# National Forest Inventories: how can they contribute to forest genetic conservation?

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### Introduction

The history of humankind is one of the modification of forested environment, which by the degradation and fragmentation of forest ecosystems, their alteration through the harvesting of forest products, use of fire, or more general environmental alteration and by the introduction of pests, pathogens, or exotic species resulted in the erosion of biodiversity. Since we do not know the long-term, broad scale cumulative effects of past and current forestry practices, we cannot expect to achieve the long-term goal of an ecological sustainability without monitoring and modification of our forest management through time. Hence, we should treat forestry as adaptive management which must be accompanied with monitoring programmes to accumulate key information. In this context, the monitoring of forest genetic resources is one important component. But meaningful and operational feasible genetic monitoring is far from simple tasks. Because complete genetic inventories are neither possible nor practical, we are forced to use surrogate measures, each of which is adequate in its own right (LINDENMAYER et al. 2000). As biodiversity monitoring is a long-term process it only rarely provides instant results of direct value for political decisions makers. Hence, funding is often lacking. Therefore, we suggests that biodiversity monitoring may be combined with national forest inventories (NFI) or closely related forest resource assessments that are traditionally performed on a regular basis in several European countries (EC 1997).

Genetic monitoring can be defined as a goal-oriented assessment which is repeatedly performed in order to reveal temporal or spatial changes in genetic parameters (Box 1). Here we face the dilemma that in most cases the natural level of genetic variation of forest tree species must remain unknown. In many European regions, the 'natural' gauge against today's genetic variation can be compared with is not (longer) available. Especially for wide-spread tree species which has been impacted primarily by translocation of reproductive forest material this holds true. In certain eastern European countries there may be still virgin or close-to-virgin forests, however, data on genetic diversity cannot be simply used as a baseline for other regions. Forest tree species have

#### Box 1. Inventoring and monitoring – some definitions.

In a strict sense the two terms 'inventorying' and monitoring have to be differentiated. **Inventorying** in relation to the assessment of biodiversity can be defined as 'the surveying, sorting, cataloguing, quantifying and mapping of entities such as genes, individuals, populations, species, habitats, biotopes, ecosystems, landscapes or their components, and the synthesis of the presence/absence, relative abundance, and patterns of variation ...' (STORK & SAMWAYS 1995). While inventories merely provide snapshots of the actual biodiversity status, **monitoring** can be defined as a goal-oriented assessment which is repeatedly performed in order to reveal temporal or spatial changes in particular parameters. For long-term monitoring of biodiversity change, information must be comparable over time and space. Hence it is recommended that the groups that are involved in monitoring activities should coordinate use of standard protocols in study design, sampling procedures, sample and data analysis and reporting methods. Biodiversity monitoring at the genetic or species level usually aims to develop a framework for predicting the development of the genetic or species composition in order to improve management or to serve as an early warning systems.

a natural geographic genetic pattern. Forests close to former ice-age refugia, for instance in the Balkans, generally harbour more genetic diversity at least at neutral or semineutral gene markers than virgin forests in central or northern Europe formerly did (*e.g.*, COMPS *et al.* 2001).

The objective of this paper is to describe briefly how aspects of a genetic diversity assessment may be incorporated into NFI or similar forest assessments. Emphasis is laid upon easy-to-use applications.

## Indicators of genetic erosion

In principle, a successful biodiversity inventory (monitoring) should rely on two basic principles. Firstly, we need to identify the **criterion** which may be defined as 'the principal function and processes that genetic diversity is maintained'. Secondly, we then focus on those components that are most relevant achieving the criterion being either subject to major threats to be mitigated or in focus by the management targets. They are called **indicators**. Important and often completely missing is the establishment of threshold values (critical values) of a certain indicator (**verifier**). However, changes at the genetic level are extremely difficult to assess in practice. Mainly for the forest stand level those indicators tackling genetic drift, selection, gene flow or the reproductive system have been proposed (*e.g.*, BOYLE 2000). However, those genetic criteria and indicators are not always technically or operationally feasible and cannot be easily applied in NFIs. Following list of indicators that could be measured singly or in combinations on individuals and populations of a given species in a defined area as part of a systematic effort to monitor changes at the genetic level for the forest tree species may be helpful (cf. BROWN *et al.* 1997):

- Species distribution and number of sub-specific entities A useful genetic approximation is the assessment of formal taxa such as sub-species, varieties or entities such as ecotypes, chromosome races and landraces. The measurement of intraspecific morphological variation is an easily obtained indicator of genetic diversity. Morphological measurements can be obtained in the field or from field specimens, not requiring laboratory studies. Another advantage is that morphological characters may be ecologically adaptive (SCHAAL *et al.* 1991).
- Natural regeneration Mother Nature selects for reproductive success. That is why the occurrence of natural regeneration as part of forest stand structure is a suitable indicator whether a certain species is well thriving and its reproductive system is functioning.
- Population size, numbers and isolation Small populations are at relatively greater risk of loosing alleles, increased inbreeding and extinction due to stochastic events (see p. 413 ff., this volume). The number and isolation of populations in an area will reflect both the overall genetic diversity in the area and how this is structured.
- Environmental amplitude From provenance research is has been clearly shown that the climate is of major importance shaping the genetics of forest trees (*e.g.*, MATYAS 1996, see p. 275 ff., this volume) while edaphic components are less important (*e.g.*, TEICH & HOLST 1974). The number of distinct habitats or environments in which a given forest tree species is found in a study area (for example based on climatic classifications or ecoregions) indicates adaptive variation.
- Genetic diversity at gene or genetic markers (generally less feasible for NFI, see below)
- Quantitative genetic variation (normally not applicable for NFI, separate specific surveys or field experiments needed)
- Inter-population genetic structure and mating pattern (normally not applicable for NFI, separate specific surveys or field experiments needed)

# What can be realistically done through NFIs

The practical fieldwork to assess genetic resources within the framework of a NFI is confined due to the prime resource assessment (normally timber). Field plots are visited only once during an inventory cycle and field data of different inventory cycles are not always collected at the same time or season. Therefore, field data on phenological variation (*e.g.*, bud burst) cannot be recorded.

## Species distribution

Knowledge of the abundance and distribution pattern of species is of great importance in its attempts to preserve and utilize (autochthonous) plant genetic resources and a NFI

can provide these data. Examples of actual tree species distribution may be found for Switzerland (BRÄNDLI 1996), Austria (SCHADAUER 1994) or many other countries. The actual distribution pattern can then be compared with the natural range of a species and an area outside this range can be identified as introduced. Knowledge where a forest tree species has been artificially introduced is an important piece of information for the management of genetic resources. Non-autochthonous populations can jeopardize autochthonous ones by hybridization and introgression either through purposeful introduction by humans or through habitat modification, bringing formerly reproductively isolated populations into contact (CARNEY *et al.* 2000). Especially species with small local population sizes are threatened such as *Populus nigra* L. by genetic swamping through widespread cultivation of *P.* × *euramericana* Guinier or ornamental clones (CAGELLI & LEFÈVRE 1995).

In determining the natural distribution of a tree species some prerequisites are essential. In an ideal case, the potential natural occurrence (potential natural vegetation, PNV) is at hand for each inventory plot allowing more subtle inferences. The PNV determines the climax vegetation assuming no human influence (TÜXEN 1958). For several European countries such maps are available (e.g., Czech Republic – NEUHÄUSLOVÁ & MORAVEC (1997) (Fig. 1). However, often such maps developed by plant sociologists are not sufficiently fine-grained to be useful for a NFI. Therefore, an assessment on the plot level by the field staff may be needed. An operational derivation of the PNV applicable for field staff, which is usually not specialized in plant sociology premises could be: (1) aggregation of single PNVs to coherent groups of PNVs (e.g., 126 PNVs are pooled to 26 PNV groups used for field assessment in the Austrian NFI), (2) an expert system or some kind of key that allows the derivation of these PNV groups from easily assessable parameters such as growth region, altitude, relief, soil type, geology, and regional climate. The field staff determines the mentioned parameters and uses them as input variables for the expert system, which suggests a PNV type that is checked for plausibility. For the Austrian NFI these techniques have been successfully used for many years.

With this information at hand the comparison between actual and natural forest communities becomes feasible in the field. There are two ways of possible comparison:

(1) Comparison of the two communities by means of the **quantitative** tree species' share; the actual proportions of trees species can be estimated easily, whereas estimation of potential natural proportions is rather sophisticated and not easy to obtain. For instance, the share of European beech (*Fagus sylvatica* L.) in the PNV type *Abieti fagetum* is variable according to special site conditions and developmental phases.

(2) Comparing the actual and potential occurrence of the **qualitative** tree species' share; focusing on the main tree species of a natural forest community this method is operational for NFI. The most relevant case is that a tree species is found at a plot, however, this species is not characteristic for the respective PNV and *vice versa*.

#### Subspecific entities

There are different subspecific entities: subspecies, varieties, races, *etc*. These taxa refer to populations restricted to geographical areas that differs from others in identifiable



**Figure 1**. Map of the potential natural vegetation of the Czech Republic [simplified from NEUHÄUS-LOVÁ & MORAVEC (1997), reproduced with friendly permission of authors and Institute of Botany, Academy of Sciences of the Czech Republic].

characteristics of the same forest tree species, but not to an extent of being classified as a separate species. Generally, emphasis should be laid on those characteristics that are predominantly genetically controlled (see p. 221 ff., this volume).

Since the infancy of forest genetics, certain morphological traits have been attractive to researchers. Thus, cone length, shape of cone scales, crown shape or other morphs have been studied across regions in many forest trees. Unfortunately, we often do not know how (strongly) those traits are genetically controlled. In spite of this limitation, data may be helpful. Morphological differences often used to identify subspecies or other subspecific entities may be applicable for surveys. For the genus *Quercus*, for instance, MAGIC (2002) provided a detailed (sub)species description which may be especially helpful in assessing genetic resources in the Q. petraea-robur complex in the Balkan Peninsula. Early attention of forest geneticists attracted Picea abies (L.) Karst. It has been known for a long time that cone length varies drastically with elevation (KIENITZ 1879). However, we can learn from seed orchards established with high elevation clones planted in low elevation, that cone length is only moderately genetically controlled while shape of the cone scales is not modified by the 'new' environment (Th. Geburek, unpublished data). However, different cone scales have been correctly used to identify varieties (PRIEHÄUSSER 1956, Fig. 2). Furthermore, differences of the indumenta (pubescence) of young spruce shoots vary within European populations (PRIEHÄUSSER



**Figure 2**. Different morphs of cone scales in *Picea abies* (according to PRIEHÄUSSER 1956).

1958, Fig. 3). While shoots of Baltic and northern European populations are more hairy, populations from the Central Alps or Balkan shown less pubescence as evidenced in common garden experiments (LINES 1960). Unfortunately these traits are only applicable for inventories covering major parts of the distribution range since variation within regions [*e.g.*, the Alps (cf. SCHMIDT-VOGT 1972)] is normally missing. In this conifer, different crown shapes (branch habit types) differing with elevation are obvious in their native environment (SCHMIDT 1952) and the



**Figure 3.** Different pubescence of young shoots in *Picea abies* (according to PRIEHÄUSSER 1958).

crown shape is maintained under different environmental condition (Th. Geburek, unpublished data). In Austria for instance, crown shape was surveyed for the first time during the period of 1971-80 and has been recorded again in order to detect differences which may have taken place in the last decades.

In *Larix decidua* Mill. the length of stomata rows on the upper surface of needles on short shoots relative to needle length may be assessed. This ratio increases with altitude and is largely under genetic control. Low-altitude provenances (*e.g.*, from Poland or Sudetes) can be clearly distinguished from the high-altitude populations in the Alps and Tatra Mountains) (MAIER 1992). Also in larch, cone size and shape vary considerably within the native range. More spherical forms are mostly found in the Carpathians (cone length approx. to 2 cm) while in the Alps more longitudinal stretched cones (cone length approx. to 3 cm) are typical (RUBNER & SVOBODA 1944). In areas where one suspects a heavy historic seed and plant transfer, this trait may be also applicable.

Other morphs such as spiral grain in *Fagus sylvatica* L. (TEISSIER DU CROS *et al.* 1980) or *Picea abies* (CAHALAN 2002) may also be also included in NFI.

#### Natural regeneration

Mother Nature selects for reproductive success. That is why the occurrence of natural regeneration is a suitable indicator whether a forest tree species is well thriving and the

reproductive system is functioning. However, the reverse is not necessarily true. First one has to assess whether in a certain forest the natural regeneration is 'necessary' at the time of field inspection and secondly if, where appropriate, the extent of the natural regeneration is to be evaluated with respect to the possibility whether a new stand can be established based on the current seedlings abundance and distribution.

Two key questions should be answered in this context:

(1) What is the current status of the area considered as natural regeneration?

- percentage and distribution pattern of the regenerated area;
- distribution of seedling height classes;
- existence of seed trees and small seedlings 10 cm).
- (2) What is the potential of the young plants?
  - vitality;
  - browsing characteristics and other damages.

There are several intricate problems linked to the inventory of natural regeneration. It is particularly important to determine the minimum number and minimum height of young plants per surface unit to define whether the existing regeneration should or should not be assessed. Identifying such threshold numbers is a difficult task. For the field staff the method must be operationable, but the minimum number of plants having a certain growth necessary for a successful regeneration differs from site to site and from species to species. Depending on the average height, different threshold numbers (minimum number of seedlings in order to identify an area as naturally regenerated) are used in the Austrian NFI , as illustrated in Fig. 4.

The final phase of regeneration has to be defined as well. In many European countries the natural regeneration is affected by heavy game browsing. The final phase may be defined when the seedlings have reached a certain height not longer accessible by game.

For roe deer this height may be set as 130 cm. In many European countries browsing (game and domestic stock) threatens natural regeneration. А feasible procedure could be the combination of two sampling methods: the fixed area plot and the assessments on a subsample therein. Subsampling is appropriate because the number of damaged seedlings on the whole plot can be very high. For instance, in a fixed plot area plot of 300 m<sup>2</sup> a certain number of sample trees (e.g., 5 individuals) are selected according to their height and their spatial distribution taking into account their significance for the further development of the regeneration. This can be done by selecting the highest seedling of each species, as long as they have a certain



**Figure 4.** Threshold seedling numbers for the assessment of regeneration according to tree height, example from the Austrian Forest Inventory for 300 m<sup>2</sup> field plots.

minimum distance to each other. Only on these subsamples browsing damages are assessed. This approach will provide reliable estimates on the further development of the regeneration and is more efficient than an assessment of all seedling of the plot, because the majority of the plants will later die due to growth competition.

## Proportion of natural versus artificial regeneration

Another important aspect which can be tackled by NFIs that include regeneration surveys is the proportion of natural versus artificial regeneration. There is one hurdle that has to be considered when the areas of natural and artificial regeneration are compared. The probability that a certain developmental phase will be detected is proportional to the duration of such a phase. As natural regenerations last normally much longer than artificial ones, detection probabilities differ. Therefore, area-related estimates of natural and artificial regeneration are not meaningful. The following example may further illustrate this. If the phase of a natural regeneration lasts 20 years and only 5 years for an artificial one, respectively, the estimate for the area of the natural regeneration will be fourfold biased assuming an identical proportion of the two regeneration regimes in reality. If the proportion of different time spans required can be estimated like in this example, this ratio can be used for a correction. However, this ratio often varies erratically or is unknown. Another possibility is to consider only those natural regeneration plots beyond that phase which mark the beginning of the artificial one.

## Data collection for specific genes

Field data for specific genes can normally not be recorded through NFI. Of course, within a NFI plant material may be collected that is to be used in genetic surveys such as in Quercus spp. (PETIT et al. 2002) or Picea abies (SPERISSEN et al. 2001). However, morphs that are gene markers in forest trees are very scarce. A trait to be potentially used in conifers, is the colour of immature female cones which is considered to have adaptive significance. In Pinus monticola Douglas ex D. Don (STEINHOFF 1974) and Picea glauca (Moench) Voss (TEICH 1970) immature cone colour is encoded by a single gene, while both in Pseudotsuga menziesii (Mirb.) Franco (COPES 1972) and Cryptomeria japonica D. Don (TSUMURI et al. 1988) this morph is controlled by two or more genes. Adaptive coloration in animals has long received serious consideration (e.g., HAMILTON 1973). In plants, discussion on colour pattern primarily stems from the attraction of pollinators to flowers and to dispersal of seeds (fruits) (e.g., MURRAY et al. 1993). However, different coloration of female cones in conifers suggests a thermoregulatory function. The greenish-coned variant attains lower external temperatures than do reddish ones of comparable size (e.g., Abies concolor (Gord. et Glend.] Lindl. - STURGEON & MITTON 1980). Such a thermoregulatory function is also suggested for Pinus ponderosa Dougl. (SMITH 1980), Larix decidua L. (GEBUREK, unpublished data) and Picea abies (Th. Geburek, unpublished data). In early studies it was presumed that greenish-coned variants in Picea abies are late-flushers, while reddish

-coned variants are early developers (SCHRÖTER 1898). A later more detailed study did not support this view (DENGLER 1955). It must be noted that in *Picea abies* only the immature cone colour is strongly correlated with elevation and not the colour of the fullsized cone (Th. Geburek, unpublished data). Coloration of male inflorescenes in conifers may have been similar adaptive function. However knowledge is much more limited and genetic control still remains presumptive (CARLISE & TEICH 1970).

In the most recent Austrian NFI, female cone colour polymorphisms in *Picea abies* and *Larix decidua* was used and was recorded in 1500 field plots for more than 4,000 sampled trees (Figs. 5 and 6). The field assessments were restricted to spring and early summer because later in the year different cone colours cannot be clearly distinguished.

Generally selective effects due to a global change are extremely difficult to quantify in natural forest stands. At this thermoregulative gene we expect changes in the genetic structure along elevations in the long-term and in future Austrian NFIs this trait will be recorded again.

### Socio-economic and political aspects

Before commencing *in situ* conservation of forest genetic resources a sound plan including the reserve planning and establishment, future management and utilization should be clear for those mandated to carry out the conservation. Besides genetic aspects



**Figure 5.** Colour of female cones is an adaptive trait and differs in many conifers as exemplarily depicted in *Larix decidua*.



**Figure 6.** Proportion of different female cone colour (green, green-reddish, red) in *Larix decidua* along different elevations in the Austrian Alps (*e.g.*, 5 = 450-550 m, 17 = 1,650-1,750 m).

also non-genetical (socioeconomic and political) ones are of high relevance that may be furnished by a NFI. Among others these include the continuity of the ownership, right of utilization of the genetic resource and access right. Generally in public forests action can be more easily taken than in private forests. Moreover, size of the private forest enterprise may further affect the in situ management. Goal conflicts that may arise from different ways of utilization such as area protection or potential forest clearance due to settlement and

traffic routes have to be taken into account. Hence regional forest utilization plans and other land utilization plans are helpful instruments.

#### Forest history and management regime

For the conservation of forest genetic resources both the forest history and the current management regime are important component. For instance, in areas in which historically heavy seed and plant transfer occurred (see p. 437 ff., this volume) are to be excluded from *in situ* means when natural forest genetic resources are to be conserved. Furthermore, forests which were primarily artificially regenerated are less suited than areas in which forests were naturally regenerated.

## **Outlook: Remote sensing**

Many different forms of remote sensing are available. While lately the emphasis on laser scanner and synthetic aperture radar data has increased, most work to date has used photographs and digital optical imagery, primarily from airborne and space borne platforms. Remote sensing provides one of the most efficient tools available for determining landscape-scale elements of forest biodiversity, such as the relative proportion of matrix and patches and their physical arrangement (for review see INNES & KOCH 1998). Remote sensing thus provides a means to make assessments across several different spatial scales, and is also critical for assessments of changes in ecosystem pattern over time. At intermediate scales, remote sensing provides an ideal tool for evaluating the presence of corridors and the nature of edges (forest

fragmentation) (RIITTERS *et al.* 2000). At the stand scale, remote sensing technologies are likely to deliver an increasing amount of information about the structural attributes of forest stands, such as the species composition and nature of the canopy surface the presence of layering within the canopy, the presence of (very) coarse woody debris on the forest floor (*e.g.*, GERYLO *et al.* 1998) and health status (ADAMS *et al.* 1999). So far remote sensing is still very limited as far as the assessment of genetic resources is concerned. For an early warning system for the genetic erosion of agricultural crops remote sensing has been already proposed in order to collect data on the introduction of crop varieties, reduction of habitat, socio-economic factors, environmental degradation and disasters (HUTCHINSON & WEISS 1999). For the assessment certain forest tree species that depend on the availability of certain habitats, such as *Populus nigra* L., to gather other area-related data for instance in the socio-economic and policy sector, or for an assessment of environmental threats, remote sensing is a very promising tool.

# Conclusions

Any activity to conserve forest biodiversity must be based on reliable information about the current status of resources, their likely development and - of course - the conservation objective. Inventories and monitoring programmes can play a pivotal role but in order to optimize efforts it must be first decided which biodiversity level (genes, species), geographical scale, and time frame are aimed at. Secondly, availability of adequate resources and sound understanding of ecological dynamics in forests are cornerstones for an accurate evaluation and, thirdly, standardized protocols wherever possible make inventories and monitoring comparable and allow later the validation and calibration of findings. Therefore, a statistical framework is essential and should be planned ahead of any field work. While in many European countries an exclusive biodiversity assessment on a regional scale is not realistic, it may be - at least in part combined with ongoing NFIs or related surveys. There are no general technical guidelines that have to be completely implemented at the national level. However, probably the most important information facing conservation and management efforts for forest tree species are adequate inventory data on their distribution and abundance and this type of information can be surely furnished. Forests of the former Soviet Union, for example, cover approximately 28 % of the global forests harbouring more than 570 species and subspecies of forest trees holding genetic resources of global importance. A first important step towards forest genetic conservation in this region would be the data collection on forest tree species abundance and distribution. Generally, information on the natural range and the potential natural vegetation also would come in handy to identify and declare in situ conservation areas (see p. 535 ff., this volume).

While it is already difficult to monitor species diversity, an evaluation of the genetic level is even more intricate and forest genetic conservation is partly suffering a backlash from unrealistic expectations from molecular genetics or conservation ecology. But certain morphological traits that are genetically controlled can be observed in the field and plant material used for genetic analyses may be also collected. Many scientists will argue that such information is of low practical value. Indeed, it is not possible yet to

assess the adaptive potential of forest tree species at a regional scale, but if we do not deal with genetic implications of conservation management explicitly, then they become simply buried in the assumptions of the decision-making progress. The advantage of a NFI accounting for genetic diversity is that it forces managers to explicate about genetic effects through the reproductive system, translocation or forest reproductive material and plausible interactions of demographic attribute and genetic compositions.

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