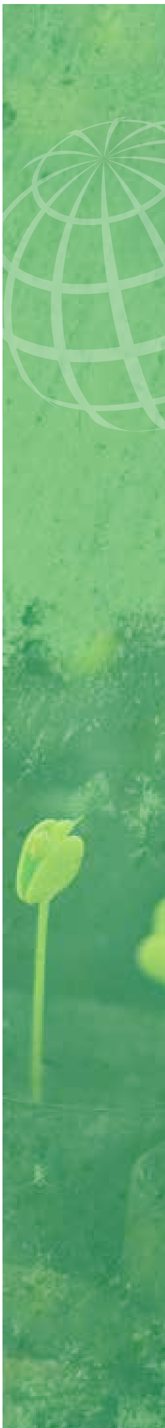
Food and Agriculture
Organization of the
United Nations

COMMISSION ON
GENETIC RESOURCES
FOR FOOD AND
AGRICULTURE

THE STATE
OF THE WORLD'S
FOREST GENETIC RESOURCES
THEMATIC STUDY



INDICATORS OF THE GENETIC DIVERSITY OF TREES - STATE, PRESSURE, BENEFIT AND RESPONSE

THE STATE OF THE WORLD'S FOREST GENETIC RESOURCES – THEMATIC STUDY

INDICATORS OF THE GENETIC DIVERSITY OF TREES - STATE, PRESSURE, BENEFIT AND RESPONSE

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FOOD AND AGRICULTURE ORGANIZATION OF THE UNITED NATIONS
Rome, 2020

Required citation:
Graudal,L.,Loo,J.,Fady,B.,Vendramin,G.,Aravanopoulos,F.A.,Baldinelli,G.,Bennadji,Z.,Ramamonjisoa,L., Changtragoon, S. and Kjær, E.D. 2020.*Indicators of the genetic diversity of trees - State, Pressure, benefit and response*. State of the World's Forest Genetic Resources - Thematic study. Rome, FAO. https://doi.org/10.4060/cb2492en

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ISBN 978-92-5-133759-2

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About this publication

At its 12th Session in 2009, the Commission on Genetic Resources for Food and Agriculture (the Commission) requested the Food and Agriculture Organization of the United Nations (FAO) to prepare *The State of the World's Forest Genetic Resources*. It stressed that the preparation of this global assessment should be based primarily on country reports on forest genetic resources (i.e. heritable materials maintained within and among tree and other woody plant species that are of actual or potential economic, environmental, scientific or societal value), supported by thematic studies and other available information and knowledge on these resources.

Between 2009 and 2010, FAO, in collaboration with Bioversity International and the World Agroforestry Centre (ICRAF), informed and consulted the scientific community on the preparation of a series of thematic studies. Groups of experts were established for this purpose and the coordinators of the groups met twice in 2011-2012 to share information and to coordinate the work.

The Commission considered a draft of the global assessment at its 14th Session in April 2013 and, based on its findings, agreed on the *Global Plan of Action for the Conservation, Sustainable Use and Development of Forest Genetic Resources* (Global Plan of Action). Subsequently, the FAO Conference adopted the Global Plan of Action at its 38th Session in June 2013. FAO then published *The State of the World's Forest Genetic Resources* (FAO, 2014a) and the Global Plan of Action (FAO, 2014b). In the same year, the expert groups also published the key findings of the thematic studies in a special issue of the journal *Forest Ecology and Management* (see Loo, Souvannavong and Dawson, 2014).

Several of the thematic studies included more analyses and in-depth discussions on various aspects related to the conservation, use and development of forest genetic resources than was possible to publish as scientific articles. Moreover, it was not possible to present in *The State of the World's Forest Genetic Resources* the wealth of information from the country reports and the thematic studies. Therefore, the Commission requested, at its 15th Session in 2015, FAO to make the country reports and the thematic studies available on its website.

This publication presents the thematic study on the indicators of genetic diversity of trees. It includes a historical account of the development of science-based indicators for tree genetic diversity that embrace ecological surrogates for genetic diversity, the genecological approach, genetic monitoring of management units, the use of molecular markers, as well as relevant experience from other organisms and policy processes. In addition, it includes a section on relevant data, data sources and databases. This information, with the twists of modern technologies (from genetics as well as geographical information systems), can enlighten the otherwise scarce knowledge on actual tree genetic diversity.

The content of this publication is entirely the responsibility of the authors, and does not necessarily represent the views of FAO, or its Members.

Acknowledgements

The study was supported by the institutions of the authors, FAO and the CGIAR Consortium Research Programme on Forests, Trees and Agroforestry (FTA).

Abbreviations and acronyms

ABS	Access and benefit sharing
ACT	Amazon Cooperation Treaty
ACTO	Amazon Cooperation Treaty Organisation
AHTEG	Ad-hoc Technical Expert Group on Indicators for Biodiversity
APFORGEN	Asia-Pacific Forest Genetic Resources Programme
ATO	African Timber Organisation
B	Benefit (type of indicator)
BIP	Biodiverstity Indicators Partnership
BLUP	Best Linear Unbiased Prediction
C&I	Criteria and indicators
CAB	Commenwealth Agricultural Bureau
CBD	Convention on Biological Diversity
CGIAR	Consultative Group on International Agricultural Research
CGRFA	Commission on Genetic Resources for Food and Agriculture
CIFOR	Center for Internatonal Forestry Research
CILSS	Comité Inter-Etate pour la Lutte contre la Sécheresse au Sahel (Permanent Inter-State Committee for Drought Control in the Sahel)
CITES	Convention on International Trade in Endangered Species of Wild Fauna and Flora
CNR	Consiglio Nazionale delle Ricerche (Italian National Research Council)
COP	Conference of the Parties
DFSC	Danida Forest Seed Centre (now FLD)
DNA	Deoxyribonucleic acid
DPKM	Diversity-productivity-knowledge-management (indicator set)
EU	European Union
EUFGIS	European Forest Genetic Resources Information System
EUFORGEN	European Forest Genetic Resources Programme
EVOLTREE	EVOLution of TREEs as drivers of terrestrial biodiversity– European Research Group faciliatated by the European Forest Institute (EFI)
FAO	Food and Agriculture Organization of the United Nations
FBD	Forest biological diversity
FGR	Forest genetic resources
FLD	Forest & Landscape Denmark, Department of Geosciences and Natural Resource Management, University of Copenhagen
FORGEN	FAO Panel of Experts on Forest Gene Resources
FRA	Global Forest Resources Assessment
FRB	Foundation for Research on Biodiversity (France)
FSC	Forest Stewardship Council
GBO	Global Biodiversity Outlook
GES	Good Environmnetal Status
GMO	Genetically modified organism
IBPGR	International Board for Plant Genetic Resources (now Bioversity International)
ICRAF	International Centre for Research in Agroforestry (World Agroforestry Centre)

INIA	Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (National Institute of Agrarian and Food Research and Technology), Spain
INRA	L'Institut National de la Recherche Agronomique (the French National Institute for Agricultural Research)
IPCC	Intergovernmental Panel on Climate Change
IPGRI	International Plant Genetic Resources Institute (now Bioversity International)
ITTO	International Tropical Timber Organization
IUCN	World Conservation Union (International Union for Conservation of Nature)
LAFORGEN	Latin America Forest Genetic Resources Network
MAPFORGEN	Atlas for the conservation of forest genetic resources in Latin America and the Caribbean
MDG	Millenium Development Goals
MEA	Millenium Ecosystem Assessment
NFI	National forest inventory
NFP	National forest programme
NGS	Next generation sequencing
OECD	Organisation for Economic Co-operation and Development
P	Pressure (type of indicator)
PEFC	Programme for the Endorsement of Forest Certification
QTL	Quantitative trait loci
R	Response (type of indicator)
REFORGEN	FAO worldwide information system on forest genetic resources
S	State (type of indicator)
SAFORGEN	Sub-Saharan Africa Forest Genetic Resources Programme
SCBD	Secretariat of CBD
SEBI	Streamlining European Biodiversity Indicators
SFM	Sustainable forest management
SNP	Single-nucleotide polymorphism
SPBR	State-Pressure-Benefit-Response
SSR	Simple sequence repeat
TREEBREEDEX	A working model network of tree improvement for competitive, multifunctional and sustainable European forestry (European research project 2006–2011)
UNCCD	United Nations Convention to Combat Desertification
UNCED	United Nations Conference on Environment and Development
UNECE	United Nations Economic Commission for Europe
UNEP	United Nations Environment Programme
UNFF	United Nations Forum on Forests
VECEA	Vegetation and Climate Change Eastern Africa
WCMC	World Conservation Monitoring Centre
WWF	World Wide Fund for Nature

Executive summary

The last two decades have seen numerous developments for tracking the rate of loss of the world's biodiversity. First was the Convention on Biological Diversity (CBD) adopted in 1992, followed in 2002 by the agreement on targets to reduce the loss of biological diversity by 2010 (the 2010 Biodiversity Target), and then in 2010, the adoption of the Aichi Targets for the Strategic Plan for Biodiversity 2011–2020.

Although very important progress has been made overall, there is "still a considerable gap in the widespread use of indicators for many of the multiple components of biodiversity and ecosystem services, and a need to develop common monitoring scheme within and across habitats" (Feld *et al.*, 2009). And genetic diversity is probably the element of biodiversity where developing relevant indicators has lagged behind the most. Identifying and operationalizing indicators of genetic diversity, including tree genetic diversity, remains a major challenge.

The purpose of the indicators of tree genetic diversity is to identify trends in maintaining and enhancing the adaptive potential of tree species. The indicators should, therefore, be built to monitor trends reflecting this purpose, which is of crucial importance for the long-term sustainability of the forest and other tree-based sectors as a whole.

Indicators should ideally provide answers or shed light on four basic questions that could help to identify and prioritize possible actions related to using and conserving genetic diversity, enhancing the adaptive potential of tree species. Indicators are grouped into four types depending on the basic question they are intended to address and actions that society can implement:

Basic question	Type of indicator	Intended significance of indicator
How is the status of biodiversity changing?	S – State	Analysing the conditions and status – are we losing genetic diversity? Where, which and how?
Why is biodiversity being lost?	P - Pressure	Monitoring the extent and intensity of the causes of loss
What are the implications for society?	B - Benefit	Quantifying the benefits that humans derive from biodiversity
What does society do about it?	R - Response	Measuring the implementation of policies or actions to prevent or reduce loss

Since trends in genetic diversity (and, therefore, long-term adaptive potential) need to be known before the impact of any type of pressure can be assessed, providing a relevant state indicator is the most crucial step of the assessment procedure. Response, pressure or benefit indicators cannot, and should not, be used independently of state indicators. Drawing from quantitative and population genetics, substantial theoretical progress has been made over the past 20 years in identifying relevant state indicators of tree genetic diversity. However, these scientifically sound indicators have so far proven difficult to apply in practice. Pressure indicators of genetic diversity are intrinsically linked with state indicators and have, therefore, not been identified on their own. Benefit indicators for genetic diversity can only be implemented if the valuation of genetic diversity is available. Apart from the value of breeding, such valuation is rare. Response indicators are generally much easier to define because recognition and even quantification of, for example, breeding, conservation, research, education and regulation actions and programmes are relatively straightforward.

The attempts of the forest sector to use indicators of genetic diversity in practice have in general been limited to response indicators, which do not provide any real understanding of the status of the genetic resources of trees on the planet, apart from assessments of threat at the species level provided by the common (and important) red lists of threatened taxa.

It is important to emphasize the link between species diversity and genetic diversity, making species level indicators relevant to genetic diversity. However, this is true only up to a certain point. Thus, to effectively conserve the genetic diversity of a species, the diversity should be known. For most species, though, knowledge of genetic variation is minimal, pointing to the central dilemma of gene resource conservation, which is to recognize the need for conservation without knowing exactly what to conserve. Knowledge of genetic variation must therefore, to a large extent, be derived from surrogates as the species' ecological diversity (habitat diversity, diversity of ecological requirements).

Although considered unrealistic 20 years ago, many state indicators can now be proposed for immediate implementation because of scientific breakthroughs such as geographical information systems, high throughput molecular techniques and the ability to handle large amounts of data (e.g. presence/absence species data). Concurrently, ecological monitoring and sustainable management (including management of genetic resources) have made significant progress.

The four major operational indicators presented in this report make use of these recent changes and discoveries. They are as follows:

Operational indicator	Implications	Possible primary sources of data and information
Trends in species and population distribution and diversity patterns for selected species	The state of the genetic *diversity* of trees: what is really happening to the resource?	International, regional and national databases, FAO's Global Forest Resources Assessment (FRA)
Trends in plantation performance of selected species	The *productivity* of the genetic resource of trees in current use; also reflecting the possible potential of mobilizing the resource further	National forest inventories, economic valuation studies, FAO's Planted Forest Programme, FRA
Trends in knowledge on genetic diversity of species and in education and awareness	Current *knowledge* and potential capacity for development of the genetic resource	Scientific literature, various databases and national institutions
Trends in management (sustainable use and conservation) of tree genetic resources	Current *management* of the genetic resource: how well are we actually doing?	National and international institutions and networks

The theoretical basis of this diversity-productivity-knowledge-management (DPKM) set of four indicators is the genecological approach, where there are three factors that are the major forces of evolution at the ecosystem/population microscale: natural selection, genetic drift and gene flow. The effects of natural selection can lead to differentiation associated with local adaptation, while genetic drift can lead to differentiation associated with stochastic changes and genetic erosion, both being mediated by the action of gene flow that can lead to genetic homogenization.

The DPKM set can be applied to appropriate groups of tree species, both in the wild and under cultivation, representing different regions and different climates, present as well as future. It is flexible enough to accommodate additional knowledge as it becomes available and it is easy and cost effective for management to implement.

The DPKM set could possibly provide a realistic picture of the state, trends and potentials of the world's tree genetic resources. Efficient implementation strategies for managing these resources worldwide include establishing links with provision, rules and regulations of forest reproductive material, and forest certification schemes. Furthermore, the indicators proposed in this report could be considered when developing indicators for the post-2020 global biodiversity framework.

1. Introduction

Biodiversity indicators, tree genetic diversity indicators and the international context

1.1 The subject: Indicators and the conservation of forest genetic resources for sustainable use

Criteria and indicators

Criteria and indicators are used in different fields to define priorities and measure the extent to which the priorities are met (e.g. Prabhu *et al.*, 1999). A criterion will usually reflect an objective (goal or target[1]). Here it represents the conservation of the world's forest genetic resources (FGR) for sustainable use. Practical and informative indicators that can be measured periodically to reveal the direction of change of genetic diversity are, therefore, required. Indicators are, by definition, used to track progress and should always be defined in relation to their objective (Feld *et al.*, 2009). The measure of an indicator is commonly referred to as a verifier.

For any indicator to be useful in practice, the data must be relatively easy and inexpensive to collect and its significance for achieving the target must be clear. Most institutions cannot afford to implement indicator systems that require substantial resources for data collection or expensive analytical techniques (e.g. McKinnell, 2002).

Levels of consideration: global, regional, national and local

For an indicator to be of significant importance for achieving any target it must be scientifically sound, realistic and relevant to policy, for defining the baseline and for monitoring. The type of policy relevance will depend on the context, e.g. whether efforts are made at the global, regional, national or local level. The notions of global and national are straightforward. The meanings of regional and local are more ambiguous. Henceforth, we use the term "regional" in the physical geographical sense for larger areas that are considered homogenous units in terms of environment across political borders, which, depending on the context, can be large areas (e.g. temperate and boreal forest or dry zone Africa, see Chapter 2) or small areas (e.g. the regions of distribution of a specific species). The term "local" is thought of as a smaller area appropriate for applying very specific management interventions that may vary in size from a few to over thousands of hectares (from management unit to landscape).

The level of consideration, from the global down to the local management unit, also has implications for the indicator's level of detail. At the local management unit, it may be possible to deal with individual trees (genotypes) or even genes, whereas at the global level it usually will be necessary to deal with an aggregation of individuals in the form of populations, species or ecosystems.

The importance of diversity indicators is that they will provide evidence for the state (in terms of conservation status) and the trend in changes of the object under consideration (improving or degrading status of conservation). This provides

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[1] Criteria, objectives, goals and targets are essentially used as synonyms, depending on the context.

a basis for policy and management decisions to maintain and enable the sustainable use of the genetic resources considered.

Delimitation of forest genetic resources: genetic diversity of trees

In this study, we refer to indicators of genetic diversity of trees rather than to indicators of FGR. FGR typically refer to the genetic variation of forest trees of present or potential value for mankind. The notion of potential value in a likely different future (see e.g. Alfaro *et al.*, 2014) implies that different species than those currently harvested and used will benefit mankind. This includes not only forest trees but also trees and other woody perennials outside forests. Therefore, the full spectrum of genetic diversity, not only currently known important adaptive genes (genetic resources of present value), will be considered here. In fact, the resource cannot be distinguished from the diversity. For the sake of simplicity, we refer to the "genetic diversity of trees" as the area of interest of this study.

Value, present or potential, means that indicators must also address economic value. Although very few valuation studies of genetic diversity exist (but see, for example, Hein and Gatzweiler, 2006, see also Section 3.3), the indicators in our study will be related to natural processes, management response to present and potential threats, as well as to the present and potential benefits humans derive from genetic diversity.

Plantation, semi-domesticated and wild tree species

In agricultural plants there is a distinction between crop genetic resources and the genetic resources of crop wild relatives (e.g. Brown, 2008). Such a distinction is less prominent and less relevant in forest tree species, as most of them are not domesticated or subject to limited levels of domestication. However, evidence of long-lasting domestication has emerged recently in areas of the tropics where people have lived for millennia, such as in the Amazon Basin (Clement, 1999). Many tree species that were - and in some cases still are - valuable for food have been subject to some degree of incipient or semi-domestication over the centuries, but little is known about how the patterns and levels of genetic diversity may have changed as a result. In addition, some tree plantation species (mainly timber species, but also some multipurpose species) have been and are in the process of more intensive domestication, involving breeding as well as conservation programmes. For these species, much more is known about their genetics, and more specific indicators of their state of genetic diversity will, therefore, be available. It is relevant to distinguish between the more intensively used plantation species (a few hundred) and the vast majority of wild tree species (many thousands), which no doubt harbour large untapped potentials, but of which very little is known.

Types of indicators: state, pressure, response and benefit

Indicators can be used to measure the achievement of the criterion in different ways. It can be a direct measurement of genetic parameters or proxies hereof, providing a direct indication of the state of the resource as such. These types of indicators are called state indicators (S). An indicator can also be an indirect measure of incidents or activities that pose a threat to the genetic resource, e.g. deforestation, which are referred to as pressure indicators (P). Or it can be an indirect measure that reflects an action towards improving the state of the diversity, like *ex situ* or *in situ* conservation stands, legislation and regulation that enhance the genetic resource, or capacity building in planning and implementation of genetic resource management programmes. Such indirect measures are referred to as response indicators (R). In the work on indicators it has been common to distinguish between these three types of indicators, state (S), response (R) and pressure (P), in a coherent framework (e.g. Namkoong *et al.*, 2002[2]).

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[2] Namkoong *et al.* (2002) present a conceptual model of the relation between pressure, state and response indicators in a context

More recently, benefit (B), understood here as the amount and change in benefits that humans derive from genetic diversity, has been coined as a type of indicator (e.g. Sparks *et al.*, 2011 or UNEP/WCMC, 2011). Benefit indicators would be intended to grasp the issue of value of genetic diversity, briefly mentioned above.

Sparks *et al.* (2011) emphasized that linked sets of indicators constituting a response-pressure-state-benefit framework (the RPSB loop) would facilitate an understanding of the relationships between policy actions, anthropogenic threats, the status of biodiversity and the benefits that people derive from it.[3] Sparks et al. (2011) argue that "explicitly linked sets of indicators offer a more useful framework than do individual indicators because the former are easier to understand, communicate and interpret to guide policy... Such an approach is appropriate at global, regional, national and local scales but for many systems it is easier to demonstrate causal linkages and use them to aid decision making at national and local scales."

In accordance with Sparks *et al.* (2011), the *Ad Hoc* Technical Expert Group on Indicators for Biodiversity under the Convention on Biological Diversity (CBD) has agreed that a framework for communicating biodiversity information should respond to the following four logical policy questions (UNEP/CBD/AHTEG, 2011):

- How is the status of biodiversity changing? (state);
- Why are we losing biodiversity? (pressure and underlying causes)
- What are the implications? (benefit); and
- What do we do about it? (response).

The assessment of change in status over time is typically done to monitor the loss of diversity, also referred to as genetic erosion (Brown and Hodgkin, 2015). One of the values of diversity (benefit) is that it may provide for adaptation to a variety of conditions. Conversely, loss of diversity may cause lack of ability to withstand environmental change or susceptibility to pests and diseases, summarised in the concept of genetic vulnerability (see further in Brown and Hodgkin, 2015).

1.2 What should a relevant indicator of tree genetic diversity reveal?

There are at least 60 000 tree species on Earth (Grantner, 2005; Beech *et al.*, 2017) and perhaps even as many as 100 000 (Oldfield *et al.*, 1998, see also Petit and Hampe, 2006). It is still an open question, how many of these species are useful, or perhaps rather how many are known to be useful, or how many may become useful to human societies in the future. Some 2 500 to 3 500 of these species have been registered as forestry or agroforestry species (Burley and Carlowitz, 1984; Simons and Leakey, 2004). Many of these are used to a large extent in their wild stage and a limited number have been brought into cultivation. Even fewer of them have ever been tested for the performance of their populations in different environments and very little is known about their genetic variation. The Food and Agriculture Organization of the United Nations (FAO) Panel of Experts on Forest Gene Resources lists almost 500 species identified as of high global, regional and/or national priority for exploration, collection, conservation and use (FAO, 2001b). The 500 species were selected mostly for their economic importance for food and wood production, and less for their ecological importance or dominance (FAO, 2001b).

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where response is the response of biodiversity itself (called process by Brown *et al.*, 1997) and not the response by man, i.e. different from the RPSB loop that is now gaining prominence (see also Chapter 3).

[3] In the Marine Sector, where relevant conservation efforts have been well advanced, the Marine Strategy Framework Directive within the EU, operates with indicators of State, Pressure and Impact. Where State and Pressure are similar to the standards used by CBD, Impact is understood as the effect of a pressure on the state and thus provides an explanation of impact seen in relation to a defined overall goal of good environmental status (GES) of the marine environment (European Commission, 2011).

Very few of these species have been subjected to intraspecific variation studies and very little documentation is available on their distribution (Feeley and Silman, 2011). In addition, many of these species are considered threatened. The Intergovernmental Panel on Climate Change (IPCC) estimates that 20 to 30 percent of plant and animal species will be at risk of extinction if global average temperature increases 1.5°–2.5°C (IPCC, 2007; see also Ruhl, 2008, and Warren *et al*., 2018).

To identify and understand indicators for tree genetic diversity is obviously not an easy task. Apart from their large number, species vary in their biological attributes in the plant communities where they grow and in their interaction with environmental and anthropogenic factors. When thinking in terms of indicators, it is necessary to focus not only on genetic variation *per se*, but also to include the genetic processes within the plant communities in which trees grow (e.g. Eriksson *et al*., 1993). Relevant indicators of tree genetic diversity should reveal both genetic patterns and genetic processes.

Genetic patterns of variation occur at different hierarchical levels. Variation between ecosystems might reflect an important adaptation to different environmental conditions. Many studies have revealed substantial geographic differentiation of trees in ecotypes, thus suitable for different planting sites.

Variation between trees within populations may reflect the presence of an important genetic variation in terms of polymorphisms in expressed genes. The expected genetic response to selection is proportional to the level of genetic diversity, and the presence of genetic variation is, therefore, crucial for the species' ability to react to changing climates, newly occurring pests, or simply to the ongoing competition with other species.[4] This level of variation is also important in terms of genetic variation in the traits of commercial importance because such variation allows efficient breeding.

The genetic processes are important for continued adaptation. Continued genetic differentiation through ongoing natural selection allows species and populations to maintain their adaptation at various sites. It is important to note that anthropogenic influence does not *per se* hinder the efficiency of natural selection. Processes also protect species and populations against the adverse effects of small population sizes, i.e. protect against inbreeding, genetic erosion and/or random genetic drift. This is important because mating (gene flow) occurs between individuals and/or forest fragments to an extent that allows the maintenance of viable population sizes.

Neither of the two above aspects (patterns and processes) are (or should be) static, and rather than looking for an indicator for the status quo, we must look for indicators that infer (i) the extent to which hierarchical diversity levels (within and between populations and ecosystems) are expected to change substantially in the short (and intermediate) timeframe, and (ii) the extent to which sound genetic processes are expected to continue to work efficiently.

Such indicators must be state indicators (see discussion above). Indirect indicators of pressure, response or benefit will never be able on their own to reveal the state and development of the two fundamental aspects of maintaining genetic diversity. This does not mean that pressure, response and benefit indicators *per se* are of less interest, but the state indicators are required to interpret the other types of indicators.

Identifying ideal state indicators of genetic diversity of trees has for quite a long period of time been considered an almost impossible task. This has been especially true when trying to span the level from management units of relatively few priority species to the global level of thousands of species with widespread distribution. Progress at the management unit is, however, now well underway, whereas global indicators continue to be more distant (see further in Chapter 3).

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[4] In general, this is true, but levels of inbreeding within some tropical broadleaf species are high. The expected genetic response through selection and breeding, in these cases, would not be proportional to the level of genetic diversity.

The recent and rapid development of molecular marker techniques (Allendorf *et al.*, 2010) has facilitated considerably the identification of state indicators at the management unit of identified priority species (Schwartz *et al.*, 2007; Laikre *et al.*, 2008; Geburek *et al.*, 2010; Luikart *et al.*, 2010; Aravanopoulos, 2011; Konnert *et al.*, 2011; Stetz *et al.*, 2011; Hansen *et al.*, 2012; Bruford *et al.* 2017). At least where facilities are available, such scientific techniques are within practical reach. However, in practice availability depends on access to resources and facilities, which varies enormously among countries and world regions. In Europe, work by the European Forest Genetic Resources Programme (EUFORGEN), has reached a point where implementation is likely to begin within a few years[5] (see Chapter 3).

The major challenge remaining would seem to be how to identify global state indicators, which are also highly relevant to policy. However, we will argue below (Chapters 3 and 4) that this (at least in principle) can be done by applying different, simple demographic verifiers, because an indicator for the exact status quo is not required. Rather, indicators for the presence of multiple, genetically viable populations (*in situ* or *ex situ* managed) - that reasonably represent the gene pool of a given species - are to be targeted.

1.3 The international context: global biodiversity indicators

Biodiversity is the diversity of life at all levels of organization, from genes to populations, species and ecosystems (CBD article 2). As biodiversity appears to be declining, the international community has developed relevant targets for reducing the loss and indicators to reach these targets. Genetic diversity is a basic key element of biological diversity, which also supports such ecosystem services (MEA, 2005) as providing food and other primary production, controlling pests and diseases, and for scientific discovery.

International collaboration in developing global indicators of biodiversity

The 2010 Biodiversity Target

In the framework of the CBD global targets for reducing the loss of biological diversity by 2010 (the 2010 Biodiversity Target), and ways to track progress in achieving this goal were adopted by more than 180 of the world's governments in 2002. Twenty-one sub-targets were set to be reached by 2010, towards 11 principal goals related to biodiversity (see e.g. SCBD, 2010).

Since 2002, global indicators of biodiversity set to assess the state and trends of the various biodiversity components and the goals and targets to be reached have been identified and are at different stages of development and implementation. A global initiative, the Biodiversity Indicators Partnership (BIP), was established to promote and coordinate development and delivery of biodiversity indicators in support of the CBD and other sectors (see www.bipindicators.net).

BIP brings together more than 40 organizations working internationally on indicator development to provide the most comprehensive information on biodiversity trends.

The indicators related to the 2010 Biodiversity Target were developed under seven focal areas. Of 22 preliminary headline indicators relating to the seven focal areas (BIP, 2010), the status of 14 headline indicators are reported in the Global Biodiversity Outlook 3 (SCBD, 2010) (see Box 1[6]).

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[5] In Europe, the fishery sector is also advanced with the EU Marine Strategy Framework Directive, according to which member states must take the necessary measures to achieve or maintain good environmental status (GES) in the marine environment by the year 2020 at the latest; and are required to adopt marine strategies. A Commission Staff Working Paper on the relationship between the initial assessment of marine waters and the criteria for good environmental status includes indicators of genetic diversity (European Commission, 2011). See further in Chapter 3, Box 5.

[6] At European level, 26 indicators have been proposed (SEBI, 2011).

Box 1
The 2010 Biodiversity Indicators

The set of indicators developed to assess progress towards the 2010 Biodiversity Target of reducing the loss of biodiversity (agreed upon in 2002) is summarized in the table below. Focal area headline indicator and proposed indicators (each of which has 1–3 measures, not specified in the table) are given as presented in the CBD decision VIII/15 (2006), here according to UNEP-WCMC (2009). Of the 22 proposed indicators, 13 were considered for immediate testing and use (in 2006) and 8 (those in brackets) requiring further development (UNEP-WCMC, 2009). Status of the indicator development (column 3, using the labels ❶,❷, and ❸) is also according to UNEP-WCMC (2009): ❶ fully developed with well-established methodologies and global time-series data, ❷ under development, ❸ not being developed. Multiple labels in column 3 indicate multiple measures under each Focal Area Headline Indicator (UNEP-WCMC, 2009 adapted from Walpole *et al.*, 2009). The assessment of the indicator and its degree of certainty is quoted from the Global Biodiversity Outlook 3 (SCBD, 2010) and covers 14 of the originally proposed 22 indicators.

Focal Area Headline Indicator	Biodiversity 2010 Indicator	Status of indicator development	Assessment of Indicator GBO 3 2010	Degree of certainty of indicator
Status and trends of the components of biological diversity	1. Trends in extent of selected biomes, ecosystems and habitats	❶❷	Most habitats in most parts of the world are declining in extent, although forest area expands in some regions, and the loss of mangroves has slowed significantly, except in Asia.	Medium
	2. Trends in abundance and distribution of selected species	❶❷❷	Most species with limited population size and distribution are being further reduced, while some common and invasive species become more common.	High (but limited number of taxa assessed)
	3. Coverage of protected areas	❶❷❷	There has been a significant increase in coverage of protected areas, both terrestrial and marine, over the past decade. However, many ecological regions, particularly in marine ecosystems, remain under-protected, and the management effectiveness of protected areas remains variable.	High
	4. Change in status of threatened species	❶	The risk of extinction increases for many threatened species, although some species recovery programmes have been very successful.	High (for those species assessed)
	5. Trends in genetic diversity of domesticated animals, cultivated plants and fish species of major socioeconomic importance	❷❷	It is likely that the genetic variety of cultivated species is declining, but the extent of such decline and its overall impacts are not well understood.	Low (although many case studies with a high degree of certainty are available)

▶▶

Focal Area Headline Indicator	Biodiversity 2010 Indicator	Status of indicator development	Assessment of Indicator GBO 3 2010	Degree of certainty of indicator
Sustainable use	6. Area of forest, agricultural and aquaculture ecosystems under sustainable management	❷❷❷	There are considerable efforts under way to increase the extent of areas of land under sustainable management. Regional efforts on sustainable forest management are expected to contribute to this. Traditional agricultural practices are being maintained and revitalized as the demand for ethical and healthy products increases. However, these are still relatively small niches and major efforts are required to substantially increase the areas under sustainable management.	Low
	(7. Proportion of products derived from sustainable sources)	❶❷❷		
	(8. Ecological footprint and related concepts)	❶	The ecological footprint of humanity is increasing. Efforts at increasing resource efficiency are more than compensated by increased consumption by a growing and more prosperous human population.	High
Threats to biodiversity	9. Nitrogen deposition	❶	Human activity has doubled the rate of creation of reactive nitrogen on the planet's surface. Pressure on biodiversity from nutrient pollution continues to increase, although some measures to use nutrients more efficiently, to reduce their release into water and the atmosphere, are beginning to show positive effects.	
	10. Trends in invasive alien species	❶	The number and rate of spread of alien species is increasing in all continents and all ecosystem types.	Medium (although many case studies with a high degree of certainty are available)
Ecosystem integrity and ecosystem goods and services	11. Marine Trophic Index	❶	Despite intense pressure, the Marine Trophic Index has shown a modest increase globally since 1970. However, there is substantial regional variation with declines being recorded in half the marine areas with data. Although the global increases may indicate a recovery, it is more likely a consequence of fishing fleets expanding their areas of activity, thus encountering fish stocks in which larger predators have not yet been removed in large numbers.	High
	12. Water quality of freshwater ecosystems	❶	Most parts of the world are likely to be suffering from declines in water quality, although quality in some areas has improved through control of point-source pollution.	High
	(13. Trophic integrity of other ecosystems)	❸		
	14. Connectivity / fragmentation of ecosystems	❷❷	Most terrestrial and aquatic ecosystems are becoming increasingly fragmented, despite an increased recognition of the value of corridors and connections, especially in climate change adaptation.	High

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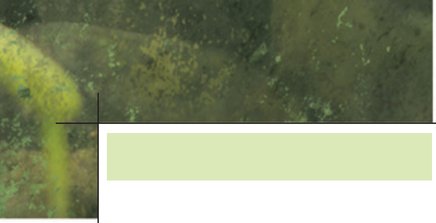

Focal Area Headline Indicator	Biodiversity 2010 Indicator	Status of indicator development	Assessment of Indicator GBO 3 2010	Degree of certainty of indicator
	(15. Incidence of human-induced ecosystem failure)	❸		
	(16. Health and well-being of communities who depend directly on local ecosystem goods and services)	❷		
	(17. Biodiversity for food and medicine)	❷❷		
Status of traditional knowledge, innovations and practices	18. Status and trends of linguistic diversity and numbers of speakers of indigenous languages	❷	Many minority languages are believed to be in danger of disappearing, and linguistic diversity is very likely declining.	Low (although case studies with a high degree of certainty are available)
	(19. Other indicator of the status of indigenous and traditional knowledge)	❸		
Status of access and benefit-sharing	(20. Indicator of access and benefit-sharing)	❸	The need and possible options for additional indicators are being examined by the Ad Hoc Open-ended Working Group on Access and Benefit-sharing.	
Status of resource transfers	21. Official development assistance (ODA) provided in support of the Convention	❷	The volume of ODA for biodiversity has increased over the past few years.	High
	(22. Indicator of technology transfer)	❸		

In a scientific assessment, Butchart *et al.* (2010) compiled 31 indicators to report on the progress of the 2010 Biodiversity Target. They concluded that despite some local successes and increasing responses, the rate of biodiversity loss does not appear to be slowing (Butchart *et al.*, 2010), as is also clear from the assessment in the Global Biodiversity Outlook 3 (SCBD, 2010). None of the indicators has so far measured tree genetic diversity.

The Aichi Biodiversity Targets

A revised and updated Strategic Plan for Biodiversity for the period 2011–2020 was adopted in 2010 (see www.cbd.int/sp). It contains twenty targets, the Aichi Biodiversity Targets, organized under five strategic goals (Box 2). The five strategic goals directly address the four policy questions quoted above (Section1.1). Strategic goals A and B cover the question of underlying causes and direct pressures causing loss of diversity. Strategic goal C deals with the conservation status of biodiversity and the improvement thereof. Strategic goal D covers benefits and strategic goal E responses to enhance the implementation of the Strategic Plan.

Box 2
The twenty Aichi Targets and the five Strategic Goals

Strategic Goal A: Address the underlying causes of biodiversity loss by mainstreaming biodiversity across government and society

Target 1: By 2020, at the latest, people are aware of the values of biodiversity and the steps they can take to conserve and use it sustainably.

Target 2: By 2020, at the latest, biodiversity values have been integrated into national and local development and poverty reduction strategies and planning processes and are being incorporated into national accounting, as appropriate, and reporting systems.

Target 3: By 2020, at the latest, incentives, including subsidies, harmful to biodiversity are eliminated, phased out or reformed in order to minimize or avoid negative impacts, and positive incentives for the conservation and sustainable use of biodiversity are developed and applied, consistent and in harmony with the Convention and other relevant international obligations, taking into account national socio-economic conditions.

Target 4: By 2020, at the latest, Governments, business and stakeholders at all levels have taken steps to achieve or have implemented plans for sustainable production and consumption and have kept the impacts of use of natural resources well within safe ecological limits.

Strategic Goal B: Reduce the direct pressures on biodiversity and promote sustainable use

Target 5: By 2020, the rate of loss of all natural habitats, including forests, is at least halved and where feasible brought close to zero, and degradation and fragmentation is significantly reduced.

Target 6: By 2020 all fish and invertebrate stocks and aquatic plants are managed and harvested sustainably, legally and applying ecosystem based approaches, so that overfishing is avoided, recovery plans and measures are in place for all depleted species, fisheries have no significant adverse impacts on threatened species and vulnerable ecosystems and the impacts of fisheries on stocks, species and ecosystems are within safe ecological limits.

Target 7: By 2020 areas under agriculture, aquaculture and forestry are managed sustainably, ensuring conservation of biodiversity.

Target 8: By 2020, pollution, including from excess nutrients, has been brought to levels that are not detrimental to ecosystem function and biodiversity.

Target 9: By 2020, invasive alien species and pathways are identified and prioritized, priority species are controlled or eradicated, and measures are in place to manage pathways to prevent their introduction and establishment.

Target 10: By 2015, the multiple anthropogenic pressures on coral reefs, and other vulnerable ecosystems impacted by climate change or ocean acidification are minimized, so as to maintain their integrity and functioning.

Strategic Goal C: To improve the status of biodiversity by safeguarding ecosystems, species and genetic diversity

Target 11: By 2020, at least 17 per cent of terrestrial and inland water, and 10 per cent of coastal and marine areas, especially areas of particular importance for biodiversity and ecosystem services, are conserved through effectively and equitably managed, ecologically representative and well connected systems of protected areas and other effective area-based conservation measures, and integrated into the wider landscapes and seascapes.

Target 12: By 2020 the extinction of known threatened species has been prevented and their conservation status, particularly of those most in decline, has been improved and sustained.

Target 13: By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species, is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity.

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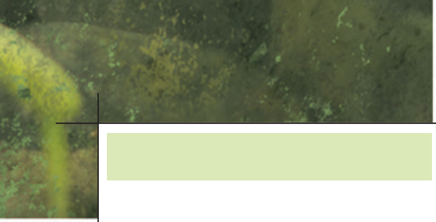

Strategic Goal D: Enhance the benefits to all from biodiversity and ecosystem services

Target 14: By 2020, ecosystems that provide essential services, including services related to water, and contribute to health, livelihoods and well-being, are restored and safeguarded, taking into account the needs of women, indigenous and local communities, and the poor and vulnerable.

Target 15: By 2020, ecosystem resilience and the contribution of biodiversity to carbon stocks has been enhanced, through conservation and restoration, including restoration of at least 15 per cent of degraded ecosystems, thereby contributing to climate change mitigation and adaptation and to combating desertification.

Target 16: By 2015, the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization is in force and operational, consistent with national legislation.

Strategic Goal E: Enhance implementation through participatory planning, knowledge management and capacity building

Target 17: By 2015 each Party has developed, adopted as a policy instrument, and has commenced implementing an effective, participatory and updated national biodiversity strategy and action plan.

Target 18: By 2020, the traditional knowledge, innovations and practices of indigenous and local communities relevant for the conservation and sustainable use of biodiversity, and their customary use of biological resources, are respected, subject to national legislation and relevant international obligations, and fully integrated and reflected in the implementation of the Convention with the full and effective participation of indigenous and local communities, at all relevant levels.

Target 19_ By 2020, knowledge, the science base and technologies relating to biodiversity, its values, functioning, status and trends, and the consequences of its loss, are improved, widely shared and transferred, and applied.

Target 20: By 2020, at the latest, the mobilization of financial resources for effectively implementing the Strategic Plan for Biodiversity 2011-2020 from all sources, and in accordance with the consolidated and agreed process in the Strategy for Resource Mobilization, should increase substantially from the current levels. This target will be subject to changes contingent to resource needs assessments to be developed and reported by Parties.

Indicators for these targets and goals have also been identified and developed (UNEP/CBD/AHTEG, 2011; UNEP/WCMC, 2011; UNEP/CBD/COP, 2016).

Targets and indicators for genetic resources for food and agriculture

The Commission on Genetic Resources for Food and Agriculture (CGRFA) and FAO have contributed to the development and use of targets and indicators that are related to genetic resources for food and agriculture (which in its broader sense includes forestry) and that are relevant to the work of the CBD, in particular Aichi Target 13. The CGRFA has adopted targets and indicators for monitoring the implementation of the Global Plans of Action on plant, animal and forest genetic resources. Part of the data on plant and animal genetic resources that countries report to FAO is also used for monitoring progress towards achieving Aichi Target 13. More recently, the CGRFA has also been discussing the development of targets and indicators for aquatic genetic resources.

After the adoption of the 2030 Agenda for Sustainable Development with its 17 Sustainable Development Goals and 169 targets in 2015, FAO has contributed to the development of indicators for these goals and targets. Currently FAO serves as a custodian agency for 21 global indicators (including the indicators on plant and animal genetic resources) spanning across six Sustainable Development Goals.

1.4 Current coverage of genetic diversity by the global indicators

Genetic diversity and coverage by the 2010 Biodiversity Indicators

One of the seven focal areas used for indicators under the 2010 Biodiversity Targets was "reducing the rate of loss of the components of biodiversity (Box 1), including (i) biomes, habitats and ecosystems; (ii) species and populations; and (iii) genetic diversity", under which tree genetic diversity, as described in the introduction, would belong.

However, no specific indicator on tree genetic diversity was identified. One of the headline indicators under this focal area is "Trends in genetic diversity of domesticated animals, cultivated plants, and fish species of major socio-economic importance" (Number 5, Box 1).

The formulation of the headline indicator on trends in genetic diversity implies a utilitarian focus, which fits well within the ecosystem service framework of the Millennium Ecosystem Assessment (MEA, 2005). Genetic diversity in this context is considered a resource as something useful being bred, planted and/or harvested, including from the wild. Trees are not specifically mentioned in the focal area but are of course included in plants.[7] Trees do, however, fall in all the categories of use mentioned. Trees are domesticated, planted and harvested from plantings or from natural occurrences. It is important to note that many tree species are important for other products besides timber. Harvest may be done as part of sustainable management systems but is often in the form of so-called mining. Nevertheless, the headline indicator would seem to include only the group of planted tree species referred to in the introduction and not to the vast majority of wild tree species. A relevant indicator of tree genetic diversity would go beyond this headline.

Two specific indicators have so far been identified under this headline:

- The *Ex-situ* Crop Collection Enrichment Index; and
- The genetic diversity of terrestrial domesticated animals (proportion of the world's breeds at risk).

Scientists (e.g. Laikre *et al.*, 2010) have pointed out the insufficiency of these indicators, since they neither monitor the genetic diversity within breeds nor the genetic diversity in domesticated plants or any wild species. The importance of genetic variation for evolutionary processes should be taken into consideration in developing international policy to conserve biological diversity. Without meaningful indicators and targets for conservation of this critical component of biodiversity, the adaptive potential of all wild and domesticated species is likely to continue to erode (Laikre *et al.,* 2010).

The Secretariat of the Convention on Biological Diversity (SCBD) recognized that the first set of indicators were incomplete in many areas, e.g. wild genetic resources, and that many of the indicators were patchy in their coverage (SCBD, 2010; see also Walpole *et al.*, 2009).

Coverage by the indicators for the Strategic Plan 2011–2020

The work initiated on indicators for the Strategic Plan for Biodiversity 2011–2020 generated proposals for new indicators related to genetic diversity. The *Ad Hoc* Technical Expert Group (AHTEG) on the subject adopted the following proposals for most relevant operational indicators (UNEP/CBD/AHTEG, 2011a)[8] under Target 13 (see above and further below):

- Trends in the genetic diversity of cultivated plants, and farmed and domesticated animals and their wild relatives (class B);
- Trends in the number of effective policy mechanisms implemented to reduce genetic

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[7] In the work of Streamlining European 2010 Biodiversity Indicators (SEBI, 2010), tree species have occasionally been specifically added to this headline.

[8] An updated set of indicators was adopted at COP 13 in 2016 (UNEP/CBD/COP, 2016). The analysis of coverage given here is based on the originally proposed indicators of 2011.

erosion and safeguard genetic diversity related to plant and animal genetic resources (class B); and

- Trends in genetic diversity of selected species (class C).

These were then incorporated into the indicators for the Strategic Plan for 2011-2020. A fourth indicator on the access to genetic resources and sharing of benefits arising from their utilization (under Target 16) was not yet formulated in 2011 but was later included (UNEP/CBD/COP, 2016).

Compared to the headline indicator on genetic diversity of the 2010 Biodiversity Indicators, information on wild relatives are now incorporated. From a tree species point of view, as stated above, it is important to include the wild species. The first and third of the three indicators, in the context of tree species, might be considered identical.

To which extent these indicators are sufficient will depend on how they are translated into specific sub-topic indicators. For that purpose, it is necessary to consider what the indicators are supposed to reveal (see Section 1.2 above).

1.5 Relation of tree genetic diversity to other areas of indicator development

The 2010 Biodiversity Indicators

The development of an indicator on tree genetic diversity relates to several of the 2010 biodiversity headline indicators (see Box 1):[9]

- No. 1. Trends in extent of biomes, ecosystems and habitats
- No. 2. Trends in abundance and distribution of species
- No. 4. Change in status of threatened species
- No. 6. Area of forest, agricultural and aquaculture ecosystems under sustainable management
- No. 10. Trends in invasive alien species

Trees are constituents of habitats, and a trend in the first headline indicator (No. 1) will, obviously, also *sine qua non* reflect an overall trend in tree genetic diversity. A trend in the distribution of a species (No. 2) is normally also an indicator for a trend in the genetic diversity of the species. A similar direct relation exists for No. 4; a threatened tree species will often have limited distribution and, therefore, possibly also limited (or reduced) genetic variation. Some tree species may be invasive (No. 10), and where such species spread at the expense of other species, it likely implies a negative trend in genetic diversity for these species. Ideally, sustainable management implies management of the genetic resources. Whether a tree species is grown under a sustainable management system (No. 6) or not, should, at least in principle, also provide a trend in terms of genetic diversity.

Of the above measures, the trend in distribution of a species (No. 2) is probably the single measure most directly related to genetic diversity, and thus an indicator that could be used also for indirect assessment of genetic diversity (see further below).

Indicators for the Strategic Plan 2011–2020

Developing indicators for tree genetic diversity should relate to the new (or revised) set of indicators being developed for the Strategic Plan 2011–2020. In the new plan indicators are organized in relation to the 20 Aichi Biodiversity Targets (see Box 2) (UNEP/CBD/AHTEG, 2011a; 2011b).

The indicator framework is quite complex, as is shown in Figure 1. A tabular relationship between the policy questions, headline indicators, sub-topics, Strategic Goals and the Aichi Biodiversity Targets is presented in Appendix IV of UNEP/CBD/AHTEG (2011a), which for convenience is reproduced as Appendix 1 to this Thematic Study.

In addition to the four indicators on genetic diversity mentioned above (Section 1.4, Coverage by the proposed new set of indicators for 2011–2020), a number of other proposed indicators will relate to genetic diversity. In the new set of

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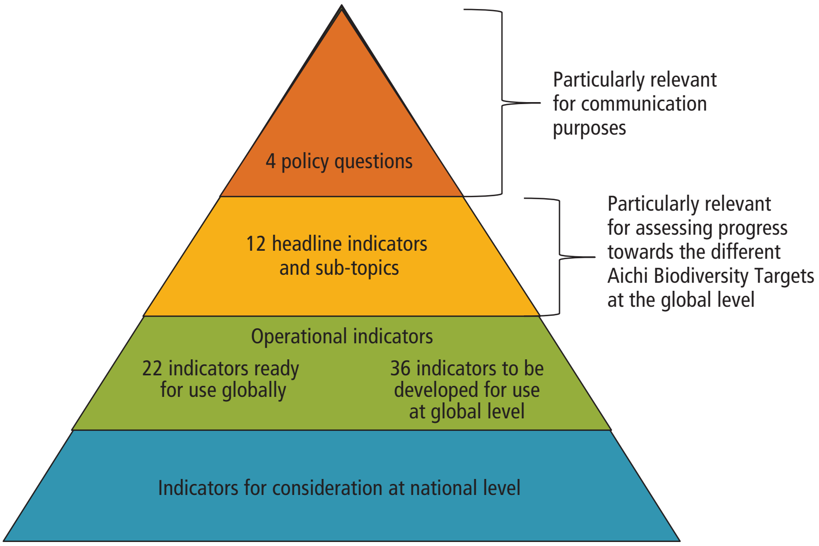
[9] Numbering is in accordance with BIP, 2010.

proposed indicators, we find a similar pattern of relationship to a possible indicator of tree genetic diversity as for the 2010 Biodiversity Indicators discussed above (Section 1.5). Again, it is "trends in distribution of species" that can be considered most relevant as a possible additional expression of genetic diversity.

An attempt to identify and summarize all the currently proposed indicators (including the four listed above) in the Strategic Plan for Biodiversity 2011–2020 of relevance for tree genetic diversity are given in Table 1 below.

In constructing the table, we have followed the suggestions for headline indicators and operational indicators considered relevant ("most relevant" or "other relevant") by UNEP/CBD/AHTEG (2011a) under Aichi Targets 13 and 16 (Section 1.4), providing 14 operational indicators. These comprise only state and response indicators. We added the operational indicators that address distribution, population trends and extinction risks of relevance for populations of trees and that target intraspecific variation (but not mentioned as such by UNEP/CBD/AHTEG), providing an additional eight operational indicators of which one is classified as a state indicator, five are classified as pressure indicators, one as a benefit indicator and one as a response indicator. We have further included three operational benefit indicators that reflect the benefit, value and condition of ecosystem services to enable adequate coverage of the benefits of genetic diversity. Finally, we have included one operational response indicator covering capacity building, knowledge

FIGURE 1
Relationship between the different elements of the indicator framework for assessing progress towards the Strategic Plan for Biodiversity 2011–2020 and the Aichi Biodiversity Targets (Source: Appendix 2 in UNEP/CBD/AHTEG, 2011a, see also Box 2). Indicators ready for use globally, to be developed for use at the global level, and for consideration at the national level are labelled A, B, and C, respectively, in Table 1.



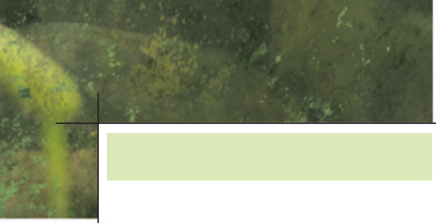


TABLE 1
Relationship between the types of indicators (in the sequence of UNEP/CBD/AHTEG: S: state, P: pressure, B: benefit, and R: response, corresponding to the four logical policy questions (see Section 1.1) and the five strategic goals of the Aichi Targets (see Box 2), headline indicators and operational indicators of relevance for genetic diversity of trees (Source: extracted and adapted from Appendix V in UNEP, CBD and AHTEG, 2011a).[10] A: ready for use at the global level, B: recommended for development at the global level, C: proposed for consideration/development at the sub-global level. Aichi Target: "most relevant target" first; if Target 13 or 16, among "other relevant targets", listed subsequently. The level of diversity (ecosystem, species, genes or general biodiversity) in focus has been added.

Type of indicator	Headline indicator	Level and readiness for use	Operational indicator	Aichi Target	Focus
S	Trends in abundance, distribution and extinction risk of species	A	Trends in abundance of selected species (UNCCD indicator)	12,13	Species
		A	Trends in extinction risk of species (MDG indicator 7.7) (also used by CMS)	12,13	Species
		B	Trends in distribution of selected species (also used by UNCCD)	12	Species
S	Trends in genetic diversity of species	B	Trends in genetic diversity of cultivated plants, and of farmed and domesticated animals and their wild relatives	13	Genes
		C	Trends in genetic diversity of selected species	13	Genes
P	Trends in pressures from unsustainable agriculture, forestry, fisheries and aquaculture	A	Trends in population and extinction risk of utilized species, including species in trade (also used by CITES)	4	Species
		B	Trends in population of forest and agriculture-dependent species in production systems	7	Species
P	Trends in pressures from habitat conversion, pollution, invasive species, climate change, overexploitation and underlying drivers	A	Population trends of habitat-dependent species in each major habitat type	5	Species
		A	Trends in the impact of invasive alien species on extinction risk trends	9	Species
		B	Trends in climate change impacts on extinction risk	10	Biodiversity
B	Trends in distribution, condition and sustainability of ecosystem services for equitable human well-being	A	Trends in benefits that humans derive from selected ecosystem services	14	Ecosystem
		A	Population trends and extinction risk trends of species that provide ecosystem services	14	Species
		B	Trends in economic and non-economic values of selected ecosystem services	14	Ecosystem
		C	Trends in the condition of selected ecosystem services	14	Ecosystem

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[10] The updated set of indicators from 2016 (UNEP/CBD/COP, 2016) operates with generic indicators and specific indicators instead of headline and operational indicators. The 2016 set of indicators is expanded and further differentiated compared to the 2011 set of indicators.

Type of indicator	Headline indicator	Level and readiness for use	Operational indicator	Aichi Target	Focus
R	Trends in integration of biodiversity, ecosystem services and benefits sharing into planning, policy formulation and implementation and incentives	B	Trends in number of effective policy mechanisms implemented to reduce genetic erosion and safeguard genetic diversity related to plant and animal genetic resources	13	Genes
		B	Trends in implementation of National Biodiversity Strategies and Action Plans, including development, comprehensiveness, adoption and implementation	17,13, 16	Biodiversity
R	Trends in access and equity of benefit sharing of genetic resources	B	ABS indicator to be specified through the ABS process	16	Genes
R	Trends in accessibility of scientific/ technical/traditional knowledge and its application	B	Trends in degree to which traditional knowledge and practices are respected through full integration, participation and safeguards in national implementation of the Strategic Plan	18,13	Biodiversity
		B	Trends in coverage of comprehensive policy-relevant sub-global assessments including related capacity building and knowledge transfer, plus trends in uptake into policy	19	Biodiversity
		C	Number of maintained species inventories being used to implement the Convention (CBD)	19,13	Species
R	Trends in coverage, condition, representativeness and effectiveness of protected areas and other area-based approaches	A	Trends in protected area condition and/or management effectiveness including more equitable management (decision X/31)	11,13	Biodiversity (protected areas)
		A	Trends in representative coverage of protected areas and other area-based approaches, including sites of particular importance for biodiversity, and of terrestrial, marine and inland water systems	11,13	Ecosystem
		B	Trends in the connectivity of protected and other area-based approaches integrated into land and seascapes (decision VII/30 and VIII/15)	11,13	Biodiversity (protected areas)
		C	Population trends of forest-dependent species in forests under restoration	15	Species
		C	Trends in the delivery of ecosystem services and equitable benefits from protected areas	11,13	Ecosystem
R	Trends in mobilization of financial resources	Not specified	Trends in financial flow of funding for implementation of the Strategic Plan (Indicators agreed in decision X/3 of CBD COP)	20,16	Biodiversity

transfer and uptake into policy, areas which are of importance for the conservation, management and use of genetic diversity.

There are thus 10 proposed headline indicators and 26 proposed operational indicators of the indicators proposed by the Ad Hoc Technical Expert Group of UNEP, which are considered relevant for genetic diversity in the context of this study.

Of the 26 proposed operational indicators, nine are considered ready for use at the global level (class A), 11 are suggested for development at the global level (class B), five are proposed for consideration/development at sub-global level (class C, *i.e.* regional, national or local), and one is unclassified in terms of level, but relevant in general for all areas.

Of the 26 operational indicators, five relate primarily to the ecosystem level, 10 focus mainly on the species level, four on the genetic level, and seven cut across the diversity levels.

The challenge of translating the acknowledged headline and operational indicators of species distribution and their genetic diversity into specific verifiable sub-topic indicators (see Sections 1.2 and 1.4) remains.[11]

1.6 The continued need to identify operational indicators for tree genetic diversity

A number of indicators have been proposed to address the internationally recognized need to monitor the loss of biodiversity and its implications for the sustainable provision of ecosystem services (MEA, 2005). As a result, and thanks to a concerted international effort, numerous monitoring systems are emerging. However, for some areas they are either still too limited in scope or incompatible.

In their 2009 review of 617 peer-reviewed journal articles between 1997 and 2007, Feld *et al.* (2009) listed 531 indicators for biodiversity and ecosystem services encompassing a wide range of ecosystems (forests, grasslands scrublands, wetlands, rivers, lakes, soils and agro-ecosystems) and spatial scales (from patch to global scale). They found that "despite its multiple dimensions, biodiversity is usually equated with species richness only", mostly at regional and finer spatial scales. Regional to global scale indicators were less frequent than local indicators and mostly made of physical and area fragmentation measures. Despite their role and potential value across scales and habitats, "functional, structural and genetic components of biodiversity [are] poorly addressed". Genetic diversity, for example, was included in less than five percent of the 531 biodiversity indicators that were analysed.

Although progress has been made (Walpole *et al.*, 2009; Butchart *et al.*, 2010; Sparks *et al.*, 2011), the conclusion of Feld *et al.* (2009) can still generally be considered valid: "Despite great effort to develop indicator systems over the past decade, there is still a considerable gap in the widespread use of indicators for many of the multiple components of biodiversity and ecosystem services, and a need to develop common monitoring schemes within and across habitats. Filling these gaps is a prerequisite for linking biodiversity dynamics with ecosystem service delivery and to achieving the goals of global and sub-global initiatives to halt the loss of biodiversity."

Not only would there seem to be too many incompatible monitoring systems with sometimes too limited scopes making cross-sector uses difficult, there are also too few relevant indicators for operational purposes. So far, none of the indicators that stem from the CBD have been used in the forestry sector and the different attempts that have been made to implement indicators have been based on forest sector initiatives as it appears from the following chapter.

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[11] This is valid also when comparing with the updated set of indicators from 2016.

Chapter 2

Attempts to implement indicators for tree genetic diversity in practice

2.1 Criteria and indicators for sustainable forest management

The United Nations Conference on Environment and Development (UNCED), held in 1992, adopted a non-legally binding "Authoritative Statement of Principles for a Global Consensus on the Management, Conservation and Sustainable Development of All Types of Forests" (Forest Principles) in addition to the three conventions on biological diversity, climate change and desertification. This led to a somewhat separate, but parallel, process for monitoring (and associated indicator development) and promoting conservation of forest biodiversity through sustainable forest management. The Intergovernmental Panel on Forests was established in 1995 and the international policy dialogue on sustainable forest management continued through the Intergovernmental Forum on Forests from 1997 to 2000 (Rosendal, 2001).

The UN Forest Forum (UNFF) was established in 2000 to continue the work and was given the task to "monitor and assess progress at the national, regional and global levels through reporting by governments, as well as by regional and international organizations, institutions and instruments, and on this basis consider future actions needed." Countries agreed in 2001 that, among other things, the UNFF would monitor "Progress towards sustainable forest management of all types of forests" stressing "the importance of the use of regional and national criteria and indicators for sustainable forest management as a basis for reporting on sustainable forest management" (FAO, 2002). To that end, by the mid-1990s at least nine regional and eco-regional criteria and indicator processes had been initiated to monitor progress towards sustainable forest management. Most of these processes attempted to identify indicators of genetic diversity as part of a larger set of biodiversity indicators (see Table 2).

The Montreal Process was initiated in 1993 and it developed criteria and indicators in 1995 to provide a reporting framework for progress towards sustainable forest management in boreal and temperate forests. In addition to Canada, the Montreal Process includes Argentina, Australia, Chile, China, Japan, Mexico, New Zealand, Republic of Korea, Russian Federation, the United States of America and Uruguay. It has been an active international player in promoting sustainable forest management approaches as well as methods to monitor them. Each member country has its own internal set of criteria and indicators and its own process for collecting the information to report on them.

The Pan-European Process (which began as the Helsinki Process in 1993) under the Ministerial Conference on the Protection of Forests in Europe includes 44 countries. The criteria and indicator set developed through this process is used for reporting on the State of Europe's Forests (Forest Europe, UNECE and FAO, 2011).

The Tarapoto Proposal for criteria and indicators of sustainable forest management was drafted by member countries of the Amazon Cooperation Treaty in 1995: Bolivia, Brazil, Colombia, Ecuador, Guyana, Peru, Suriname and Venezuela. Although 77 indicators were identified, only 15 priority indicators, which were judged to be feasible, have been tested for use (ACTO, 2004).

Several processes, including the Near East Process (covering 30 countries extending from Algeria to Kyrgyzstan), the Lepaterique Process (the countries in Central America), the Dry Forests Asia Process (covering Bangladesh, Bhutan, China, India, Mongolia, Myanmar, Nepal, Sri Lanka and Thailand), the African Timber Organization (mostly Central and West African timber producing countries), and Dry Zone Africa (29 countries from all parts of the continent where arid or semi-arid conditions prevail) have elaborated sets of criteria and indicators for sustainable forest management. However, it is not clear to what extent they have been rigorously tested or measured, at least as part of these processes (Rametsteiner, 2006).

The International Tropical Timber Organization (ITTO) developed a set of criteria and indicators that cover much of the world's tropical forest area. Many of the ITTO member countries are also involved in one or more of the other processes (FAO, 2002). However, the reporting requirements under the ITTO are "legally binding" in as much as countries are obligated to follow up on their commitments to report on mutually agreed SFM goals using ITTO's criteria and indicators (Rametsteiner, 2006). None of the other processes has legally binding requirements.

Although the list of indicators presented in Table 2 is impressive in its breadth and intentions, few of these genetic diversity indicators are actually being measured and monitored. As Chun (2005) noted, applying the Lepaterique Process has been more theoretical than practical. As an example, although 11 countries are officially involved in the Montreal Process, which represents 83 percent of the world's boreal and temperate forest cover and 49 percent of world's forest (Anon., 2009), only Canada, Australia and New Zealand have seriously attempted to implement the criteria and indicators (McDonald and Lane, 2004). In fact, they do not usually measure all the indicators, and are notably reasonably efficient on species and ecosystem level indicators of biodiversity (FAO, 2002), but do not do so well on those at the genetic level.

Australia is an exception in that two genetic indicators of sustainable forest management are reported (Montreal Process Implementation Group for Australia 2008):

Element 1.3 (of the Biodiversity Criterion): Genetic diversity

- Indicator 1.3a. The number of forest dependent species at risk from isolation that may lead to loss of genetic variation
- Indicator 1.3b. The number of *in situ* and *ex situ* conservation efforts for forest dependent species

Australia reported the number of species for which data on genetic variation had increased over the previous five years and listed the number of species within the major taxa that are potentially at risk from isolation in Tasmania. They also listed tree species that are in genetic resource conservation and tree improvement programmes, including more than 40 native timber and oil-producing plant species, and discussed the approach taken to avoid negative impacts of gene flow from plantations.

Many of the indicators of genetic diversity themselves are problematic either in measurement or interpretation. Two of the three Montreal Process indicators are intended to measure the state of genetic diversity, but both are open to interpretation and do not provide guidance on which or how many species to monitor. Most of the indicators adopted by other processes are response indicators and some are only tangentially related to genetic diversity, for example "Area, by forest type, in categories of protected areas, in relation to total forest area". Some are two steps away from state indicators, for example, "Existence of mechanisms for the conservation of genetic resources" refers to the existence of policies or other mechanisms and stops short of determining whether or not they are implemented. Once implemented, substantial efforts would still be required to measure whether the actions are positively affecting the resource. Others, such as "Existence of the number of seed provenance" are vague, at least when written in English.

TABLE 2

Genetic diversity indicators associated with biodiversity-related criteria for major regional sustainable forest management monitoring processes (from Graudal *et al*., 2014). Year refers to the date of the indicator version presented. Number refers to the number of the indicator in the original source of information. Type: classification of type of indicator (S: state, R: response).

Process, region and year initiated	Year	Number	Text	Type
Montreal Process *Temperate and Boreal Forests* 1995 (Anon., 2009)	2007	1.3 a	Number and geographic distribution of forest associated species at risk of losing genetic variation and locally adapted genotypes	S
		1.3 b	Population levels of selected representative forest associated species to describe genetic diversity	S
		1.3 c	Status of on site and off site efforts focused on conservation of genetic diversity	R
Pan-European Forest Process (previously Helsinki Process) *Europe* (Forest Europe *et al*., 2011)	2002	4.6	Area managed for conservation and utilization of forest tree genetic resources (*in situ* and *ex situ* gene conservation) and area managed for seed production	R
Tarapoto Proposal *Amazon Forest* (ACT, 1995)	1995	4.3	Measures for conserving genetic resources	R
The Near East Process *Near East* 1996 (FAO, 1999)	1996	2.9	Existence of the number of seed provenance	R
		2.10	Number of forest dependent species with reduced range	S
		2.11	Population levels of key species across their range	S
Dry Forests Asia Process *South & Central Asia* 1999 (FAO, 2002)	1999	3.6	Existence of mechanisms for conserving genetic resources	R
African Timber Organization, *West and Central Africa* 1993 (Anon., 1998)	1994	IIA.1.3	In harvesting, the standards are explicit on minimum number of large trees to be retained as seed producers (mother trees) per ha and species	R
The Dry-Zone Africa *North, East and Southern Africa* 1995 (Anon., 1999)	1999	2.9	Average number of provenances	R
		2.10	Number of forest dependent species with reduced range	S
		2.11	Population levels of key species across their range	S
		2.12	Management of genetic resources	R
International Tropical Timber Organization *Humid tropics* 1992 (Anon., 2005)	2005	5.5	Measures for *in situ* and/or *ex situ* conservation of genetic variation within commercial, endangered, rare and threatened species of forest flora and fauna	R
Lepaterique Process *Central America* (Anon., 1997)	1997	5.6	Number of species conserved *ex-situ* (e.g. in seed banks)	R

Among the 16 genetic diversity indicators listed in Table 2, only six refer to the state of the resource while the other 10 correspond to a management or policy response. Taken together, only two state and four response indicators can be considered unique and non-overlapping among the different sets. More than half of the indicators relate directly to genetic diversity whereas the others relate indirectly to genetic diversity, for example, by measuring trends in species diversity.

The two distinct state indicators are (Graudal *et al*., 2014):

- number and geographic distribution of forest associated species at risk of losing genetic variation and locally adapted genotypes (also, “Number of forest dependent species with reduced range”); and

- population levels of selected representative forest associated species to describe genetic diversity (also, “Population levels of key species across their range”).

In principle such indicators could have been part of the 2010 Biodiversity Indicators of CBD, but no indicators of this kind were explicitly included (see Section 1.3 and 1.4). There is room for inclusion and adoption in the framework proposed for 2011–2020 (see Table 1, Section 1.5).

The four response indicators are (Graudal *et al*., 2014):

- status of on-site and off-site efforts focused on conservation of genetic diversity (also “area managed for...”, “mechanisms for...”, “measures for...”);
- existence of the number of seed provenance (also “average number of…”);
- in harvesting, the standards are explicit on minimum number of large trees to be retained as seed producers (mother trees) per ha and species; and
- management of genetic resources.

No such response indicators were assessed as part of the 2010 Biodiversity Indicators either, but if better defined, they would be well suited to assess “trends in number of effective policy mechanisms implemented to reduce genetic erosion and safeguard genetic diversity” (Table 1, Section 1.5).

Except for the “existence of the number of seed provenance”, which is unclear as stated (may be a translation issue), information on this set of unique state and response indicators would provide a reasonable assessment of the status of genetic resources as well as the management responses. However, with a few exceptions, the data has not been collected on any of the indicators (Wijewardana, 2008).

Forest Europe reported on the criteria and indicators set of the Pan-European Process (Forest Europe, UNECE and FAO, 2011) and is one of the few of the processes to attempt to measure and report on a genetic indicator. The areas managed for *ex situ* conservation and seed production were found to have increased during the reporting period (from 1990 to 2010). More than 450 000 hectares of forest were reported to be managed for *in situ* conservation in Europe outside of Russian Federation, covering a total of 142 tree taxa, including species, sub-species and hybrids. The report noted that “there are significant gaps in the geographical representativeness of *in situ* gene conservation areas as compared to the distribution maps of European tree species”, and furthermore, that “wide coverage of areas for gene resources ensures the capacity of forest trees to adapt to climate change”. Overall the assessment shows positive trends. Although it is laudable that an assessment of the genetic indicator was included in the report, it illustrates the weakness of reporting only on response indicators without measuring state indicators. An increase in the area reported for *in situ* and *ex situ* conservation does not reveal much, if anything, about the status of the forest genetic resource itself. A proposed revised indicator on genetic resources is currently (2017–2020) being prepared by EUFORGEN for the pan-European criteria and indicators for sustainable forest management.

The indicators listed in Table 2 include only those that were specifically intended as indicators of genetic diversity (although some fall more into the species-level indicator category). Other indicators that are not listed but were adopted by the processes to measure biodiversity at the ecosystem and species levels refer to characteristics that have a direct bearing on genetic diversity of forest tree species as well. For example, indicators relating to the extent of protected areas, forest cover and fragmentation, and to the degree of destructive harvest are relevant for genetic resources and, in some cases, have been assessed more successfully than those that are specific for genetic diversity. Considering that population size might be the most important indicator of genetic diversity and a close second would be degree of fragmentation, the ecological or species level indicators may be more useful indicators of the state of genetic resources for many species than the genetic indicators themselves (which are rarely assessed).

At a Joint Workshop (October 2011, Victoria, British Columbia, Canada) to "Streamline Global Forest Reporting and Strengthen Collaboration among International Criteria and Indicator Processes", with Montreal Process, ITTO, Forest Europe and FAO representatives, although many successes were discussed, it was noted that the national and regional SFM criteria and indicator processes are facing challenges for several reasons (Anon., 2011). Chief among them is the competition from other fora outside of forestry, such as the CBD, and the report called for closer collaboration with such efforts. The proceedings also recorded that it has become increasingly difficult to maintain political awareness of SFM and to make strong links between the use of criteria and indicators and policy development. Despite the urgency of calls to combat deforestation, enthusiasm for using criteria and indicators to monitor sustainability of forestry practices seems to be declining; in fact, interest in sustainable forestry seems to be falling in priority in the national policies of some countries (Wijewardana, 2008). The recent global attention to forest landscape restoration as an important component of climate change mitigation and adaptation (e.g. Stanturf *et al.*, 2015) may contribute to reverse this trend.

Indicators relating to biodiversity have been noted to be difficult and issues that were identified by participating countries to the Montreal Process included "no scientific agreement on how the data should be collected" and "little or no understanding of how to measure an indicator" (Parviainen and Lier, 2006).

2.2 Indicators of forest certification schemes

Forest certification schemes have adopted indicator sets (though sometimes using different terminology) to monitor forest resources at the management unit level. The two largest schemes are the Forest Stewardship Council (FSC) and the Programme for the Endorsement of Forest Certification (PEFC). Both have generic criteria and/or indicators for genetic diversity. The FSC in its 10 generic principles and criteria has two criteria that relate to genetic diversity, as follows:[12]

> "6.3 Ecological functions and values shall be maintained intact, enhanced, or restored, including:
>
> a) Forest regeneration and succession.
>
> b) Genetic, species, and ecosystem diversity."
>
> and
>
> "10.3 Diversity in the composition of plantations is preferred, so as to enhance economic, ecological and social stability. Such diversity may include the size and spatial distribution of management units within the landscape, number and genetic composition of species, age classes and structures."

Under the FSC certification, the specific indicators vary by country and region, so adoption of specific wording relating to genetic diversity is optional. But the 10 principles must be applied as a condition for certification in any management unit.

The PEFC is an international umbrella organization under which independent forest certification schemes are mutually recognized. Several of the generic PEFC indicators within the "Criterion 4: Maintenance, conservation and appropriate enhancement of biological diversity in forest ecosystems" relate to genetic diversity (PEFC, 2010):

> "4.1 Forest management planning shall aim to maintain, conserve and enhance biodiversity on ecosystem, species and genetic levels and, where appropriate, diversity at landscape level.
>
> 4.2 Forest management planning, inventory and mapping of forest resources shall identify, protect and/or conserve ecologically important forest areas containing significant concentrations of:
>
> a) protected, rare, sensitive or representative forest ecosystems such as riparian areas and wetland biotopes;

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[12] See www.fsc.org

b) areas containing endemic species and habitats of threatened species, as defined in recognised reference lists;

c) endangered or protected genetic *in situ* resources;

d) globally, regionally and nationally significant large landscape areas with natural distribution and abundance of naturally occurring species.

4.3 Protected and endangered plant and animal species shall not be exploited for commercial purposes. Where necessary, measures shall be taken for their protection and, where relevant, to increase their population.

4.4 Forest management shall ensure successful regeneration through natural regeneration or, where not appropriate, planting that is adequate to ensure the quantity and quality of the forest resources.

4.5 For reforestation and afforestation, origins of native species and local provenances that are well-adapted to site conditions shall be preferred, where appropriate. Only those introduced species, provenances or varieties shall be used whose impacts on the ecosystem and on the genetic integrity of native species and local provenances have been evaluated, and if negative impacts can be avoided or minimised."

The two forest certification schemes and their indicators are applicable at the management unit and are not intended to be expanded to provide information at a regional, national or international level.

For example, an indicator related to genetic resources in the Finland FSC Standard is: "The forest owner shall favour naturally regenerated seedlings when silviculturally or economically justified. In artificial regeneration, the suitability of the origin of seedling and seed material shall be confirmed (Board of the Finnish FSC Association Standard Working Group, 2010)." The Canadian Boreal FSC Standard includes the following: "The genetic diversity of tree species is maintained during forest management through: the maintenance of species at the limits of their range, use of natural regeneration, local collection of seeds for seedling stock and seed broadcasting, adherence to seed zones, and appropriate selection of seed trees and advanced regeneration." (Forest Stewardship Council – Canada, 2004).

Although the PEFC generic indicators appear to be more specific than the FSC's, the FSC, at least as it is applied in Western Canada is a closer match to the forest genetic resource policy in British Columbia, Canada with more direct applicability to the genetic resources within a management unit, according to Auld and Aitken (2003). They noted that the province's policy with respect to FGR addresses:

- genetic diversity (the variability within a species in a natural or artificially regenerated stand compared with the baseline);
- adaptation (the ability of trees to grow in local conditions);
- quality (the beneficial character of traits that bred trees are selected for); and
- the use of genetically modified (GM) trees.

Both certification systems fall short of the provincial requirements, having a stronger emphasis on biodiversity in general than genetic diversity (Auld and Aitken, 2003).

Both FSC and PEFC encourage management practices that promote natural regeneration and preserve phenotypic variation, but the FSC differentiates between "natural" and "plantation" in its assessment of forest management operations; and within natural forests, natural regeneration and conservation set-asides (e.g. buffer zones) are required by FSC.

On the other hand, PEFC is alone in encouraging that planting material be well adapted to the target sites and that if planting material is not local, the potential for damage should be assessed and the non-local material is allowable only if its negative effects can be avoided or minimized.

2.3 Major issues and gaps for application of indicators in practice

Considerable time and effort have been spent on developing and testing genetic indicators as part of SFM criteria and indicators processes and forest certification schemes. However, there have been few attempts to implement any of them and those that have been measured and reported are response indicators.

Reporting on response indicators alone without measuring state indicators can lead to misleading conclusions because well-intended policies and management practices do not necessarily result in improved conservation status (see Section 3.4). Reasons for the dearth of reported results for genetic indicators include the difficulty, real or perceived, in interpreting and measuring them, disagreement among the experts on the minimal set of indicators required in order to provide useful and usable information, lack of resources to add additional variables to the standard forest inventory data collection procedures, and a lack of understanding among the forest management practitioners about the relevance of genetic resources to forest sustainability.

A common practical framework is needed to reduce the number of indicators that appear in the various processes to several that are unique, informative, and practically applicable. They must be based on science and geneticists must provide the necessary support to demonstrate the applicability and value of the indicators in a way that non-geneticist managers and other practitioners can understand and appreciate.

Certification bodies such as FSC and PEFC can play an important role in guiding the implementation of sustainable forest management at the management unit level. However, the indicators must be both more specific and practically applicable, at least in the national or regional standards, to be meaningful.

Chapter 3

Development of scientifically based indicators for tree genetic diversity

Criteria and indicators have been developed for various aspects of sustainable forest management (e.g. Castañeda, 2000). The genetic variation within tree species is one of these aspects (see above and further below). In an international context, work on criteria and indicators for assessment and monitoring genetic variation of trees has been led by FAO since the early 1990s with important contributions in the early years by CIFOR and more recently Bioversity International, particularly in Europe through EUFORGEN. Also, many regional and national programmes exist and have made attempts to identify criteria, indicators and verifiers for monitoring FGR (Chapter 2), but documentation of experiences in the scientific literature is only patchy.

In Section 1.1, we expressed our criterion as the conservation of the world's forest (or tree) genetic diversity for sustainable use; and in Section 1.2 we put forward our thesis that the indicators we are looking for should reflect the extent to which (i) the genetic diversity within and between populations and ecosystems is expected to change; and (ii) sound genetic processes are expected to continue to work efficiently.

Here we discuss the identification of indicators of tree genetic diversity that can realistically be used to assess the status and development of within-species genetic diversity world-wide. For practical application purposes the identification of verifiers becomes important. Verifiers should be measurable and provide "data or information that enhances the specificity or the ease of assessment of an indicator" (Prabhu, 1999).

Namkoong *et al.* (2002) present a conceptual model of the relation between pressure, state and response indicators in a context where response is the response of biodiversity itself (called process by Brown *et al.*, 1997) and not the response by man, i.e. different from the RPSB loop that is now gaining prominence (Section 1.1).

It is useful to recall the definitions provided by Sparks *et al.* (2011):

- "Responses: indicators measuring the implementation of policies or actions to prevent or reduce biodiversity loss.
- Pressures: indicators monitoring the extent and intensity of the causes of biodiversity loss that responses aim to address
- State: indicators analysing the condition and status of aspects of biodiversity
- Benefits: indicators quantifying the benefits that humans derive from biodiversity."

We approach the problem from three different angles:

1. How far are we towards developing indicators for tree genetic diversity (Section 3.1)?
2. What is the current thinking on the utility and practicality of state, pressure, response and benefit indicators in a world-wide context (Section 3.2–3.3)?
3. What are the most appropriate data sources for developing usable practical indicators (Section 3.4)?

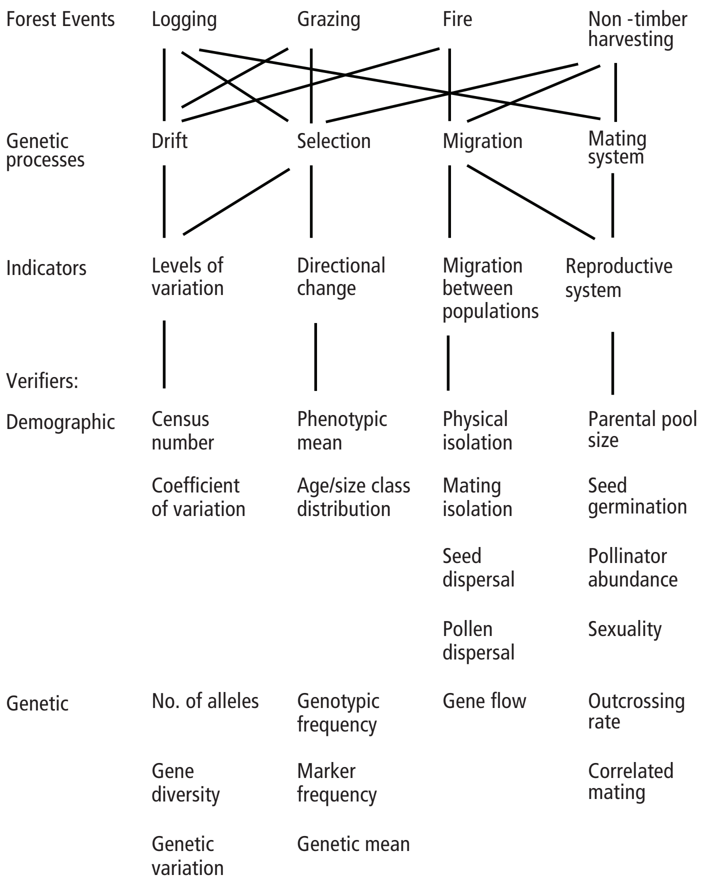
Given that indicators should reflect trends, we will also touch upon the baseline problem (Section 3.4): to what extent can we establish a meaningful baseline from where we can assess the development of the indicators?

3.1 Development of indicators for tree genetic diversity

The most elaborate and authoritative work on criteria and indicators for assessing and monitoring tree genetic variation was made in the period from the mid-1990s to the early 2000s. Namkoong *et al.* (1996, 2002) suggested one criterion for conservation of FGR: "conservation of the processes that maintain genetic variation" and four indicators related to the processes that maintain genetic diversity. Several demographic (12) and genetic (9) verifiers related to the four indicators were identified. The hierarchy of criterion, indicators and verifiers is shown in Figure 2.

FIGURE 2

Relationship between forest events, genetic processes and their indicators (from Namkoong *et al.*, 2002).*



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* The diagram is limited to natural forests so the ability to grow (propagate) a species would have to be added in the case of plantations, e.g. many dipterocarps cannot at present be propagated.

The indicators have the obvious advantage that they conceptually link to generally agreed population genetic thinking. Also, a fair number of case studies of different tree species in different ecosystems have tried to qualify and quantify the relations between the specific "Forest events", and "Genetic verifiers" by applying genetic markers (previously allozymes, in recent years usually DNA based techniques). However, a general application, *scaling-up* the genetic verifiers proposed by Namkoong *et al.* (2002) would be a significant task for any single species, not to mention for any proportion of the (relatively small) sample of tree species that may be classified as cultivated, or for most species in the wild (see above). Also, it would not be easy to establish a suitable base line for all the indicators. The demographic verifiers seem easier to assess - at least a reasonable subset of the indicators in a reasonable subset of populations.

At the request of FAO, McKinnell (2002) made a comprehensive review of indicators on tree genetic diversity, and reviewed the work of Namkoong *et al.* (1996, 2002) as well as other international and national processes that have led to suggestions for tree genetic diversity indicators.

McKinnell (2002) made the following six major conclusions:[13]

1. For any indicator to be useful in practice the data must be easy and cheap to collect and the significance for sustainability of the ecosystem must be clear. Most forest management agencies simply cannot afford to implement indicator systems that require large resources for data collection or expensive analytical techniques.
2. The current indicators in the various criteria and indicator processes are generally ineffective for measuring the status and trends in genetic diversity in forest ecosystems.
3. Since it is not feasible to monitor every aspect of biological diversity, suitable surrogate measures must be sought. The most appropriate surrogates are those ecological processes that control genetic diversity.[14] Recent developments appear to be heading in that direction.
4. Direct quantitative assessment of genetic diversity by biochemical means is not yet, and probably will never be, capable of use for routine operational purposes.[15] However, biochemical techniques are invaluable tools for research to support the identification of suitable surrogate attributes. A great deal more research is required before we can be confident that we have the most effective surrogates. Since we are basically looking for ecological processes as surrogates, there are potentially indicators that will be common to most forest types.
5. Though the criteria and indicator approach as a whole holds so much promise as a spur to better forest management, it seems to have lost impetus in some processes.
6. With respect to forest genetic diversity, we may have to be satisfied, for the foreseeable future, with a qualitative approach that requires forest managers to have in place an appropriate strategy for its management. Such strategies themselves are not easy to develop and implement and will vary greatly according to local circumstances.

There does not seem to have been much work toward developing indicators for tree genetic diversity between the review of McKinnell (2002), testifying his point 5 (Sigaud, 2005; Laikre *et al.*, 2010), and a few recent studies (e.g. Aravanopoulos, 2011; Konnert *et al.*, 2011). However, in some areas, work is underway. EUFORGEN has made a remarkable achievement over the last decade by establishing a pan-European network of gene conservation stands for a considerable number of forest tree species (Koskela *et al.*, 2013; de Vries

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[13] McKinnell (2002) did not number his conclusions. The text has been slightly abbreviated but is otherwise quoted from McKinnell (2002).

[14] Performance of populations in field trials could help to identify the genetic variation as well as to delineate genecological zones (e.g. Graudal *et al.,* 1997).

[15] This assumption has proven to be false; see further in the text.

et al., 2015). A programme for monitoring these stands is currently being developed (Aravanopoulos *et al.*, 2015).

Molecular markers are developing rapidly and the assumption of McKinnell (2002) under point 4 is no longer valid. The use of molecular markers to construct indicators is much more likely today - not to say inevitable – than it was ten years ago, where they almost *a priori* would be rejected. Molecular markers provide information on risk status that maps do not (for example large population size, but little diversity because of recent colonization or centuries old introduction using uniform material). Molecular data are rapidly becoming less expensive, and as we increase the amount of gene sequences available (both neutral markers to test for demographic parameters, and adaptive genes to test for adaptation), monitoring such genes in natural populations of selected species are becoming feasible at no great cost (Funk *et al.*, 2012).

With reference to Spellman *et al.* (2001) and Jennings *et al.* (2001), McKinnell (2002) seems to favour the idea of identifying ecological process surrogates of genetic diversity as possible quantitative indicators (point 3). With further reference to Jennings *et al.* (2001) and to ITTO (1998), McKinnell (2002) points to the qualitative approach under point 6 as probably more likely. Point 3 of McKinnell (2002) would represent a state indicator (S), whereas point 6 would represent a response indicator (R). We have seen that response indicators so far are the ones that have been mainly used in practice (Chapter 2).

Following the review of McKinnell (2002), Bariteau (2003) analysed the feasibility of evaluating the state of the world's FGR. The main conclusions by Bariteau (2003) were:

1. There are various reasons to think that a project on the state of the world's forest tree genetic resources coordinated by FAO, in close collaboration with national and international partners, would be desirable.
2. The feasibility of the project relies on the existence of intraspecific genetic diversity indicators with an acceptable applicability level for a global study of this type, and does not require large financial investments.
3. One of the proposed options consists of turning to genecological zonation to distinguish the variability within species.
4. This approach would have the additional advantage of placing knowledge of species diversity in a broader ecological context through knowledge of the ecosystems that provide their habitat. An eco-regional approach would be necessary to compare information between neighbouring countries. This step would be compatible with the ecosystem approach recommended by the CBD and would allow synergies to begin to be developed between forest genetics and environmental sciences.

The proposal by Bariteau (2003) to use genecological zonation to assess genetic diversity, which is made with reference to Graudal *et al.* (1997), comply with the conclusions of McKinnell (2002) given above, specifically point 6. Today, we are fortunate to be able to combine such an approach with the use of molecular markers (see also Pierson *et al.*, 2015).

The proposal was discussed by the FAO Panel of Experts on Forest Gene Resources (the FORGEN Panel) at its 13th session in November 2003 (FAO, 2004). According to the FORGEN Panel, the lack of a global assessment of the status and trends of forest genetic diversity and the lack of estimators of the rate of genetic diversity loss were limiting factors in decision-making at international, national and institutional levels.

A global FGR evaluation should constitute a long-term objective and rolling process, rather than a short-term set of disconnected activities (FAO, 2004). The strategic objective should be combined with a pragmatic, step-by-step implementation, using top-down and bottom-up approaches as appropriate, combined with specialized thematic case studies. Priority should be given to identifying and validating measurable forest genetic parameters, identifying values attached to the use of trees and to agreements on priority-setting methodologies.

The FORGEN Panel revisited the above issue at its 14th Session in February 2007 (FAO, 2007), based on a comprehensive technical review of status and trends of the world's FGR (Palmberg-Lerche, 2007) and an unpublished secretariat note dealing with the identification of global indicators of tree genetic diversity (L. Graudal and E.D. Kjær, personal communication, 2007), in which a proposal for development of an indicator on tree genetic diversity based on genecological zonation was described. The contents of this note have been updated and incorporated in this thematic study.

The FORGEN Panel recommended that indicators be further elaborated to help monitor changes in types and levels of forest biological diversity and FGR, which should be fully integrated with those developed and implemented in other fields or sectors. The FORGEN Panel further suggested a minimum set of information on genetic diversity of planted tree species, which is reproduced in Appendix 2 (FAO, 2007).

It was also noted that using reliable indicators will improve: (a) the precision of the State of the World assessment, (b) national monitoring of changes over time, (c) related management actions, and (d) the future ability of FAO to technically assist countries and local communities to manage FGR effectively, focusing on critically important areas, species and issues (FAO, 2007). Ecogeographic and genecological zonation were specifically mentioned as tools to support the definition of priorities for conservation and the early application of genetic resource management (FAO, 2007).

Scientific work has focused mainly on the state indicators because they provide the only direct measure of the diversity itself (Section 1.1 and 1.2). Pressure indicators are intrinsically linked with state indicators and can often be expressed by the same verifiers. For example, a dwindling population may indicate loss of genetic variation as well as anthropogenic or environmental change. In the following, we discuss state and pressure indicators together, followed by a section dealing with response and benefit indicators.

3.2 State and pressure indicators

Following up on the work of Namkoong *et al.* (1996, 2002), McKinnell (2002) and Bariteau (2003), we discuss several indicators for monitoring the state and pressure of tree genetic diversity, whether directly related to genetic processes (selection and gene flow) or their ecological surrogates. It is possible to use surrogates because ecological processes affect genetic processes, usually by manipulating population sizes via fluctuations in selection intensity and mating system variability. In turn, genetic changes will affect adaptation potential and demography, and thus ecological processes.

The interactions between demographic and genetic processes are summarized in Figure 3, and a detailed explanation of their effects can be found in the simulation papers of Le Corre and Krémer (2003, 2012). Such indicators have never been put into practice.

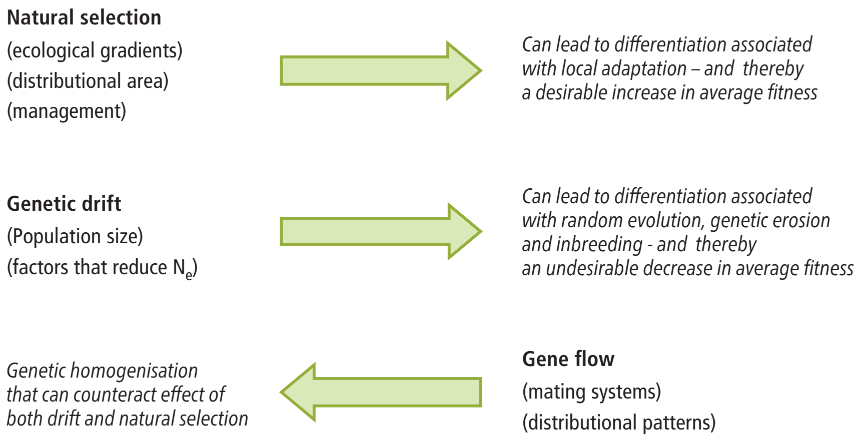
An ecological surrogate approach

As McKinnell (2002) pointed out, ecological factors meaningful for genetic diversity might be more easily measured and monitored than genetic parameters, thus they might also be more easily implemented by forest managers, forest owners or monitoring agencies.

At the regional level (or ecosystem scale), abiotic ecological factors can affect population size and genetic diversity. In a study of the correlation of environmental proxies on the adaptive genetic diversity of *Eucalyptus delegatensis* grown in common gardens, Garnier-Géré and Ades (2001) found that solar radiation and temperature range each explained more than 50 percent of the total genetic variance of growth performance as a result of local adaptation in the local natural habitat. In *Populus nigra*, hydroperiod, sediment type and area of available habitat all affect regeneration and demographic structure, thus selection and gene flow (Lefèvre *et al*., 2001).

At the local scale (or management unit), biotic ecological factors, such as the amount of inter-specific competitors and hybridogeneous congeners

FIGURE 3
Genetic diversity in populations results from the interaction between natural selection, gene flow and genetic drift. Scientifically based indicators are necessary to monitor the state of this subtle balance and threats that menace it from local to regional and global scales.



(related organisms that may hybridize), occurrence of pests and diseases were also found to be good surrogates of genetic diversity in *Populus nigra* as they affect demography and selection (Lefèvre *et al.*, 2001). For *Eucalyptus delegatensis*, Garnier-Géré and Ades (2001) found understorey type to be correlated to adaptive genetic diversity, thus reflecting local or region wide selection.

Ecological surrogates of genetic diversity can apply at least at two different spatial scales, local and regional (and/or national depending on species distribution range). However, they could be species-specific and lack the generalization abilities needed for indicators. Even when global biodiversity indices are created, their idiosyncrasy might remain. Geburek *et al.* (2010) created such an index, easily usable by management services for monitoring, encompassing multiple levels of biodiversity. However, its use is limited to the forests of Austria, thus making it difficult to handle at the world level. In general, ecological surrogates and multi-level-based indices are hard to translate to "averaging" approaches and, therefore, are very difficult to interpret.

A genecological approach

The genecological approach addresses genetic diversity at the regional scale where species have their distribution range defined (from entire continents down to national and subnational levels).

The perception of tree species consisting of a series of locally differentiated populations has been supported by numerous studies (e.g. Rogers and Ledig, 1996). It has stimulated the development of experimental methods since the eighteenth century based on common garden experiments where trees of different origin were planted in the same environment to reveal the genetic component of variation. The high level of differentiation observed in the adaptive genetic diversity among populations, especially for growth capacity, justified developing forest genetics in the twentieth century by making foresters aware of the need to conserve the genetic diversity of forest trees.

Bariteau (2003), therefore, poses this question: "Should not this method for identifying variability based on genecological zonation be the starting point for activities targeting genetic resources, and be generalized to the set of species considered as priority in the world?"[16]

Conceptually, the genecological approach builds on any tree species being perceived as a series of metapopulations,[17] differentiated through the balance between gene flow (between populations at different frequency according to the landscape scale) versus natural selection (reflecting different local conditions within the natural distribution area).

The ability to disperse genes over long distances by pollen or seed is a common feature of many tree species (Smouse and Sork, 2004) and this will act towards homogenizing differentiation due to divergent natural selection (Kremer *et al.*, 2012). The local scale of differentiation is, therefore, only expected to occur if selective forces are strong over small distances (Eriksson *et al.*, 2012). In the presence of moderate ecological gradients, the adaptive genetic differentiation within a species is, therefore, expected to be manifested at a regional rather than a local level (e.g. Graudal *et al.*, 1997). The empirical evidence for the presence of local adaption is substantial in tree species where provenance and common garden tests over the last century have provided ample evidence of adaptation on a regional scale and development of clinal patterns in species with continuous distribution range across ecological gradients, even in the presence of substantial gene flow (Alberto *et al.*, 2013). Most published studies are from temperate and boreal forests, but several studies in tropical tree species have identified similar levels of adaptation (Finkeldey and Hattemer, 2007; Ræbild *et al.*, 2012). The genecological concept builds on an expectation that genetic differentiation in adaptive traits will reflect the variation in ecological conditions at a regional level, at least as long as the species in question has a fairly continuous distribution containing viable populations. Based on this assumption, the idea behind the genecological zonation approach is to develop a frame for predicting patterns of genetic variation between populations in traits of adaptive significance. As the approach is based on the expectation that genetic patterns are generated from the balance between gene flow and selection, it will be less relevant for species predominantly present in small fragmented populations where drift and inbreeding may have played a prominent role in developing genetic patterns.

In areas with substantial plantations, the gene pools could sometimes consist of islands of indigenous populations separated by cultivated land filled with planted individuals of non-native genetic origin. In this context, gene flow through pollen (or seed) into the native populations could be problematic due the risk of "swamping" ("polluting") the native gene pool (McKay *et al.*, 2005). In such cases, applying the genecological approach for sampling within-species diversity must be combined with identifying "locally, genetically sound and un-swamped populations" (McKay *et al.*, 2005).

In addition to strong theoretical ecological and evolutionary reasons, there are well-documented empirical results that "point to potentially important links between two of the most fundamental levels of biodiversity: species diversity and genetic diversity" (Vellend and Geber, 2005). Vellend (2006) further indicates that scientific results "point to the importance of considering

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[16] Here, priority is viewed from a utilitarian perspective. See also "Identification of priority species" in the technical review of status and trends of the world's FGR prepared for the FORGEN Panel meeting in 2007 (Palmberg-Lerche, 2007).

[17] A group of spatially separated populations of the same species with potential genetic connectivity (Levins, 1969; Hanski and Simberloff, 1997; Baguette and Stevens, 2003).

the genetic origin and diversity of material used in ecological experiments and in restoration efforts, in addition to highlighting potentially important community consequences of the loss of genetic diversity in natural populations.” Factors such as selection, migration and habitat range could affect species diversity and genetic diversity in the same direction (Vellend and Geber, 2005). However, the links between genetic diversity, species diversity, composition of communities and distribution are far from trivial (e.g. Alonso *et al*., 2006). For example, restricted habitat and distribution ranges often lead to low species diversity in communities (islands for example), but responses in terms of genetic diversity can vary widely: for example, the California endemic *Pinus torreyana* (Ledig and Conkle, 1983) is genetically narrow (“depauperate”) but *Cedrus brevifolia* (Eliades *et al*., 2011) with limited distribution in Cyprus is one of the most diverse conifers. Conversely, widely distributed species such as the Mediterranean *Pinus pinea* (Vendramin *et al*., 2008) and the North American *Pinus resinosa* (Mosseler, 1991 and 1992; Allendorf *et al*., 1982) are genetically depauperate species. Bottleneck related evolutionary factors may explain such discrepancies (e.g. Fady and Conord, 2010).

In a recent study, ter Steege *et al.* (2015) estimated the global conservation status of more than 15 000 Amazonian tree species (see also Feeley, 2016). They find that between 36-57% of all Amazonian tree species qualify as globally threatened according to IUCN Red List criteria. They further estimate that if trends observed in Amazonia apply to all trees in the tropics, more than 40 000 tropical tree species may qualify as globally threatened. Their estimations are based on the effects of forest loss on tree populations and can thus be interpreted as loss of intraspecific variation in all the species assessed.

Genetic monitoring of management units

Conserving genetic resources is most practically done at the local level where conservation units are defined and management plans with specific requirements are implemented to protect local resources (e.g. Koskela *et al.,* 2013). At this scale, indicators need to monitor temporal changes in population genetic variation and structure relevant to the long-term adaptive potential of the population, using appropriate measurements (verifiers) derived from the field of population genetics (Aravanopoulos, 2011; Konnert *et al*., 2011). Namkoong *et al*. (1996, 2002), Aravanopoulos (2011) and Konnert *et al*. (2011) proposed a series of indicators to evaluate genetic variation, selection, gene flow and genetic drift using demographic and genetic parameters as verifiers (Box 3 and Table 3).

Use of molecular markers and next generation sequencing for genetic monitoring

The use of molecular tools for genetic monitoring have moved from an era of scepticism (McKinnell, 2002), where studies were limited to reveal patterns of neutral genetic diversity and provide genetic parameters to characterize such diversity, to a point of great promise of surmising also adaptive genetic variation (Schwartz *et al*., 2007; Hansen *et al*., 2012; Funk *et al.*, 2012; Fady *et al.,* 2016; Dawson *et al.,* 2017). Applications in practice are being promoted (e.g. Stetz *et al.,* 2011) in genomic and metagenomic approaches. The promises of molecular markers are described in Box 4.

In a recent study on wheat by the Foundation for Research on Biodiversity (FRB) in France (Goffaux *et al.,* 2011), trends in genetic diversity were monitored using a combined measure of: (1) number of varieties used over time, (2) how varieties are used in space (a landscape x variety heterogeneity measure), and (3) genetic diversity of each variety. Basically, the indicator combines diversity within and diversity among varieties over a given landscape (regional within country, country, continental (= range-wide), global). The study showed a decreasing trend of genetic diversity in wheat in France during the twentieth century that was not visible when only part (1) of the indicator was used.

Box 3
Using indicators to monitor conservation efficiency at the local level of the management unit

A gene conservation unit refers to a population of a geographical location selected because of its potential for adaptive evolution through maintaining population and metapopulation stability (Moritz, 1999). Genetic monitoring of a gene conservation unit is defined as the quantification of temporal changes in population genetic variation and structure relevant to the long-term adaptive potential of the population, generated by measurements of appropriate parameters (Aravanopoulos, 2011). It refers to the observation of the dynamics of transition from the present to the future genetic status of a gene conservation unit (Konnert *et al.*, 2011). The aim of genetic monitoring is to assess the status of genetic resources and quantify relevant changes in light of preserving the long-term adaptive evolutionary potential of a species. Genetic monitoring encompasses something more than a study method, especially under changing environmental conditions. By observing temporal changes in populations, causal components can be inferred, and their relative importance can be evaluated. Such an early detection mechanism would maximize the chances of implementing management decisions that could alleviate potential harmful effects before irreversible damage occurs. Hence, genetic monitoring of gene conservation units includes a prognostic value as well and forms a method to secure the conservation of processes that maintain genetic variation in natural populations (Aravanopoulos, 2011).

Several studies have considered indicators and verifiers related to population genetic diversity (e.g. Allendorf *et al.*, 2008; Bariteau, 2003; Graudal and Kjaer, 2007 (unpublished); Laikre *et al.*, 2008; McKinnell, 2002; Namkoong *et al.*, 1996, 2002), nevertheless only

TABLE 3
Parameters for evaluating temporal changes in genetic monitoring of gene conservation units proposed by Aravanopoulos (2011) and Konnert *et al.* (2011).

Indicator	Verifier
Aravanopoulos, 2011	
Selection	Age and size class distribution, Reproductive fitness - percentage of filled seeds and percentage of germination, Regeneration abundance
Genetic drift and genetic diversity	Effective population size, Allelic richness, Latent genetic potential
Gene flow	Outcrossing/actual inbreeding rate
Konnert *et al.*, 2011	
Directional change in gene or genotypic frequencies	Differences between cohorts in allele, genotype and phenotype frequencies, and in the distribution of age classes
Levels of genetic variation	Gene frequencies, genetic diversity, percent polymorphic loci, average number of alleles per locus, variation in phenological parameters, Fixation index, Number of potential parent trees
Gene migration between populations	Dispersion of pollen and seeds, differentiation between populations of the same age, isolation, family structures
Changes in mating system processes	Mating system, rate of cross-fertilization, rate of biparental inbreeding, number of effective pollen donors, proportion of empty/full seed and germinability

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a few have focused on gene conservation units of forest trees (Aravanopoulos, 2011; Konnert *et al.*, 2011).

Aravanopoulos (2011) proposed the use of the minimum number of indicators and verifiers needed to implement the gene-ecological approach for population genetic monitoring that was suggested by Graudal and Kjaer (unpublished, 2007). Three indicators and seven verifiers were proposed (Table 3). Konnert *et al.* (2011) indicators were based on the Namkoong *et al.* (1996) work. In total, four indicators and 18 verifiers were proposed (Table 3). Evidently, both the Aravanopoulos (2011) and the Konnert *et al.* (2011) approaches suggest the combined use of demographic and genetic parameters to evaluate genetic variation, selection, gene flow and genetic drift. The proposed indicators are practically the same, while most of the proposed verifiers are congruent as well. The scientific reasoning for indicator and verifier selection is explicitly presented in both works.

In theory, genetic monitoring is indispensable for every species. In practice, species selected for monitoring should be organized by priority. Aravanopoulos (2011) has suggested that genetic monitoring should focus on keystone perennial plant species of biological and economic importance, starting from ecologically dominant species (aiming at prevention), and rare or endangered species (aiming at restoration). Konnert et al. (2011) have recommended choosing species according to their usability, existence and indicator capacity starting from species for which genetic markers are available for routine testing.

Both studies also deal with the practical implementation of genetic monitoring. The Konnert *et al.* (2011) study provides two examples of initial (base line) assessment for beech (*Fagus sylvatica*) and wild cherry (*Prunus avium*). Aravanopoulos (2011) proposes a periodicity of one assessment per decade with phenological data and sample material (mature trees and seeds) being collected in a single visit in the field. Konnert *et al.* (2011) on the other hand, suggest several visits in the monitoring plots and propose a periodicity of one to two years for phenological parameters, five years for the genetic analysis of seeds and 10–15 years for assessing genetic parameters. Konnert *et al.* (2011) also suggest a particular design of a monitoring plot covering a 4-hectare area for stand forming species and a minimum requirement of 150 trees for monitoring plots of scattered species. They also suggest geo-referencing the monitoring plot in addition to individual trees and recording tree social classification as well as site environmental data. The difference in the field level engagement by the two approaches lies in their different goals. Aravanopoulos (2011) aims at the genetic monitoring of, possibly remote, gene conservation units at an international scale, where repeated visits may be costly and demanding. Konnert et al. (2011), on the contrary, are interested in developing a genetic monitoring system applicable in the German forests, therefore considering areas where repeated visits and more formal plot delineation can be more straightforward. In addition, Aravanopoulos (2011) suggested particular sample sizes to be used and numbers of loci to be analysed for simple sequence repeat (SSR) and single-nucleotide polymorphism (SNP) approaches, as well as levels of critical differences between assessments that should indicate drastic change.

3.3 Response and benefit indicators

Response policies or actions to manage tree genetic diversity

Response indicators should measure the implementation of policies or actions to prevent or reduce biodiversity loss (Sparks *et al.*, 2011). Responses are measures that correct or remedy the loss taking place. Some concrete examples of response indicators were discussed in Chapter 2. An indicator of response will usually provide a measure for the response itself, but not necessarily for the efficiency or the impact of the response on the degree of loss. As already discussed above (Section1.2 and Chapter 2), the significance of response indicators should, therefore, be interpreted cautiously and preferably be combined with state indicators to assess their impact on the

Box 4

The promises of molecular markers for genetic monitoring at different spatial scales: new tools available for monitoring evolutionary processes involved in adaptation

Accurate biodiversity analysis poses an on-going challenge for the success of monitoring programmes. This is especially important because monitoring applications require repeated sampling and timely analysis. A morphology-based identification of bio indicators is time consuming. On the other hand, new laboratory and statistical techniques now enable the efficient use of molecular markers for genetic monitoring.

Assessment of the current distribution of genetic diversity provides a useful baseline, but only if repeated measurements (monitoring) can reveal changes in genetic diversity and the processes responsible for them (Schwartz *et al.*, 2007). Such genetic monitoring is also the only way to evaluate the long-term sustainability of forest management. To assess genetic diversity, it is necessary to develop a sound and common monitoring protocol that can be applied for all tree species. Monitoring can include quantitative assessments of molecular genetic variation at either the neutral and adaptive level to estimate most genetic parameters. Put simply, molecular marker choices for the estimation of indicators would be the highly variable multi-allelic microsatellites (SSRs) and the highly abundant bi-allelic SNPs.

Forest trees have been proposed as excellent experimental systems for understanding the relationship between naturally occurring genotypic and phenotypic diversity in plants (Neale and Savolainen, 2004; González-Martínez *et al.*, 2006; Neale and Ingvarsson, 2008). For economically important species, common garden experiments (provenance, progeny and clonal tests) are available, allowing for an estimation of ecotypic variation in growth and functional traits. Furthermore, many forest tree species are in the early stages of domestication, which implies that large numbers of different genotypes can be found in replicated genetic tests for trait evaluation and selection. During the last years, the improvement in genomic resources of trees has also allowed many loci underlying phenotypic variation in trees to be identified (see González-Martínez *et al.*, 2011 review for conifers). High-throughput DNA sequencing and genotyping technologies have enabled comparative studies of natural variation at the molecular level, and have yielded important insights into the genetic mechanisms underlying adaptation and speciation (Gilad *et al.*, 2009). Developing experimental approaches, such as genetic association studies assessing the correlations between allelic variants and trait differences, has been very helpful for dissecting individual genes underlying complex traits (Neale and Savolainen, 2004). Next generation sequencing (NGS) tools have made existing techniques cheaper and faster, and more importantly, they have enabled genomic studies to be conducted in any organism, including relevant ecological non-model plants (Stapley *et al.*, 2010).

A single run on an NGS machine can generate more data than was stored on GenBank a decade ago, so that even from a starting point of no genetic resources in the target species and no whole genome sequence in a closely related species, the tools required to understand the role of demography and selection in shaping diversity and, more generally, to monitor long-term adaptation, can be generated rapidly (Stapley *et al.*, 2010).

The options for monitoring genetic variation using molecular markers have so far been limited primarily to analysing neutral and/or candidate *loci* known to encode ecologically important genes. Previously identified quantitative trait loci (QTLs) represent another source of genes for monitoring, with the caveat that QTLs might be population and environment specific and that the effects of selection on individual QTLs could be small. Since most adaptive traits have a polygenic genetic architecture, failure to demonstrate genetic change at a specific candidate *locus* does not rule out that change has occurred at other *loci* affecting the same trait. This complexity argues for analysing many *loci* (hundreds to thousands) to

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densely cover the genome and possibly identify other *loci* under selection from the same environmental stressors. Fortunately, this approach is now becoming feasible with the advent of NGS methods (Margulies *et al.*, 2005). Transcriptome sequencing provides rich sources of SNPs (Barbazuk *et al.*, 2007), facilitating identification of the genes involved in adaptive change (e.g. Renaut *et al.*, 2010; Williams and Oleksiak, 2011). An exciting recent development is the use of reduced-representation genome-wide sequencing; thousands of short fragments are sequenced throughout the genome, allowing for genotyping by sequencing of thousands of SNPs and narrowing the gap between model and non-model species (Allendorf *et al.*, 2010; Davey *et al.*, 2011). Of course, there are still some technical challenges. The benefits of NGS sequencing will not be fully appreciated until extremely high-performance computing and intensive bioinformatics support is available. But significant progress has been made during the last years. The continuing developments in quantitative genetics, bioinformatics and population genomics are expected to improve dramatically the efficiency for genetic monitoring, thus increasing the understanding of evolutionary processes and providing novel tools for the practical conservation of biodiversity.

state of the genetic diversity. Response can be related to the generation of relevant knowledge and capacity or to the actual management of the resource.

The proposed headline indicators listed in Table 1 (Section 1.5) reflect five different kinds of response:

i. integration of response measures in policy, planning and implementation of programmes, including legislation;
ii. availability, accessibility and uptake of adequate knowledge and capacity in policy as well as practice;
iii. the extent of physical management and conservation activities in the field;
iv. the complicated issue of access and benefit sharing of genetic resources (where response related to benefit rather than state of the resource is considered); and
v. the general response issue of mobilizing adequate financial resources for the different measures required to reduce loss to acceptable levels.

In the early 1960s, FAO initiated a global programme to conserve and manage FGR largely embracing the five kinds of response (FAO, 1975; Palmberg-Lerche, 2007) and several regional networks on FGR have been established at the initiative of Bioversity International and FAO since the 1990s.[18] The ability of the different networks to cover the challenges posed by the needs for response has varied considerably and has been very dependent on the availability of resources. EUFORGEN has been one of the more successful networks in this respect (Section 3.4, the case of EUFGIS/EUFORGEN below).

Furthermore, there are several national programmes that attempt to integrate the five kinds of response (e.g. Graudal and Kjær, 1999). However, many of these programmes initiated in the 1970s have suffered from a lack of public support and are, therefore, often limited or no longer functional (Graudal and Lillesø, 2007; Lillesø *et al.*, 2011b). Worldwide, many national research, education and management programmes dealing with the management of genetic resources of trees have been considerably downscaled over the last two decades. A similar erosion of taxonomic knowhow has taken place (Hoagland, 1996; Kim and Byrne, 2006; Drew, 2011). Also, the obvious importance of quality nursery facilities in support of large scale forest landscape restoration seems to lack adequate attention (Haase and Davis, 2017).

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[18] Asia-Pacific Forest Genetic Resources Programme (APFORGEN), European Forest Genetic Resources Programme (EUFORGEN), Latin America Forest Genetic Resources Network (LAFORGEN), Sub-Saharan African Forest Genetic Resources Programme (SAFORGEN).

At present, there is no coherent framework of an adequate response to the loss of tree genetic diversity in place. However, it may be possible to learn from the Marine Waters Sector in Europe where the Marine Strategy Framework Directive prepared by the European Commission has formed the basis for a Commission Decision on criteria and methodological standards on good environmental status of marine waters, including biological diversity (EU, 2010; Cochrane *et al.*, 2010; European Commission, 2011) (see Box 5).

Box 5
Assessment of marine waters and the criteria for good environmental status

The Marine Strategy Framework Directive provides a framework for European Union (EU) member states to take the necessary steps to achieve or maintain "good environmental status" (GES) by the year 2020. EU member states must adopt action plans to be reviewed every six years and apply an ecosystem-based approach to managing human activities (European Commission, 2011).

The framework provides a holistic approach for assessing marine waters. State characteristics as well as pressures and impacts (Footnote 5 in Section 1.1) of physical, chemical and biological features and disturbance, habitat types and ecosystems are defined and assessed. Drivers and costs of degradation are considered (European Commission, 2011).

It is particularly interesting that genetic diversity is included in the framework of criteria and indicators, see the following table:

TABLE 4

Relevant criteria and indicators about biological features of individual species in the marine environment (source: extracted from Table 4 in European Commission, 2011). Criteria here roughly correspond to the concept of headline indicators and operational indicators of CBD in Table 1, and indicators to specific verifiable sub-topic indicators (Section 1.5)

Component	Criteria	Indicators
Fish Mammals Reptiles Seabirds Other species of EU legislation and international agreements Genetically distinct forms of native species	1.1 species distribution	1.1.1 species distribution range 1.1.2 species distribution pattern 1.1.3 area covered by species
	1.2 population size	1.2.1 population abundance
	1.3 population condition	1.3.2 population demographics 1.3.3 population genetic structure
Commercially exploited fish and shellfish – additional criteria/indicators	3.2 reproductive capacity of the stock	3.2.1 spawning stock biomass 3.2.2 biomass indices
	3.3 population age and size distribution	3.3.1 proportion of large fish 3.3.2 mean max. length 3.3.3 fish length distribution 3.3.4 size at first sexual maturation
Non-indigenous species	Special considerations (related to pressure and impact)	

Benefits of tree genetic diversity and its sustainable management

Benefit is the most recently emerged indicator of biodiversity. It has direct links with the notion of ecosystem services of the Millennium Ecosystem Assessment (MEA, 2005). It has been identified as an indicator to understand and evaluate the amount and change in benefits that society derives from biodiversity (Sparks *et al.*, 2011). A benefit indicator should help answer the question: What are the implications of biodiversity changes for society (UNEP/CBD/AHTEG, 2011a)? In terms of tree genetic diversity, this indicator should be intended to quantify the benefits society derives from existing genetic diversity (Sparks *et al.*, 2011), genetic diversity being both an essential component of ecosystem sustainability and a service that ecosystems provide (for example for breeding in forestry, horticulture, etc.).

The notion of benefit is rooted in the economic valuation of the biodiversity framework, which should make it possible for impacts on different ecosystems to be compared (Ferraro *et al.*, 2012). For a benefit indicator to exist requires that an "adequate compensation" for the loss of ecosystem services provided can be measured (Boyd and Wainger, 2002). In the case of tree genetic diversity, such compensation could be estimated from the loss of food production in agro-forestry systems under pest attacks, loss of water and soil protection under climate change, loss of timber under extreme weather conditions, etc., when tree genetic diversity is not or is insufficiently taken into consideration. However, although different methods are available to estimate the value of genetic resources (Sarr *et al.*, 2008), few have been used to ascribe a value to FGR (Bosselmann *et al.*, 2008; Hein and Gatzweiler, 2006) which remain mostly uncharacterized (Elsasser, 2005).

The benefit of genetic diversity as a resource is directly expressed in the value of tree breeding. The profitability of breeding is well established (e.g. Daniels, 1984; Willan, 1988; Foster *et al.*, 1995; McKeand *et al.*, 2006; Rosvall, 2011). Seed source selection can provide physical gains of 10–30 percent. Selection within a seed source may add 10–25 percent and a further gain of 15–25 percent can be added by breeding. Through a fairly simple process, it is possible to achieve a 35–80 percent gain with very high returns of investment (e.g. Foster *et al.*, 1995). A basic requirement is, of course, that the genetic diversity is present. Nevertheless, it is apparent that public programmes managing FGR have been severely reduced over a couple of decades. In some parts of the world tree breeding has been taken over by private industry, in other parts it has virtually disappeared outside the public domain. With the increasing focus on the need for developing a so-called green, bio-based economy, there would seem to be a dire need to return to focusing on the societal benefits of breeding (Graudal and Kjær, 1999), not only to increase production but also to alleviate the negative impact of harvesting natural forests and reducing illegal exploitation of even some conservation areas (e.g. WWF, 2012).

Nevertheless, two recent studies (Jalonen *et al.*, 2018; Roshetko *et al.*, 2018) verify and document a common and often quoted suspicion that many plantings and regenerations for restoration and/or conservation do not pay adequate attention to the genetic quality of the reproductive material. This is likely to be one of the most important factors of success for the huge global agenda of forest landscape restoration and with very significant implications for conservation of biodiversity.

A meaningful valuation of FGR in the context of climate change should extend beyond traditional measures such as wood production to include indicators related to societal use and ecosystem function (Thorsen and Kjær, 2007). It is crucial that benefit indicators should be based both on private and public valuations. A valuation of FGR only based on market interests might seriously underestimate societal benefits (e.g. Goeschl and Swanson, 2002). As the study by Hein *et al.* (2002) shows for coffee, a sector where economic value relies heavily on genetic diversity, the market has failed to protect genetic resources in the wild, notably in the "Ethiopian highland forests which, at current deforestation rates, will have disappeared in some 10 years".

Benefit indicators for genetic diversity can only be implemented if the valuation of genetic information is available (currently only attempted for land races (e.g. Brush and Meng, 1998)). This step is urgently awaited as "Valuation of genetic information may increase the awareness of local and national stakeholders on the economic value of forests, and may be instrumental in setting up a payment mechanism for the sustainable use of genetic information" (Hein *et al*., 2002).

3.4 Data, data sources and databases

In the technical review of status and trends of the world's FGR prepared for the FORGEN Panel in 2007, Palmberg-Lerche (2007) discuss sources and availability of information on the status of and trends in FGR, and cover *inter alia* national forest programmes, FAO's Global Forest Resources Assessment (FRA), the Convention on Biological Diversity, the Panel of Experts on Forest Gene Resources, regional workshops on FGR, country reports and databases on FGR. The discussion below complements this account.

A general condition for developing the CBD indicators has been that they should be based on existing data (to the extent possible). In the case of the genetic diversity of trees, this is not completely possible. But there are sources of data that can be used: various international and regional databases, studies of adaptive as well as neutral genetic diversity, national forest inventories, remote sensing data, various land zonation systems, vegetation maps and botanical surveys and studies. The different types of data and data sources and their possible use for providing indicators of genetic diversity are briefly discussed below.

International databases and the baseline issue

It has been recommended that existing data on provenances (e.g. in REFORGEN) and seed sources (e.g. in OECD and EU databases) be used as indicators of genetic diversity within forest tree species. As discussed in Chapter 2, number of provenances and seed sources could represent a response indicator. At the same time, by nature these measures do reflect variation in genecology.

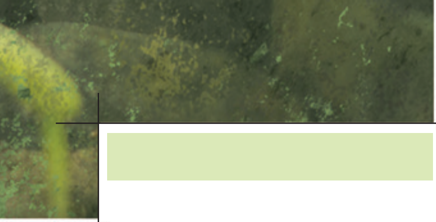
None of them relate, however, to any baseline or benchmark of past, current or potential genetic variation of a given species and they are, therefore, not immediately usable.

The number of identified and registered provenances or seed sources will probably reflect the commercial importance of a species rather than its genetic variation. An increase of seed sources may be a sign of (economic) development rather than an increase in variation. A decrease may similarly be a sign of decreasing economic importance rather than a decrease in variation. Furthermore, the concepts of provenance and seed source are used in different ways in forestry practice as well as in legislation in different countries. Simple counts are not suitable, either in time series in individual countries or for attempts to make comparisons among countries.

If counts can be benchmarked and related to genecological variation as an indirect measure of genetic variation, such counts may, however, be part of a possible indicator (Chapter 4).

Using existing data that has been compiled for other purposes to derive indicator parameters is an advantage, but it is not always easy. In Europe, work on identifying headline indicators for the 2010 Biodiversity target took place in a regional process on "Streamlining European 2010 Biodiversity Indicators", called SEBI2010. In relation to the headline indicator on genetic diversity an attempt was made to link suggestions for relevant parameters with existing sources of data and assess whether they could be extended beyond Europe and the OECD (see Box 6).

Important recent work on providing more information includes the first complete global database of tree species and their country distributions (Beech *et al.,* 2017, BGCI 2019) and the expansion of the agroforestry species switchboard documenting the presence of a total of 172,395 plant species, and 3,979 taxa at intraspecific level, across 35 web-based information sources (Kindt *et al.,* 2019).



Box 6
Linking relevant indicators of tree genetic diversity with possible sources of data in the SEBI2010 process

The Working Group 3 (WG3) under SEBI2010 discussed the headline indicator on genetic diversity for three groups of organisms: (i) mammals and poultry, (ii) crops and crop wild relatives, and (iii) trees. WG3 tried to identify a common framework of parameters for the three groups of organisms as a basis for identifying a common headline indicator. The draft parameters suggested by WG3 and possible data sources for trees are summarized in Table 5, including also some more recent references.

Only the parameters listed as number 1.3 and 2.3 in Table 5 relate to intraspecific variation. Only one parameter (no. 3.1) was retained in the final study, i.e. number of breeds per country for livestock genetic diversity (EEA, 2009).

TABLE 5

Overview of possible draft parameters and data sources suggested for a SEBI2010 indicator on genetic diversity, based on a discussion in WG3 on Genetic Resources in European Environment Agency (EEA), November 2006 (SEBI2010 WG3, updated January 2007). Parameters were identified in common for animals, crops and trees. Only trees are covered in this table. A column showing the possible availability of similar data at the global level has been added.

No.	Type[19]	Possible parameters to assess status on diversity of genetic resources, by country (SEBI2010 WG3)	Availability and data sources for trees in Europe (SEBI2010 WG3)	Possible availability at global level
Possible parameters to assess status on diversity of genetic resources by country				
1.1	S	Species, number total	Numbers and areas of species distribution available for almost all European countries (EUFORGEN[20])	FAO, 2006a; Beech *et al.*, 2017; and BGCI, 2019
1.2	S	Indigenous species, number total (according to national definition)	As above (EUFORGEN); also naturalized species; in general, relatively few introduced tree species	FAO, 2006a; Beech *et al.*, 2017; BGCI, 2019
1.3	S	Breeds, varieties, provenances, number total (according to national definition)	May to some extent be extracted from EU and OECD sources	REFORGEN
Possible parameters to assess importance and protection status of species and breeds, by country				
2.1	S	Species, share • top 5 most widely used • no of species making up 85% of production	Information available, compiled by all participants in EUFORGEN; share in area (km 2, %). Source: EUFORGEN annual national reports + National data	FAO, 2006a; Beech *et al.*, 2017; BGCI, 2019
2.2	S	Breeds/varieties/landraces/ provenances, share • top 5 most widely used by most widely used species • no of breeds of species making up 85% of production	For species on EU list, share in area (km 2, %). Source: EUFORGEN annual national reports; EU	FAO, 2006a (only at species level)
2.3	S	Share of threatened native breeds, varieties, etc.	List including all the threatened "status" of *tree species* compiled within EUFORGEN. Cross-check with IUCN list	FAO, 2006a (only at species level)

▶▶

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[19] S: State, R: Response.

[20] Source: the EUFORGEN web-site (http://www.euforgen.org), annual reports for EUFORGEN countries, and for several species, technical guidelines for the conservation of FGR.

No.	Type[19]	Possible parameters to assess status on diversity of genetic resources, by country (SEBI2010 WG3)	Availability and data sources for trees in Europe (SEBI2010 WG3)	Possible availability at global level
Protection and conservation of species and genetic diversity by country				
3.1	R	National conservation programmes for species and breeds/varieties, etc. (exist: yes/no)	Source: EUFORGEN, National Focal Point	Information may become available as part of the State of the World's Forest Genetic Resources
3.2	R	*In situ* protection: National conservation programmes for species and breeds/varieties, etc. (exist: yes/no)	Information can be extracted from country reports within EUFORGEN	
3.3	R	*In situ* protection: share of species or breeds/ varieties/landraces/provenances protected (in vivo plantations and stands)	Number + Number of sites or area (km 2)	
3.4	R	*Ex situ* protection: National conservation programmes for species and breeds/varieties, etc. (exist: yes/no)	Information can be extracted from country reports within EUFORGEN	
3.5	R	*Ex situ* protection: share of species or breeds/ varieties/landraces/provenances protected (by conservation method)	Number + Number of sites or area (km 2)	
12	R	Gene bank existence, number of banks or yes/no	Information can be extracted from country reports within EUFORGEN	

In the CBD2010 process *ex situ* crop collections (corresponding to no. 12 in Table 5) was used as an indicator for trends in genetic diversity (composed of sub-indicators on: (a) the quantity of accessions, genera, species and crops conserved in *ex situ* collections, (b) the quality of *ex situ* collections, and (c) the capacity to conserve crop genetic diversity in *ex situ* collections in terms of conservation facilities and human resources (BIP, 2010).

Ex situ crop collections have been regarded as a key tool for conserving crop plant varieties and their wild relatives. As an indicator they show changes in the crop genetic diversity that are available for sustainable agricultural production, and changes in the efforts to collect specimens and conserve that diversity. The indicator would reflect changes in the number and identities of crop species, and in the number of accessions of each of those species.

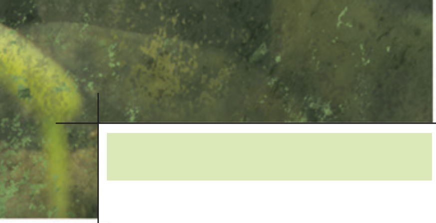
Whereas this type of indicator may be valid for certain cultivated crops, it will not provide significant information about intraspecific variation in trees.

Examples of regional databases

The European Information System on Forest Genetic Resources (http://portal.eufgis.org) is particularly relevant for monitoring genetic diversity. It was developed as part of a project supported by the European Commission (http://www.eufgis.org). The EUFGIS database is maintained as part of the activities of the European Forest Genetic Resources Programme (EUFORGEN).

The EUFGIS database contains geo-referenced information on genetic conservation units based on 26 data parameters at unit level and 18 data parameters at population level. As of December 2019, EUFGIS contained data on 3 593 genetic conservation units and 108 tree species in 35 countries.

Other European databases are TREEBREEDEX and EVOLTREE. The TREEBREEDEX (www.treebreedex.eu; www.trees4future.eu) database offers an extensive and up-dated inventory of the various types of germplasm (provenances, progenies, clones, varieties) collected and tested by breeders over more than 50 years, as well as of field experimental genetic trials (provenance, progeny, clonal, variety, demonstration trials, seed orchards, clonal archives, etc.). It provides key metadata on genotypes and experimental sites.



The EVOLTREE (www.evoltree.eu) database consists of different databases from the laboratories of the network partners that have been linked together. A centralized search engine allows the user to define queries against the whole set of databases. The databases contain information about molecular markers and sequences, population genetic diversity and phenotypic data, mapping and association populations, pedigrees of several forest tree species.

These European databases are relevant for genetic monitoring, but so far, no such monitoring has taken place, though proposals for indicators and verifiers for the genetic monitoring units are presently underway (Aravanopoulos *et al.*, 2015).

Outside Europe, relevant databases are also being established. The MAPFORGEN portal (www.mapforgen.org) presents the distribution, conservation status of and threats to 100 tree species of socio-economic importance in Latin America and the Caribbean. Molecular marker data and genetic diversity maps are available for nine of the species. As additional data becomes available it will be added, including genetic information for other species among the 100 listed and extension to other continents.

The potential natural vegetation map of Eastern Africa (VECEA, www.vegetationmap4africa.org) contains information on the distribution and use of tree species (see also section on vegetation maps and botanical literature below).

The North America based Dendrome project is a collection of forest tree genome databases and other forest genetic information resources for the international forest genetics community. Dendrome is part of a larger collaborative effort to construct genome databases for major crop and forest species (see https://dendrome.ucdavis.edu/index.php).

A prerequisite for the utility of the databases as a basis for providing verifiers of indicators is that they are generally accessible, which often is not the case. Most databases established for scientific purposes (e.g. EVOLTREE) will have limited access at least for a period of time, whereas databases established for public monitoring generally will be open (like NFIs).

A wealth of data is available in many institutions across the world, although often not readily available for the scientific community for many reasons including technical (data stored on paper, as annex to publication or under inappropriate electronic formats, lack of meta-data), legal (no agreement on data sharing) and personal (lack of scientific recognition for data collection and sharing).

Use of national forest inventories

Another relevant source of data could be national forest inventories (NFI), which have the advantage of being publicly available. Geburek and Shadauer (2005) provide a concise systematic overview of the use of NFI in a genetic resource management context. In many European countries NFIs are based on a network of sample plots where data are collected periodically. Geburek and Shadauer (2005) conclude, *inter alia*:

- Inventories and monitoring programmes can play a pivotal role. To optimize efforts, targets must be decided for biodiversity level (genes, species), geographical scale and time frame.
- 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 on-going NFIs or related surveys.
- 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 furnished.

The value of these data compared to the parameters discussed above lies in the fact that they enable qualification in a relevant context. The problem would be that such NFIs are only available from a selection of countries and that NFIs normally are done only over a fairly large time span. In Europe it seems to be a feasible way forward. There has been considerable work on the contributions of NFIs to forest biodiversity assessments over the last decade (Winter *et al.*, 2008; Chirici *et al.*, 2011), but there has been no specific general proposal for the assessment of genetic diversity based on NFIs, apart from the Austrian forest biodiversity index proposed by Geburek *et al.* (2010). However, the Austrian index is composed of several different state and response indicator values, weighted according to their perceived significance for maintaining species richness and genetic diversity; and is, therefore, not easily applicable outside the Austrian context.

Genetic studies based on field trials and molecular techniques

Genetic studies based on field trials as well as molecular techniques have already been mentioned several times (Sections 1.2, 3.1 and 3.2). Only such studies contribute direct measures of intraspecific diversity and are, therefore, indispensable as a basis for providing indicators to monitor the state of genetic diversity. In combination with vegetation maps and other ecological maps, genetic studies can be used to surmise genetic variation and thus provide direct, as well as indirect, indicators of the state of genetic diversity.

Although field trials in general are limited to relatively few species, usually of commercial importance, there exist a wealth of trials covering hundreds of species (Rogers and Ledig, 1996: Bariteau, 2003). The traditional aim of such trials is to evaluate the performance of the genetic units (provenances, families, genotypes) being tested, but they can also be used to characterize the environment for zonation (Graudal *et al.*, 1997) and thus provide not only direct measures of adaptive genetic variation but also contribute to estimated genecological variation. There is a wealth of data that, if made available and with modern computational power, could reveal new insights and knowledge.

The rapid development of molecular markers allows fast and comprehensive surveys of genetic diversity within and between populations. As explained above, recent progress in high-throughput sequencing and genotyping technologies have enabled a transition of studies away from patterns of neutral genetic diversity to studying putative adaptive genes across complex environmental gradients. In combination with high-performance computing, among other things, it is expected to provide novel tools for genetic monitoring and for practical conservation of biodiversity (Section 3.2, Box 4). The almost explosive increase in genetic studies (e.g. Allendorf *et al.*, 2010) will constitute an important source of data for genetic monitoring. The basic descriptive information of the thousands of taxa at stake continues to be essential and the lack of data (e.g. Feeley and Silman, 2011) and an apparent worldwide decline in taxonomic competence is worrying (Hoagland, 1996; Kim and Byrne, 2006; Drew, 2011; Section 3.3).

A recent meta-analysis of molecular marker genetic datasets for eastern African trees supports the utility of potential natural vegetation maps for planning climate-smart restoration initiatives (Dawson *et al.*, 2017). The authors suggest that the type of data used, from molecular marker studies combined with field trials should be pooled to support more across-species analyses to facilitate and strengthen the kind of meta-analysis that can be useful for applied restoration and genetic resource conservation activities.

Use of remote sensing

Geburek and Shadauer (2005) point also to the future utility of remote sensing, which is likely to deliver an increasing amount of information about the structure and composition of forest stands. So far, use of remote sensing for assessing genetic resources is limited. However, it is possible to identify and map some species (e.g. Larsen, 2007; Gillespie *et al.*, 2008; Féret and Asner, 2012) and thus enable monitoring of their distribution as a primary indicator of genecological variation. Remote sensing can also be used to predict or model species distribution or potential distribution using indirect links to climate and remote sensing data (e.g. Buermann *et al.*, 2008; Feilhauer *et al.*, 2012). The combination of mapping actual current distribution and modelling potential natural distribution will provide a potentially powerful tool to assess the state of a species intraspecific variation in the form of genecological variation. Although not yet immediately applicable at scale, it will most likely be possible to use this tool for some species within a few years (Lillesø *et al.*, 2011). Such an approach will be like that which we propose for applying genecological zonation.

Use of zonation

Genecological zonation is one way of denoting the comparison of species distribution with well-defined ecological zones. Ecogeographical surveys have, for example, been used to identify conservation needs for crops' wild relatives (IBPGR, 1985; Hoyt, 1988; Maxted *et al.*, 1995), to identify agroecological zones for major crops (FAO, 1978/80), and to define tree seed zones with specific recommendations for collecting (seed procurement zones) and using (seed deployment zones or tree planting zones) seed sources of tree and shrub species, (e.g. Barner and Willan, 1983; Buijtenen, 1992; Lillesø *et al.*, 2001).

There are many different types of seed zone systems used in different countries, of which the oldest date back to the 1930s (e.g. Ledig, 1996). A few examples are Haddock and Sziklai (1966), Barner and Willan (1983), Robbins and Hughes (1983), Campell (1986), Olsen and Aalbæk (1991), Aalbæk (1993), Aalbæk and Kananji (1995) and Lillesø *et al.* (2001). There is a vast amount of information and data around to assist in surmising the distribution of intraspecific variation.

Care should be taken in the use of seed zones or regions of provenance, since in many countries they could reflect trade regulations rather than well-defined ecogeographic variation.

This type of information has already been used to prepare national FGR conservation plans, as well as species-specific genetic conservation plans. Examples of national plans targeting intraspecific variation for many species are the Sudan (Graudal *et. al.,* 1997), Denmark (Graudal *et al.,* 1995), and Cambodia (Moestrup *et al.*, 2006). Examples of species-specific plans are *Tectona grandis* (Graudal *et al.*, 1999), *Pinus merkusii* (Theilade *et al.*, 2000) and *Baikiaea plurijuga* (Theilade *et al.*, 2002).[21]

Vegetation maps, botanical literature and genecologcial baselines

Any mapping of intraspecific variation will rely on the knowledge of species distribution. Geo-referenced representative collections would constitute the most reliable source for mapping distribution of species; however, such collections are not available for many species, and when available the records often remain unpublished (Feeley and Silman, 2011).

Another source of information is vegetation maps and accompanying source material with a description of vegetation types and their constituent species. Creating botanical surveys and preparing vegetation maps were of high priority in many countries in the past. However, for long periods of time such maps had limited use. In more recent years, national vegetation maps and regional composite maps (like White's vegetation map of Africa (White, 1983)) have attracted renewed interest to serve as tools for identifying conservation priorities (e.g. Olson *et al.*, 2001; Kier *et al.*, 2005; van Breugel *et al.*, 2015; Dinerstein *et al.*, 2017). In most cases, the detailed species-specific information of the botanical surveys and the national maps and the information underlying these maps including criteria to define the vegetation classes and delimit them spatially have remained very difficult to access, because the composite maps exclude this level of detail (Lillesø *et al.*, 2011). Current attempts to make such information available in digital form are emerging, and several natural vegetation maps and potential natural vegetation maps from different parts of the world are being published (Bohn *et al.*, 2002/3, 2007; Lillesø *et al.*, 2005; Kindt *et al.*, 2005, 2007a,b; Mucina *et al.*, 2006; Friis *et al.*, 2009; Lillesø *et al.*, 2011; Kindt *et al.*, 2011a,b,c,d; van Breugel *et al.*, 2011a,b; Breugel *et al.*, 2015b; de Sousa *et al.*, 2017).

In this context, the great advantage of these "higher resolutions" is that they model, or provide the possibility to model, the potential natural distribution of species in the landscapes and, therefore, can be used as a tool to identify the genecological baseline of the species considered (Lillesø *et al.*, 2011). They provide the possibility for assessing the status of the intraspecific variation of a much larger number of species than would otherwise be considered realistic (see above under remote sensing).

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[21] The examples mentioned here are examples where the Danida Forest Seed Centre has been involved. A systematic review would most probably reveal many others. Some can be found in FAO/DFSC/IPGRI, 2001; FAO/FLD/IPGRI, 2004a and 2004b.

Chapter 4

Discussion, conclusions and recommendations

4.1 Progress and the way ahead in identifying relevant and practical indicators

The development of biodiversity indicators to track the rate of loss of biodiversity on a global scale has been underway for two decades. Although undeniable progress has been made overall, there is "still a considerable gap in the widespread use of indicators for many of the multiple components of biodiversity and ecosystem services, and a need to develop common monitoring schemes within and across habitats" (Feld *et al.*, 2009).

Establishing the Biodiversity Indicators Partnership (BIP, https://www.bipindicators.net/) to promote and coordinate development and delivery of biodiversity indicators in support of CBD and other sectors has been an important step to close this gap. In the need for further harmonization, there will also be an important role for the Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES, http://www.ipbes.net).

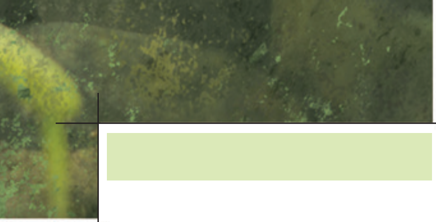
Genetic diversity is probably the element of biodiversity where the development of relevant indicators has lagged most behind. This has repeatedly been pointed out by the scientific community (e.g. Laikre *et al.*, 2010). Recognized by the CBD Secretariat (SCBD, 2010; Walpole, 2009), the Strategic Plan for Biodiversity 2011–2020 allows for improved coverage. Nevertheless, it remains a major challenge to identify and operationalize indicators of genetic diversity, including tree genetic diversity.

In the forest sector, considerable theoretical progress in identifying relevant indicators has been made over the past 20 years (e.g. Namkoong *et al.*, 1996, 2002; McKinnell, 2002; Bariteau, 2003; Aravanopoulos, 2011). However, practice has been somewhat detached from theory. It has been difficult and costly in practice to satisfy the scientific requirements of implementing the assessment and monitoring, in particular of state indicators. The attempts of the sector to use indicators in practice have, therefore, often been limited to response indicators.

However, the indirect indicators of response, pressure or benefit cannot on their own reveal the extent to which the processes that maintain genetic variation are conserved. Response, pressure or benefit indicators cannot and should not be used independently of state indicators.

The overall goal of genetic diversity indicators is to identify trends in maintaining and enhancing the adaptive potential of tree species. The indicators should be built to monitor trends reflecting this target. The target is of crucial importance for the long-term sustainability of forest and other tree-based sectors as a whole. From an operational viewpoint, sustainability certification schemes (like FSC and PEFC) may offer the possibility of using state indicators to monitor genetic diversity.

The response-pressure-state-benefit-(RPSB) loop (Sparks *et al.*, 2011) provides an appropriate framework to ensure that the suggested set of indicators meet the requirements of being scientifically sound, realistic, as well as policy relevant. Identifying indicators of tree genetic



diversity should, preferably, be done within such a framework and result in a set of RPSB indicators. However, as the state represents the most crucial step for monitoring processes related to genetic diversity and long term adaptive potential trends under different types of pressures, we argue here that the most relevant framework for designing and implementing genetic diversity indicators should be a state-pressure-response-benefit (SPRB) loop. Creating and implementing scientifically sound, realistic and policy relevant state indicators for genetic diversity remains a major challenge and a necessary target for the forestry sector.

4.2 Proposing a set of relevant possible indicators

Although the indicators developed so far have proven difficult to apply in practice, the considerable scientific advances of the past two decades provide the basis for both new and previously considered unfeasible approaches to be tested and applied at different scales, from the global over the regional/national, down to the local. For implementation purposes and adoption by managers and policy makers, it is crucial that indicators are listed following a hierarchical approach within the SPRB framework.

Table 6 below shows a first attempt to list indicators and their type (state, pressure, response, benefit) in a cross tabular format with the levels considered (global, regional/national and local). Table 6 is not necessarily exhaustive, but contains a set of possible examples. The practical use of the information presented in Table 6 may seem unattainable given the number of operational indicators listed. However, a closer look at the hierarchical composition of the table, shows that different levels are connected, and the resolution of knowledge and data required to assess an indicator is increasing when stepping down from one level to the next. There is a hierarchy in terms of scale, moving from the global level down to the

TABLE 6

Some possible operational indicators at different scales under the headline indicator: Trends in genetic diversity (adaptive potential) of tree species. Primary measures (parameters) are listed, derived (proportional) figures will, in some cases, have to be calculated to provide information on trends (see also Box 6). The table is not considered exhaustive. SPRB indicator codes refer to state, pressure, response and benefit.

Scale	Operational indicator	Type of Indicator (SPRB)	Verifiable indicator	Verifiable measure (direct or proxy)
Global	Trends in knowledge of genetic diversity of species	R, B	Increase in number of species that are described for which distribution and/or genetic parameters are known	Same Increase in number of articles in genetic diversity by species
Global	Trends in genetic diversity for selected species	S	Number of species with known distribution for which allelic diversity is declining	Number of species with known distribution for which distribution is declining
Global	Trends in genetic conservation	R	Number of tree species directly targeted in conservation programmes	Same
Global	Trends in sustainable use of tree genetic diversity	R, B	Number of tree species for which regulation of use of forest reproductive material exist	Same
Global	Trends in education and awareness	R	The change in number of tree geneticists and tree breeders Existence of networks Presence in NFIs and NFPs	Number of university courses/ training courses offered in forest genetics related subjects FGR networks (function/operation) Use in NFIs and NFPs

Scale	Operational indicator	Type of Indicator (SPRB)	Verifiable indicator	Verifiable measure (direct or proxy)
Global/ regional/ national	Species distribution of selected species	S	Natural distributional range	Geographic and climatic range
Global/ regional/ national	Population distribution pattern of selected species Population size	S	Distributional pattern within the latter, where appropriate Representation within the natural range No. of populations, their area and density (abundance)	Geographic, climatic and eco-geographic distribution of populations No. of populations relative to their potential genecological distribution Area and density of populations
Regional/ national	Trends in knowledge of genecology	R, S	No. of species with mapped genecological variation	Same
Regional/ national	Trends in knowledge of among population genetic diversity	R, S	Among population genetic diversity (of selected species)	Parameters of genetic differentiation among populations
Regional/ national	Size of plantation programme	B	Hectares planted by species/provenance either locally or as an exotic	Same
Regional/ national	Status of genetic improvement	B, R	Number and type of improved seed sources traded/exchanged	Same Certification scheme in place
Regional/ national Local	*In situ* and *ex situ* conservation measures in place	R, B	Conservation action taken for species/ populations at risk	Existence of a national strategy/programme Number and area of conservation units
Regional/ national Local	Use of adapted seed sources	B, R	Guidelines/regulations in place for matching seed source and planting site (ecological conditions)	Seed source performance (growth and survival) Certification scheme in place
Regional/ national Local	Use of diverse seed sources	R, B	Guidelines/regulations for composition and harvest of seed sources (number of mother trees)	Seed source performance (growth and survival)
Local (management unit/ landscape)	Plantation resilience, option values and improved production	B	Profit from breeding vs. loss from ill-adapted plantations	Seed source performance (growth and survival), realized gain and profit
Local (management unit/ landscape)	Population condition	S, P	Demographic condition of selected populations (diversity in adaptive traits/genes)	Age/size class distribution Number of reproducing trees Abundance of regeneration Environmental heterogeneity Number of filled seeds Percentage of germination (see Box 3 and Box 4)
Local (management unit/ landscape)	Population condition	S, P	Genetic condition of selected populations (population) genetic structure where appropriate)	Genetic parameters: Effective population size (Ne) Allelic richness Outcrossing/inbreeding rate Spatial Genetic Structure, Hybridization/ introgression (see Box 3 and Box 4)

local level. There is also a hierarchy in terms of the level of genetic diversity considered, when moving from among species diversity to within-species diversity expressed at different resolution, from variation among populations to variation among genotypes within a population, all the way to the diversity present within a genotype.

Note that for the global, regional and national scales, no pressure indicator is mentioned in Table 6. At these scales, state and pressure indicators are intimately linked, and a relevant pressure indicator would be “loss of forest habitat” or “increase of forest habitat fragmentation” which is not specifically a genetic diversity indicator and is already considered under other headline indicators (see also Table 1).

The very detailed Table 6, where each SPRB indicator is addressed at each spatial scale, can be made simpler for facilitating implementation under the headline indicator "Trends in genetic diversity (adaptive potential) of tree species". A condensed version of the proposed indicators is given in Table 7, where the indicators are aggregated by type and summarized in fewer major operational indicator lines (Graudal *et al.*, 2014).

4.3 A state-pressure indicator

Providing a relevant state indicator represents the most crucial step within the SPRB loop, because trends in genetic diversity (and, therefore, long term adaptive potential) need to be known before the impact of any type of pressure can be assessed.

A relevant state indicator for trends in genetic diversity must include components at different scales (local/landscape/regional/national), i.e. the amount of diversity and how it is distributed in space. Therefore, a more detailed proposal for a

TABLE 7

Types of possible operational indicators under the headline indicator (from Graudal *et al.*, 2014): Trends in genetic diversity (adaptive potential) of tree species. Primary measures (parameters) are listed, derived (proportional) figures will, in some cases, have to be calculated to provide information on trends (see also Box 6). An attempt to provide the primary scale of measure and indicator is also given.

Operational indicator	Verifiable indicator	Verifier (direct or proxy)	Primary scale of measure and indicator
State-Pressure			
Trends in species and population distribution pattern of selected species	• Number of species with known distribution for which allelic diversity is declining • Natural distributional range • Distributional pattern within the natural distribution range, where appropriate • Representation within the natural range • No. of populations, their area and density (abundance)	• Number of species with known distribution for which distribution is declining • Geographic and climatic range • Geographic, climatic and eco-geographic distribution of populations • No. of populations relative to their potential genecological distribution • No. of populations, their area and density (abundance)	Global/ regional/ national
Trends in population condition	• Demographic condition of selected populations (diversity in adaptive traits/ genes) • Genetic condition of selected populations (population genetic structure where appropriate)	• Demographic parameters measured in the field • Genetic parameters measured in the laboratory	Local
Benefit			
Trends in plantation performance of selected species	• Hectares planted by species/provenance either locally or as an exotic • Profit from breeding vs. loss from ill-adapted plantations	• Hectares planted by species/provenance either locally or as an exotic • Seed source performance (growth and survival, realized genetic gain and profit)	Local/ national/ regional/ global
Response-Benefit			
Trends in knowledge of genetic diversity of species	• Increase in number of species that are described for which distribution and/or genetic parameters are known • No. of species with mapped genecological variation • Among population genetic diversity (of selected species)	• Increase in number of species that are described for which distribution and/or genetic parameters are known • No. of species with mapped genecological variation • (Increase in number of articles on genetic diversity by species) • Parameters of genetic differentiation among populations	Global/ regional/ national/ local

Operational indicator	Verifiable indicator	Verifier (direct or proxy)	Primary scale of measure and indicator
Trends in education and awareness	• The change in number of tree geneticists and tree breeders • Existence of networks • Presence in NFIs and NFPs	• Directories of Forest Geneticists and Tree Breeders • Number of university courses/ training courses offered in forest genetics related subjects • FGR networks (function/operation) • Use in NFIs and NFPs	National/ regional/ global
Trends in sustainable use of tree genetic diversity	• Number of tree species for which regulation of use of forest reproductive material exist • Number and type of improved seed sources traded/exchanged • Guidelines/regulations for matching seed source and planting site • Guidelines/regulations for composition and harvest of seed sources (number of mother trees)	• Number of tree species for which regulation of use of forest reproductive material exist • Certification scheme in place • Seed source performance (growth and survival) • Certification scheme in place • Use of diverse seed sources	National/ regional/ global
Trends in genetic conservation	• Number of tree species directly targeted in conservation programmes • Conservation action taken for species/ populations at risk *(in situ* and *ex situ)*	• Existence of a national strategy/programme • Number and area of conservation units	National/ regional/ global

state indicator on tree genetic diversity based on genecological zonation is presented in Box 7.

It is important to emphasize that species diversity and genetic diversity are generally linked and that species-rich areas are also genetic diversity-rich areas (Vellend and Geber, 2005; Vellend, 2006; Alonso *et al*., 2006; Fady and Conord, 2010), thus making species level indicators relevant to genetics, although only up to a certain extent. Ideally, to conserve the diversity of a species, its diversity should be known. For most species our knowledge of genetic variation is minimal, pointing to the central dilemma of gene resource conservation: a recognized need of conservation without knowing exactly what to conserve. The genetic variation will to a large extent have to be extrapolated based on ecological factors and the autoecology of the species (Graudal *et al*., 1995 and 1997).

4.4 Testing indicators

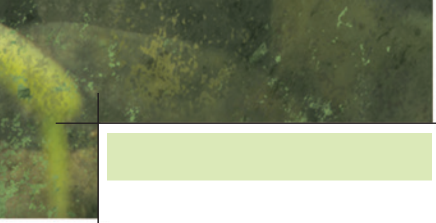
Although we are at a stage where many indicators can be proposed for immediate implementation, there is still a need to test the implementation of genetic diversity indicators in different forest zones, and for different categories of species (autoecology). The implementation of the proposal provided in Box 7 would constitute a test in itself.

An initiative of the CGIAR Research Programme on Forest, Trees and Agroforestry (FTA, CGIAR CRP6, http://www.cifor.org/crp6/), called Sentinel Landscapes, provides an opportunity for testing and applying the indicators. Sentinel Landscapes are in Africa, Asia and Latin America, each one spanning national boundaries and including forest-to-farm and environmental gradients. They are intended to provide sites for long term research and monitoring. At present it has, however, not been possible to mobilise support for implementation of such a scheme for testing indicators.

In Phase II of FTA, 2017-2022, a separate flagship on Tree Genetic Resources to Bridge Production Gaps and Promote Resilience has been introduced, providing for higher priority given to work on tree genetic resources, which may lead to strengthening the further development of indicators of tree genetic diversity.

4.5 Soliciting data for a realistic set of proposed indicators

Table 6 lists several proposed possible indicators, which were discussed by the FAO Intergovernmental Technical Working Group on Forest Genetic Resources in January 2013 (FAO, 2013a), and by the



Box 7
Proposal for an indicator on tree genetic diversity based on genecological zonation

Currently, there is enough genetic information available to define a quantitative indicator based on genecological zonation that may fulfil the criterion of a usable indicator. Below we discuss and suggest such an indicator, and the process needed to test and verify it.

Requirements of an indicator

An indicator for tree genetic diversity should fulfil the following criteria:

- It should reflect the genetic processes and be interpretable.
- It should be measurable and be valid across species and landscapes.
- Its validity should be generally accepted by experts and managers.
- Data must be easy and cheap to collect.

Proposed definition/principle of an indicator

Phase 1:

- Development/application of a world-wide terrestrial eco-geographic zonation (common for all domesticated/utilized plant species – to be based on existing work (see Section 3.4, Vegetation maps and botanical literature) or planned work (FRA 2010 indicator Extent of Forests and Forest Types)).
- Distribution of important tree species across these zones (mainly based on existing distribution maps). The baseline point in time reflecting the original natural distribution in the current climate will vary and has to be decided. Expected/potential distribution in 1960 or earlier will be relevant to draw a base line back in time.

Phase 2:

- Evaluate to what extent the species have genetically viable populations in each of the zones according to a set of defined criteria (drawing on *i.e.* Namkoong *et al.,* 2002; McKinnell, 2002; Bariteau, 2003; Lefèvre *et al.,* 2013; plus, work on genecological zones by Forest & Landscape Denmark of the University of Copenhagen (and formerly Danida Forest Seed Centre) and the World Agroforestry Centre (ICRAF)).

  For each species in each zone the status can be assessed, e.g. in classes such as:

  2= genetically viable populations (according to specified criteria) present in the given zone, and with good protection status
  1 = genetically viable populations (according to specified criteria) present in the given zone but conservation status not optimal
  0 = species present, but no genetically sound populations (according to specified criteria) present
  -1 = species is not expected to be present with more than a few trees from the original gene pool

Populations might here be *in situ* or *ex situ* as defined in the criteria for genetically viable populations.

Phase 3:

- Index delivery: The number of zones in which major species maintain viable genetic gene pools will be compared to the total number of zones where the species occurs/occurred. The index will be evaluated at three levels according to the corresponding hierarchical zones.

How well does the proposed indicator fulfil requirements?

The indicator should reflect the genetic processes and be interpretable. Genetic diversity within a species occurs between and within populations. A change in the geographical distribution area will reflect diversity between populations. To assess diversity within populations, it is necessary to know if they are genetically viable, i.e. to have an estimate of their size (area, census number) and if any dysgenic selection takes place.

The proposed indicator should be measurable. Wide experience with zonation systems and mapping of species distribution is available (from e.g. Europe, North America, Cambodia, Thailand, Nepal, Burkina Faso, East Africa). Knowledge of change in a geographical distribution area will be available for many important tree species. Information about the genetic viability of the individual populations is often harder to get, but some experience to build on is available (e.g. from *Eucalyptus spp*., teak [*Tectona grandis*], merkus pine [*Pinus merkusii*], zambesi teak [*Baikiaea plurijuga*], gum arabic [*Senegalia* [earlier *Acacia*] *senegal*], and many European and North American species). An identification phase database like REFORGEN, MAPFORGEN, OECD and EUFGIS will be useful on this point.

The validity of the indicator should be generally accepted. As already indicated, the idea of using the genecological approach appears to be accepted by experts and managers. The approach is closely associated with several of the verifiers identified in the more elaborate scientific approach identified by Namkoong *et al.* (1996, 2002, see above). It is equally important that it is accepted by practitioners who will implement the scheme.

The most difficult requirement to fulfil is obviously that the indicator should be inexpensive to measure. If the process model recommended by the FORGEN Panel (Section 3.1) is used, it should be possible to test, verify and modify the model on a number of species, and from there gradually expand coverage, e.g. within the framework of FRA.

A model based on a limited number of species

The process to develop a model that can be used in the 2020 process would include:

- testing the approach for a small number of case studies;
- adapting methodology if necessary;
- identifying relevant tree species (50–100) – use past species prioritization exercises, FORGEN Panel list, REFORGEN, FRA;
- outsourcing to a network of international institutions that will be jointly responsible for the assessment and evaluation;
- Identifying species natural distribution to ecozones (or a sample of their distribution). Assess their conservation status at different reference points (e.g. >1960, 1990, 2000, 2010, 2020).

The intensity of the work that can be done will depend on the level of financial input it is possible to raise and the availability of data, e.g. the digital vegetation map that has been developed for eight countries in Africa and the EUFORGEN/EUFGIS database would readily enable the three phases suggested for a selection of the registered species.

The approach can already be implemented for many species using available information, while additional information (such as that which comes from genomic studies) can be added on a continuous basis.

(Expanded from L. Graudal and E.D. Kjær, personal communication, 2007)

FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) in April 2013 (FAO, 2013b; FAO, 2013c). The Commission requested that FAO continue working on the provisional list of indicators to monitor the state of the world's FGR and the status of implementation of the Global Plan of Action for the Conservation, Sustainable Use and Development of Forest Genetic Resources. In the same session, the Commission agreed to the Global Plan of Action (as presented in Appendix F of FAO, 2013c), and it was then adopted by the FAO Conference in June 2013 (FAO, 2013d).

The Global Plan of Action has identified 27 strategic priorities within four major priority areas (FAO, 2013d). The Plan does not in itself provide any indicators but makes developing such indicators a strategic priority. The strategic priorities will themselves require monitoring, which, however, is considered beyond the scope of the current report.

In 2015, the Commission again discussed draft indicators for FGR and recognized that more work was needed to finalize the draft list of indicators for monitoring the implementation of the Global Plan of Action. Subsequently, FAO and the Intergovernmental Technical Working Group continued their work, and in 2017 the Commission adopted targets, indicators (response) and verifiers for monitoring the implementation of the Global Plan of Action. The targets, indicators and verifiers have been identified in four priority areas (FAO, 2017):

- improving the availability of, and access to, information on FGR;
- *in situ* and *ex situ* conservation of FGR;
- sustainable use, development and management of FGR; and
- policies, institutions and capacity-building.

In Box 7, the criteria for a state indicator were listed as follows:

- It should reflect the genetic processes and be interpretable.
- It should be measurable and be valid across species and landscapes.
- Validity should be generally accepted by experts and managers.
- Data must be easy and cheap to collect.

The reference to the genetic processes in the first of these criteria is particular for state indicators, but otherwise the criteria would be generally valuable for all types of indicators.

As stated earlier, for any indicator to be useful in practice, the data must be relatively easy and inexpensive to collect, and its significance must be clear. Also, as shown throughout the report, there are many indicators proposed by several different international initiatives. For a commonly acceptable workable indicator to emerge, the challenge will be to identify a manageable number of indicators for which data can be solicited.

For facilitating implementation, the indicators proposed in Table 7 can be further aggregated by type into four major operational indicator lines addressing the entire SPRB framework:

- trends in species and population distribution and diversity patterns for selected species (S, P);
- trends in plantation performance of selected species (B);
- trends in knowledge of genetic diversity of species and in education and awareness (R, B); and
- trends in management (sustainable use and conservation) of tree genetic diversity (R, B).

Below, indicators are briefly discussed under these four headings.

Trends in species and population distribution and diversity patterns for selected species

In Table 7, this major state-pressure indicator is divided into two operational indicators, one at the species level and one at the population level. Three global forest resource assessments made by FAO have, in different ways, dealt with the species level, by assessing endangered or threatened species, number of native tree species and the tree species composition of the growing stock (FAO, 2001a, 2006, 2010). It should be noted that such parameters in themselves are generally of little value as indicators of genetic diversity. For parameters to be useful as indicators they must not only be quantified and available in time series, but also qualified in a relevant context (see FAO, 2001a). For example, a general problem is the apparent discrepancy between a seemingly well-known number of endangered species and much more uncertainty about the total number of species (see Section 1.2). One way forward would be to quantify and qualify the past and present distribution of selected species, e.g. as proposed in Box 7, based on data currently being brought to light by the scientific community (like EUFORGEN, MAPFORGEN and VECEA, see Section 3.4).

The population level will most likely be more resource demanding to deal with. It can be done, but it will require a commitment of significant means at the national and regional levels. A promising model underway is the European work on developing genetic monitoring methods for genetic conservation units of forest trees (Aravanopoulos *et al.*, 2015).

There is a need to identify genetically appropriate indicators, and, at the same time, not to inflate the already large number of indicators that exist at the global and regional scale. For lesser known species, independently of their economic and ecological value, using species level information on distribution may be a first step towards including genetic information in an indicator. However, the relationship between species diversity and genetic diversity is not always straightforward. Thus, an indicator based on genecological zones within species (e.g. number of regions of provenance or ecoregions) and how their size changes in time would be the next best step to take. Finally, following the model applied by EUFORGEN (Lefèvre *et al.*, 2013), an indicator based on the number of forests conserved for their genetic diversity per country/region (species range), where the minimum requirements are met for the dynamic conservation of genetic diversity, would also be highly relevant.

A comparison of the past and present genecological distribution of selected species is a realistic way of assessing the trend of intraspecific variation, and it provides a state indicator of tree genetic diversity. Moreover, such a comparison also permits an analysis of the causes of anticipated loss and thereby reveals relevant pressures. Data for many tree species enabling such analysis are currently brought to light by the international scientific community. Further work could be outsourced to a network of international institutions that will be jointly responsible for assessment and evaluation.

Trends in plantation performance of selected species

Though work towards developing state, pressure and response indicators of tree genetic diversity has been ongoing for some time, little has been done on benefit indicators.

Tree planting, in plantations and on farms, will be one of the major assets of a future global and local economy relying on renewable resources. By appropriately managing genetic resources, the benefits of tree planting can be increased many fold. A valuation of this effort in terms of the extent and development of selected tree planting activities and the use of relevant reproductive material can provide a direct indicator of benefit.

In Table 7, the trends in plantation performance is suggested as the primary benefit indicator. The Planted Forest Programme of FAO (see http://www.fao.org/forestry/plantedforests/en) has compiled and analysed information on planted forests over more than a decade. In addition, an increasing amount of information on trees outside forests is becoming available. The relative contribution of planted forests to the global production of wood serves as a general indicator of the importance of tree plantations. In 2005, the world's forest plantations covered some 260 million ha or 7 percent of the global forest area, but produced 1.2 billion m^3 of industrial round wood or about two thirds of the total global round wood production (Evans, 2009). By 2030, the production from plantations could surpass 2 billion m^3 of industrial round wood. Given the increasing importance of planted forests, information on trends in genetic diversity, deployment and productivity of a selection of planted tree species could be a feasible indicator of benefit (see FAO, 2007 and Appendix 2).

Indicators of the subtler benefits related to ecosystem services are still some way ahead. There is a clear need to link genetic variability and ecosystem services, but we should also be aware of the dual nature of genetic diversity as, on the one hand, a necessary precondition for future evolution and adaptability of local populations, entire species and ecosystems, and, on the other, a service provider. Additional work in this area is required.

Trends in knowledge of genetic diversity of species and in education and awareness

Knowledge, education and communication are closely linked. Scientific knowledge can be gathered from the literature, whereas traditional knowledge can be more difficult to trace. The state of education might, to some extent, be available from national statistics and could be gathered through national surveys. Assessment of trends will probably have to rely on special studies. Knowledge on within-species diversity can be immediately connected to the two indicator areas discussed above under Trends in species and population distribution patterns and condition and Trends in plantation performance.

The increasing utility and the decreasing costs of using molecular techniques and genomic approaches to map genetic variation show great promise as an efficient means for monitoring genetic diversity, but it is imperative that we not neglect the basic importance of taxonomy, ecology and field testing in this context.

The fading priority of sustainable forest management in the national policies of some countries (Wijewardana, 2008), the diminishing competence in taxonomy (Drew, 2011) and the erosion of applied programmes of genetic resource management (Graudal and Lillesø, 2007) are, therefore, of great concern. There seems to be an on-going trend world-wide towards the loss of practical knowledge and of the ability to identify tree species, of tree seed handling, tree breeding and tree genetic resource conservation management, which will be an impediment to implementing any programme to use and conserve tree genetic diversity. A similar problem has emerged for developing and supporting quality tree nursery facilities in the context of meeting global forest and landscape restoration needs (Haase and Davis, 2017); and awareness of the importance of choosing the right planting material continues in many cases to be low (Jalonen *et al.*, 2017; Roshetko *et al.*, 2018; Lillesø *et al*., 2018). Indicators to monitor these areas of response policy would be highly relevant and can be achieved through national surveys.

Trends in management (sustainable use and conservation) of tree genetic diversity

Management response can be measured by the extent of physical management and conservation activities in the field, and by the integration of response measures in policy, planning and implementation of programmes, including legislation. Some of these elements are straightforward in principle and can be elucidated through quantification of breeding and gene conservation activities at the national level and are already available and are being used for some geographical areas. The indicators adopted by the CGRFA for monitoring the Global Plan of Action implementation (cf. above) largely cover these issues (FAO, 2017).

The issue of response in terms of legislation and regulation is probably the more difficult to address, but one way to approach it would be to quantify adopting certification schemes for distribution and exchange of reproductive material. Schemes exist for some areas where this can be done, but it is important to validate that those schemes introduced are relevant for the purpose before they are used as a positive measure of action.

Table 7 provides indicators for managing reproductive material coupled with breeding programmes, and for implementing specific gene conservation programmes. This is like the current reporting by Forest Europe mentioned in Chapter 2 (Forest Europe, UNECE and FAO, 2011). It would be important to connect such reporting with a relevant genecological baseline.

The genecological approach suggested is similar to the approach used by the EU as part of the Marine Strategy Framework Directive (Box 5). The comparison between these widely different habitats makes all the more sense because marine organisms and trees have similar life history traits such as a long lifespan, high dispersal and large distribution areas. Like marine organisms, forest trees provide ecosystem services of disproportionally large importance relative to their distribution and frequency. Monitoring aquatic genetic resources in the marine environment is backed by legislation in the form of a European Commission decision. The feasibility of applying legislative measures in support of monitoring genetic diversity of other areas of biodiversity, including forest trees, should be considered.

In the forest sector, such an approach could be combined with regulating forest reproductive material. Statistics on the use of forest reproductive material (or seed sources) over time would not be enough to assess trends in tree genetic diversity. However, when statistics exist on the use and trade of forest reproductive material, when regions of provenances are delineated, and their diversity is estimated, such an indicator can be used. In terms of an indicator, this leads to recommending that regions of provenances (or a similar scheme that makes passport data on geographic origin mandatory) should be established where they do not exist, that statistics on the reproductive material collection and trade should be compiled and that some characterization of this material within regions of provenances should be done (using marker and/or phenotypic traits at the region of provenance level).

4.6 Towards scientifically sound, realistic and implementable tree genetic diversity indicators

The vast array of indicators that have been proposed for monitoring genetic diversity can be reduced to a set of four indicators that cover the SPRB spectrum of Sparks *et al.* (2001). This DPKM set of indicators derives mostly from the genecological approach to genetic diversity and can be addressed at multiple scales, from global to local. Table 8 gives a brief characterization of the proposed set of indicators.

The DPKM set can be applied on appropriate groups of tree species in the wild and in cultivation representing different regions and different climates, present as well as future. It is flexible enough to accommodate additional knowledge as such knowledge becomes available and is easy and cost effective for management to implement. It holds the potential of providing a realistic picture of the state, trends and potentials of the world's tree genetic diversity.

TABLE 8

A brief characterization of a proposed set of four indicators, the "diversity-productivity-knowledge-management" (DPKM) set of indicators (from Graudal *et al*., 2014).

Operational indicator	Implications	Possible primary sources of data and information
Trends in species and population distribution and diversity patterns for selected species	The state of the genetic diversity of trees: what is really happening to the resource?	International, regional and national data bases, FRA
Trends in plantation performance of selected species	The productivity of the genetic resource of trees in current use; also reflecting the possible potential of further mobilizing the resource	National forest inventories, FAO Planted Forest Programme, FRA
Trends in knowledge of genetic diversity of species and in education and awareness	Current knowledge and potential capacity for developing the genetic resource	Scientific literature, various databases and national institutions
Trends in management (sustainable use and conservation) of tree genetic diversity	Current management of the genetic resource: how well are we doing?	National and international institutions and networks

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Appendix 1

Relationship between the policy questions, headline indicators, sub-topics, Strategic Goals and the Aichi Biodiversity Targets (taken from Appendix IV of UNEP/CBD/AHTEG, 2011a). Note that some indicator sub-topics are repeated under different policy questions and headline indicators. This is because some sub-topics are relevant to different aspects of the proposed indicator framework.

Policy Questions[22]	Headline Indicators	Indicator Sub-topics	Strategic Goals[23]	Most relevant Aichi Targets
State – How is the state of biodiversity changing?	Trends in extent, condition and vulnerability of ecosystems, biomes and habitats	Trends in degradation of natural habitats	B, C	5, 12
		Trends in extent of natural habitats	B	5
		Trends in fragmentation of natural habitats	B	5
	Trends in abundance, distribution and extinction risk of species	Trends in abundance, distribution and extinction risk of species	C	12
	Trends in genetic diversity of species	Trends in genetic diversity of species	C	13
Pressures and underlying causes - Why are we losing biodiversity?	Trends in pressures from unsustainable agriculture, forestry, fisheries and aquaculture	Trends in degradation of natural habitats	B	5
		Trends in sustainability of agriculture, forestry and aquaculture	B	7
		Trends in sustainable consumption and production of goods and services	A, B	4, 7
		Trends in sustainable utilization of target and bycatch populations	B	6
	Trends in pressures from habitat conversion, pollution, invasive species, climate change, overexploitation and underlying drivers	Trends in degradation of natural habitats	B	4, 5
		Trends in impact of invasive alien species	B	9
		Trends in number/extent of invasive alien species	B	9
		Trends in integrity of ecosystems vulnerable to climate change	B	10
		Trends in pollutant releases to the environment	B	8
Benefits - What are the implications of biodiversity loss?	Trends in distribution, condition and sustainability of ecosystem services for equitable human well-being	Trends in benefits that humans derive from biodiversity and ecosystem services	D	14
		Trends in consequences of benefits derived from ecosystem services for human wellbeing	D	14
		Trends in natural capital that delivers multiple ecosystem services	D	14, 15

Policy Questions[26]	Headline Indicators	Indicator Sub-topics	Strategic Goals[27]	Most relevant Aichi Targets
Responses - What do we do about biodiversity loss?	Trends in awareness, attitudes and public engagement in support of biological diversity and ecosystem services	Trends in awareness, attitudes and public engagement in support of biological diversity	A	1
		Trends in sustainable consumption and production of goods and services	A	1
	Trends in integration of biodiversity, ecosystem services and benefits sharing into planning, policy formulation and implementation and incentives	Trends in degree to which traditional knowledge and practices are fully respected in implementation of the Strategic Plan	E	18
		Trends in genetic diversity of species	C	13
		Trends in impact of invasive alien species	B	9
		Trends in implementation of National Biodiversity Strategy and Action Plans (NBSAP)	E	17
		Trends in incorporation of biodiversity and ecosystem services into incentive systems	A	3
		Trends in knowledge of values of biodiversity and ecosystem services	A	2
		Trends in proportion of production landscapes sustainably managed	B	7
		Trends in reflection of biodiversity and ecosystem services in policy decisions, planning and reporting processes	A	2
		Trends in responses to invasive alien species	B	9
		Trends in sustainable consumption and production of goods and services	A	4
		Trends in sustainable utilization of target and bycatch populations	B	6
	Trends in access and equity of benefit sharing of genetic resources	Trends in access and equity of benefit sharing of genetic resources	D	16
	Trends in accessibility of scientific/technical/traditional knowledge and its application	Trends in degree to which traditional knowledge and practices are fully respected in implementation of the Strategic Plan.	E	18
		Trends in improvement, sharing, transfer and application of knowledge	E	19
	Trends in coverage, condition, representativeness and effectiveness of protected areas and other area-based approaches	Trends in area of sustainably used ecosystems	C	11
		Trends in natural capital that delivers multiple ecosystem services	D	14, 15
		Trends in protected areas coverage, representation and condition	C	11
	Trends in mobilization of financial resources	Trends in financial flows of funding for implementation of the Strategic Plan	E	20

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22 It should be noted that, depending on the context, a State indicator could also be a Pressure or Response indicator, etc. The categorization should, therefore, not be considered rigid but dependent on the key questions that are being asked.

23 A, B, C, D, and E refer to the five strategic goals of the Aichi Targets (see Box 2).

Appendix 2

Proposed minimum set of information on genetic diversity of planted tree species (from Appendix 4 in FAO, 2007).

Selection of 25 to 30 of the most economically important planted tree species
For each species:

1. Geographic range
2. Climatic range (maximum/minimum values needed)
3. Trends in provenance results (BLUP analysis (best linear unbiased prediction))
4. Conservation status of provenances sampled
5. Estimated percentage of the natural range sampled
6. Genetic diversity estimate by species/population
7. Hectares planted by species/provenance either locally or as an exotic
8. Status of genetic improvement (seed stand? orchards? clonal deployment?)
9. Information of seed availability/natural stands/seed orchards
10. Are there regional restrictions that limit germplasm transfer?
11. Do *ex situ* conservation stands exist/status?

The last two decades have seen numerous efforts in developing indicators for monitoring the world's biological diversity. Considerable progress has been made in this regard for tracking habitat and species diversity while genetic diversity is the element of biodiversity for which the indicator development has often lagged behind. This is partly because identifying and operationalizing indicators for genetic diversity, including tree genetic diversity, remains a major challenge.

In the forest sector, considerable theoretical progress has been made in identifying relevant indicators for tree genetic diversity over the past 20 years in parallel with developing indicators for sustainable forest management. However, it has been difficult and costly to meet in practice the scientific requirements for assessing and monitoring tree genetic diversity. The purpose of the indicators of tree genetic diversity is to identify trends in maintaining and enhancing the adaptive potential of tree species. The indicators should thus be designed to monitor relevant trends, which are crucial for the long-term sustainability of the forest and other tree-based sectors as a whole.

This study, prepared within the ambit of *The State of the World's Forest Genetic Resources*, reviews issues related to the development of indicators for tree genetic diversity. It includes a historical account of the development of science-based indicators for tree genetic diversity that embrace ecological surrogates for genetic diversity, the genecological approach, genetic monitoring of management units, the use of molecular markers, as well as relevant experience from other organisms and policy processes. It also includes a section on relevant data, data sources and databases. Finally, the study proposes a set of four operational indicators for monitoring tree genetic diversity. The proposed indicators could support efforts towards sustainable forest management, as well as the development of indicators for the post-2020 global biodiversity framework.

ISBN 978-92-5-133759-2

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CB2492EN/1/12.20