

ENHANCING THE RESILIENCE OF NORDIC FORESTS – AIDED BY MICROBIOTA, EPIGENETICS AND TREE BREEDING

The ongoing global change calls for increasing resilience of forest trees. Active breeding can be used as a tool to improve tree resistance as here exemplified with Norway spruce against the main causal root rot fungus, *Heterobasidion*. Besides the use of breeding to improve resistance, future research and forest management should take into account the potential impact of the tree microbiome and epigenetic mechanisms on resilience.

Introduction

Forests constitute one of the main natural resources in the Nordic countries. They provide raw material for industries, habitat for important biodiversity, outdoor activities, and a major sink for carbon. A healthy forest is a prerequisite for contributing all the desired services in a sustainable way. Increased pressure caused by human disturbance, global warming, and increasing numbers of invasive species on Nordic forest tree species are likely to weaken the trees and make them susceptible to diseases and pests.

The genetic adaptation, directed by natural selection and survival of the fittest, gradually makes tree populations better adapted. In addition to this relatively slow process, the trees possess - or can be assisted by - other means to improve their resilience in the changing conditions. In this context, the role of forest microbiota, the epigenetic mechanisms of trees and active resistance breeding should be given more attention in research and forestry, in order to develop forestry measures, which enhance their positive effects, and to avoid the harmful ones.

A forest tree is much more than a tree

It is well-known that trees rely on their interaction with mycorrhizal fungi. However, in

recent years the forest tree microbiome has received growing attention as a key component in forest health and ecosystem functioning far beyond the role in procuring the trees with nutrients and water.

Trees are associated with thousands of microorganisms that can serve as a reservoir of extra genes and functions that can benefit the host. The recent explosive development of high-throughput molecular sequencing technologies has enabled a new level and scale of evolutionary and environmental studies into the complex and poorly understood interactions. New fine-scale studies have revealed a microbiome taxonomic signature on individual tree species and variation from tree to tree that may potentially determine the fitness of the host. For instance, the microbial composition of forest trees stressed by pathogenic diseases can differ between healthy and unhealthy trees.

The complicated, mutual interactions between forest trees and their microbes are still poorly understood, and even less is known on the influence of global climate change on these interactions. Future research that addresses the impact of the forest microbiome on trees' growth and resistance to environmental stresses is therefore important in order to safeguard resilience and sustainability of our future forests.

Potential application of Epigenetics for Tree Breeding, Genetic Resources Conservation and Forest Management

Recent studies have highlighted the pivotal role of epigenetic mechanisms linking environment, gene expression and phenotypes in forest tree species. Epigenetics refers to all the processes affecting the expression of genes and the activity of transposable elements without altering the DNA sequence that is heritable both during individual's development and across genera-

tions. Epigenetic mechanisms are encoded by genes in the genome itself and form an essential part of genomic diversity, significantly extending the regulatory abilities of genomes.

Epigenetic mechanisms contribute significantly to phenotypic plasticity, stress responses, disease resistance, acclimation and adaptation to habitat conditions for plants and especially forest trees during their lifetime but also across multiple generations. Most of the studies on forest trees have focused on the role of epigenetics in tree development, and response to environmental changes and priming of defense responses. More recently studies have pointed out the potential relevance of epigenetics in tree improvement.

Potential use of epigenetic approaches could be realized in three main directions: 1) explore and use of natural or environmentally-induced epigenetic diversity (e.g. epigenetic memory in Norway spruce or in poplar); 2) use of epigenetic marks in addition to classic genetic markers for trait improvement (e.g. methylation marks in poplar and spruce), and 3) develop of methods for editing of trees epigenome (e.g. CRISPR-dCas9 approaches).

These three directions could also be consecutive stages for study and implementation of epigenetics in practical forestry and breeding.

Despite there is still a long way to go on to decipher the role of epigenetics in environmental responses, epigenetics should be considered and included into the breeding programs and forest management.

Breeding for resistance against root rot in Conifers

Today the forests are challenged by a number of biotic and abiotic threats of which root rot to conifers is the economically most serious with yearly losses exceeding 100 million Euros in the Nordic countries. The last decade's research has established that there is sufficient genetic variation in resistance against the main causal rot fungus, *Heterobasidion*, in Norway spruce for substantial progress to be made through incorporating resistance into breeding programs. Furthermore, there is minimal trade-off between resistance traits and growth- or wood properties traits, suggesting that improved resistance likely could be attained without sacrificing gains in terms of growth.

Recent advances in genomic research of conifers have provided us genetic markers to help to map the resistance traits and defense pathways in forest trees. This allows for developing breeding strategies with early selection for resistance also against disease problems normally associated with older trees, such as root rot.

Arguably, exploiting genetic variation associated with pest or disease resistance into operational breeding and deployment programs would strengthen the position for Nordic forestry to meet future challenges associated with climate change and globalization. This could be done e.g. via selection strategies including phenotypic or genomic selection and make use of technologies such as somatic embryogenesis. Besides recent developments in genomic research, a deeper insight into epigenetics and into the understanding of host-microbe relationships may prove important for a more efficient selection of trees for a resilient future forest.

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