

# Within stand relatedness and genetic diversity

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#### We have a dream....

to know all sequences by all trees what we have and their relations with all traits.



#### Why to study?

- For determining stand or population structure and diversity
- For evaluating population viability
- For having material for evaluation the influence of breeding on diversity/relatedness
- For determining origin of forest trees
- For any other purpose which could help us understand how trees are behave and use such information by silvicultural or conservation actions



## Such information is very interesting but...

- We are not able to get it
- We must use less sources for getting such information
- It the purpose will be investigaton of single stand (or few stands) then how we could define a term "stand"?
- Do we have enough finances for getting that?



### What is a stand in this case?

- There are many tree species on good site types: number of target individuals per ha could be low
- How old the stand must be? Can we consider two years old stand as a stand?
- Shall we consider some number of trees of the target species as one unit stand? Some average number of effective population size?



#### Background – how to get money? CBD

- **CBD** article 2: "Biological diversity" means the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems.
- Article 6. General measures: Each Contracting Party shall, in accordance with its particular conditions and capabilities: (a) Develop national strategies, plans or programmes for the conservation and sustainable use of biological diversity or adapt for this purpose existing strategies, plans or programmes which shall reflect, inter alia, the measures set out in this Convention relevant to the Contracting Party concerned; and (b) Integrate, as far as possible and as appropriate, the conservation and sustainable use of biological diversity into relevant sectoral or cross-sectoral plans, programmes and policies.
- **CBD** article 12: Research and Training: The Contracting Parties, taking into account the special needs of developing countries, shall: b) Promote and encourage research which contributes to the conservation and sustainable use of biological diversity, particularly in developing countries, inter alia, in accordance with decisions of the Conference of the Parties taken in consequence of recommendations of the Subsidiary Body on Scientific, Technical and Technological Advice;



#### Background – how to get money? MCPFE

- S2: considering that, above and beyond the conservation of forest species, the essential objective is the conservation of the genetic diversity of these species, which are an essential part of mankind's heritage.
- S2: recognizing, also that the use of genetically-improved materials is of great importance for afforestation and restocking, in particular where this is for the purpose of the production of timber.
- H4: (Areas for research) Studies on genetic variability of regionally important tree species in response to changes in climate and increased concentration of carbon dioxide, and on the degree and rate of evolutionary processes and adaptation, by means of genetic changes.



#### Strasbourg 2 resolution:

- Research for conservation
- Research for breeding (silviculture)



#### Conservation of FGR in Europe

- EUFGIS database available <u>www.eufgis.org</u>
- It was compiled on the basis of minimum requirements for gene conservation units



#### GCU-s

The units should have a designated status as gene conservation areas of forest trees at national level. The units can be located in forests managed for multiple uses, protected areas or seed stands. The minimum size of a unit depends on tree species and conservation objectives as follows;

- 1) 500 or more reproducing trees (when the objective is to conserve gene diversity of widely occurring and stand-forming conifers or broadleaf species),
- 2) 50 reproducing trees (when the objective is to conserve adaptive or other traits in marginal or scattered tree populations) or 50 seed bearing trees (scattered tree species with sexual dimorphism), and
- 3) 15 unrelated reproducing trees (when the objective is to conserve remaining populations of rare or endangered tree species).

In light of presented minimum requirements, we are facing the same problem: how define a stand and how many samples do we need for determination the genetic structure and level of relatedness by single stand



#### Short overview about literature



#### Papers available

- Common fashion by papers: 5-40 samples per stand or per population analysed, different variables calculated
- In some cases all trees analysed, usually in case where stands are very small and/or rare, especially in the Mediterranean region
- One paper where bigger number of forest trees per one stand analysed (Chybicki *et al.*, 2008).



One problem:

Genome size (bp):	No of genes,	% of coding DNA
Escherichia coli - $4,7 \ge 10^6$	4 000	100
Arabidopsis th. $-125 \ge 10^6$	25 500	50
<i>Picea abies</i> – 30 000 x 10 <sup>6</sup>	25 000 - 50 000	<3
<i>Fritillaria</i> sp. <b>– 85 000 x 10</b> <sup>6</sup>	25 000	0,02
Homo sapiens – 3 000 x 10 <sup>6</sup>	40 000	<2



#### Spatial Genetic Structure Within Two Contrasting Stands of Scots Pine (*Pinus sylvestris L.*)

The spatial genetic structure of two contrasting stands of Scots pine located within one continuous population investigated: (i) the even aged qualified seed-tree stand utilized for commercial seed collections (321 trees) and (ii) the naturally established unevenaged and unmanaged stand (173 trees). Genetic variation at 14 allozyme loci (*Fest, Gdh, Aat-1, Aat-2, Aat-3, Mdh-1, Mdh-3, Mdh-4, 6Pgdh-1, 6Pgdh-2, Pgi-2, Pgm-1 and Shdh-1*) studied Two stands differed substantially in the levels of inbreeding. The estimated *FST coefficients also showed that the* two studied stands genetically are not very differentiated at the single locus level (although at the multilocus genotypic level they are)

In spite of such strong differences there were only slight differences either in genetic diversity and spatial genetic structure.



#### Common conclusion by investigations of Scots pine populations

Despite periodic interstadial fragmentation episodes, Scots pine biology provides for the long –term maintenance of high within-population and low amongpopulation genetic diversity at neutral genetic markers (Robledo-Arnuncio *et al.*, 2005)

This conclusion was made on the basis of cpSSR analyses



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Tollefsrud *et al.*, 2008. Genetic consequences of glacial survival and postglacial colonization in Norway spruce: combined analysis of mitochondrial DNA and fossil pollen – Molecular Ecology, 17, 4134 - 4150







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Combined analysis of nuclear and mitochondrial markers provide new insight into the genetic structure of North European Picea abies (*Tollefsrud* et al. 2009 (*Heredity*))

### **Thanks!**

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