



Simple to sample: Vascular plants as surrogate group in a nature reserve

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Summary

One of the basic tools to quantify biodiversity is based on the use of surrogate species. Such groups of species are easily assessed and may reflect the diversity of other important and less easily detectable taxa (cross-taxon surrogacy). Among these key groups of species, the vascular plant flora has great potential in determining diversity of other groups, since in terrestrial ecosystems it constitutes the bulk of total biomass and provides the physical structure for other organisms. The cross-taxon congruence of species diversity (species richness and species composition) among vascular plants, bryophytes, lichens, fungi, oligochaetes, butterflies and birds was investigated with special attention to testing the potential role of vegetation as surrogate for the other studied taxa. The 271 ha Nature Reserve “Bosco di S. Agnese” (Tuscany, Italy) characterised by evergreen Mediterranean woodlands, scrublands, garigues, xeric grasslands and cultivations was used as study area. A multi-scale sampling design, based on a restricted random selection of plots, was used to get information about vascular plants, bryophytes, lichens, fungi, oligochaetes, butterflies and birds. The congruence in species richness and composition among the different taxa was tested by Spearman rank correlation coefficient. Most of the pair-wise comparisons showed weak and statistically not significant correlations for both species richness and compositional data, indicating a limited cross-taxon congruence. Species richness of vascular plants was significantly correlated only to that of birds and butterflies. Compositional patterns were congruent only between vascular plants and butterflies. The results of this study

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indicated that neither vascular plants nor any other taxonomic group is a valid surrogate in this nature reserve.

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Introduction

The growing impact of human activities on natural ecosystems leads to a pressing need for development of straightforward methodologies for quantifying and monitoring biodiversity (Colwell & Coddington 1994; Gaston 2000; Harper & Hawksworth 1994; Kati et al. 2004). The proper management and monitoring of ecosystems and nature reserves require high-quality biological data, but time and costs often prevent the collection of a great amount of such data. The quantification of total species richness is practically impossible because of (i) the high number of species found in several habitats (Gaston 1996; Palmer 1995); and (ii) the impossibility of applying complete and objective species inventories (Palmer et al. 2002). Moreover, an apparent flaw in the systematic knowledge of certain taxonomic groups inevitably hampers the use of such groups for monitoring aims (Chiarucci et al. 2007; Palmer 1995).

In conservation biology, one of the basic tools for quick and economic measurements involves the use of surrogate species (Caro & O'Doherty 1999; Favreau et al. 2006; Lindenmayer et al. 2000). Taxon surrogacy hypothesis is based on the assumption of a concordance among the species richness or compositional patterns across different taxonomic groups (i.e. cross-taxon congruence, Howard et al. 1998; Lamoreux et al. 2006; Lund & Rahbek 2002; Prendergast et al. 1993; Su et al. 2004). In particular, some groups of organisms seem to be correlated with the diversity of the other groups. Among these, vascular plants are certainly a fundamental component for the structuring and functioning of terrestrial ecosystems; they constitute the bulk of net primary productivity and they represent an important taxon for the selection of nature reserves (see Rytí 1992). Moreover, sampling vascular plants is relatively easy (Pharo et al. 2000) and their taxonomy is sufficiently well described and standardised. Vascular plant species richness has been positively correlated with species richness of bryophytes (Sætersdal et al. 2003; Sauberer et al. 2004), lichens (Dynesius & Zinko 2006; Sætersdal et al. 2003), fungi (Sætersdal et al. 2003) and animal groups such as butterflies (Hawkins & Porter 2003; Howard et al. 1998) and birds (Kati et al. 2004; Qian 2007; Vessby et al. 2002).

The importance of compositional data has recently been demonstrated by Su et al. (2004) and by Similä et al. (2006), who found a high correlation between patterns of species composition of different taxa, despite their incongruence in species richness. Vascular plants species composition has been positively correlated with that of bryophytes (Chiarucci et al. 2007; Sætersdal et al. 2003), lichens (Pharo et al. 2000; Sætersdal et al. 2003), fungi (Chiarucci et al. 2005; Packham et al. 2002), butterflies (Howard et al. 1998; Maccherini et al. 2009; Su et al. 2004) and birds (Howard et al. 1998; Su et al. 2004). Reyers and Jaarsveld (2000) suggest that different techniques can produce dissimilar and even contrasting results for the same data set, but not necessarily contradictory because different techniques assess different aspects of species diversity. However few researchers have directly compared patterns of cross-taxon congruence in species richness and community composition (Howard et al. 1998; Oertli et al. 2005; Similä et al. 2006; Su et al. 2004). Many authors have analysed cross-taxon congruence, but the results are fragmentary and only partially in agreement even with respect to the same taxa (Howard et al. 1998; Kati et al. 2004; Negi & Gadgil 2002; Oertli et al. 2005; Prendergast et al. 1993; Ricketts et al. 2002; Schouten et al. 2009; Similä et al. 2006; Su et al. 2004; Vessby et al. 2002). Because of these contrasting results, the practical value of biodiversity indicators requires rigorous testing before implementation (Gustafsson 2000).

Following this view, cross-taxon congruence can be investigated by comparing species richness at individual site (α -diversity), or the variation in species composition among sites (β -diversity, Whittaker 1972). Some authors (e.g. Legendre 2007) considered β -diversity an interesting "currency" for comparing different ecological communities. Ordination methods have largely been used to partition the variation of community composition matrices, structuring the β -diversity of the system into orthogonal axes, which can be used to produce ordination plots (Legendre 2007). The ordination axes obtained for different taxa can then be compared by calculating pair-wise correlations (e.g. Hajek et al. 2002; ter Braak & Shaffers 2004).

The aim of this paper is to investigate the degree of congruence between species richness and compositional patterns (presence/absence of species)

of seven taxonomic groups (vascular plants, bryophytes, lichens, fungi, oligochaetes, butterflies, birds) in a nature reserve, to test whether vascular plants can be a potential surrogate group for predicting diversity of the other taxonomic groups at local scale.

Materials and methods

Study area

The study area is the Nature Reserve “Bosco di Sant’Agnese” (λ 11°13’00”E, ϕ 43°29’00”N, WGS84), in southern Tuscany (Italy). The Reserve covers 271 ha, with an elevation range from 246 to 419 m and a geological substrate formed by limestones and marls. Mean annual rainfall amounts to about 782 mm, while the average annual temperature is 12.4 °C.

The landscape is dominated by evergreen Mediterranean woodlands and scrublands, in which *Cupressus sempervirens* L., *Quercus ilex* L. and *Arbutus unedo* L. are the most abundant species. Garigues and xeric grasslands are present on eroded slopes, while cultivations (mostly olive and vineyards) cover a small proportion of the area. In general, the soils are very shallow and poor in organic matter.

Sampling design and field data collection

The spatial grains adopted for collecting information on species composition were 1 m², 100 m² and 10 000 m², but for the purposes of the present study only data relative to 10 000 m² (hereafter referred to as macroplot) were used. The adopted sampling design was the same as those described by [Kalkhan et al. \(2007\)](#) and [Baffetta et al. \(2007\)](#). In particular, the study area was overlaid with a square grid with cells of 500 × 500 m (25 ha), extracted from the kilometric UTM (ED50) grid and within each of such cells, one macroplot of 100 × 100 m (1 ha) was randomly selected, yielding a total amount of 12 macroplots ([Figure 1](#)). Each macroplot was in turn divided into four quadrants of 50 × 50 m and within each quadrant a plot of 10 × 10 m was randomly chosen, yielding a total amount of 48 plots. Finally, within each plot four subplots of 1 × 1 m were selected using an analogous procedure, yielding a total of 192 subplots. In order to locate sampling units as accurately as possible, static GPS methodology with differential correction was used for locating macroplots and plots, while the subplots were located by using a metric tape within the plot.

The presence of each species of vascular plant was recorded within the 1 × 1 m subplots and the 10 × 10 m plots. Bryophytes, fungi, lichens and oligochaetes were recorded within the 1 × 1 m subplots, while birds and butterflies were recorded within the 100 × 100 m macroplots. Vascular plants were sampled in May and June 2004. Bryophytes (liverworts and mosses) and lichens were sampled on bare soil, rocks, dead wood, trees and shrubs located at an height of up to 2 m above the ground, during May and June 2004. Fungi (macromycetes, either saprobes or parasites, with fruiting structure visible by naked eye) were recorded on tree bases (up to 2 m height) and dead wood in June 2004. Oligochaetes (*Lumbricidae* and *Enchytraeidae*) were sampled in June 2004, by using four square soil cores (12.5 × 12.5 × 12.5 cm) within each 1 × 1 m subplot; the oligochaetes were then extracted from soil by a modified version of the wet-funnel method ([Healy & Rota 1992](#); [O’Connor 1955](#)). Adult butterflies were sampled using Pollard-Yates observation technique ([Pollard & Yates 1993](#)), consisting in a visual census of 10 min along a rectangular transect of 100 × 10 m located in the centre of each macroplot; this sampling was conducted between 11:00AM and 15:00PM in July and August 2004. The breeding bird species were identified by the point-count method ([Bibby et al. 1992](#)); a sampling point was established in the centre of each macroplot and all the species visually or acoustically identified within a radius of 50 m were listed by a 10-min census, this sampling was performed in May and June 2004 always between 05:00AM and 9:00AM.

Species richness and composition (presence of all species) of each 100 × 100 m macroplot of vascular plants, lichens, bryophytes, fungi and oligochaetes at macroplot scale were obtained from the pooled list of species found in the 16 subplots or four plots (for vascular plants) nested within each of the 12 macroplots. Lists of butterfly and bird species were obtained by pooling the respective lists obtained in the two sampling dates within each macroplot.

Data analysis

The Spearman *rho* rank correlation coefficient was used, with presence-absence data, in order to test if species richness of the seven taxa was correlated. Multivariate analysis was used in order to evaluate the congruence of species composition of considered taxa. In particular, ordination analysis has earlier been used to address the congruence among taxonomic groups ([Anand et al. 2005](#); [Chiarucci et al. 2005, 2007](#); [Lee & Rotenberry 2005](#); [Pharo](#)

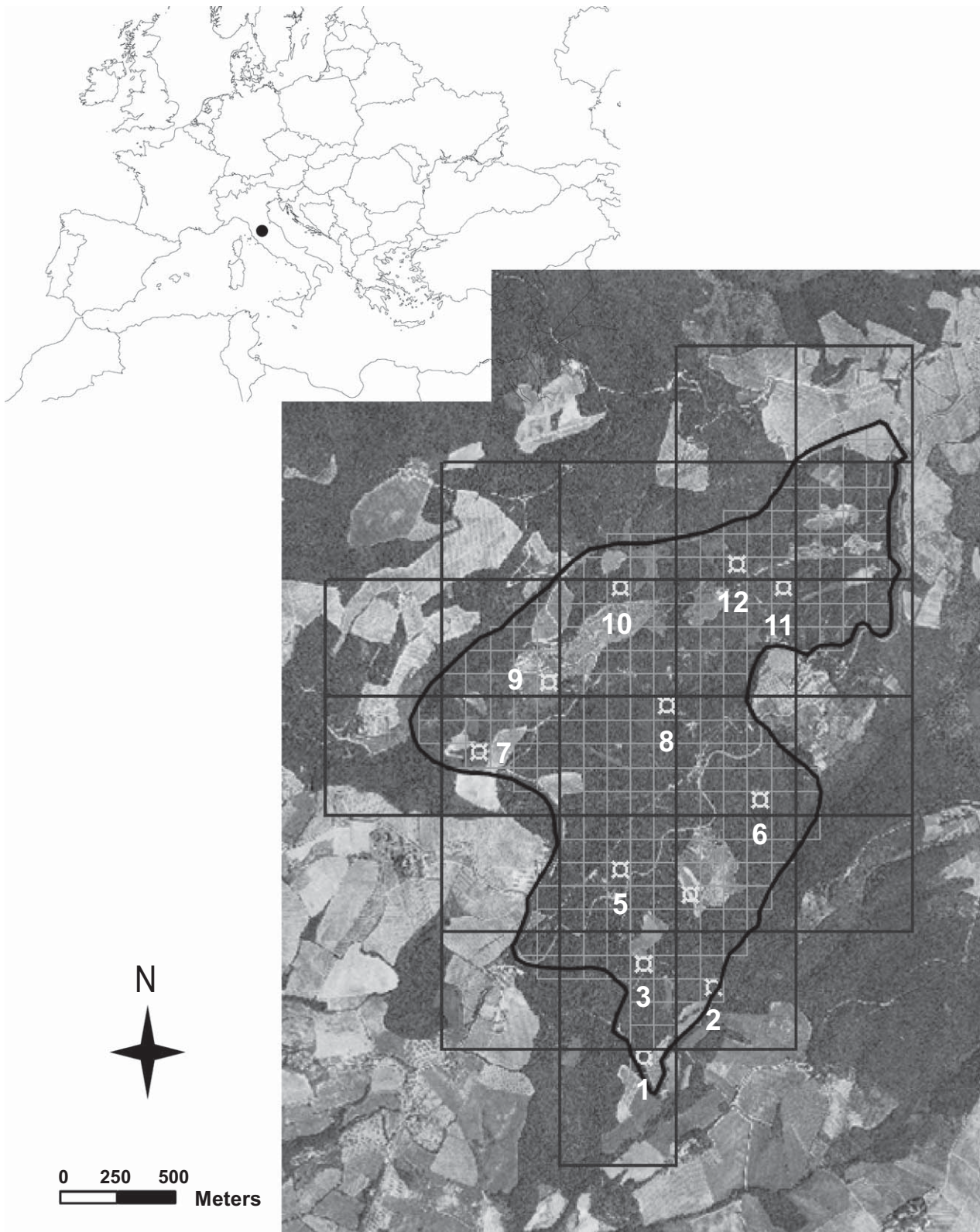


Figure 1. Location of the study area “Bosco di Sant’Agnese” Nature Reserve in central Italy and the kilometric UTM (ED50) grid divided into 500×500 m cells, within which one macroplot of 100×100 m (1 ha) was randomly selected, yielding a total amount of 12 macroplots.

Table 1. Summary statistics for each taxonomic group in all 12 macroplots (each macroplot was 100 × 100 m).

Taxonomic group	Mean number of species (SD)	Minimum number of species	Maximum number of species	Pooled number of species in the macroplots
Vascular plants	32.7 (10.8)	17	54	144
Bryophytes	17.3 (4.2)	8	22	44
Lichens	18.5 (11.9)	0	34	68
Fungi	7 (3.8)	2	16	46
Oligochaetes	8.4 (7.5)	0	22	34
Butterflies	6 (5.7)	1	18	32
Birds	11.5 (3.8)	5	17	31

Table 2. Spearman rank correlation coefficient (*Spearman rho*) among the species richness of all taxonomic groups at the macroplot scale.

	Vascular plants	Bryophytes	Lichens	Fungi	Oligochaetes	Butterflies	Birds
Vascular plants	–	0.003 (0.991)	–0.233 (0.467)	–0.470 (0.123)	–0.178 (0.580)	0.638 (0.026)	0.729 (0.007)
Bryophytes		–	0.201 (0.531)	0.297 (0.348)	0.357 (0.255)	0.093 (0.775)	–0.280 (0.379)
Lichens			–	0.096 (0.763)	0.071 (0.826)	–0.054 (0.867)	0.017 (0.957)
Fungi				–	0.562 (0.057)	–0.089 (0.783)	–0.463 (0.129)
Oligochaetes					–	0.091 (0.779)	–0.075 (0.817)
Butterflies						–	0.647 (0.023)
Birds							–

Parentheses show the *P*-value.

et al. 1999, 2000; Sætersdal et al. 2003; Similä et al. 2006). We relied on Principal Component Analysis (PCA-ordination) based on presence/absence data. We used linear methods because of (i) their potential use with empty samples contrary to unimodal methods (Lepš & Šmilauer 2003); and (ii) the relatively short length of the compositional gradients. Multivariate analysis was performed by using the CANOCO 4.5 software package (ter Braak & Šmilauer 2002). The potential use of the compositional pattern of each taxon as a surrogate of that of all others was tested by the Spearman *rho* correlation of the sample scores along the PC axes. Significant (positive or negative) correlation indicates parallel variation in the species composition among taxonomic groups.

Results

Species richness

The 12 sampled macroplots were largely composed of woodlands and scrublands (eight macroplots) and, to a lesser extent, by grasslands and cultivation fields with small patches of included

woodlands (four macroplots). The total number of species recorded in the 12 macroplots (Table 1) was highly variable across the seven taxa: 144 for vascular plants; 44 for bryophytes (six liverworts and 38 mosses); 68 for lichens; 46 for fungi; 34 for oligochaetes (two *Lumbricidae* and 32 *Enchytraeidae*); 32 for butterflies; and 31 for birds. Vascular plants were the most species-rich group while birds were the least species-rich group (Table 1).

Correlations of the species richness among the seven taxonomic groups were generally weak and statistically not significant for most comparisons (Table 2). In particular, the species richness of vascular plants was significantly correlated to that of butterflies and birds only, while these two latter groups were also significantly correlated to each other (Table 2). Furthermore, some correlation results were negative but not significant.

Species composition

The correlations between the sample scores of PC axis 1 (correlations between PC axis 2 were not significant for all comparisons) for the different taxonomic groups were low and not statistically significant for most of the comparisons (Table 3):

Table 3. Spearman rank correlation coefficient (*Spearman rho*) among sample score relative to the PC1 for all taxonomic groups at the macroplot scale.

	Vascular plants	Bryophytes	Lichens	Fungi	Oligochaetes	Butterflies	Birds
Vascular plants	–	0.023 (0.994)	0.047 (0.884)	0.166 (0.606)	–0.112 (0.708)	0.759 (0.004)	–0.182 (0.572)
Bryophytes		–	0.00 (1.000)	0.014 (0.966)	–0.040 (0.902)	0.100 (0.758)	–0.582 (0.047)
Lichens			–	0.084 (0.794)	–0.061 (0.851)	–0.051 (0.876)	0.005 (0.987)
Fungi				–	0.555 (0.061)	0.177 (0.583)	0.264 (0.407)
Oligochaetes					–	0.095 (0.770)	0.300 (0.344)
Butterflies						–	–0.283 (0.372)
Birds							–

Parentheses show the *P*-value.

only the correlation between vascular plants and butterflies was significant. The seven taxonomic groups did not follow comparable compositional gradients, and they were characterised by rather different orderings of the macroplots in the PCA scatter plot (Figure 2). With regard to the PCA scatter plot obtained for vascular plants, the first axis can be interpreted as a gradient from shrubland and woodland communities (macroplots 5, 10, 11, 6, 3, 12, 8 and 2) to open habitats such as xeric grasslands and cultivation fields (macroplot 9). The PCA scatter plot of the other taxa did not present the same ordering of macroplots (Figure 2, but see also Figure 1). The correlation performed on the sample scores of axis 1 confirmed results achieved for species richness albeit birds showed a statistically non-significant correlation in such a case.

Discussion

Surrogates are needed because it is unfeasible to measure the overall biodiversity of an area taking into account all the taxonomic groups (Margules et al. 2002). Surrogate can be used to reduce costs in the survey process or to represent different taxa in the conservation planning process. In particular, identifying efficient surrogate species, in the context of conservation biology, could be useful to (i) establish biodiversity priority areas (Favreau et al. 2006; Margules & Pressey 2000), (ii) manage for biodiversity conservation (Kati et al. 2004), (iii) monitor restoration programs (Anand et al. 2005), etc. An increasing need to test cross-taxon congruence at the local scale is evident (Kati et al. 2004; Su et al. 2004), since conservation actions (e.g. management and ecological restoration programs) are mainly performed at this scale. Nonetheless, there is much debate regarding the

selection and use of surrogates, and there are also many conflicting research findings because the publication bias gives more visibility to positive results and thus to existing correlations (Wolters et al. 2006).

The results of this study suggest that it is difficult to find a surrogate taxon useful to predict the biodiversity of other taxa. In fact, none of the investigated taxa was a valid surrogate for both species richness and composition. In particular, vascular plants were not an adequate surrogate species group to be used at the observed scale, because they did not fully represent the richness and compositional patterns of the other taxa.

The species richness patterns observed in this study showed a low congruence among the considered taxa. If a *rho* value of 0.70 is considered as threshold to indicate a certain level of congruence among taxa (Lovell et al. 2007), only the correlation between vascular plants and birds was significantly positive in this study. Moreover, several taxa showed a tendency for correlation but without significance.

Some authors indicated that testing congruence in community similarity is more appropriate than testing congruence in species richness (Lovell et al. 2007; Oliver et al. 1998; Su et al. 2004). Contrary to those findings, in this paper both types of data (composition and richness) indicated a scarce cross-taxon congruence. The observed patterns of species composition demonstrated a general incongruence among the investigated taxa, with the correlation between vascular plants and butterflies being the only significant.

Several studies at many different spatial scales of investigation have reported a low degree of congruence between the species richness and species composition of vascular plants and that of bryophytes (Jonsson & Jonsell 1999; Pharo et al. 1999; Söderström 1981), lichens (Anand et al. 2005;

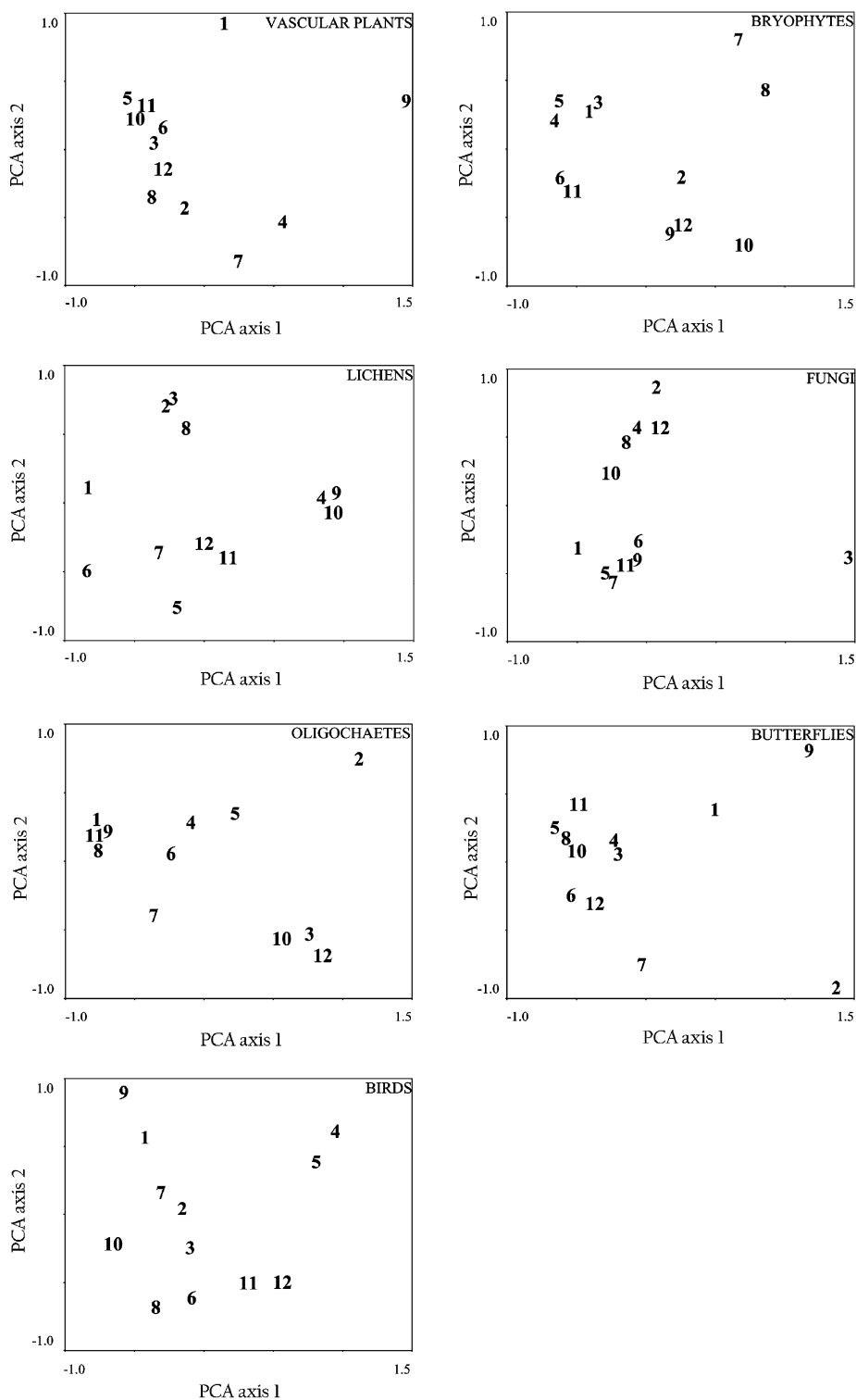


Figure 2. Principal component analysis (PCA) diagram of the 12 macroplots based on each taxonomic group (labels indicate individual macroplots).

Jonsson & Jonsell 1999; Negi & Gadgil 2002), fungi (Sætersdal et al. 2003; Virolainen et al. 2000) and species composition of birds (Anand et al. 2005). In the same way several studies, which are in agreement with the findings of this paper, have

reported a high correlation between species richness and species composition of vascular plants and that of butterflies (Hawkins & Porter 2003; Howard et al. 1998; Similä et al. 2006; Su et al. 2004) and species richness of birds (Kati et al. 2004; Qian

2007; Vessby et al. 2002). The close relationships between vascular plant and butterfly diversity can be due to both the evolutionary bonds (i.e. pollination co-evolution) and the consumer-resource interactions between these two taxa, since several butterflies are obligatorily associated with vascular plants during their larval stage (see Ehrlich & Raven 1964). In the same way the richness of vascular plants and birds can be linked to consumer-resource interactions and evolutionary bonds (i.e. seed dissemination). In general, plant species diversity can influence animal species diversity in several ways; a greater variety of plants is expected to lead to a greater variety of trophic levels, which in turn can lead to a greater variety of consumers (MacArthur 1972; Rosenzweig 1995). Moreover vascular plants provide food and nesting sites, and it is reasonable to hypothesise that plant diversity is associated with diversity of different major groups of animals (Hawkins & Porter 2003).

Although several studies showed that species richness patterns of bryophytes, lichens, fungi and oligochaetes are linked to environmental features, which also determine, in the same way, the vegetation (Campana et al. 2002; Dynesius & Zinko 2006; Sætersdal et al. 2003; Similä et al. 2006), the vascular plant species richness was not an appropriate predictor for those taxa. In fact bryophytes and lichens species richness has been found to be related to soil nutrient richness and humidity (Økland 1996; Sætersdal et al. 2003), the richness of polypore species to the total volume of dead wood (Sætersdal et al. 2003; Similä et al. 2006) and earthworm species richness to the total vegetation cover (Campana et al. 2002).

The lack of similar patterns of species richness or composition among taxa could be explained by the fact that cross-taxon congruence is highly variable and depends on different factors, such as (i) the considered spatial scale (Flather et al. 1997; Hess et al. 2006), (ii) the analysed taxa and (iii) the environmental heterogeneity of the area (Margules & Pressey 2000), but also (iv) the type of investigation (e.g. measures of species richness versus measures of community similarity, Cushman & McGarigal 2004). In fact, the incongruence emerged in this study could be due to the fact that the study area shows a high degree of landscape homogeneity with no evident gradients, with evergreen Mediterranean woodlands and scrublands dominating the whole area.

As emerged from this study, the vegetation-driven conservation planning, and consequently the habitat-based approach, is likely to be an ineffective means to protect other taxa (maybe with the

exclusion of butterflies and birds). This study confirmed that cross-taxon congruence patterns are highly complex and call for extensive locality and taxon specific assessments.

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