Hierarchical analysis of mite community structures in Irish forests—A study of the relative contribution of location, forest type and microhabitat

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ABSTRACT

In determining the overall γ-diversity within a land use type or when assessing the impact of a land use on biodiversity one has to consider the hierarchically nested nature of the γ-diversity. In this study we used a hierarchical approach to examine the diversity of mites, Oribatei and Mesostigmata, in various forest types in Ireland. The study included sampling at regional, stand, individual tree and microhabitat scales. α- and β-diversity (species richness) was examined at each of these scales and the proportional contribution to the variation accounted for by each level of the hierarchy was quantified. β-Diversity generally accounted for at least 50% of the γ-diversity at all levels of the habitat hierarchy with average values varying from 34% between regions, to 57.5% between forest types within region, to 63% between trees within forest type and 63% between microhabitats within a forest type. Differences between the fauna of microhabitats within a forest type accounted for approximately 30% of the total variation while that of forest types within regions accounted for 10.5%. These results are similar to those reported in several other studies but the study quantifies the variation by examining the relative contributions of α- and β-diversity to species richness. Redundancy Analysis allowed the identification of the proportional contribution of the hierarchical components to the variation in community structure in a manner which has not been used before for these systems.

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1. Introduction

Comparatively little is known of the invertebrate biodiversity in Irish forests (Bolger, 2004). In particular, it is not known how invertebrate diversity varies between forest types. This is of importance because, in Ireland, following centuries of deforestation, which reduced forest cover to 1.2% of the land area at the beginning of the 20th century, a rapid expansion forest cover has lead to approximately 10% of the land area (Forest Service, 2007). However, the trees planted during this period are largely non-native species such as Sitka spruce, which is native to North America, and represents 52% of the forests area. This has lead to a concern about potentially low biodiversity in these forests due to the absence of coevolved animal species and the forest management practices used.

In determining the overall γ-diversity within a land use type or when assessing the impact of a land use on the biodiversity and community structure in a landscape one has to consider spatial aspects of the diversity and, in particular, understand the hierarchically nested nature of the γ-diversity, i.e. the contributions of both the α and β components of the diversity should be taken into account (Whittaker, 1972). In other words, in addition to considering the diversity within patches or microhabitats (α-diversity) it is important to understand the species turnover between patches (β-diversity) and thus their importance in determining the total (γ) diversity within the landscape. In this study we used a hierarchical approach to examine the diversity of mites, Oribatei and Mesostigmata, in various forest types in Ireland.

Mites are good indicators of habitat and management practices (Ruf, 1998; Aspetti et al., 2010) are an ideal taxon to use when examining hierarchical aspects of biodiversity. They are generally believed to be a hyperdiverse taxon, with current estimates of the number of living species ranging from 500,000 to a million (Hammond, 1992; Walter and Behan-Pelletier, 1999; Ødegaard, 2000). In addition, they are extremely abundant and perform important functions in terrestrial ecosystems. They play a major role in decomposition and nutrient cycling and the composition of the fauna affects their ability to perform these roles (Heneghan and Bolger, 1997, 1999).

The Oribatei are often the most abundant microarthropods in forest soils and canopies (Petersen and Luxton, 1982; Behan-Pelletier and Walter, 2000; Lindo and Winchester, 2006) and may be distributed in a highly aggregated manner in this

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three-dimensional environment (Usher, 1975). Mesostigmata are among the species frequently collected from forest microhabitats such as fungal sporophores (O'Connell and Bolger, 1997a,b) but also occur in soil and canopies (Recher et al., 1996; Lindo and Winchester, 2006; Lindo and Stevenson, 2007; Arroyo et al., 2010a). Non-predatory species seem to predominate in the Uropodina and many species appear to be microphytophagous or possibly panphytophagous, feeding on fungi, bacteria, yeast and decaying organic matter. All Gamasina, on the other hand, with only a few notable exceptions are considered to be predatory or parasitic in their feeding habits.

In addition, there is an accumulating literature showing that the fauna varies significantly between different microhabitats within forests. For example, distinct assemblages of moss inhabiting oribatids occur in the canopy and forest floor (Winchester, 1997; Arroyo et al., 2010a,b; Beaulieu, 2012); suspended moss and soil mats in the canopy of Sitka spruce have a distinct oribatid assemblages (Winchester et al., 1999); the bark of different tree species can also support distinct oribatid communities (Nicolai, 1986) and the species richness of Mesostigmata in forests is strongly related to the number of microhabitats examined (Madej et al., 2011).

A multiscale approach was therefore adopted to address the biodiversity of mites in Irish forests and to assess the hierarchical relationships between the local, regional and national scale components of mite biodiversity. This involved sampling at regional, stand, individual tree and microhabitat scales, examining the α- and β-diversity (species richness) at each of these scales and quantifying the proportions of the variation in the total (γ) accounted for at each level of the hierarchy.

2. Methods

2.1. Design of study

This work was designed primarily to assess the variability in mite assemblage structures between five forest types in Ireland – oak, ash, Scots pine, and first and second rotation Sitka spruce. A hierarchical design was adopted in which a single stand of each forest type was selected in each of five different regions of Ireland. Within each stand, five individual trees were sampled and associated with each tree nine microhabitats were sampled. These were moss on the upper, middle and lower canopy, branches from the upper middle and lower canopy (for examination of the fauna of bark), moss from the base of the tree, and the soil organic horizon and of the upper five centimetres of mineral soil under the tree. Therefore there were 5 regions $\times$ 5 forest types $\times$ 9 microhabitats $\times$ 5 trees giving a total of 1125 samples. Details of the sites are provided in Arroyo et al. (2012).

2.2. Sampling

Following the protocol of Finnamore et al. (1998) climbers collected five sections of a single branch (approximately 40 cm in length) from the top of the living crown, mid-crown and at the bottom of the living canopy in each tree. The epiphytic moss cover was removed and the branches and twigs were bathed in a dilute solution of NaOH for 48 h. The liquid was then filtered and the animals collected. Samples from a particular height of a tree were pooled to give a single sample. Thus, there were three compound samples for each tree.

Samples of the moss occurring in the canopy were collected at each of the heights on each tree using a scraper and pooled for each height and tree. The sizes of these samples varied depending on the amounts of moss present on the trees. Finally, one moss sample was collected from the mats on the bark at the base (0–50 cm) of each

of the trees sampled. All the fauna inhabiting moss microhabitats were extracted using a Macfadyen extractor. Samples of the organic and mineral soil horizons were collected using a 5 cm diameter corer and the animals extracted from these using the Macfadyen extractor.

2.3. Data analysis

The contributions of various levels of the hierarchy to the species richness of the system was examined by determining the proportional contribution of β-diversity at each level and Redundancy Analysis was used to identify hierarchical components of variation. The determination of α, β and γ species richness followed Lande (1996). In this construct the total species richness (γ) in a pooled set of assemblages (S_T) is the total number of species found in the communities under consideration. The richness in an assemblage j is S_j and the turnover among assemblages (β) is defined as $S_T - \bar{S}_{within} = \sum_j q_j(S_T - S_j)$ where $S_T - S_j$ is the difference between the total species richness (γ) and the species richness in assemblage j. This is weighted by the proportional "weight" of the assemblage (q_j) determined by the number of individuals in each assemblage such that $\sum_j q_j = 1$. The average α species richness ($\bar{S}_{within}$) is a weighted average again using q_j as a weighting.

The determination of the hierarchical components of variation follows (Lepš and Šmilauer, 2003). This was carried out using CANOCO for Windows version 4.02 (ter Braak and Šmilauer, 1998). A separate CANOCO project was used for each level of the hierarchy and the contribution of a particular level in the hierarchy determined using individual units in the levels immediately above it as covariables and levels immediately below as split blocks. Although the β-diversity was high (Length of first axis of DCA = 7.747), as recommended by Lepš and Šmilauer (2003) Redundancy Analysis was used because, as is generally the case for microarthropod data, the data matrix was sparse with only 7092 non-zero entries (4% of total).

3. Results

3.1. β-Diversity at each level of the hierarchy

One hundred and fifty-four species were found in the study (Arroyo et al., 2012) but β-diversity represented a large proportion of the variation at all levels of the hierarchy thus the diversity recovered from any forest type or region was considerably lower than the total. Even when all of the data within individual regions were amalgamated, the species turnover between regions represented approximately one third of the total richness (Table 1). The number of species recovered within regions varied between 81 and 109 but the proportional contribution of β-diversity among forest types was generally at least equal to the contributions of α-diversity and in one region it reached 69.1% of the total, i.e. there was a turnover of at least half of the diversity as one moved from one forest type to another within a particular region. When this is extended to a comparison of individual trees within a region the turnover from tree to tree is of the order of 75% with the β-diversity in one region reaching 88.5%.

There was also large β-diversity between trees within each of the forest types. The greatest variation was among the oak trees where $\beta = 93.2$ but this only represented 71.9% of the total species richness while this proportion was over 80% among individual Scots pine and Sitka spruce (Rotation 1) (Table 1).

There was a significant difference between the species richness associated with the different forest types. The greatest species richness occurred in the oak and Scots pine forests with total richness of 119 and 114 species respectively (c.f. Arroyo et al., 2012).