Genomic Selection: Towards more Efficient, Financially Viable and Resilient Wood Production (GenoWood)

Bioeconomy aims at a society that strongly relies on renewable biological sources, while achieving economic growth efficiently and sustainably. In Finland, forest industry has a key role in bioeconomy. Demand for wood will be increasing, as well as demand for tailor-made trees with specific chemical and physical wood characteristics. In the near future, climate change and associated natural disturbances (pests, pathogens, changing length of growing season and associated frost damage) may negatively affect the productivity of forests. Increased wood production must further be combined with ecological and societal demands for biodiversity and multiple uses of forests. These demands put pressure to radically enhance and speed up forest tree breeding.

Our goal in the project is to utilize novel genomic and phenotyping methods and examine the feasibility of conducting genomic selection in Nordic conifer species. The proposed research makes use of unique resources for Scots pine that have been developed in Finland during decades of research in forest tree genetics, breeding and biotechnology. Our project brings together research groups with complementary skills in molecular biology, population genetics and breeding, forest pathology, and economics.

Tree populations have large variation in many adaptive and economically important characteristics, enabling tree breeding based on natural genetic variation. Changes in the environment and in the use of wood put pressure to include new traits in breeding programs. On one hand, resilience of trees against changing climate and resistance against pests and pathogens must be included in the programs. On the other hand, forest industry demands more uniform and specific chemical and physical characteristics of wood that can be tailored by tree breeding.

Genomic tools are increasingly being used for breeding of both animals and plants. Genomic selection uses genomewide markers to predict phenotypes. In order to associate genomic markers with phenotypes, we started in the summer 2018 an experiment where ca. 10,000 pine seedlings originating from different populations were grown in greenhouse conditions. Their growth rate was measured, as well as the timing of their budset, indicating preparation for wintering. In November, a subset of the seedlings was subjected to freezing stress and their recovery was monitored by automatic color measurement (brown vs. green). Preliminary analyses of data were conducted and showed that experiment produced qood quality phenotypic data that will be used for genomic selection analyses when data from genotyping part will be ready. This spring, when the seedlings had overwintered successfully, 2000 seedlings were repotted in the greenhouse and will be challenged with annosum root rot to measure their resistance, and with UV-C irradiation to measure their chemical response. Variations in resistance of pine seedling populations in response to annosum infection is apparent. Susceptible seedlings had strong necrotic brown reactions as well as marked decreases in photosynthesis efficiency. In pine, UV-C induces synthesis of stilbenes (pinosylvin and its monomethyl ether) in the needles, the same compounds that are responsible for hereditary decay resistance of pine heartwood. DNA markers for further analysis have been developed based on sequence data from this and earlier projects. Using DNA isolated from needles, the goal is to score 50,000 genetic markers will be determined for 500-700 and their association to phenotypic traits is calculated. These data will also be used for genomic prediction and examining potential of selection. The breeding population data are being compared to a natural population using these same markers.

During the project we will further analyze the economic (financial gains) and societal outcome (carbon balance) of present and future breeding for volume production (growth) and quality (decay resistant timber as an example).

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