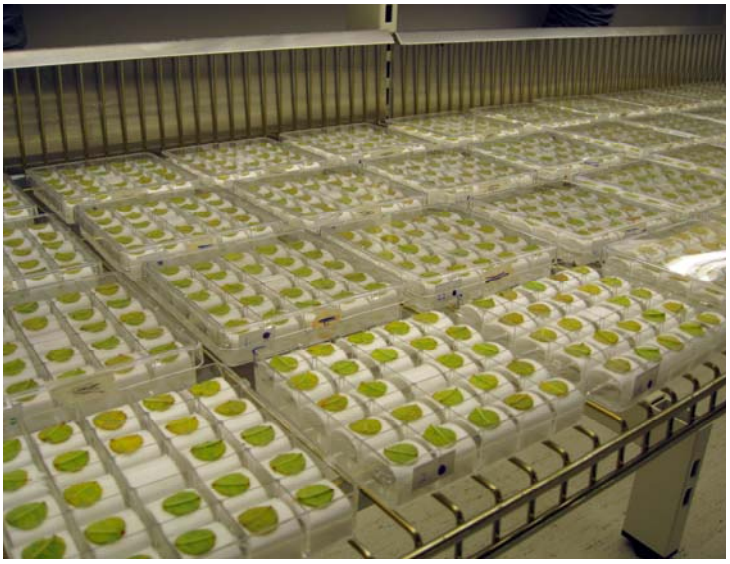
Improved resistance against willow leaf rust

The willow leaf rust fungus (*Melampsora larici-epitea*) can cause large damage in biomass willow plantations. Production losses of up to 40% have been estimated in susceptible clones. A high rust resistance is therefore one of the most important breeding goals, and improvements of resistance have also been achieved in the breeding programs during the years.

A lasting problem is that the willow leaf rust fungus, like many other rust fungi, has a high capacity to change and overcome resistance of the plant. This is especially true for the kind of resistance that is governed by a single major gene, which is common in many crops. It is therefore preferable to utilize also other types of resistances that are based on several minor genes (i.e. quantitative resistance) and hence more complicated for the fungus to adapt to. The aim is that the cultivated willow clones should have many different resistance genes and that it should be possible to combine these resistance genes in various ways in the varieties. The purpose of this project is to develop molecular markers for resistance genes that can be used as a tool in the plant breeding.

Infection experiments to identify resistance components

We are now working on developing molecular markers for the various resistance genes in *Salix*. To achieve this, we have studied two *Salix* families, by doing controlled infection experiments in growth chambers. Resistance measurements were made of latent period, number and size of rust pustules and necrotic flecking.



Measurements:

Number of pustules

Pustule size

Necrotic flecking

Latent period

Infection experiments were performed on approx. 300 genotypes in each of the two Salix families. Four different rust fungal isolates were used. In total, 9200 leaf discs were assessed in the experiments.

Field inventories

We are also doing assessments of rust resistance in the field on the same *Salix* genotypes that are used in the infections experiments. By comparing the results we can see how the resistance pattern from the infection experiments agree with those under field conditions.

*The figure shows a field trial of Salix family S1 (*a *S. viminalis* x *S. schwerinii* backcross) *in September 2008. The trial was planted in June the same year.*

Locating resistance genes on genetic maps by QTL mapping

The data on resistance reactions was combined with the molecular data from the genetic maps that have been created within the SAMBA project. By QTL mapping (mapping of quantitative trait loci), QTLs or genes that affect resistance reactions can be located on the genetic maps. We have identified a number of genomic regions that are important for rust resistance in the two *Salix* families. In two cases, QTLs were located close to markers for rust resistance genes from the *Populus* genome. The next step will be to evaluate the resistance markers identified in the QTL mapping on unrelated willow clones of various genetic backgrounds. Further fine-mapping might be necessary in order to find molecular markers that are tightly linked to the genes of interest.

Gene detective

BAC libraries – an approach to identify the actual resistance genes

A valuable resource constructed within the SAMBA project is two BAC libraries (Bacterial Artificial Chromosome libraries). A BAC library is a collection of DNA fragments that is stored in bacteria. In our case the whole genomes of the two parents of mapping family S1 are available as thousands of DNA fragments in such BAC libraries. We will screen the BAC libraries with help of the molecular markers from the QTL mapping. Interesting DNA fragments will be sequenced, and this will help us to map the resistance QTLs more precisely and possibly identify the actual resistance genes. This will also facilitate the development of stable markers for future breeding purposes.

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