

Dear steering committee et al.

I would like to keep you updated about what has been/is/will be going on here at WSL in respect to the silverfir project. We (especially Sabine, but also myself, René, Christoph, and our gardeners) have put a major effort into this in the last 3 months.

The tree [Pictured Separately] is located in a forest next to WSL and is marked. the forest manager is informed. they are not planning to cut it in the near future ;-) the official name is: "AA_WSL01".

We prepared around 50 megagametophytes. finally, 2 megagametophyte DNA samples (each 3.7 microg) were sent to CNAG end of february. passed the QC tests there. these samples are for paired-end sequencing and should not be combined (different genotypes).

Eight needle DNA samples (10-13 microg each) were sent to CNAG yesterday and safely arrived today. these samples are for paired-end sequencing and can be combined, they all represent the same genotype.

Megagametophyte and needle samples were genotyped with 11 nSSRs and 2 cpSSRs. by doing this, we could verify if the tree is a silverfir at all (it is!) and whether it is a typical genotype of the region (it is also). it also helped us to check for contamination and to check if we are analysing the right samples at all. additionally, the tree is included in a SNP analysis (502 loci) of katalin csillery which is being analysed right now.

We already sampled needles and needle buds for RNA-Seq from the original tree. flower buds will follow soon. we are planning to repeat this sampling in spring and summer, and are also thinking about sampling bark and roots (very challenging). christoph is working on the planning of future steps regarding tissue sampling, in close collaboration with berthold.

We stratified some hundred seeds of the original tree and have put them already into soil. they are germinating right now. these seedlings will be for additional RNA-seq with different treatments applied (e.g., drought/cold).

We sampled twigs for grafting (cloning). at the moment, we are planning to have max. 10 clones, emphasis here is put on a) having a backup and b) having easier access to the genotype. grafting starts these days. if anybody plans experiments with clones, then we can think about making a major grafting effort next winter/spring.

If you have any questions, don't hesitate to contact me.

Have a nice week, Christian