B4EST

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

Deliverable D6.4

Report on training courses

Planned delivery date (as in DoA): M24

Actual submission date of this updated version: 29/11/2022, month M55

Workpackage: WP6

Workpackage leader: EFI

Deliverable leader: UPS, updated by EFI M55

Version: 2.0

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

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1   Summary

Key scientific results, new tools and new methodological developments produced in the framework of B4EST were initially foreseen to be disseminated via three hands-on training events (from M30-M45) to Masters and PhD students and post-doctorate fellows. These events were to be organized by the academic partners (UPS; SLU; CIRAD; NIBIO; UU; INRAE; UOULU; CNR) and open stakeholders interested by the topics.

Due to the COVID-19 limitations occurring since March 2020, it was initially thought that the courses would be organized remotely in the form of videos/online tutorials. Training session 1 was therefore organized online by SLU in October 2021. However, a lack of online interest from students in winter 2021 led to training sessions 2 and 3 being organized in-person in June 2023, back-to-back with the B4EST international conference in Lisbon.

The presentations from these two in-person courses have been made available on the B4EST website, to enable durable resources and target a larger audience, including stakeholders interested in the topics.

This document was therefore updated in September 2022 (M53).

2   Introduction

The programme of these three courses was discussed among the eight partners involved during the 2nd Annual Meeting of the B4EST project in April 2020, and in two other web-meetings (June 23th & October 6th 2020), held in visio-conference because of the COVID-19 crisis.

The training courses were linked to university curricula and highly relevant, existing other training initiatives (e.g., EVOLTREE or HOMED training courses). The courses covered: i) phenotypic plasticity evaluation and norms of reaction modelling (linked to WP1, 3 days), ii) Contribution of GWAS to the understanding of the evolution of quantitative traits under natural selection (linked to WP2, 3 days), iii) The impact of integration of biological information (gene networks) on the accuracy of genomic prediction (linked to WP3, 3 days).

3   Results

3.1   Training session 1

A specific session at B4EST 2nd annual meeting in April 2020 was dedicated to the preparation of this training session that will disseminate results and analytic tools from WP1, especially from Task 1.3.

Phenotypic plasticity evaluation and norms of reaction modelling was held online from 5-7 October, 2021.

Information is available on the B4EST website: https://b4est.eu/training-course-phenotypic-plasticity-and-norms-of-reaction-modelling

This 3-day course organized by SLU under the responsibility of Prof. Harry Wu was initially foreseen to be held in October 2020 in Umeå, but due to COVID issues was rescheduled for October 2021 online. The training course was organized into three consecutive days, including six lectures, plus several case studies about 75 minutes per lecture/case study (3.5-4 hours per day), using Zoom as a meeting format. Some lecturers gave their lecture from North America and hands-on demonstration with R was included in some lectures.

Course instructors included: Harry Wu/Zhiqiang Chen (SLU, Sweden), Tongli Wang (UBC, Canada), Tore Skrøppa/Arne Steffenrem (NIBIO, Norway), Laurent Bouffier (INRAE, France), Philippe Rozenberg (INRAE, France), Marie Denis (CIRAD, France), Jean-Marc Gion/Alexandre Bosc (CIRAD/INRAE, France), Maurizio Marchi (CNR, Italy).

The topics related to WP1 were the following:

(1) Introduction to genecology.
(2) Response functions – norm of reactions (in link with Task1.3 and Deliverable D1.2).
(3) Integration of genetic and environmental effects into a linear mixed model or a universal response function (URF) (in link with Task1.4).
(4) Model comparisons and selection.
(5) Case studies of Norway spruce provenance, family and clonal plasticity and norm of reaction.
(6) Reaction norm estimated on microdendrometer data on an annual and daily basis for Maritime pine, Douglas-fir, and Eucalyptus (in link with case-studies developed in Task 1.3).
(7) New modelling method on plasticity and norm of reaction including genomic base of norm of reactions.

Programme:
Day 1 (5th, October)
Lecture 1: From genotype by environment interactions to norm of reactions (Wu) (9:00-10:30)
Lecture 2: Climate modelling (Marchi) (10:45-12:15)
Lecture 3: Response functions – norm of reactions (Wang) (16:00-17:30)

Day 2 (6th, October)
Case study 1: Norway spruce (Skrøppa & Chen) (10:45-12:15)
Lecture 4: Bayesian varying coefficient model with selection: An application to functional mapping (Denis) (14:15-15:45)
Lecture 5: Integration of genetic and environmental effects into a linear mixed model or a universal response function (URF) (Wang) (16:00-17:30)

Day 3 (7th, October)
Case study 2: New modeling method on plasticity and norm of reaction for Larch and Douglas-fir (Rozenberg) (9:00-10:30)
Case study 3: Norm of reaction and genomic selection for Maritime pine (Bouffier & Papin) (10:45-12:15)
Case study 4: Reaction norms related to tree water status: a case study in eucalyptus and maritime pine (Bosc & Gion) (13:15-14:45)

The targeted audience was graduate students and postdocs from B4EST project and outside (e.g. SLU and Umeå University, publicity from EVOLTREE, publicity from B4EST). It will be also open to researchers and tree breeders interested in the topic. There were a total of 25 participants from EU countries for the training. There were 16 male and nine female participants with eight PhD students, six postdocs and 11 researchers. The case studies of the course were efficiently and successfully delivered with high praise by participants. Many participants expressed thanks to the lecturers for their careful preparation of the teaching and an impressive amount of knowledge in each topic, and all cases were related to the B4EST project.

3.2   Training session 2

This training session disseminated results and analytic tools from WP2 especially from Task 2.2.

"Genetic basis of quantitative traits and multitrait association" was originally foreseen to be organized by UU in Uppsala for 20-30 students under the responsibility of Prof. Martin Lascoux. This 3-day course was planned to be held in Spring 2021 either in Uppsala or organized as a web-course in autumn 2021. The targeted audience was graduate students and postdocs from the B4EST project and outside (e.g. Uppsala EBC graduate school, publicity from EVOLTREE, publicity from B4EST). It was also open to researchers, tree breeders.

The 3-day course planned to reflect the understanding of quantitative traits and the main current models, understanding concepts rather than particular packages, i.e. more a state-of-the-art at theoretical levels in genetics of quantitative traits. The first day the "infinitesimal to the omnigenic model" will be presented, the second day will be dedicated to the "omnigenic model and the evolution of quantitative traits architecture" and in the third day, the consequences of the omnigenic model for genome wide association will be evaluated from what we already know and what needs to be known.

However, when a web version of the course was advertised in autumn 2021, there was a lack of interest from students. Consequently, the decision was taken to instead run a short, focused course in-person, back-to-back with the B4EST international conference in Lisbon, in June 2022.

Polygenicity and population genetics was held on 22 June 2022, at the Instituto Superior de Agronomia, Lisbon, Portugal.

Information is available on the B4EST website: https://b4est.eu/b4est-conference/programme/training-courses

Course instructors included: Santiago C. González-Martínez (INRAE), Marina de Miguel (Universite de Bordeaux), Juliette Archambeau (INRAE), Sam Yeaman (University of Calgary), Martin Lascoux (UU).

The course consisted of 4 lectures followed by discussions.

In contrast to quantitative genetics that, from the start, has been built on the assumption that evolution was inherently acting on polygenic traits, population genetics has, by and large, been

a single locus affair. However, this is slowly changing and there has been a strong interest lately in developing models of change in allele frequencies that are intrinsically assuming a multilocus response to selection. The present short course will be constructed around two series of studies, that we hope, are just the beginning of exciting new developments. First, the course will present recent applications of the omnigenic model and discuss their implications for breeding and evolutionary inferences, including modelling approaches. Secondly, we will focus on a newly developed approach to infer selection from genomewide temporal change in allele frequencies. In both cases, applications to trees will be presented.

Programme
• Lecture 1: 13:30- 14:30 Polygenic Adaptation: Introduction and Case Study (maritime pine) (pdf) Santiago C. González-Martínez, Marina de Miguel
• Lecture 2: 14:30-15:30 Applications to modelling and landscape genomics (pdf) Juliette Archambeau
• Lecture 3: 16:00-17:00 Local vs. global adaptation and the importance of genotypic redundancy (pdf) Sam Yeaman
• Lecture 4: 17:00-18:00 The linked selection signature of rapid adaptation in temporal genomic data: An application to oaks (pdf) Martin Lascoux
• Practical demo (pdf)

The course was held in partnership with the EVOLTREE Network, and advertised also through their channels. Approximately 15-20 students and researchers attended.

Photo of Training session 2: Santiago C. González-Martínez

3.3   Training session 3

This training session disseminated results and analytic tools from WP3 especially from the innovative Task 3.3. The provisional title of this training course was foreseen to be **"The impact of integration of functional genomic information on the accuracy of genomic prediction**", and it was aimed to be organized during 3-4 days in Summer 2021 in Toulouse by UPS under the responsibility of Jacqueline Grima-Pettenati and Fabien Mounet. A web meeting early 2021 was dedicated to the preparation of this training session.

The targeted audience was graduate students and postdocs from B4EST project and outside (publicity from EVOLTREE, publicity from B4EST). It was also open to researchers.

Due to the COVID-19 limitations occurring since March 2020, and the extension of the B4EST project duration, the course was postponed until summer 2022. It ran in a revised format as a short, focused course, back-to-back with the B4EST international conference in Lisbon in June 2022.

Data integration for prediction and breeding – new tools for obtaining, processing and integrating phenomic and genomic data was held on 23 June 2022, at the Instituto Superior de Agronomia, Lisbon, Portugal.

Information is available on the B4EST website: https://b4est.eu/b4est-conference/b4est-short-course-data-integration-for-prediction-and-breeding-new-tools-for-obtaining-processing-and-integrating-phenomic-and-genomic-data

Course instructors included: Patricia Faivre-Rampant (INRAE), Véronique Jorge (INRAE), Fabien Mounet (University of Toulouse), Raphael Ployet (Oakridge, USA), Abdou Wade (INRAE), Harold Duruflé (INRAE), Leopoldo Sanchez (INRAE), Victor Papin (INRAE), Laurent Bouffier (INRAE)

The course ran for a half, day, in addition, half-day individual web-based "coaching sessions" were offered in September 2022.

System biology approaches are becoming rapidly the goal of analytical frameworks aiming at developing comprehensive studies of the biological reaction to the changing environment. Under such analytical frameworks, we find a combination of computational and mathematical approaches that are applied typically to multilayered datasets covering different levels of integration between the phenome and the genome. The final aims of such integrative framework are: to reveal the architecture of interactions within biological systems, to comprehend the functioning of the system and to predict accurately the phenome.

This short course is not intended to offer a detailed overview of system biology techniques. Indeed, this is a rapidly expanding interdisciplinary field, where new methodologies are been developed every day, with still no clear mainstream method. This course intends to be a first hands-on introduction to the subject, through some cases studies in trees that propose some of the most simple and robust approaches to data integration. Most of the lectures will be illustrated with R scripts showing the key analytical steps and tools.

Programme

Introduction, 8:30 – 8:40 (LS)
Lecture 1, 8:40 – 9:20, obtaining the omics (PFR, VJ)

Obtaining "omics" datasets, latest genotyping and sequencing methodologies explained. *Overview of the classical and novel methodologies for genotyping and sequencing that help to populate the omics multilayered datasets*

Lecture 2, 9:20 – 10:15, omics integration (FM, RP)

Transcriptomic, metabolomic and phenomic data integration – a case study for Eucalyptus. *Through a case study in Eucalyptus, we will discuss different strategies to integrate transcriptomic, metabolomics, phenomic, together with targeted analyses. The objective is to identify key regulatory hubs, investigate co-regulation networks hidden behind norms of reaction, and pave the way to include this knowledge in breeding strategies."*

The presentation: [Combining systems biology and artificial intelligence to dissect the regulatory networks of wood formation in Eucalyptus](#) (Raphael Ployet) is available on the B4EST YouTube channel.
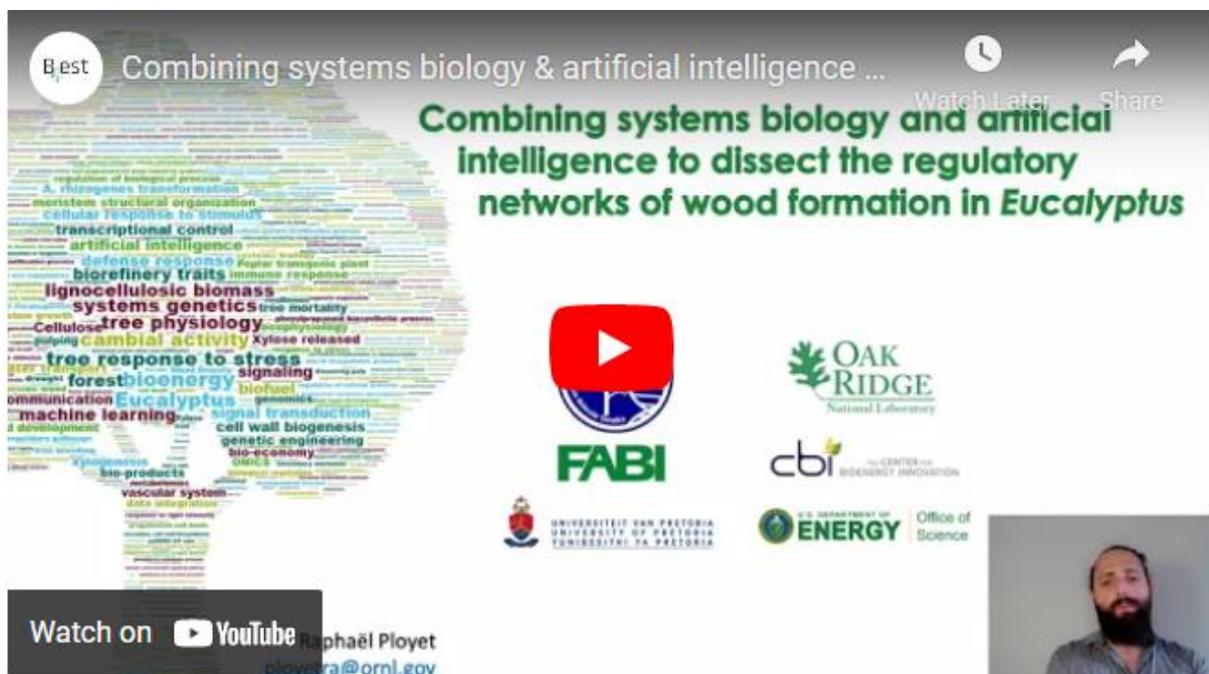
Break, 10:15 – 10:35

Lecture 3, 10:35 – 11:30, multiomics prediction (AW, HD, LS)

Simple ways to combine transcriptomics and genomic polymorphisms for phenotype prediction. *Through a case study in Poplar, we illustrate here an omics integration approach involving transcriptomics and SNP polymorphisms, and aimed at predicting phenotypes in a context of genomic selection.*
[Multiomics prediction](#) (Abdou Wade, Harold Duruflé and Leopoldo Sanchez)

Lecture 4, 11:30 – 12:25, integration for norms of reaction (VP, LB, LS)

Piling up longitudinal phenotypic data to construct genomic reaction norms. *We present here another way of data integration equally useful when it comes to quantify the role of environment in tree reactions. The strategy illustrated here combines into a single modelling approach genomic polymorphisms and climatic and environmental records associated to candidate trees, with the aim of predicting individual genomic norms of reaction in a case*

study of maritime pine from the breeding population.
[Construction of norms of reaction – Case study : Maritime pine (Pinus pinaster)](#)
(Victor Papin, Laurent Bouffier, Leopoldo Sanchez-Rodriguez)

(Part II): Customized web-based training sessions dedicated to phenomic and genomic data analyses and integration

For those attending B4EST "Data integration for prediction and breeding: new tools for obtaining, processing and integrating phenomic and genomic data" (Part I), we proposed half-day individual web based "coaching sessions" (September 2022). Considering your objectives, one or several lecturers involved in this training session will dedicate their time to provide you competent advices / strategies, and propose the most appropriate analytical pipelines to process and analyze your own datasets.

PhD students, postdoctoral fellows and researchers with background in at least one of the following fields: quantitative genetics, functional genomics, bio-informatics, statistics were targeted. 13-15 participants attended.

4   Conclusions

Despite the problems caused by the COVID-19 situation, all three training courses were successfully delivered.

Unfortunately technical issues at the Lisbon venue meant that it was not possible to record the on-site training courses for later use. However, the detailed powerpoint presentations have been made available on the B4EST website.

5   Partners involved in the work

Eight academic partners of B4EST were involved in the preparation of these courses:

UPS, SLU; CIRAD; NIBIO; UU; INRAE; UOULU; CNR