

Concept on the Genetic Monitoring for Forest Tree Species in the Federal Republic of Germany ¹

elaborated by the Expert-group "*Genetic Monitoring*" ² German Federal-State-Working Group "*Forest Genetic Resources and Forest Seed Law*"

Preliminary remarks

In the framework of the international efforts for safe-guarding biological diversity worldwide, the preservation of genetic multiplicity (*resp.* genetic diversity) of forest tree populations by protecting the genetic systems is of crucial importance. Genetic diversity determines adaptability and efficiency of forest trees; it is the base for the sustainable development of forests. Consequently genetic diversity is an essential prerequisite for multi-functional forestry including the source of the renewable raw material wood.

Both on the national and international level, conserving the woodlands and securing the forest functions in natural and managed forests in a sustainable way are the objectives of several monitoring programmes in forest ecosystems. At present however, the genetic level as the essential base of genetic diversity is regarded rather insufficiently within the scope of such programmes. A genetic monitoring is an essential base for securing and controlling the sustainable management of forest stands by maintaining genetic diversity.

Results obtained from punctual and short-term case studies make obvious that natural and anthropogenic influences can change populational-genetic processes. In order to be able to follow these changes in the genetic systems, it is necessary to record these states repeatedly as well as to document any progress by time series. Thus, it is urgently required to have integrated genetic aspects as a focal point into the forest monitoring.

The "*Concept for the Conservation and the Sustainable Utilization of Forest Genetic Resources in the Federal Republic of Germany*" as revised in the year 2000 and authenticated by the Forest Chief Conference (PAUL *et al.* 2000) postulates the development of fundamentals for a genetic monitoring in the forest. This action is regarded as an essential step for implementing the Convention on Biological Diversity which claims in its paragraph 7b for the surveillance of the distinct constituents of biological diversity (ANONYMOUS 1993).

Objectives

Genetic monitoring aims at the registration of the status and the development of genetic systems by means of criteria, indicators, and verifiers. It contributes essentially to the estimation and valuation of the influence of factors which affect the genetic system of forests. By means of criteria and indicators, it is possible to formulate examples, plan measures and control the success. Discerning changes in the genetic system which become only visible in succeeding forest generations on superior monitoring levels (*e.g.* stand structure, vitality, and natural regeneration), genetic monitoring provides a decisive contribution as an early warning and controlling system for changes in the ecosystem.

The results of the genetic monitoring subserve forest practice, nature protection, consultation of politics, science as well as the exchange of information with other monitoring systems. This monitoring complies with the demands of the Convention on Biological Diversity [CBD; Earth Summit, Rio Declaration 1992] (ANONYMOUS 1993).

Realization

Genetic monitoring includes the periodical, randomized or plot-specific inspection of genetic structures and characteristics of the genetic system (*e.g.* population size, flowering, and sexual system).

Criteria of populational-genetic processes should be gathered in view of defined indicators by verifiers (*cf.* Appendix 1).

Genetic monitoring must involve both managed as well as unmanaged forests. The choice of the tree species is carried out according to their importance concerning usability, existence, and indicator capacity. It is recommended to work first on such tree species for which genetic markers are available for routine serial tests.

For reasons of comparability, genetic monitoring should be performed according to tree species-specific uniform methods, particularly regarding sampling strategy, inventory procedures, analyzing techniques, documentation, and data evaluation (*cf.* Appendix 2). The data are to be recorded in such a way that will be useful in simulation processes.

The scientific-technical conditions for implementing such a genetic monitoring are preexisting in the German Federal and State forest research institutions. The Federal-State-Working Group "*Forest Genetic Resources and Forest Seed Law*" based on the "*Concept for the Conservation and Sustainable Utilization of Forest Genetic Resources in the Federal Republic of Germany*" as published in 2000 (*cf.* PAUL *et al.* 2000) is responsible for the coordination of the genetic monitoring programme.

Implementation

For realizing the genetic monitoring concept, it may be drawn on

- existing plots (*e.g.* permanent observation plots, nature forests, experimental plots *etc.*),
- environmental and forest data,
- existing marker systems,
- studies already performed on the sample strategy,
- database systems,
- evaluation algorithms, and
- computer simulation models.

Reporting

The actual state of the genetic monitoring is documented in the periodical reports of the Federal-State-Working Group "*Forest Genetic Resources and Forest Seed Law*" and the forest environmental control of the German Federal Ministry of Food, Agriculture and Consumer Protection [BMELV, formerly BMVEL].

Application of the results

The results of the genetic monitoring supply information on the current state of the genetic system of the forest tree species under surveillance. Moreover, they are useful for

- estimating genetic implications of silvicultural measures;
- developing practical strategies for the conservation of forest genetic resources;

- integrating genetic aspects in the strategic utilization of different monitoring programmes, as well as
- optimizing the genetic management in view of the sustainable utilization of forest ecosystems.

¹Original German version "*Konzept zum genetischen Monitoring für Waldbaumarten in der Bundesrepublik Deutschland*" translated into English and revised in February 2006 by WERNER D. MAURER;

² Members of the Expert-group "*Genetic Monitoring*", cf. below

References

ANONYMOUS (1993): Gesetz zum Übereinkommen über die biologische Vielfalt. Bundesgesetzblatt BGBI II, S. 1741 und Übereinkommen über die biologische Vielfalt. BGBI. II, S. 1742-1772.

PAUL, M.; HINRICHS, T.; JANSSEN, A.; SCHMITT, H.P.; SOPPA, B.; STEPHAN, B.R. & DÖRFLINGER, H. (2000): Concept for the Conservation and Sustainable Utilization of Forest Genetic Resource in the Federal Republic of Germany (in collaboration with W. ARENHÖVEL, A. FRANKE, R. KÄTZEL, J. KLEINSCHMIT, H.-J MUHS, E. NATZKE, W. RUETZ, W. SCHILLING & U. TABEL). Sächsische Landesanstalt für Forsten [LAF] Pirna-Graupa, Hrsg., ISBN 3-932967-25-9, 66 pages.

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Appendix 1 – Criteria, indicators and verifiers for genetic monitoring in forests

The prime objective of managing forest ecosystems is to preserve these biospheres and safeguard their functions in a sustainable manner. This aim is supported by conserving genetic diversity and protecting the genetic systems of the species present. The genetic system is to be understood by those mechanisms which serve the generation, maintenance, and modification of genetic variation as well as passing the genetic variation on to the next generation. Forest ecosystems are to be managed in such a way that genetic diversity is maintained by securing the genetic system of the species.

Genetic monitoring seizes the conditions of the genetic systems by means of criteria, indicators, and verifiers. It aims at pursuing developments, estimating influential factors, formulating examples, planning measures, as well as allowing control of success.

The intactness of the genetic system and the availability of genetic variation are a prerequisite for sustainability. Therefore it is important to specify criteria, indicators, and verifiers for the intactness of the genetic system:

- criteria are essential characteristics of the system,
- indicators signify their status regarding intactness, and
- verifiers serve the examination of the assessment made for the genetic system.

The intactness *resp.* functionality of the genetic system of a species is characterized by the populational-genetic processes drift, selection, mating system, and migration. Thus, maintaining these processes represents each the criterion for the conservation of genetic variation. NAMKOONG *et al.* (1996) suggested as indicators for populational-genetic processes (*cf. Table 1.1 Indicators of uninfluenced genetic processes*):

- level of genetic variation,
- change in genic and genotypic frequencies,
- changes in the mating system, and
- changes in gene migration.

In Tab. 1.1 the symbol (-) denotes where **no** influence of the relevant genetic process is indicated.

Table 1.1 Indicators of uninfluenced genetic processes

<i>Processes</i>	<i>Indicators</i>			
	Level of genetic variation	No directional changes in the genic <i>resp.</i> genotypic frequencies	No changes in the mating system	No changes in gene migration
genetic drift	-			
direct selection	-	-		

indirect selection	-	-		
mating system			-	
gene flow			-	-

By means of the given indicators, genetic monitoring aims to the assessment of the conditions, and by repeating this procedure, on the dynamics of the processes of the genetic system. For this, the common populational-genetic data and the parameters deduced hereof are estimated. These represent the verifiers of the given indicators. Table 1.2 *Keywords for the indicators of the verifiers of genetic processes* summarizes keywords characterizing the verifiers for the respective indicators as suggested by NAMKOONG *et al.* (1996).

Table 1.2 Keywords for the verifiers of the indicators of genetic processes

<i>Indicators</i>	<i>Verifiers</i>				
	1	2	3	4	5
Level of genetic variation	genetic diversity; percentage of polymorphic loci	effective numbers of alleles	genetic variation of traits important for adaptation	fixation index	number of potential parent trees
Directional change in genic resp. genotypic frequencies	differences in the genotype frequencies of different cohorts	differences in the phenotype frequencies of different cohorts	differences in the age-class distribution	--	--
Mating system	selfing	sexual system	abundance of pollinators	pool of potential parents	proportion of empty seeds and germinability
Migration	extent of genetic differentiation between populations	pollen dispersal	seed dispersal	isolation by barriers	spatial aggregation of different mating types

It will be necessary for the definite implementation of the monitoring concept to operationalize the given verifiers. For this purpose, linking to monitoring concepts of different organizational levels of ecosystems should be aimed at.

Reference

NAMKOONG, G., BOYLE, T., GREGORIUS, H.-R., JOLY, H., SAVOLAINEN, O., WICKNESWARI, R.

& YOUNG A. (1996): Testing criteria and indicators for assessing the sustainability of forest management: Genetic criteria and indicators. Center for International Forestry Research (CIFOR) Working Paper No. 10, Bogor, Indonesia, 12 pages. *Trippstadt, 30. October 2004; revised 18. February 2006 sgd. Dr. Werner Maurer, Coordinator*

Appendix 2 – Methodical approaches

2.1 Selection of suitable tree species

The tree species to be analyzed are to be valued in view of their suitability for the genetic monitoring according to their importance concerning usability, existence, and indicator capacity. Based on the twenty forestry species for which genetic studies had been carried out successfully in the German Federal and State forestry research institutions so far, nine criteria for valuating their suitability are compiled in the following.

2.1.1 Criteria including valuation scale:

1. Status of endangering: 1 = no, 2 = medial, 3 = high
2. Rarity: 1 = no, 2 = medial, 3 = high

3. Economic significance: 1 = low, 2 = medial, 3 = high
4. Manner of pollination: W = wind, I = insects
5. Range of seed dispersal: F = far, M = medial, N = near
6. Availability of primary data from different monitoring programmes *resp.* from nature forest research: 1 = no, 2 = medial, 3 = high
7. Availability of methods for identifying genetic markers: 1 = no, 2 = limited, 3 = unproblematic
8. Plot representativity of the tree species in Germany: 1 = low, 2 = medial, 3 = high
9. Share relevance for the stand: P = principal tree species, M = mixed tree species

The mean value calculated on this base gives the ranking list based on the priorities (1 = high, 2 = medial, and 3 = low) as presented in Table 2.1 *Selection of suitable species resp. genera of forest trees*. A distinct valuation for deciduous tree species, coniferous tree species, insectpollinated tree species and relict tree species is defined.

2.1.2 Results of the evaluation procedure and recommendation for considering the following tree species

Immediate focus is put on

- | | |
|------------------------------------|--------------------------------------|
| two deciduous tree species | : European beech, oak |
| two coniferous tree species | : European silver fir, Norway spruce |
| two insect-pollinated tree species | : Small-leaved linden, wild cherry |
| two relict tree species | : Black poplar, elm |

Table 2.1 Selection of suitable species resp. genera of forest trees

	Status of endangering	Rarity	Economic significance	Pollination	Seed dispersal	Availability of primary data	Markers	Representativity of plots	Share relevance for the stand	Priority
Sycamore maple (<i>Acer pseudoplatanus</i>)	1	2	2-3*	W	F	1	3	2	M	3
European beech (<i>Fagus sylvatica</i>)	1	1	3	W	F/N	3	3	3	P	1
Oak (<i>Quercus spec.</i>)	1	1	3	W	F/N	3	3	3	P	1
Wild cherry (<i>Prunus avium</i>)	2	2	2	I	F/N	1	2	1	M	3
Small-leaved linden (<i>Tilia cordata</i>)	2	2	2	I	M	1	2	1	M	3
Wild apple (<i>Malus sylvestris</i>)	3	3	1	I	N	1	2	1	M	3
Wild pear (<i>Pyrus pyraster</i>)	3	3	1	I	N	1	2	1	M	3
Black poplar (<i>Populus nigra</i>)	3	3	1	W	F	1	3	1	M/P	2
Elm (<i>Ulmus spec.</i>)	3	3	1	W	M	1	2	1	M	3
European ash (<i>Fraxinus excelsior</i>)	1	1	2	W	M	1	3	1-2	M	3
Birch (<i>Betula spec.</i>)	1	1	2	W	F	1	1	2	M	3
Black alder (<i>Alnus glutinosa</i>)	3	1	2	W	M	2	2	2	P/M	2
Wild service tree (<i>Sorbus torminalis</i>)	3	3	2	I	N	1	2	1	M	2
Service tree (<i>Sorbus domestica</i>)	3	3	2*	I	N	1	2	1	M	2
European silver fir (<i>Abies alba</i>)	1	2	3	W	M	3	3	2	P	1
Norway spruce (<i>Picea abies</i>)	1	1	3	W	M	3	3	3	P	1
Scots pine (<i>Pinus sylvestris</i>)	1	1	3	W	M	3	3	3	P	1
European larch (<i>Larix decidua</i>)	1	2	3	W	M	3	2	2	P	2
Douglas-fir (<i>Pseudotsuga menziesii</i>)	1	1	3	W	M	2	3	2	P	2
Yew (<i>Taxus baccata</i>)	3	3	1	W	F/N	1	2	1	M	3

*regionally specific

grey shaded: recommended tree species

2.2 Selecting and establishing monitoring plots

A tree species-related number of populations sufficing statistical criteria are selected within the Federal Republic of Germany from both managed and unmanaged forest ecosystems that belong to the different basic ecological units. Within these populations genetic monitoring plots are established including tree species-specific numbers of individuals / minimum sizes (the number of individuals of the mature stand determines the size of the plot).

The plots must be in a reproducible age, and they should include natural regeneration at least in part.

When selecting monitoring plots, those plots should be given top priority for which a high data density and precise plot documentation is already available, like e.g. genetic experimental plots, nature forest reserves, and yield and growth permanent observation plots. The following plot parameters, collective parameters, and tree parameters have to be documented for the selected genetic monitoring plots:

2.2.1 Plot parameters:

- monitoring tree species
- basic ecological unit
- natural forest community
- brief description for plots, e.g. managed forest, nature forest, permanent observation plots
- for managed forest: planning targets?
- for nature forest: since what time taken out of management?
- coordinates of the plot (Gauss-Krüger-coordinates of the plot center)
- forest location (e.g. forest district, forest division, forest compartment, and sub-compartment)
- plot size
- sea-level
- ownership

2.2.2 Collective parameters

- Atype (e.g. mature stand, nature regeneration, seeds)
- year of surveying
- stand age
- Baumzahl
- number of trees
- horizontal structure
- horizontal structure
- isolation and fragmentation
- treatment variant
- stand history
- e.g. planting natural regeneration, origin of reproductive material

2.2.3 Tree parameters

- tree identification label
- tree coordinates (x/y)
- diameter in breast height (DBH) > 7 cm
- tree height
- social ranking position
- on selected plots:
 - crown length and diameter
 - quality traits (forking, top straightness, epicormic shoots)

Environmental data, if available from the surroundings of the plot (e.g. weather, atmospheric load, pollutant immission, soil vegetation) should be documented.

2.3 Inventory of parameters of the genetic system

For the characterization of the genetic system, phenotypic and genetic traits are to be considered as given in Table 2.2 *Parameters listed for indicators and verifiers*. An overview of the valuation of these parameters is summarized in Table 2.3 *Valuation of the parameters according to priority and costs*.

2.3.1 Data ascertainment for phenotypical traits

Inventories concerning flowering and fructification are to be performed in regular intervals on selected trees of the genetic monitoring plots. For seeds quality traits like the proportion of empty seeds and germinability are to be estimated.

2.3.2 Data ascertainment for genetic traits

On the monitoring plots the genotypes of the selected potentially reproducible individual trees are to be identified for distinct gene loci by means of gene markers. Depending on the age structure of natural regeneration, a genetic inventory has to be carried out by sampling. In some sections of the stands the seed generation of different seed years is additionally analyzed in a sample.

The choice of the markers used is specified according to the tree species under study. For isozyme gene markers this selection may be supported by the *ad-hoc*-Expert-group "*Biochemical-genetic Analysis*". Regulations regarding the application of DNA markers will be met at a later time. For DNA markers the use of identical marker systems is also urgently required.

Protocols for recording data for the verifiers according to Table 1.2 *Keywords for the indicators of the verifiers of genetic processes* in Appendix 1 have still to be set up.

Table 2.2 Parameters listed for indicators and verifiers

Indicator	Verificator	Short-cut	Parameter
Level of genetic variation	genetic diversity percentage of polymorphic loci	A1	isozymes and/or DNA-markers for a defined number of gene loci for each tree
	effective number of alleles	A2	<i>cf.</i> A1
	genetic variation of traits important for adaptation	A3	phenological parameters (begin and termination of flushing) frost hardiness (variation in the phenolic metabolism) intensity of the attack of biotic pests Crown shape
	fixation indices	A4	<i>cf.</i> A1
	number of potential parent trees	A5	tree height depending on the stand structure tree distances (coordinates) flowering intensity stand age structural isolation
Directional changes in the genic and genotypic frequencies	differences of the genotypic frequencies of different cohorts	B1	<i>cf.</i> A1, age of the tree
	differences of the phenotypic frequencies of different cohorts	B2	shape of growth, <i>cf.</i> A3
	differences in the age class distribution	B3	<i>cf.</i> A1, frequencies according to the age class distribution
Changes in the mating system	selfing rate	C1	<i>cf.</i> A1
	sexual system	C2	male and female flowering intensities pollen proliferation / pollen traps incompatibility
	abundance of the pollinators	C3	data concerning the frequency of insects
	pool of potential parents	C4	<i>cf.</i> A5
	proportion of empty seeds and germinability	C5	germinability proportion of empty seeds 1000-grain weight
Changes in the migration of the genes	extent of the genetic differentiation between populations	D1	<i>cf.</i> A1, relevant also for natural regeneration (input and output)
	pollen dispersal	D2	models not to be included in the genetic monitoring when the main wind direction is known genetic markers of pollen and seed parents
	seed dispersal	D3	genetic markers of pollen and seed parents
	isolation by barriers	D4	<i>cf.</i> stand description in chapter 2.2
	spatial aggregation of different mating types	D5	<i>cf.</i> A1; tree coordinates (<i>cf.</i> stand description in chapter 2.2)

Table 2.3 Valuation of the parameters according to priority and costs

No.	Parameter	Priority	Costs per year
1	Isozymes for a defined number of gene loci for each tree	1	2
2	Phenological parameters (begin and termination of flushing)	1	1

3	Vitality (Forest Health Inventory)	1	1
4	Intensity of the attack of biotic pests	2	3
5	Crown shape (depending on the tree species)	2	1
6	Tree height depending on the stand structure*	2	2
7	Social position of the individual tree	1	1
8	Tree distances (coordinates)	1	3
9	Flowering intensity	1	2
10	Stand age/tree age	1	0
11	Structural isolation of the individual tree	1	1
12	Shape of growth	1	1
13	Male and female flowering intensity	2	3
14	Pollen production/pollen traps	3	3
15	Incompatibility	3	3
16	Data concerning the frequencies of insects (depending on the tree species)	2	?
17	Germinability	1	2
18	Proportion of empty seeds	1	2
19	1000-grain weight	1	2
20	Isozymes in natural regeneration (input and output)	1	2-3
21	Molecular markers	1	3

* basic data

2.4 Data Management

A defined uniform data system is urgently required for the documentation, administration, and tending of the data (*e.g.* GENDIS).

2.5 Evaluation and modelling

The analysis and evaluation of the genetic data is carried out by applying such tested and proved evaluating routine programs like *e.g.* GSED, PopGene, and MacGen. The populational-genetic computer simulation program ECO-GENE is available for modelling. When performing populational-genetic modelling, linking to existing silvicultural models and practical management concepts is to be striven for.