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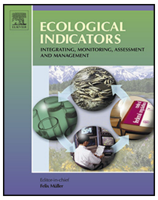

One taxon does not fit all: Herb-layer diversity and stand structural complexity are weak predictors of biodiversity in *Fagus sylvatica* forests

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ABSTRACT

Since adequate information on the distribution of biodiversity is hardly achievable, biodiversity indicators are necessary to support the management of ecosystems. These surrogates assume that either some habitat features, or the biodiversity patterns observed in a well-known taxon, can be used as a proxy of the diversity of one or more target taxa. Nevertheless, at least for certain taxa, the validity of this assumption has not yet been sufficiently demonstrated.

We investigated the effectiveness of both a habitat- and a taxa-based surrogate in six European beech forests in the Apennines. Particularly, we tested: (1) whether the stand structural complexity and the herb-layer species richness were good predictors of the fine-scale patterns of species richness of five groups of forest-dwelling organisms (beetles, saproxylic and epigeous fungi, birds and epiphytic lichens); and (2) the cross-taxon congruence in species complementarity and composition between herb-layer plants and the target taxa.

We used Generalized Linear Mixed Models (GLMMs), accumulation curves and Procrustes analysis to evaluate the effectiveness of these surrogates when species richness, complementarity and composition were considered, respectively.

Our results provided a limited support to the hypothesis that the herb-layer plants and the stand structural complexity were good surrogates of the target taxa. Although the richness of the herb-layer plants received a stronger support from the data than structural complexity as a predictor for the general patterns of species richness, the overall magnitude of this effect was weak and distinct taxa responded differently. For instance, for increasing levels of herb-layer richness, the richness of lichens showed a marked increase, while the richness of saproxylic fungi decreased. We also found significantly similar complementarity patterns between the herb-layer plants and beetles, as well as a significant congruence in species composition between herb-layer plants and saproxylic fungi. Finally, when different stand structural attributes were considered singularly, only the total amount of deadwood received support from the data as a predictor of the overall species richness.

At the fine scale of this study, herb-layer plants and stand structural complexity did not prove to be effective surrogates of multi-taxon biodiversity in well-preserved southern European beech forests. Rather than on weak surrogates, these results suggest that sound conservation decisions should be supported by the information provided by comprehensive multi-taxonomic assessments of forest biodiversity.

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1. Introduction

The prioritization of conservation and restoration efforts requires a thorough understanding of the spatial distribution of biodiversity although, unfortunately, this is still remarkably poor for most taxa, especially at fine spatial scales (Grussu et al., 2014; Westgate et al., 2014). Ecosystems are extremely complex, and an adequate knowledge of the whole biodiversity spectrum is hardly achievable. This has led to the development and use of proxies or surrogates to simplify, represent, and help the management of forest ecosystems (Lindenmayer et al., 2014).

A surrogate is defined as "[a measure] that readily reflects: the biotic or abiotic state of an environment; represents the impact of an environmental change on a habitat, community or ecosystem; the abundance of a particular species; or is indicative of the diversity of a subset of taxa, or of wholesale diversity, within an area" (Lindenmayer et al., 2014). Surrogates are usually divided into two broad types (1) habitat-based and (2) taxa-based surrogates (Lewandowski et al., 2010; Lindenmayer et al., 2014). Habitat-based surrogates assume that some habitats or environmental features are good proxies of the richness, composition or diversity of one or more taxa. Taxa-based surrogates, instead, assume that the biodiversity patterns observed in a given taxon (the surrogate), which is usually well known and/or easy to sample, can be generalized to one or more (target) taxa. Thus, taxa-based surrogates assume a high cross-taxon congruence that avoids the need to detect all species within a study area (Gioria et al., 2011; Westgate et al., 2014). The rationale behind the use of taxa-based surrogates has been explained by several hypotheses: for instance, the effect of one taxon diversity on another taxon's diversity could be mediated by cross-taxon functional interactions (e.g., trophic, mutualistic, parasitic), by a similar response to the environmental conditions or through a shared biogeographic history (Toranza and Arim, 2010; Gioria et al., 2011).

In certain ecological contexts, taxon- and habitat-based surrogates could be used jointly and return complementary information on the target taxa (Lindenmayer et al., 2014). For instance, in temperate forests both vascular plants and the forest stand structural characteristics were often considered as good surrogate candidates of forest overall biodiversity. Vascular plants are a potentially effective taxon-based surrogate, since they are relatively easy to sample and their taxonomy is sufficiently well described (Santi et al., 2010; Blasi et al., 2011). On the one hand, plants represent the bulk of both ecosystems' biomass and net primary productivity, and play a fundamental role in the trophic networks of forest ecosystems. Trophic or mutualistic interactions may account for part of the patterns of congruence between vascular plants and other forest taxa, such as insects (de Araujo, 2013) or mycorrhizal fungi. For instance, arbuscular mycorrhiza can influence the forest plant species diversity by altering the competitive balance in plant communities (Gerz et al., 2016). On the other hand, vascular plants and other taxa may respond similarly to a common disturbance history (Nordén et al., 2014) or to shared environmental conditions in the understory, e.g. forest floor humidity or light intensity. In support of these hypotheses, several works reported that richness of vascular plant species is positively correlated with that of bryophytes (Rooney and Azeria, 2015), lichens (Blasi et al., 2010), and animals such as birds (Blasi et al., 2010) and butterflies (Santi et al., 2010). Nevertheless, contrasting results were reported and thus a rigorous testing of plants as a biodiversity indicator is still needed (Lewandowski et al., 2010; Santi et al., 2010; Gao et al., 2015).

Forest structural complexity, which synthesizes the variety of structural components occurring in a stand, is also a possible candidate as a habitat-based surrogate in temperate forests. Indeed, structural complexity shows a good potential to be used as a biodiversity proxy, at least when considering those taxa that utilize specific forest structures (McElhinny et al., 2005; Gossner et al., 2014). Linking the stand structural complexity to specific taxa provides information about the proximate causes of biodiversity change, including those related to specific silvicultural practices. For instance, the lack of a certain structure may be correlated to the absence of a particular group of organisms, as it is the case with deadwood and saproxylic beetles or fungi (Bouget et al., 2014; Gossner et al., 2014).

Whatever kind of surrogate is chosen, it is necessary to carefully assess its effectiveness (Gao et al., 2015). A growing body of literature has emerged over the last decades to evaluate surrogates and synthesize the available information (Lewandowski et al., 2010; Rodrigues and Brooks, 2007; Westgate et al., 2014). For many taxa, the assumptions behind cross-taxon congruence have not yet been sufficiently tested, nor were the identity of the factors driving the huge variation observed across systems and scales (Gao et al., 2015). These factors may result in inconsistencies that may undermine the reliability of surrogacy indicators when applied to novel contexts (Kirkman et al., 2012; Westgate et al., 2014); for instance, the degree of cross-taxon congruence may vary greatly in relation to the spatial scale of the study (Lewandowski et al., 2010; Rodrigues and Brooks, 2007).

Different surrogates can also be designed to take into account different facets of biodiversity. Early works focused either on single species (e.g. umbrella species) or on the richness of a species assemblage as a proxy of the richness of a whole taxon or community (Lewandowski et al., 2010). In this case, cross-taxon congruence was measured by analyzing the existing pairwise correlations between the values of species richness of two or more taxa sampled across many sites. Nevertheless, focusing only on the species richness fails at adequately representing the various facets of biological diversity. The use of multiple measures of community structure (e.g. richness, complementarity and composition) is hence recommended to depict a comprehensive assessment of cross-taxon congruence (Gioria et al., 2011). Complementarity, for instance, accounts for the compositional difference between sites and it is therefore often considered in conservation planning, e.g. when selecting a set of sites or actions that together could preserve the maximum number of species in a given area (Ferrier, 2002; Rodrigues and Brooks, 2007; Lewandowski et al., 2010).

In this work, we tested: (1) the effectiveness of herb-layer species richness (as a taxa-based surrogate) and of stand structural complexity (as a habitat-based surrogate) at predicting simultaneously the general patterns of species richness of five groups of forest-dwelling organisms (hereafter "target taxa"), i.e., saproxylic and epigeous fungi, beetles, birds and lichens. The effect of the forest stand structural complexity was tested both using a synthetic index and considering a set of stand structural features individually. Finally, we evaluated (2) the cross-taxon congruence in species complementarity and composition between herb-layer plants and the target taxa.

2. Methods

2.1. Study area

The data here presented were collected within the context of the restoration project LIFE+ 'FAGUS' (11/NAT/IT/135, www.fagus-life-project.eu), and represent the information baseline that will be used to monitor the effects of the project's concrete conservation actions. The project focused on two habitats of European priority interest according to the EU Habitats Directive (92/43/EEC) i.e., the habitat 9210* – Apennine beech forests with *Taxus* and *Ilex*, and the habitat 9220* – Apennine beech forests with *Abies alba* and beech forests with *Abies nebrodensis*. Data were collected in six European