Original articles

Cost-efficiency of cross-taxon surrogates in temperate forests

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ABSTRACT

Cross-taxon surrogacy (between-taxon similarities in species patterns) can help conservation biologists to design simplified, standardized and efficient tools for biodiversity monitoring. Our study aims to identify potential sets of indicator taxa to be recommended in temperate forests. We focused on nine forest taxa: vascular plants, bryophytes, saproxylic beetles, polypores, lichens, ground beetles, hoverflies, birds and bats. We assessed cross-taxon congruence patterns, in terms of both alpha and beta-diversity, using empirical biodiversity data from 206 plots in ten French forested areas. We evaluated the cost-efficiency of potential surrogate taxa using both strictly encoded expert knowledge and results of this study. The most congruent taxa in alpha-diversity were bryophytes (with bats and polypores), and ground beetles (with bats and saproxylic beetles), though levels of covariation were mostly weak. The most congruent taxon in beta-diversity was vascular plants (with bryophytes, ground beetles, lichens and forest birds). Contrary to our expectations, the subsets of forest species within a given taxon exhibited a lower surrogacy than the taxon as a whole. Four categories of taxa were delineated based on cost-efficiency scores – from costless but ineffective (bats and ground beetles) to costly but effective (saproxylic beetles and polypores). No single taxon was firmly identified as a relevant surrogate for other taxa; using a set of two or three taxa drastically increased surrogacy, compared with single-taxon approaches. Saproxylic beetles associated with vascular plants, or with both vascular plants and birds, seemed to be the most cost-efficient associations. Further research is required to up-scale our results from the short-term, local scale to the long-term, landscape scale in European temperate forests.

1. Introduction

Since the Helsinki conference in 1993, when the concept of sustainable management in forest ecosystems became mandatory, managers have been required to maintain species diversity in managed areas (FAO, 1999). However, assessing forest biodiversity is challenging due to (i) the large number of species involved, which discourages full inventories, (ii) the wide variety of species behavior and habitat requirements, which requires sampling according to multiple methods and procedures, and (iii) the difficulty of species identification for many taxa. Therefore, to reach their goals, forest managers and conservation practitioners often rely on biodiversity indicators, which are both ecologically relevant and suitable in a funds-limited context (Lindenmayer et al., 2000). However, managers would welcome other tools capable of adequately representing variations in major biodiversity components which cannot be intensively monitored. Studying biodiversity patterns and levels of congruence between taxa is informative and can help conservation biologists design efficient tools to monitor biodiversity in a context of habitat loss and species extinctions (Gaston, 1996). Two main approaches have been put forward in this perspective (Larsson, 2001): the indirect approach uses key environmental variables, such as habitat structural complexity (Lindenmayer et al., 2000), to evaluate biodiversity levels, while the taxonomic approach uses indicator taxa whose presence and population dynamics are

Table 1
Taxonomic variables, number of plots and geographic areas with available data, and field procedures used to sample them.

Variable	Taxon and definition	Number of plots	Geographic area	Trap type or area sampled	Number of sampling years	Median plot species richness (min-max)	Total species richness
s.beetles	Saproxylic beetles	199	1, 2, 3, 4, 5, 6, 7, 8, 9, 10	1–4 PolytrapTM (window trap)	1–3	40 (5–112)	551
g.beetles	Ground bettles	136	1, 2, 3, 4, 5, 7, 10	3 or 9 Barber (pitfall trap)	1	8 (2–26)	76
bryophytes	Corticolous and saproxylic Bryophytes	142	1, 2, 3, 4, 5, 9, 10	Deadwood and living trees, 1250 m^2	1	15 (2–43)	174
lichens	Corticolous macro-lichens	26	9	1 ha	1	40 (34–49)	136
bats	Bats	117	1, 2, 3, 4, 7	Ultrasound recording; 30 mn	1 (3 runs)	2 (0 − 13)	24
birds	Birds	119	1, 2, 3, 4, 5, 10	Point count method Blondel et al. (1970); 5 mn	1 (2 runs)	11 (4–18)	58
vascular plants	Terricolous phanerogams	147	1, 2, 3, 4, 5, 9, 10	600–1018 m^2	1 (1 run)	35 (9–70)	381
hoverflies	Hoverflies (Diptera Syrphidae)	11	8, 9	1 Malaise trap	2	47 (14–77)	163
polypores	Polypores s.l.	156	1, 2, 4, 7, 9, 10	0.125-0.3 ha	1–3 (1–3 total runs)	7 (1–34)	254

assumed to reflect those of other species in the community (Landres et al., 1988). The relative values of environmental variables and forest indicator taxa were reviewed by Gao et al. in 2015.

Well-known and easily recordable taxa have been suggested as surrogates for lesser known or more difficult-to-record congruent taxa (Noss, 1990). Congruence between taxa can be evaluated using species richness (alpha-diversity) or composition (beta-diversity). Alpha diversity has been the most used approach to date. However, beta-diversity can provide a different pattern for cross-taxon congruence from alpha-diversity (e.g. Cabra-Garcia et al., 2012) and allows researchers to highlight processes which generate and maintain biodiversity within ecosystems (Legendre and De Caceres 2013). Unfortunately, cross-taxon congruence is generally statistically weak (Gaston, 1996) and rarely consistent (Westgate et al., 2014). Moreover, relationships between potential indicator taxa and overall biodiversity have not yet been well established (Favreau et al., 2006; Gosselin and Dallari, 2007; Lindenmayer et al., 2000). However, several studies have shown congruent patterns in species richness or composition, and have proposed indicator taxa in forest ecosystems (Fensham and Streimann, 1997; Kati et al., 2004; Pharo et al., 1999; Saetersdal et al., 2003) and in agricultural (Sauberer et al., 2004) and urban contexts (Bräuniger et al., 2010). Some studies have highlighted the relevant role that a single umbrella species (e.g Ranius, 2002) or ecosystem engineer (Buse et al., 2008) can sometimes play as an indicator in very specific conditions; however, this shortcut does not appear to be efficient in predicting the diversity of all taxa (e.g. Sebek et al., 2012; Similä et al., 2006). Several reasons for this have been highlighted in the literature: (i) the wide range of behaviors (Berger, 1997) and relevant spatial scales (Simberloff, 1998) for species belonging to the same community, (ii) the absence of empirical data and evidence-based results showing the indicator function of potential indicator species (Simberloff, 1998), and (iii) contrasts in taxon ecology and therefore in their responses to environmental conditions (e.g. Pharo et al., 1999). Brin et al. (2009) suggested using several taxa together as bio-indicators. In this approach, it may be more efficient to use a set of non-congruent taxa, since their complementarity increases the quantity of information provided by the dataset (Kati et al., 2004; Westgate et al., 2017).

In terms of cost, using a set of taxa is often more expensive since this approach requires specific methods and additional specialists to record and identify the taxa (Nageleisen et al., 2009; Puumalainen et al., 2003). In a funds-limited context, partial approaches using only taxon subgroups (e.g. Sebek et al., 2012) or higher taxon levels (i.e. "taxonomic sufficiency", Ellis, 1985), or which ignore species requiring a disproportionate detection or identification effort (Vellend et al., 2008) are promising (Gaston, 2000; Williams and Gaston, 1994). Globally speaking, however, the economic feasibility of ecologically relevant indicator taxa has rarely been assessed (Mandelik et al., 2010).

This study aims to identify potential sets of indicator taxa to recommend in temperate forest biodiversity monitoring. We used previously available taxonomic data recorded at the stand level over a wide geographical area. Our dataset covers a large, contrasted forest gradient. Firstly, we quantified congruence patterns, both in terms of alpha- and beta-diversity, among nine forest taxa covering a wide range of life-history traits. Secondly, we conducted a cost-efficiency analysis of the nine forest taxa.

2. Materials and methods

Looking for an indicator first requires a clear definition of both the purpose (Noss, 1990) and the scale of its use (Heink and Kowarik, 2010). Our approach targets the conservation of forest species diversity, i.e. among species strictly or mainly associated with forest ecosystems. We recorded data at the stand level since that is the main operational scale for forest managers (Failing and Gregory, 2003). A wide range of forest contexts were sampled in the Atlantic and Continental zones, from lowland (plains and hills) to highland (montane and subalpine levels) forests, and in broadleaved-, mixed- and conifer-dominated stands (see Table A1 in Supplementary Material). Environmental and taxonomic data were recorded according to standardized procedures on 206 plots in ten forested geographic areas in France (Supp. Mat. Fig. A1).

2.1. Taxonomic data

We selected nine taxa in order to cover, *a priori*, a wide range of species behaviors and habitat requirements. Some taxa were (strictly or mainly) associated with forest, tree or woody substrates or forest-buffered climatic conditions, for example, corticolous lichens, corticolous and saproxylic bryophytes, polypores and saproxylic beetles (Table 1). Other taxa encompassed non-forest or non-tree-associated species, i.e. bats, ground beetles, birds and hoverflies. For the latter taxa, we built subsets of dendro-specialist species from the whole set of sampled species (Table 2), since dendro-specialists are more ecologically relevant and more at stake in forest conservation. In addition, for birds, subsets of forest-specific species could be less costly to inventory, since operators would be able to focus on the forest species subset instead of the whole group during sampling. However, for plants, most species are linked to open habitats (e.g. moors) and, according to most trait databases, can potentially occur along the edges or in clearings of natural forests (Rameau et al., 1989; Rameau et al., 1993). Therefore we considered all the vascular plants recorded to be forest-dwelling taxa and did not built a subset of forest species for plants. Ultimately, we gathered data from two to seven taxa per plot (Supp. Mat. Table A2).