Breeding for resistance
To Heterobasidion spp
Decreased value of timber

120-150 Skr/m³  

500-600 Skr/m³
More economic losses….
Heterobasidion annosum
Heterobasidion parviporum
Spridning
Stump treatment
Resistance testing to solve the problem
Inoculation experiments

Plants - mycelium

Branches mycelium

Trees - mycelium

Stumps - spores
Results from inoculation experiments

- Resistance is present and shows the same pattern on all materials
- Genetic factors are large enough for breeding-15-30 percent heritability
- Economic gain is considerable (15% less decay than average if top 10 clones are chosen)
- Possible to include in existing breeding programs (where genetic gain gives ca 25% higher yield)
Test somatic embryos and Heterobasidion

Resultat av embryotest omgång 2

Tid (dagar)

Embryostatus (3=vital, 0=död)
Natural infection.
Map of rot frequency in a 25 years old clonal stand in southern Sweden

- Healthy trees
- Decayed trees (46.5%)

• Heritability 0.18
• Genetic gain 15%
Increased value from production: 15-25%
* We need reliable markers for resistance to the pathogen
Chemical and transcriptional markers for resistance

- We had the opportunity to use our resistance defined material from natural infection in southern Sweden. The same clones exist on 4 locations.
- Wounded tree roots (constitutive defence) and inoculated (induced defence) tree roots.
- Analyzed transcriptional regulations and chemical profiles (terpenes and phenols).
Results chemical markers

• Resistant clones had higher constitutive conc. of astringin and its dimers: May be candidates as a constitutive markers for resistance.

• Concentration of specific phenols increased during infection period

• Constitutive concentrations of terpenes does not seem to be specific for trees more or less resistant to *Heterobasidion*.

• Terpene conc. increased during infection
Transcriptional results

- The transcriptome always shows the same pattern in the same spruce clones when inoculated with *Heterobasidion*.
- Transcriptome data correlated well with chemical profiles
- Two of the resistant clones showed different “strategies” for resistance
Future……

• Identifying high priority candidate pathogen genes in *Heterobasidion spp.*
• QTL mapping of pathogenicity
• Looking for signs of selection and diversity in a sequenced population of *H. spp*
• Identifying pathogenicity candidates in the genome from comparisons with other plant pathogens.
Future

• Secondary metabolite and toxin production in *Heterobasidion spp*
• Functional analysis of pathogenicity genes.
• QTL mapping of resistance in *Picea abies*.
• Transcript profiling of host genotypes with high and low resistance
• The mechanisms of host cell death in response to *H. annosum*
Some of us working in the project from 1992-

Bo Karlsson  
Skogforsk

Jan Stenlid  
SLU

Anna-Karin Borg  
KTH

Malin Elfstrand,  
SLU

Marie Danielsson  
KTH

Karl Lunden  
SLU