Helena	ISA - CEF	Portugal
Antoniotti	Claudia	IEFC	France
Archambeau	Juliette	BIOGECO (INRAE)	France
Bastien	Catherine	INRAE	France
Berlin	Mats	Skogforsk	Sweden
Bianchi	Simone	LUKE	Finland
Biselli	Chiara	CREA	Italy
Blanco-Ward	Daniel	Ecology and Genetics Department, Forestry Research Center (CIFOR), Madrid	Spain
Borelle	Rémi	IEFC	France
Borralho	Nuno	RAIZ Forest and Paper Research Institute	Portugal
Bozzano	Michele	EFI	Spain
Buiteveld	Joukje	Wageningen Research	Netherlands
C González-Martínez	Santiago	INRAE	France
Callejas-Díaz's	Marta	INIA-CSIC	Spain
Carrasquinho	Isabel	INIAV	Portugal
Cavers	Stephen	UKCEH	UK
Chen	ZhiQiang	Swedish University of Agricultural Sciences	Sweden
Colling	Rach	European Forest Institute	Finland
Copini	Paul	Wageningen University & Research	Netherlands
Corti	Riccardo	ISA	Portugal
Costa e Silva	Felipe	ISA	Portugal
de Guerry	Benoît	IEFC	France
de Sousa	Felipe	CE3C, Universidade de Lisboa	Portugal
Díaz Vázquez	Raquel	Centro de Investigación Forestal de Lourizán	Spain
Duruflé	Harold	INRAE	France
Faivre Rampant	Patricia	INRAE	France
Fontes	Luis	Altri Florestal	Portugal
Fricano	Agostino	Council for Agricultural Research and Economics-Research Centre for Genomics and Bioinformatics	Italy
Fugeray-Scarbel	Aline	INRAE	France
Guillardin	Laura	University of Oxford	UK

Haapanen	Matti	Luke	Finland
Hallingbäck	Henrik	Skogforsk	Sweden
Haristoy	Geoffrey	CIRAD	France
Hynynen	Jari	Luke	Finland
Inocencis	Tapace	ISA	Portugal
Janson	Liga	Latvian State Forest Research Institute "SILAVA"	Latvia
Jansons	Aris	LSFRI Silava	Latvia
Kastally	Chedly	University of Helsinki	Finland
Kondratovics	Toms	Latvian State Forest Research Institute "Silava"	Latvia
Koskela	Jarkko	FAO	Italy
Kramer	Koen	Land Life Company	Netherlands
Lascoux	Martin	Uppsala University	Sweden
Leal	Luis	Altri Florestal	Portugal
Lee	Daesung	Natural Resources Institute Finland (Luke)	Finland
Lemarié	Stéphane	INRAE-GAEL	France
Liepe	Katharina	Thuenen Institute of Forest Genetics	Germany
Marchi	Maurizio	CNR	Italy
Marques	Isabel	Higher Institute of Agronomy	Portugal
Marques	Cristina	RAIZ	Portugal
Miguel	Célia	Faculty of Sciences, University of Lisbon	Portugal
Mounet	Fabien	UPS (Université Paul Sabatier - Laboratoire LRSV)	France
Mutke	Sven	CSIC	Spain
Nervo	Giuseppe	CREA - FL	Italy
Olsson	Sanna	Forest Research Centre (INIA, CSIC)	Spain
Orazio	Christophe	IEFC	France
Papin	Victor	INRAE	France
Paulo	Octavio	Universidade de Lisboa	Portugal
Pérez	Felipe	MITECO	Spain
Perry	Annika	UKCEH	UK
Pruvost	Hubert	Cabinet d'Expertise Forestière Michel CHAVET	France
Ray	Duncan	Forest Research	UK
Ribeiro	Ana	Forest Research Center, School of Agriculture, University of Lisbon	Portugal
Sanchez-Rodriguez	Leopoldo	INRAE	France
Seabra Costa	Joana	RAIZ	Portugal
Silva	Conceição Santos	UNAC	Portugal
Steffenrem	Arne	NIBIO	Norway
Tiret	Mathieu	uppsala university	Sweden
Torres Sánchez	Esteban	Lourizán Forest Research Center	Spain
Trotter	Felix	Forest Research	UK
Tumino	Giorgio	Wageningen University & Research	Netherlands

Viegas	Mariana	CE3C, Universidade de Lisboa	Portugal
Villar Caamaño	Lucía	ARUME Foundation	Spain
Whittet	Richard	Forest Research	UK
Zeltins	Pauls	Latvian State Forest Research Institute SILAVA	Latvia

8.5 Annex 5: Training session's participants list (22-23 June)

Last name	**First Name**	**Organisation**
Alia	Ricardo	CIFOR-INIA, CSIC
Archambeau	Juliette	INRAE
Biselli	Chiara	CREA
Callejas-Díaz's	Marta	INIA-CSIC
Chianica	Diamants	ISA
Copini	Paul	WUR
Corti	Riccardo	ISA
Costa	Joana	RAIZ
Duruflé	Harold	INRAE
Faivre Rampant	Patricia	INRAE
Guillardin	Laura	University of Oxford
Kastally	Chedly	University of Helsinki
Mendes	Raquel	RAIZ
Olsson	Sanna	Forest Research Centre (INIA, CSIC)
Steffenrem	Arne	NIBIO
Tapace	Inocências	ISA
Tiret	Mathieu	Uppsala University
Torres Sánchez	Esteban	Lourizán Forest Research Center
Tumino	Giorgio	WUR
Viegas	Mariana	CE3C, Universidade de Lisboa
Villar Caamaño	Lucía	ARUME Foundation
ZhiQiang	Chen	Swedish University of Agricultural Sciences

8.6 Annex 6: Working group's participants list (22-23 June)

Last name	**First Name**	**Organisation**
Ahtikoski	Anssi	LUKE
Alia	Ricardo	INIA
Archambeau	Juliette	INRAE
Bastien	Catherine	INRAE
Benito Garzon	Marta	INRAE
Berlin	Mats	Skogforsk

Bianchi	Simone	LUKE
Biselli	Chiara	CREA
Buiteveld	Joukje	WR
Colling	Rach	EFI
Copini	Paul	WUR
de Guerry	Benoît	IEFC
Duruflé	Harold	INRAE
Faivre-Rampant	Patricia	INRAE
Fricano	Agostino	CREA
Gonzalez Martinez	Santiago	INRAE
Haapanen	Matti	LUKE
Hallingbäck	Henrik	Skogforsk
Hynynen	Jari	LUKE
Jarousse	Anne	IT
Lascoux	Martin	UU
Marchi	Maurizio	CNR
Meruo	Guiseppe	CREA
Mutke	Sven	INIA
Olsson	Sanna	INIA
Orazio	Christophe	IEFC
Ray	Duncan	FR
Sanchez	Leopoldo	INRAE
Steffenrem	Arne	NIBIO
Tiret	Mathieu	UU
Tumino	Giorgio	WUR
Whittet	Richard	FR
Zhiaqiang	Chan	SLU