

Background

To date, there is no firmly established system for genetic monitoring of gene conservation units across Europe. A genetic monitoring aims at characterizing the state and development of genetic systems by using different indicators and verifiers. Based on the monitoring concepts of Aravanopoulos *et al.* 2015 and Konnert *et al.* 2011, 16 verifiers have been chosen for testing a minimal check-list for the two deciduous species poplar and beech within the GenTree-project and using a minimal approach based on the GenTree sampling and study design.



Fig. 1: Genetic monitoring sites installed for *Fagus* and *Populus* in the GenTree-project

Minimal CHECK-LIST

suggested for genetic monitoring of conservation units in Europe

Indicator / Verifier	Poplar	Beech
Level of genetic variation		
○ number of effective alleles (A_e)	✓	✓
○ allelic richness (A_r)	✓	✓
○ latent genetic potential	✓	✓
○ Heterozygosity (H_e and H_o)	✓	✓
Change of genetic variation		
○ A_e differences between generations	✓	✓
○ A_r differences between generations	✓	✓
Mating system		
○ selfing		✓
○ inbreeding		✓
○ outcrossing		✓
○ effective of population size (N_e)	✓	✓
○ hybridization	✓	✓
○ mean no of pollen donors	✓	✓
○ clonal structures	✓	✓
○ germinability of seeds	✓	✓
Demographic constitution		
○ distribution of age classes	✓	✓
○ abundance of regeneration	✓	✓

Populus nigra

Stand composition of the German population (mixed stand with poplar-proportion of < 10%) has led to a lower total number and to a nearly complete sampling of available *P. nigra* trees and resulted in a relatively small mean number of pollen donors and effective population size.

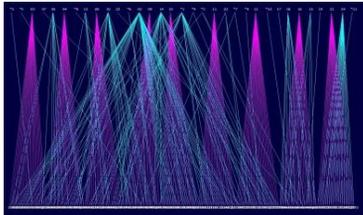


Fig.1 Result of parentage analysis for *Populus* site DE_PO_10: Pink lines connect mother trees (top) and their offspring (bottom), blue lines connect fathers (top) and their offspring (bottom)

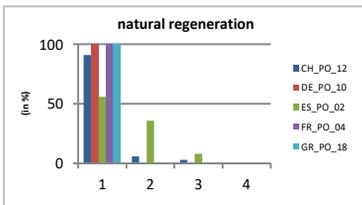
Tab. 1: Verifiers for evaluating the mating system in the five *Populus* populations based on parentage analysis of nSSR-data

Verifiers	ES_PO_02	FR_PO_04	CH_PO_12	DE_PO_10	GR_PO_18
N_e (sibship)	30	30	28	20	3
mean no. of pollen donors / family with 20 seeds	12.0	11.1	10.4	5.6	2.7
clonal structure in adults	no	no	no	no	yes
species / hybridization	no	no	no	no	yes

Populus nigra

Hardly or no natural regeneration could be found in all five poplar populations.

- 1: absence
- 2: few, scattered individuals
- 3: scattered groups
- 4: abundant



Fagus sylvatica

Comparing the two different generations offspring (seeds) and adults no hints of a significantly reduced genetic diversity are visible in the analyzed beech populations.

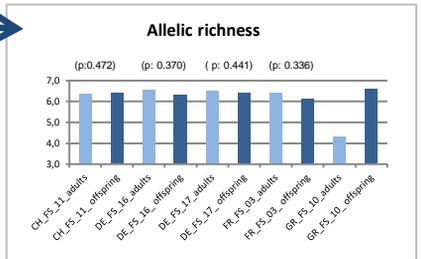


Fig.2 Allelic richness for adults (light blue) and offspring (dark blue) of five analyzed beech populations (using nSSRs); probability values (p) for the pairwise t-test between adults and offspring are given in brackets

Fagus sylvatica

There are no signs of species hybridization with *F. orientalis* in the four studied beech populations

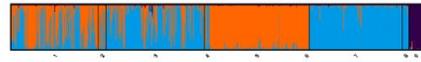


Fig. 3: STRUCTURE analysis of *Fagus* populations (K=3, 20 repeated STRUCTURE runs, computed with CLUMPAK). The *Fagus orientalis* reference (purple) is clearly separated from the analyzed populations. 1=CH_FS_11 offspring, 2=CH_FS_11 adults, 3=DE_FS_17 offspring, 4=DE_FS_17 adults, 5=FR_FS_03 offspring, 6=FR_FS_03 adults, 7=DE_FS_16 offspring, 8=DE_FS_16 adults, 9= *Fagus orientalis* reference

Take-home message

- ✓ Genetic monitoring sites for conservation units across Europe could be established for beech and poplar across Europe within the Gentree-project.
- ✓ Using the selected verifiers, populations can be evaluated and compared to each other for a genetic monitoring focusing on conservation purposes.
- ✓ Sampling: 25 adults trees per site is the lowest limit of samples and is not sufficient for meaningful dispersal studies. A minimum of 50 individuals is recommended by Horban *et al.* 2014 for evaluating genetic variation.
- ✓ A species and hybridization check is essential for evaluating conservation units, especially in species with high hybridization risk (e.g. poplar) or in areas of natural hybridization events (e.g. beech in the Balkan region).

References

- ARAVANOPOULOS, F. *et al.* (2015). Genetic monitoring methods for genetic conservation units of forest trees in Europe. *Biodiversity International*.
- HOBAN, S., SCHLARBAUM, S. (2014). Optimal sampling of seeds from plant populations for ex-situ conservation of genetic biodiversity, considering realistic population structure. *Biol. Conserv.* 177, 90–99.
- KONNERT, M., MAURER, W., DEGEN, B., & KÄTZEL, R. (2011). Genetic monitoring in forests-early warning and controlling system for ecosystemic changes. *iForest-Biogeosciences and Forestry*, 4(2), 77

Acknowledgements

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