


Molecular ecology and landscape genomics of trees



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Trees form our landscape




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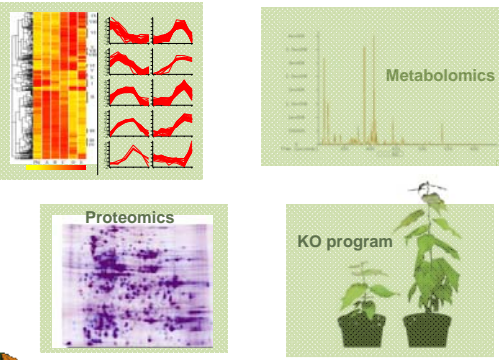
EST sequencing → PopulusDB




Sterky et al. (1998)
 PNAS 95: 13330-13335
 Sterky et al. (2004)
 PNAS 101 13951-13956





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Metabolomics



Proteomics

KO program

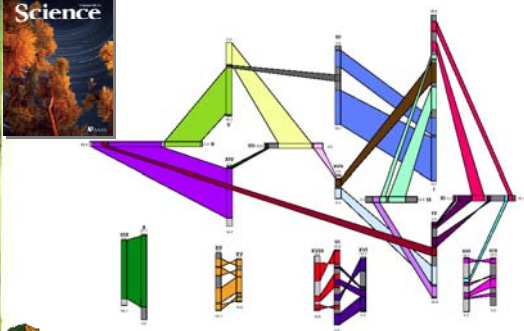

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Populus transformation

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The Populus genome

Tuskan et al. (2006)
 Science 313:1596-1604

Genetic diversity in *Populus*

- Slowly ticking molecular clock
- Dioecious
- Wind-pollinated (thousands of km)
- Wind-dispersed seeds
- "Infinite" population sizes



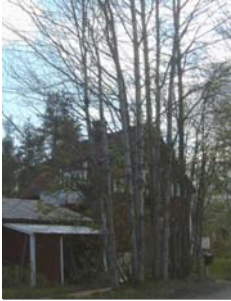

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> 1 % difference




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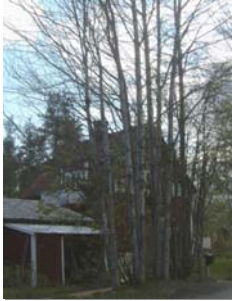




< 0.1 % difference


> 1 % difference



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< 0.1 % difference



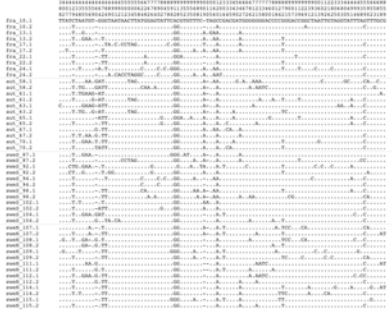

≈ 1 % difference

> 1 % difference



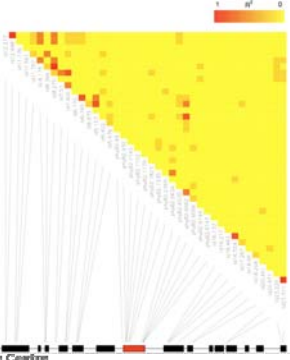

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An "infinite" number of haplotypes

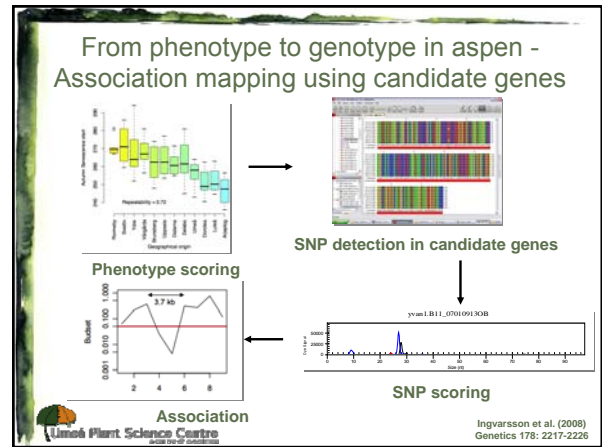
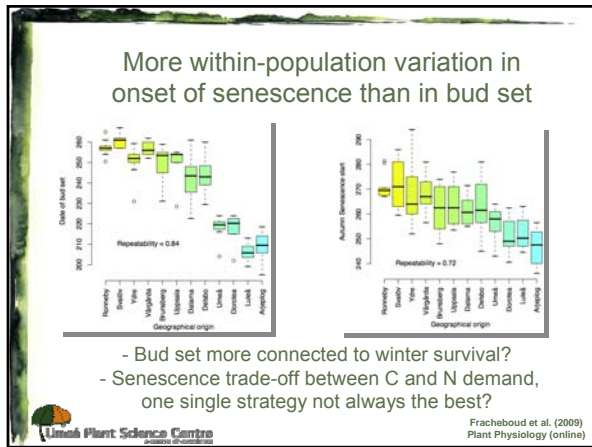
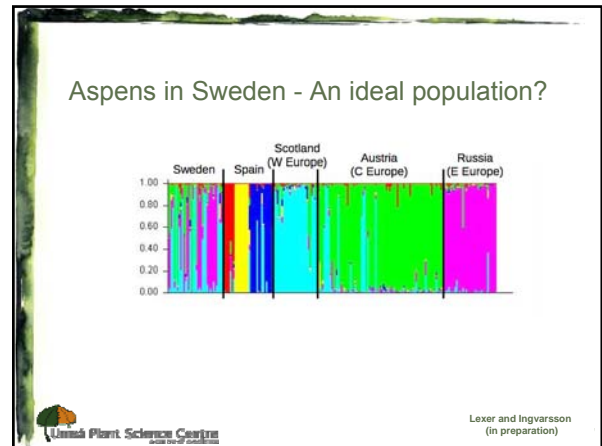
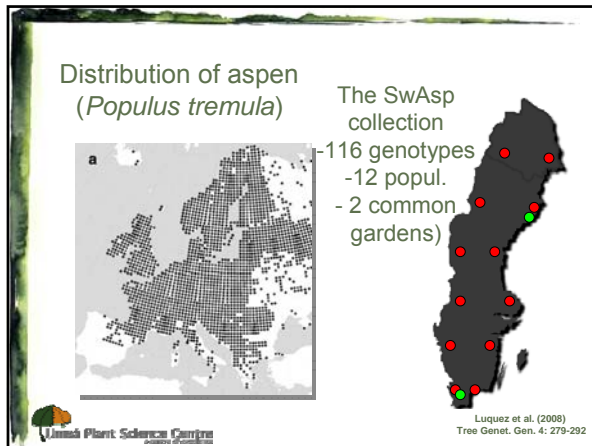



Ingvarsson et al. (2006)
Genetics 172: 1845-1853

Linkage Disequilibrium is almost absent

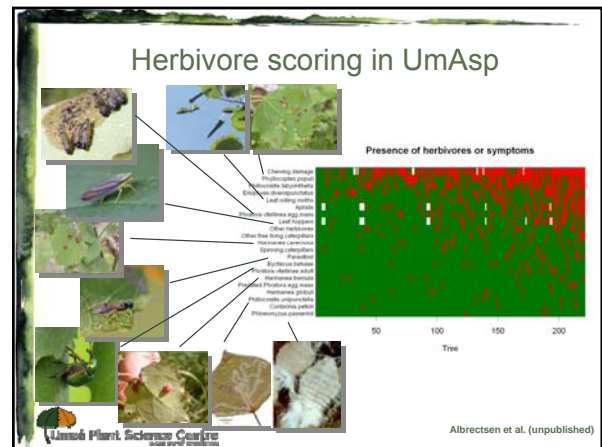
Ingvarsson et al. (2008)
Genetics 178: 2217-2226



Sequencing of six aspen genomes

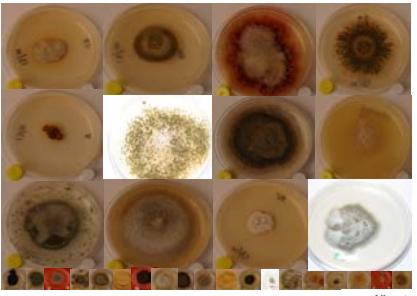
- 454/SOLiD (Illumina)
- Identify variable regions
- Estimation 10 million SNPs

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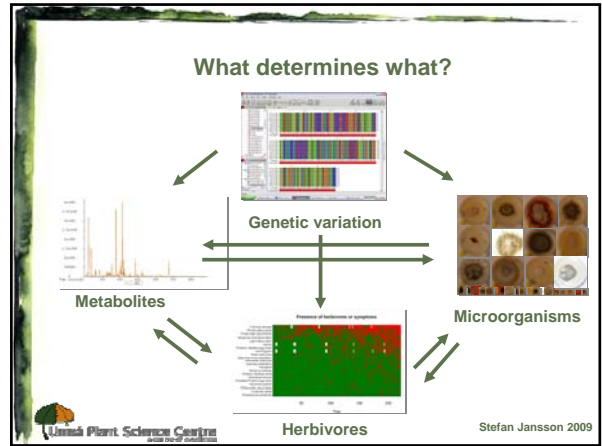


A tree - an ecosystem

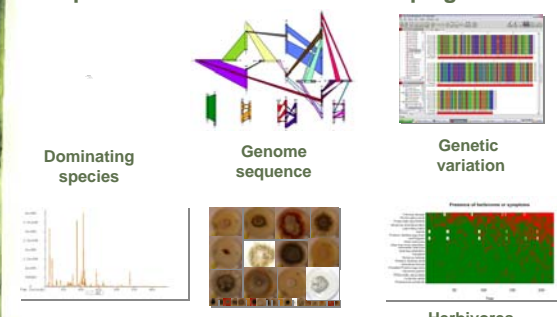
> 30 different fungal endophytes from one tree



Umeå Plant Science Centre
Albrechtsen et al.
Fungal diversity (in press)



Is aspen an ideal model for landscape genomics?



Umeå Plant Science Centre
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