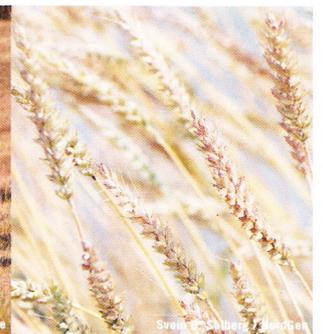
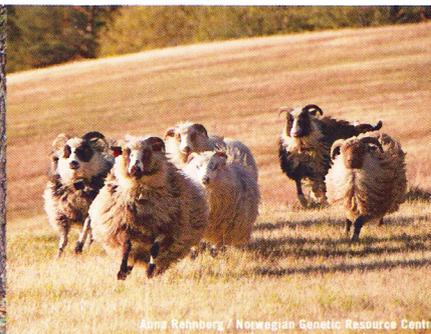
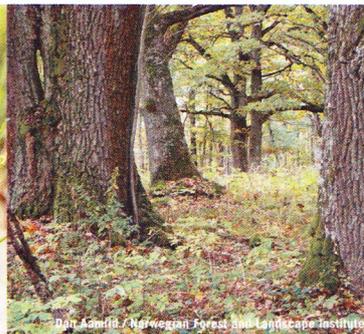
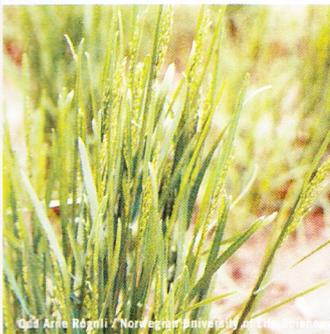


Book of Abstracts



Genetic Resources for Food and Agriculture in a Changing Climate

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Molecular and genetic analysis of plant root exudates response to phosphorus starvation

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Phosphorus (P) is an essential macronutrient for plant growth and development. The world population is expected to reach an estimated 9.2 billion by 2050, which means food production globally has to increase by 70% in order to feed the world. P starvation could be one of the major limitations to crop productivity globally. Higher plants developed various responses to P starvation, including gene expression, morphological responses such as the root architectures, physiological modification like root exudates and pH changes, as well as metabolic responses. Root exudates play an important role on releasing soil P since organic acids, a group of low molecular weight compounds, can mobilize P from mineral surfaces and from Al-, Fe- and Ca-phosphates by chelating the metals and increase P availability to plants. Hence, the root secretion of organic acids is considered as an important mechanism in alleviating P starvation. Meanwhile, the secretion of organic acids induced by P deficiency from roots of many plant species were reported previously, for example, citrate from cowpea roots, citrate and malate from *white lupin* roots etc. However, plant species, even cultivars of the same species secrete different organic acids to P starvation, indicating possible genetic diversity and adaptation. In addition, the molecular and genetic regulation mechanisms of root exudates are largely unknown to date. Here, we report our study on the effects of P supply on plant growth and organic acids secretion from the roots of *Brassica*(*HARIE*), *Wheat*(*AINO*) and *Barley*(*HEDER*), which are important crops in Norway, by using hydroponic culture. Our preliminary results showed that P starvation could cause phenotypical alterations like biomass reduction and anthocyanin accumulation. Induction of malic acid and citric acid secretion at various degrees among crops and within cultivars were also found. Moreover, P starvation seems to have affected Boron acquisition. Those results are of importance for understanding genetic diversity and adaptation of crops to P deficiency, and effective utilization of P in the future agriculture. We have carried out studies on physiology and molecular analyses. The results are in progress.

Distribution of neutral nuclear genetic diversity of European beech in two managed stands and a secondary virgin forest reserve: a case study

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The territory of present-day Slovenia was one of the main source areas for the post-glacial distribution of beech (*Fagus sylvatica* L.) and supposedly the most important glacial refugia for its re-colonisation in Europe. In the present study three autochthonous beech populations: Kamenski vrh, Osankarica and Rajhenavski Rog were examined for patterns of neutral nuclear genetic diversity. The first two populations are managed according to irregular group progressive shelter wood management with a restricted small-scale regeneration centres, and in the third one human management was banned about two centuries ago. In populations Osankarica and Rajhenavski Rog, 35 adult trees and 35 saplings, whose height was between one and three meters, were sampled, while in population Kamenski vrh only 35 adult trees were sampled, together 175 trees clustered into five samples.

Trees were analysed on 16 SSR loci. Preliminary results using SpaGeDi and Genepop showed that departures from Hardy-Weinberg equilibrium as well as association between genotypes at pairs of loci could not be confirmed (with exception for one locus in one population and two loci pairs also in one population). While allelic patterns did not differ substantially among samples, Fst and genotypic

differentiation estimates were significant ($F_{st}=0.012$; $P=0.000$ and $P=0.000$ respectively). Pairwise F_{st} values and genotypic differentiation were significant for all sample pairs except for sample pair saplings and adult trees in the virgin forest reserve. Differentiation measured as F_{st} between saplings and adult trees in population Osankarica was by tenfold lower ($F_{st}=0.006$; $P=0.029$) than differentiation between samples from different locations ($0.011 < F_{st} < 0.022$).

Further analysis focusing on spatial and temporal distribution of diversity is ongoing. Changes in genetic structure may give the evidence for disturbances in the transition from one generation to the next one in close to nature forest management regimes in beech forests.

Comparative QTL analysis of early short-time drought tolerance in Polish fodder and malting spring barleys

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Mapping populations of Polish fodder and malting spring barleys were used for QTL analysis of the traits describing short-time drought response at the seedlings stage. High throughput genotyping (DArT markers) and phenotyping techniques, including measurements of drought-induced changes in gas exchange, chlorophyll *a* fluorescence, water relations and membrane integrity were performed. The results showed a high genetic diversity of studied populations enabling the creation of high density linkage maps, as well as a high diversity in the physiological response of studied breeding materials. The analysis revealed 18 QTLs for 9 physiological traits on all of the chromosomes except for 1H in malt-type barley. In the fodder-barley population 15 QTLs for 5 physiological traits were found on chromosomes: 2H, 4H, 5H and 6H. Chromosomes 4H and 5H contained the regions explaining most of the observed phenotypic variation in the parameters analyzed in both populations. There was one major QTL for net photosynthetic rate in the malting barley mapping population located on chromosome 5H. Also two major QTL, which seem to correspond to two main genes were found for PI. One major QTL for q_p was located on chromosome 4H in the fodder barley population. Three QTL regions were common for both mapping populations but explained drought-induced changes in different traits which are in accordance with the previous studies in which different traits were shown as being responsible for the drought tolerance variation within fodder and malting barleys. It seems that the best approach for QTL analysis, effective for further evolution of marker systems, is to create mapping populations for local-adapted gene pools, even separate for different breeding directions (e.g. malting and fodder barleys) and to phenotype the well-recognized physiological characteristics responsible for the variation in tolerance among the studied group of genotypes and under local conditions.