GenMon - Implementation of a Genetic Monitoring System in European Beech (*Fagus sylvatica* L.) and Norway Spruce (*Picea abies* [L.] Karst.) Populations in Germany

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Abstract

The reduction of the loss of genetic diversity and the protection of the sustainability of forest ecosystems and all their habitats and services are objectives of high priority for forest management. Furthermore, long-term adaptability of forest stands to a changing environment must be ensured through adapted forest management. A population's adaptability is determined by genetic variation. However, established environmental monitoring systems consider biodiversity only on the species level to evaluate state and development of a forest stand. Aspects regarding the genetic system on a fundamental level have not been integrated so far, although the genetic system creates the basis of reactivity and adaptability of forest tree populations to cope with changing environmental influences. In Germany, a concept for a genetic monitoring scheme in forest tree species was elaborated, which aspires to delineate the genetic system in its entirety on the groundwork of criteria, indicators and verifiers. The implementation of the concept to the structures of German state forest institutions is the main objective of the ongoing project GenMon, which establishes a net of monitoring plots for European beech (*Fagus sylvatica*) and Norway spruce (*Picea abies*) to survey the intactness of the genetic system in observed populations.

Introduction

It is a task of today's and future generations to reduce the ongoing loss of biodiversity at global, national and local levels (GRAUDAL et al. 2014, MONASTERSKY 2014). Furthermore, the adaptability of forest ecosystems to changing environment must be ensured. The adaptability of trees to environmental factors such as climate change or outbreaks of pests and diseases depends fundamentally on their genetic variation. Therefore, the conservation and monitoring of biodiversity on all levels (species, population and genetic, CBD 1992) is essentially (GREGORIUS and DEGEN 2007). In order to allow a proper prediction of the adaptability of trees and to stop the erosion of genetic diversity, the existing monitoring has to be supplemented with a monitoring system on population level (KONNERT et al. 2011, TRÖBER et al. 2011, FUSSI et al. 2016).

Genetic variation with its inherent amplitude of allelic and genotypic structures determines adaptability and capability of forest ecosystems. It forms the fundamental basis for a sustainable development of forests and its biological diversity (GREGORIUS and DEGEN 2007). Currently, the increasing temperatures resulting from climate change may cause a directional selection within populations and result in altering genotype frequencies as evolutionary reaction (JUMP et al. 2006). It implicates a movement of efforts on national and international levels to conserve genetic diversity in situ and ex situ. In this context numerous efforts, organizations and collaborating activities like IUFRO, EUFORGEN and the CBD-process should be mentioned.

Via various pilot studies there are certain attempts in Germany. The “Concept for Conservation of Forest Genetic Resources” was published 1987 and altered in 2000 and 2010. The current version of PAUL et al. (2010) describes the necessity of an implementation of genetic monitoring in forest ecosystems. As mentioned before, genetic aspects are still lacking in environmental monitoring programs that have been established in the last 20 years. With well-considered criteria and indicators, information from genetic monitoring can serve as an early warning and controlling system, because changes in the stand structures, vitality and natural regeneration can be observed earlier than in the natural stand (KONNERT and HOSIUS 2010). From this point of view the implementation of a genetic monitoring system is overdue.

The genetic system of populations comprises all mechanisms and processes resulting in the generation, modification and maintenance of genetic variation as well as in its transfer to the following generations. The German “Concept for Genetic Monitoring in Forests” as published by the BLAG-GROUP OF EXPERTS "GENETISCHES MONITORING" (2004) is based on indicators proposed by (NAMKOONG et al. 1996) for population genetic processes concerning the following points:

- level of genetic variation,
- directional change in gene or genotypic frequencies,
- changes in mating system processes and
- gene migration between populations.

Gene frequencies and different genetic parameters based on gene frequencies, like genetic diversity, number of polymorphic loci, mean number of alleles per locus can be applied efficiently as measures for assessing the level of genetic variation. The outcrossing rate, the number of effective pollen donors, but also the quality of seed reflected by the proportion of empty seed or by germination capacity supply valuable information about the mating system. Gene migration is verified by pollen and seed dispersal distance as well as by presence or absence of family structures within a tree population.

The determination of indicators by repeated research at different times can reveal the dynamics and conditions of the processes of the genetic system (GREGORIUS and DEGEN 2007). To evaluate different methodical aspects, pilot studies have been performed for two tree species with a different mating behavior – wild cherry (*Prunus avium* L., DEGEN et al. 2008) and European beech (*Fagus sylvatica* L., MAURER et al. 2008) – resulting in a precise conception for the implementation of a genetic monitoring for forest tree species (BLAG-GROUP OF EXPERTS "GENETISCHES MONITORING" 2008).

Implementation of a genetic monitoring system

Participating institutions and choice of trees

Within the framework of the project GENMON, there are several institutions cooperating (Table 1). Presently, a net of monitoring plots for *Fagus sylvatica* L. and *Picea abies* (L.) Karst. has been established throughout Germany to evaluate the intactness of the genetic system. Both species represent about 40 % of the forest-covered area in Germany (European beech: 15.4 %, Norway spruce: 25.4 %; THÜNEN-INSTITUT 2012). They are very important tree species from the ecological and economical point of view respectively. Facing climate change, Norway spruce is considered to be potentially endangered in some regions. This expectation is caused by the fact that only a small proportion of the current distribution is formed by autochthonous, naturally regenerated populations. Spruce proveniences have been translocated over long distances and planted within and beyond the native distribution area very often on non-suitable sites, resulting in disturbed adaptation patterns. On the other hand, European beech is native all over Germany and promises to be a stable part of forest ecosystems during climate change. Both species serve as models for the implementation of a genetic monitoring in forest tree populations in Germany and presumably form a template for the introduction of suitable programmes for other forest tree species. First results will be available in summer 2019.

Table 1: Collaborating Institutions and their tasks (S: Sampling procedure, G: Genetic analyses, Q: Testing Germination Capacity of seeds, A: Analysis and evaluation of collected data)

Institution	Tasks
Bayerisches Amt für forstliche Saat- und Pflanzenzucht (ASP)	Coordination, S, G, Q
Forstliche Versuchs- und Forschungsanstalt Freiburg (FVA)	S
Landeskompetenzzentrum Forst Eberswalde	S
Landesforst Mecklenburg-Vorpommern	S
Nordwestdeutsche Forstliche Versuchsanstalt Göttingen (NW-FVA)	S, G
Forschungsanstalt für Waldökologie und Forstwirtschaft Trippstadt	S
Staatsbetrieb Sachsenforst (SBS), Kompetenzzentrum Wald und Forstwirtschaft	S, G
Thüringen Forst, Forstliches Forschungs- und Kompetenzzentrum Gotha (FFK)	S
ISOGEN am Institut für Forstgenetik der Universität Göttingen	S, G, Q
Thünen-Institut für Forstgenetik	A

Monitoring plots and sampling procedure

The establishment of the plots and the sampling procedure have already been used and characterized in pilot studies (KONNERT et al. 2011, TRÖBER et al. 2011). To ensure comparability of data, the installation of plots, sampling procedure and genetic analyses have to be similar for each investigated stand.

For European beech 14 and for Norway spruce 10 monitoring plots have been established throughout Germany (Figure 1). Every plot covers a total area of 4 hectares, with a fenced core section with 50x50 meters placed in the middle, surrounded by the intensive section, both together covering 100x100 meters (Figure 2). Within core and intensive section, each adult tree has to be sampled.

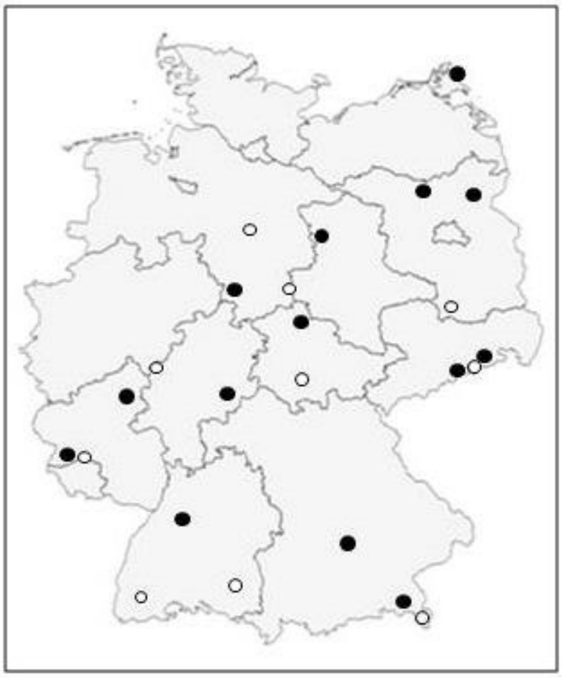

Figure 1: Location of monitoring plots (black dots: European beech, white dots: Norway spruce)

In case the number of trees in the intensive zone is insufficient, the extensive section serves to provide additional individuals up to 250 trees. Furthermore, 20 dominant trees in the intensive section (including core section) have to be chosen as seed trees. They are observed intensively to evaluate flowering phenology, leaf flushing, degree of fructification and vitality. Furthermore, at least 20 seeds per seed tree are harvested directly from the crown. Natural regeneration is characterized by sampling of 200 young plants distributed throughout the monitoring plot and of 4 clusters with 50 individuals each. The clusters enable conclusions about family structures as well as seed and pollen dispersal while the regular distributed samples provide information about the genetic diversity throughout the plot. All samples (at least 1050 per monitoring plot) are utilized for genetic analyses. A seed sample is collected from the entire plot area of 4 ha to investigate seed quality parameters. The sampling procedure is summarized in Table 2.

Table 2: Survey on the sampling procedure

Development state	**Intensive section including core section**	**Extensive section**
Genetic studies		
Adult trees	All individuals present	Additional individuals up to 250
Natural regeneration	200 young plants representative for overall plot	
	4 clusters of natural regenerations comprising 50 individuals each	
Seeds	Single tree collections of seeds from 20 adult trees	
Qualitiy structure of seeds		
Seeds	Seed mixture from entire stand area	

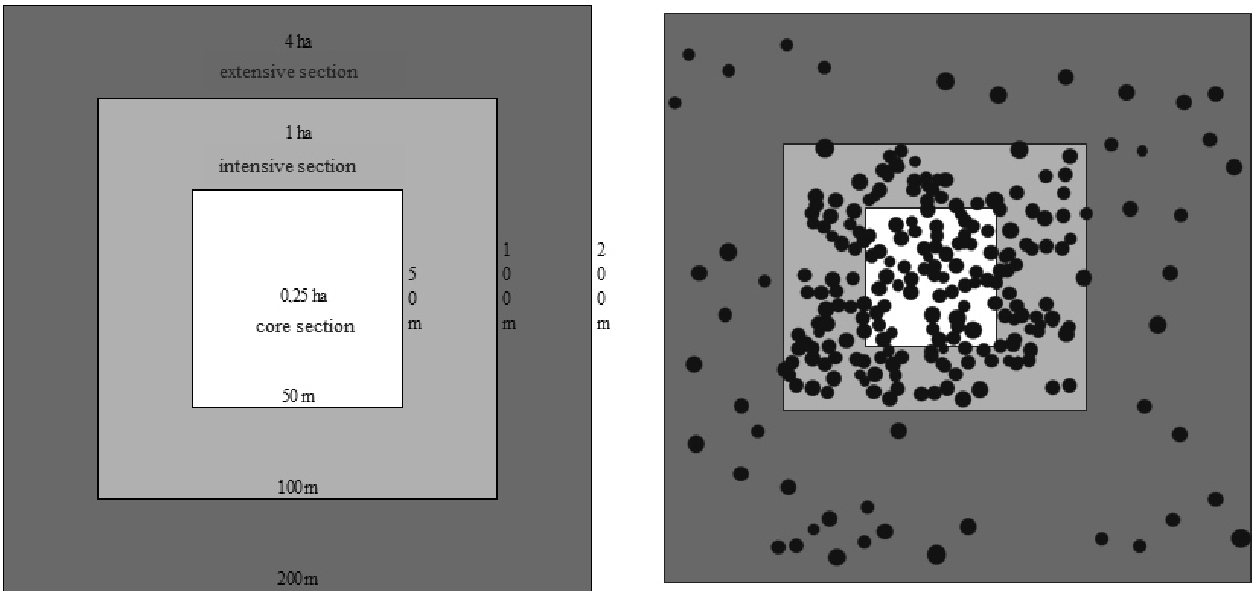

Figure 2: Schematic design of monitoring plot with core, intensive and extensive section (left) and distribution of investigated adult trees in the monitoring plot Weicholdswald (Saxony, European Beech)

Outlook

The collected data will be secured in a database. They will provide information about the intactness of the genetic system in the investigated populations and will enable estimations about the state of genetic diversity in European beech and Norway spruce for large parts of German forests. Beside information about genetic structures in a certain monitoring plot, it will be possible to prove whether there are genetic differences between different plots or between different development stages in the same plot. With appropriate software, i.e. GDA-NT (DEGEN 2008), GSED (GILLET 2008) or SGS (DEGEN et al. 2001) spatial structures and family structures will be visible and allow a deductive reasoning about pollen and seed distribution. In connection with phenotypic characteristics it may be possible to connect certain molecular markers with phenotypic attributes.

The implementation of genetic monitoring presented has also the character of a role model, pioneering application of equivalent methods for other tree species or initiating an international network of monitoring plots. It will hopefully be regarded as useful tool in the section of environmental monitoring and considered in certain programs.

For the moment, the results will represent a “snapshot” of the current condition of the investigated populations. To display the dynamics of the genetic system and its processes over time it is necessary to repeat certain investigations periodically. The “Guidance of implementation of a genetic monitoring for standforming tree species” BLAG-GROUP OF EXPERTS "GENETISCHES MONITORING" 2008) schedules seed sampling every 4 years (if fructification is sufficient) and actualizing the list of adult trees and new sampling of natural generation every 10 years. The re-estimation/re-examination of the selected indicators and verifiers allows a review of the suitability of genetic monitoring as an early warning system for ecosystem changes. It will presumably reveal reactions of the genetic system to influences of a changing environment and enlighten our understanding about mechanisms of evolutionary reactions of tree populations.

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