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Woody species diversity as predictor of vascular plant species diversity in forest ecosystems

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ABSTRACT

Despite a considerable effort of scientific community and a huge amount of literature, the capacity to assess and monitor biodiversity at coarser spatial scales in short time periods is still limited. Thus assessing indicator or surrogate information from existing data sets, such as forest inventories, is a challenge for biodiversity management and monitoring. We used two forest data sets (woody plants and all vascular plants) to test whether the diversity of woody plant species can be used as predictor of the diversity of all vascular plant species. Our study was performed in the forests of Liguria, Italy.

In order to take into account several levels of community organisation, we calculated different measures of species diversity at different levels of sampling hierarchy for both data sets (alpha, beta and gamma diversity). We used ordinary linear regression to test the predictive power of the diversity measures obtained by the occurrences of woody plant species with respect to those obtained by all vascular plant species.

Our results suggest that beta diversity and gamma diversity of woody species can be used to predict the beta diversity and the gamma diversity of all vascular plant species, at different levels of sampling hierarchy, while the alpha diversity of woody species cannot be used to predict the alpha diversity of all vascular plant species. These results point out the importance to consider measures based non only on species richness and to interpret the relation between species richness of woody plants and species richness of all vascular plants taking into account the scale dependence of this relations. Thus, our work demonstrates the feasibility of using data on woody plant species as recorded by forest inventories to predict the diversity patterns of all plant species in forest ecosystems.

1. Introduction

The lack of detailed information about spatial distribution of organisms often hampers an effective selection of conservation or management activities (Balmford et al., 1996). Complete inventories of genes, species and ecosystems are almost impossible to be achieved, given the time and cost constraints (Austin and Margules, 1986; Reyers et al., 2000). Despite a considerable amount of scientific efforts, quantifying biodiversity at coarse scales still remains difficult, especially for rich communities such as tropical invertebrates or plants (Prance et al., 2000; Novotný and Basset, 2000; Stohlgren, 2007). Standards in measuring the completeness of species lists are still lacking (Palmer et al., 2002) and this affects the capacity to assess and monitor biodiversity at coarse scales in short time periods (Chiarucci et al., 2011). As a consequence, biodiversity surrogates with easily recordable data are necessary to detect spatial and temporal patterns of biodiversity.

The demand for ecological data on forests has recently increased, especially because of the international policies aimed to assess and monitor the effects of pollution, biodiversity loss, forest degradation and climate change on these ecosystems (Corona et al., 2010; McRoberts et al., 2010). Thus, at present forest inventories represent a major source of biological, spatial and temporal data which accumulated during the years, and their potential use to investigate spatial and temporal patterns of biodiversity still

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needs to be properly understood (Palmer et al., 2002). In this context, assessing biodiversity patterns by using indirect measures, such as indicators or surrogates, is a fundamental challenge (Noss, 1990, 1999; Rodrigues and Brooks, 2007). Different studies identified general guidelines and methods to maximize the adequacy of surrogates and test their effectiveness in conservation planning (Favreau et al., 2006; Rodrigues and Brooks, 2007), especially for well studied groups, such as vascular plants, in highly diverse forest systems (Pharo et al., 2000; Macía, 2008; Thomas, 2009; Chiarucci and Bonini, 2005), and/or physiognomic features which can be easily mapped, such as vegetation types or other land classes (environmental surrogates; Faith, 2003). However, the use of surrogates or partial measures of biodiversity to evaluate biological diversity remains an open and relatively unexplored challenge (Barton et al., 2014).

To date, the predictive value of surrogates is still under debate (Van Jaarsveld et al., 1998; Panzer and Schwartz, 1998; Pharo et al., 2000; Chiarucci and Bonini, 2005; Lovell et al., 2007), depending on focus taxa, study regions, geographic scales and testing methods (Margules and Pressey, 2000). Moreover, cross-taxon surrogates have largely focused on congruency in species richness (alpha diversity), with few studies investigating the possible use of congruence surrogates for other components of biological diversity (Su et al., 2004), such as the hierarchical levels of community organisation (e.g., beta and gamma diversities). This use is particularly important because of the widespread use of diversity partitioning in ecology and conservation biology to compare diversity patterns across spatial or ecological scales (Whittaker, 1972; Peet, 1974; Gering et al., 2003; Chandy et al., 2006; Jost et al., 2010).

In this study we used two data sets recorded in Liguria, Italy, to test whether the diversity of woody species can be used as predictor of the diversity of all vascular plant species. In particular, we addressed the following questions: (1) is the woody species diversity as recorded in forest inventories a predictor of the diversity of all vascular plant species, at similar sampling effort? (2) Is the partitioning of diversity of woody species a predictor of the same partitioning of all vascular plant species?

2. Material and methods

2.1. Study area

The Liguria region is located in north-western Italy and it has a surface area of 5314 km^2. The region borders to the south on the Ligurian Sea, whereas, to the north, a continuous mountain ridge (the Ligurian Alps and the Ligurian Apennines) separates the Tyrrhenian slopes from the Po Valley basin. The 1.5 million inhabitants are mostly concentrated in coastal areas (ca. 2000 people/km^2), especially in the city of Genova.

Woodlands cover >60% of the region, and are largely used for logging, with varying intensity. The survey area is characterized by four bioclimatic units (Giordani and Incerti, 2008): (A) Montane, including some inland Alpine and Apennine areas above 1000 m a.s.l., dominated by beech forests; (B) Humid Sub-Mediterranean, occurring in the Tyrrhenian and Po valley hinterland, and along the coast, both east of Genova and near the French border, from about 400 to 1000 m a.s.l., characterized by deciduous *Quercus–Carpinus* forests; (C) Humid Mediterranean, limited to a narrow strip along the coast (less than 10 km from the sea), from 0 to 800 m a.s.l. and (D) Dry Sub-Mediterranean, occurring mainly in the valleys leading to the Po River in the western part of the region.

2.2. Data sets

We used two data sets containing data about the occurrences of woody plant and all vascular plant species. The first one (INVEN) included 2552 plots systematically sampled for the regional forest inventory (ISAFA, 1998) and provided occurrence data for 177 woody plant species (trees and shrubs) in circular plots of 600 m^2 located on a 1 × 1 km grid in forest ecosystems throughout the region. The second data set (PHYTO) included 628 phytosociological relevés carried out in the same forest area, in a subset of the INVEN sampled sites as well as additional sites. These phytosociological relevés were sampled in the same period. The PHYTO data set was sampled by performing traditional phytosociological reléves, thus recording the projection cover of all vascular species which were identified in the same plot according to the Braun-Blanquet (1928) scale. This data set included the occurrence data for 618 vascular plant species, i.e., both woody and herbaceous plants.

2.3. Analyses

In order to avoid biases due to sampling differences, all the analyses were performed using a subset of sites for which a paired plot was recorded in the INVEN as well as the PHYTO data set ($n = 380$). In this way, each plot of the INVEN data set had a corresponding plot in the PHYTO data set and vice versa. The occurrences of 137 woody species (more than 77% of species recorded by the whole INVEN data set) and 571 species (more than 92% of species recorded by the whole PHYTO data set) were included in the paired data set.

We firstly built sampled-based rarefaction curves for both INVEN and PHYTO, in order to assess the completeness of species data. We used standard (exact) rarefaction curves (Gotelli and Colwell, 2001; Chiarucci et al., 2008) and Spatially-Constrained Rarefaction curves (SCR; Chiarucci et al., 2009), to provide the expected number of accumulated species as the number of sampled plots increases from 1 to N. The use of spatially-constrained rarefaction was adopted to check for differences in the spatial autocorrelation of the species composition between the two data sets. Then, the ratio between the spatially-constrained rarefaction curves and standard rarefaction curves was used to detect the proportion of deviation from random expectations.

Secondly, we considered three levels of forest ecological organisation: the plot, the forest patch and the forest type. The plot scale was simply based on the sampling units used for data collection. The forest patches were defined on the basis of the Corine Land Cover 2006 map (European Environmental Agency; http://www.eea.europa.eu). Each polygon of each category was defined as patch. Forest types were defined by aggregating into a single class all the patches belonging to the same forest category, defined according to the Corine Land Cover (CLC) standard nomenclature (Bossard et al., 2000; APAT, 2005). The pooled species richness and composition of each forest patch and each forest type were then calculated for both INVEN and PHYTO data set. Only the forest patches having at least two sampling units and forest types having at least two patches for both the INVEN and PHYTO data sets were used for further analyses.

In order to take into account patterns of diversity across several levels of forest organisation, we calculated different measures of species diversity for each datasets: (1) the number of species per plot (alpha-plot), (2) the mean number of species per plot within each forest patch (alpha-patch) and within each forest type (alpha-forest-type), (3) the cumulative number of species recorded by the plots within each forest patch (gamma-patch), (4) the cumulative number of species recorded by the plots within each forest type (gamma-forest type), (5) the beta diversity among the plots of the same forest patch (beta-patch) and (6) the beta diversity among the plots of the same forest type (beta-forest type). Beta diversity was calculated as the according to the traditional