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Global to local genetic diversity indicators of evolutionary potential in tree species within and outside forests

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ABSTRACT

There is a general trend of biodiversity loss at global, regional, national and local levels. To monitor this trend, international policy processes have created a wealth of indicators over the last two decades. However, genetic diversity indicators are regrettably absent from comprehensive bio-monitoring schemes. Here, we provide a review and an assessment of the different attempts made to provide such indicators for tree genetic diversity from the global level down to the level of the management unit. So far, no generally accepted indicators have been provided as international standards, nor tested for their possible use in practice. We suggest that indicators for monitoring genetic diversity and dynamics should be based on ecological and demographic surrogates of adaptive diversity as well as genetic markers capable of identifying genetic erosion and gene flow. A comparison of past and present genecological distributions (patterns of genetic variation of key adaptive traits in the ecological space) of selected species is a realistic way of assessing the trend of intra-specific variation, and thus provides a *state indicator* of tree genetic diversity also able to reflect possible *pressures* threatening genetic diversity. Revealing benefits of genetic diversity related to ecosystem services is complex, but current trends in plantation performance offer the possibility of an indicator of *benefit*. *Response* indicators are generally much easier to define, because recognition and even quantification of, e.g. research, education, breeding, conservation, and regulation actions and programs are relatively straightforward. Only *state* indicators can reveal genetic patterns and processes, which are fundamental for maintaining genetic diversity. Indirect indicators of *pressure*, *benefit*, or *response* should therefore not be used independently of *state* indicators. A coherent set of indicators covering diversity–productivity–knowledge–management based on the genecological approach is proposed for application on appropriate groups of tree species in the wild and in cultivation worldwide. These indicators realistically reflect the state, trends and potentials of the world's tree genetic resources to support sustainable growth. The state of the genetic *diversity* will be based on trends in species population distribution and diversity patterns for selected species. The *productivity* of the genetic resource of trees in current use will reflect the possible potential of mobilizing the resource further. Trends in *knowledge* will underpin the potential capacity for development of the resource and current *management* of the genetic resource itself will reveal how well we are actually doing and where improvements are required.

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1. Introduction

The development of biodiversity indicators to track the rate of loss of biodiversity on a global scale has been underway for over two decades, first with the adoption of the Convention on Biological Diversity (CBD[1]) in 1992 (SCBD, 2001), followed in 2002 (SCBD, 2006) by the agreement on targets to reduce the loss of biological diversity by 2010 (the 2010 Biodiversity Target), and most recently in 2010, by the adoption of the Aichi Targets and a revised and updated Strategic Plan for Biodiversity 2011–2020 (UNEP/CBD/COP, 2010).

The rationale behind this work is a general recognition of the richness of biological diversity on Earth, the threats that human activities pose to this richness, and the negative consequences that further loss of diversity may have to mankind and to the Earth biomes as a whole. The objectives of CBD refer to intrinsic and utilitarian values of biodiversity, including their importance for evolution and maintaining life-sustaining systems (Glowka et al., 1994). Its overarching goal of sustainable development is to ensure and enhance the livelihoods of millions of people under the challenge of balancing the human appropriation of nature with the effects of global climate change and a growing world population.

According to CBD, biological diversity embraces the diversity of all life on Earth and is commonly distinguished at three levels: ecosystems, species, and genes. The values of biodiversity are generally associated with these levels. Environmental and life-support values are typically provided at ecosystem level, material goods at species level and the improvement of production depends on the availability of genetic variation (FAO, 1989). The idea of identifying biodiversity indicators is therefore not merely tracking the loss of biodiversity, although this is used as the relevant overall measure, but also to enable priority setting for conservation, development and sustainable use of biodiversity.

Criteria and indicators are used in different fields of human enterprise to define priorities and measure the extent to which these priorities are met (e.g. Prabhu et al., 1999). They have become an instrument of choice for national and international organizations to guide their members (and attract membership) towards common, quantifiable goals. The focal area of sustainable forest management for example, relies strongly on criteria and indicators to monitor progress (Wijewardana, 2006). A criterion usually reflects an objective (also termed goal or target), often rather complex and challenging to assess; in our case, the degree to which the genetic diversity of the world's forests and trees is conserved. Practical and informative indicators which can be measured periodically to reveal the direction of change of a variable (the genetic diversity of world forests in our example) are therefore required. Indicators are, by definition, used to track progress and should always be defined in relation to a given target (Feld et al., 2009). An indicator must be measurable and the metric used to measure an indicator is commonly referred to as a verifier.

Although 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 schemes within and across habitats" (Feld et al., 2009). 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 (e.g. in terms of protected area coverage), the rate of biodiversity loss does not appear to be slowing (Butchart et al., 2010).

Here, we are concerned with genetic diversity, which is not explicitly defined in CBD, and in particular, we focus on trees. Genetic diversity is defined here as the total amount of genetic differences within species. It is also referred to as intra-specific variation. Intra-specific variation can be subdivided into inter- and intra-population variation (also among and within population genetic diversity), and further into the diversity within an individual expressed by differences between alleles across chromosomes. Genetic diversity is a major element of biodiversity (CBD article 2), it is the basis for adaptation and it has been recognized by the Millennium Ecosystem Assessment (MEA, 2005) for its support to ecosystem functioning. Nevertheless it is still rarely considered and only a few global or regional indicators make reference to it (Nivet et al., 2012).

Genetic diversity is probably the element of biodiversity for which the development of relevant indicators is least advanced. In their 2009 review of 617 peer-reviewed journal articles between 1997 and 2007, Feld et al. (2009) were able to list 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 consisted of physical and area fragmentation measures. Despite their role and potential value across scales and habitats, "functional, structural and genetic components of biodiversity [were] poorly addressed". Genetic diversity was included in less than 5% of the 531 biodiversity indicators analyzed.

This lack of genetic diversity indicators has repeatedly been pointed out by the scientific community (e.g. Laikre, 2010; Laikre et al., 2010). It has been recognized by the Secretariat of the Convention on Biological Diversity (SCBD, 2010, cf. also Walpole et al., 2009) and the Strategic Plan for Biodiversity 2011–2020 allows for improved coverage of genetic diversity.

Genetic diversity is – or has been – perceived as complex and costly to measure and the task of identifying relevant indicators therefore considered close to impossible. At present, genetic diversity of terrestrial domesticated animals reported by FAO and the International Livestock Research Institute (ILRI) is the only indicator reported under Aichi Target 13 on genetic diversity (Chenery et al., 2013, Biodiversity Indicators Partnership, BIP, 2013, www.bipindicators.net). A few additional indicators of relevance to genetic diversity are reported within the BIP (cf. Chenery et al., 2013; BIP, 2013, www.bipindicators.net). Although genetic diversity continues to be poorly covered, there are promising initiatives of application, primarily related to wildlife and the marine environment (Stetz et al., 2011; European Commission, 2011; CONGRESS, 2013, www.congressgenetics.eu).

Genetic diversity can be assessed by different techniques. Morphological and adaptive traits can be studied in field trials, and biochemical, molecular and DNA variants in the laboratory. Such studies contribute direct measures of intra-specific variation. In combination with knowledge of eco-geographic variation and history, genetic studies can be used to establish possible evolutionary patterns as well as recommendation domains for deployment of reproductive material in agricultural production systems.

Molecular markers are either influenced by selection or not (in which case they are termed neutral), whereas quantitative variation measured in field trials is usually adaptive. Both types of techniques are important to gain knowledge of genetic patterns and processes. The use of molecular tools for genetic monitoring has moved from an era of scepticism (McKinnel, 2002), where studies were limited to reveal patterns of neutral genetic 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).

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[1] Abbreviations and acronyms are listed in Appendix A.

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