

Training workshop equips forest tree breeders with new tools

A training workshop for tree breeders focused on practicing use software tools for optimum selection in forest tree breeding was held in Höör, Sweden, on 29-30 October 2019. These tools, updated within the GenTree project based on the recent advancements in genomics and breeding theory, allow to optimize gains and, at the same time, maintain the level of genetic diversity in breeding populations at an acceptable level.

Tree breeders from a wide range of European countries - Croatia, Denmark, Estonia, Finland, France, Ireland, Latvia, Norway, Poland, Sweden, UK as well as one from Brazil, joined the workshop for a hands-on experience. Tim Mullin (consultant at Skogforsk) and Leopoldo Sanchez-Rodriguez (INRAE) who have a long instructional experience, led the training.

Advances in tree breeding have mimicked those made in crop and livestock improvement, where crosses are made among phenotypically selected parents, progeny-evaluated through field tests. Selection is applied to identify material for deployment. In the management of forest genetic resources, a critical challenge is to find cost-effective strategies to avoid rapid losses of diversity in breeding populations despite the selection operated in the breeding process.

The theoretical work carried out within GenTree for optimal tree selection and mating had the objective to maximize genetic gain under the constraints of relatedness between individuals. Algorithms that would account for this condition were incorporated into the tools made available to breeders: OPSEL version 2.0 and XDesign version 1.0. Updated versions of these widely accessible tools were enriched with new features and added to the POPSIM simulation software, widely used for evaluation of tree breeding programs.

Existing “traditional” breeding activities can benefit immediately by incorporating an optimization methodology such as the one described above, to achieve the highest genetic gain while conserving genetic diversity.

The use of genomic tools in breeding can be as complex as a genetic evaluation based on high-density SNPs, or as simple as establishing paternity from a small list of candidates with a rather small number of DNA markers. Genetic monitoring can be used to evaluate the impact of silvicultural operations on seeds collected from managed stands and simulation can be used in various ways to identify superior management and breeding options.

The participants, all actively involved in tree breeding, found the course extremely relevant and will have an opportunity to incorporate the newly acquired skills in their work very soon.



The course participants listen attentively to the instructor Tim Mullin.



Time for a break in the sunny weather outside the main building at the hotel Stiftsgården in Höör (Sweden).



Gearing up for the social dinner after a full day of lectures and exercises.

Programme

Monday, 28 October, 2019

- 19.00 ice breaker and registration

Tuesday, 29 October, 2019

- 8.00 Registration of late arrivals and General information
- 8.30-17.00: Classroom sessions - Overview of the tools PIDS, OPSEL, and XDesign
 - Lectures and exercises:
 - General concepts related to Identity by Descent (IBD),
 - Population parameters from pedigrees – PIDS,
 - Constraints on selection,
 - Optimal selection for deployment and breeding with Equal Contributions – OPSEL,
 - Optimal selection for deployment and breeding with Unequal Contributions - OPSEL,
 - Constraints on mating,
 - Generation of complex mating plans avoiding inbreeding – XDesign

Wednesday, 30 October, 2019

- 8.00-16.30: Classroom sessions
 - How different selection regimes affect the destiny of alleles and consequences for long-term breeding. Overview of R and Rstudio tools - breedR, SBVB, a tool for classic OCS (Optimum Contribution Selection).
 - Lectures and exercises:

- Selection regimes - pedigree-based evaluations (blups) & genomic evaluations with different genomic architectures.
- Genetic and genomic evaluation of real genomic and production data (maritime pine and poplar) – breedR,
- Genetic and genomic evaluation of subsequent generations using a genomic simulator similar to Metagene but able to work with real data as starting point – SBVB,
- Genetic and genomic evaluation of subsequent generations using classic OCS – A third tool,
- Presentation of alternatives to OCS.
- 16.30-17.00: wrap-up and course assessment

Participants

Name	Location of institute of affiliation
Tiit Maaten	Estonia
Saša Bogdan	Croatia
Marzena Niemczyk	Poland
Arnaud Dowkiw	France
Pauls Zeltins	Latvia
Haleh Hayatgheibi	Finland
Javier Herrero	Spain
Arne Steffenrem	Norway
Sara Abrahamsson	Sweden
Ainhoa Calleja-Rodriguez	Sweden
Mari Suontama	Sweden
Johan Kroon	Sweden
Mateusz Liziniewicz	Sweden
Andreas Helmersson	Sweden
Torgny Persson	Sweden
Henrik Hallingbäck	Sweden
Curt Almqvist	Sweden
Adam Klingberg	Sweden
Tomas Byrne	Ireland
Jing Xu	Denmark
Domen Finzgar	United Kingdom
Richard Whittet	United Kingdom
Gustavo Lopez	United Kingdom
Ananda Aguiar	Brazil

Lecturers and co-organizers

Leopoldo Sanchez-Rodriguez (lecturer)	France
Tim Mullin (lecturer)	Sweden
Tiret Mathieu	France
Pegard Marie	France
Johan Westin	Sweden