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Quantifying plant species diversity in a *Natura 2000* network: Old ideas and new proposals

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ABSTRACT

Assessing the effects of the spatial components on species diversity in a network of protected areas represents an important step for assessing its conservation "capacity". A clear evaluation on how α-, β-, and γ-diversity are partitioned among and within spatial scales can help to drive manager decisions and provide method for monitoring species diversity. Moving from these concepts, a probabilistic sample of plant species composition was here applied for quantifying plant species diversity within the Sites of Community Importance (SCIs) of the *Natura 2000* network in the Siena Province. All analyses were performed separately for all species and those species defined as "focal" (included in regional, national or continental "red" lists). The results indicated that species richness of the SCIs differed from one location to another one independently from the sampling efforts. Diversity partitioning indicated that most of the flora diversity within the network was given by larger-scale β-diversity, i.e. the differences in species composition among SCIs. β-diversity was then decomposed in two components: β_{Area} (due to the differences in area among SCIs) and $\beta_{Replacement}$ (due to the compositional differences across SCIs). β_{Area} was particularly important for all species, while $\beta_{Replacement}$ was the most important factor for focal species. The consequent implications for monitoring and nature conservation strategies are discussed.

1. Introduction

Due to the ever-growing impact of human activities, the biodiversity of natural habitats is rapidly being eroded, with the 13% loss estimate by Reid (1992), from 1990 to 2015, likely to be conservative (Nagendra and Gadgil, 1999). Concrete efforts for biodiversity conservation have been urged (WSSD of Johannesburg, Convention on Biological Diversity, UN Environment Programme and UN Development Programme). The objective to "*achieve by 2010 a significant reduction of the current rate of biodiversity loss at the global, regional and national level*" has been set by the convention on biological diversity and many resources are devoted to this aim. The implementation of the EU directives 92/43/EEC (Habitats Directive) and 79/409/EEC (Birds Directive) in the *Natura 2000* network is a major step towards a European strategy for nature conservation, and makes biodiversity monitoring legally binding (Bock et al., 2005). The sites of community importance (SCIs) are the main elements of the *Natura 2000* and the harmonisation of management and monitoring activities in these sites is an important challenge for local managers even though it still needs much effort (Devictor et al., 2007). Meanwhile, Habitats Directive (articles 11 and 17) focuses on monitoring of the conservation status of habitats and species of community importance, throughout the territories of all European Member States. In fact, the assessment of species diversity is crucial, since it represents a fundamental property of ecological communities and provides a tool to compare assemblages in time and space, independently from species identities (Colwell and Coddington, 1994; Olszewski, 2004). The assessment

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of species diversity could then provide useful information about the status of the *Natura 2000* network and the effects of its management, but criteria are still lacking.

Quantifying the partitioning of species diversity across spatial or ecological scales is fundamental to understand the processes structuring the biological communities (Wagner et al., 2000). Whittaker (1977) proposed a multiplicative way to link the diversity across scales, with the total diversity in a region given by the local scale diversity multiplied by the compositional change ($\gamma = \alpha * \beta$). Then, Allan (1975) introduced the additive partitioning of species diversity calculated by the Shannon index ($\gamma = \alpha + \beta$). Lande (1996) extended this latter approach to species richness and Simpson index, proposing this as a unifying way to assess the partitioning of species diversity at different organisation levels, with the advantage of using the same unit (e.g. the number of species) for quantifying the contribution of each component. Recent developments related this approach to classical techniques such as species–area curves (Crist and Veech, 2006) or rarefaction curves (Olszewski, 2004).

In order to achieve comparable results, standardized techniques are urgently needed for assessing and monitoring of biodiversity (Stohlgren et al., 1995). Probabilistic methods (Elzinga et al., 2001; Legg and Nagy, 2006) are then needed to provide a reliable inference about the species populating a large area or a network of protected areas. This is particularly true for plants, for which methods are available for assessing species diversity at a local scale (see e.g. Stohlgren, 2007), but not at a larger scale, such as a large protected area or a whole network of protected areas. At these scales, floristic data are often collected subjectively and the lists of species may be adequate for some aims (e.g. description of local habitats) but not for quantitative ones (Palmer et al., 2002). In addition, it is unlikely that one will ever get complete species lists in a large region (Robinson et al., 1994; McCollin et al., 2000). With respect to the *Natura 2000* network, even if monitoring programs single focused on animal species are ongoing, much remains to be done especially for plant species and total biodiversity.

Here, the results of a probabilistic sampling approach developed for assessing and monitoring plant species diversity within the network of SCIs of the Siena Province, Italy, are used to answer the following questions: (1) what is the relative contribution to the species diversity of the different spatial components, from the local to the regional one? (2) is the diversity partitioning of all species the same of that of focal species for which the reserve network was set up?

2. Survey sites

Seventeen SCIs are present in the Siena Province, Italy, and they range in size from 483 ha (Lago di Montepulciano) to 13,744 ha (Montagnola Senese), for a total of 58,969 ha. They range from low elevation (65 m a.s.l.) to high mountain (1,685 m a.s.l.), and host many different habitats: from open habitats to almost unmanaged forests. This network of SCIs is expected to host high plant species diversity, but the presently available floristic data are uneven.

The development phase of the monitoring program was conducted in 2005 and 2006, in eight SCIs with a variety of ecological conditions (Table 1). These SCIs host diverse plant communities, from thermophile forests dominated by *Quercus ilex*, *Quercus pubescens* or *Quercus cerris*, to mountain forests dominated by *Fagus sylvatica* or *Castanea sativa* (all the nomenclature is in accordance to Pignatti, 1982). Croplands, pastures, shrublands and conifer plantations are also present. These SCIs represent more than 35% of the *Natura 2000* surface in the Siena Province.

3. Methods

3.1. *Rationale and sampling design*

The sampling design adopted in this project was the same used for the Italian Inventory of Forests and Forest Carbon Stocks (INFC, Fattorini and Tabacchi, 2004). The sampling points were located by a restricted random selection, as follows: the whole Italy was covered by a grid of 1 × 1 km cells and one random point was selected within each cell. In the INFC project, these points were used for a three-stage sampling of forest data (De Natale et al., 2005). Here, the set of points of the INFC first sampling stage (one point per

Table 1 – Descriptive data for the eight investigated SCIs

SCI	Acronim	Area (km^2)	Altitudinal range (m)	Number of plots	All species		Focal species	
					Plot scale (mean and range)	SCI scale	Plot scale (mean and range)	SCI scale
Cono Vulcanico del Monte Amiata	AMI	17.68	782–1685	16	13.5 (4–40)	90	1.3 (0–5)	10
Alta Val di Merse	AVM	94.85	196–498	90	26.6 (6–119)	499	1.4 (0–6)	32
Bassa Val di Merse	BVM	41.40	123–459	44	29.4 (0–78)	394	0.7 (0–4)	20
Castel Vecchio	CAS	11.15	315–668	11	41.5 (12–62)	186	1.2 (0–3)	7
Valle del torrente Farma	FAR	26.29	196–498	26	30.2 (0–77)	316	1.6 (0–5)	21
Lucciolabella	LUC	14.17	315–668		25.5 (0–57)	151	1.9 (0–5)	11
Foreste del Siele e Pigelleto di Piancastagnaio	PIG	11.72	494–968	11	39.3 (16–59)	174	1.7 (1–3)	6
Ripa d'Orcia	RIP	8.31	205–522	8	29.8 (0–81)	130	1.4 (0–5)	7
All the SCIs	NETWORK	225.57	123–1685	219	28.2 (0–119)	778	1.3 (0–6)	65

1 × 1 km cell) falling within the shape of the eight SCIs and within the Siena Province was used, achieving a sample with a nominal density of 1 point per km^2 (Table 1).

A 10 × 10 m plot, divided into 16 (2.5 × 2.5 m) subplots, was installed in each sampling point, once located with a high-precision GPS. Plant species composition was recorded in each plot/subplot, together with data about slope, aspect and vegetation structure (% cover of the vegetation layers). The time spent to reach each point and to collect floristic data was also recorded.

Formally, this sampling method is based on a nested design, with four hierarchical levels: micro-scale level ($\alpha_{Subplot}$), stand level (α_{Plot}), site level (α_{SCI}) and regional level ($\alpha_{Network}$ or γ). This structure was thought to allow additive partitioning of species diversity (Allan, 1975; Lande, 1996; Veech et al., 2002; Crist et al., 2003), from the very local to the regional scale (Fig. 1). The stand level (plot scale) was considered central and then used for most of the analyses.

3.2. *Data analyses*

Annual crop species were excluded from analyses, while the cultivated tree and shrub species were maintained. Then, to test if the diversity patterns of all species were similar to those of the important species, the analyses were performed separately for "*all species*" and for the set of "*focal species*". The list of focal species included the species classified as of "*Community Importance*", "*In need of strict protection*", or "*Taking in the wild and exploitation may be subject to management measure*" (Ann. II, IV, V, Directive 92/43/EEC), or those defined as endangered in the regional database RENATO (AA.VV., 2005).

Plot-scale species richness was compared among SCIs by using a non-parametric Kruskal–Wallis one-way ANOVA, with Bonferroni correction for multiple comparisons.

To compare species richness of the eight SCIs, plot-based rarefaction curves (Sanders, 1968; Gotelli and Colwell, 2001) were calculated, by using the analytical formula (see Chiarucci et al., 2008). Some authors refer to "*species richness*" as the number of species obtained by a sample of individuals and to "*species density*" as the number of species obtained by a sample of clusters of individuals, such as a plot (see Gotelli and Colwell, 2001), but a general agreement is missing. The term species richness was used here to indicate the number of species recorded by a number of plots. Plot-based rarefaction curves were calculated for each SCI and for all the plots from the eight SCIs, to have an overall measure of the species diversity in the network of eight SCIs.

The ratio between the plot-based rarefaction curve of focal species and the corresponding one of all species was calculated to test if focal species were just a proportion of all species or followed some special pattern. Gotelli and Colwell (2001) observed that the category/subcategory taxonomic ratios used in biogeography suffer of sample-size dependence, and thus should be investigated by using the ratio of the respective rarefaction curves (see also Marignani et al., 2004). The method adopted here for analysing the focal species vs. all species pattern matches this proposal.

The total number of species recorded in each SCI was modelled as function of its area by using an Arrhenius' (1921) power function. This analysis is the classical species–area curves (Type IV in the Scheiner's, 2003 classification), with the pooled number of species recorded in each SCI as dependent variable and the number of plots as independent variable. The pooled number of species was not the true total species richness of the SCI, but an estimate based on the assumption that a comparable effort would result in higher number of species in a species rich SCI than in a species poor one. The number of plots was used as the independent variable since it represented the measure of the sampling effort within each SCI, but it is analogous to using the SCI area.

Plot-based and SCI-based rarefaction curves were calculated for the whole data set. The first gives the mean number

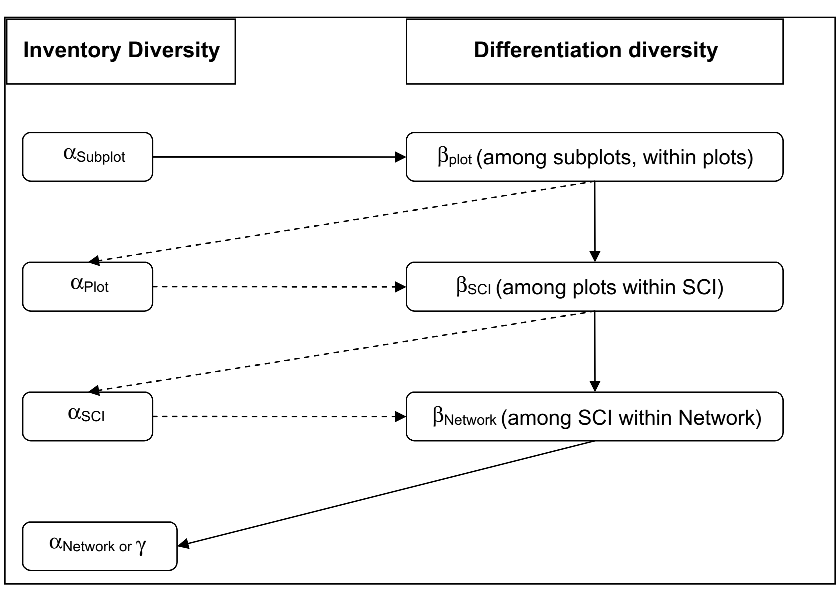

Fig. 1 – Additive partitioning model of species diversity including all the different hierarchical levels adopted for the eight investigated SCIs.

of species expected for a given number of plots, while the second gives the mean number of species for a given number of SCIs. To make the two figures comparable, the x-axis of the SCI-based rarefaction curves were scaled in terms of mean number of plots. These two curves are expected to overlap when species are randomly distributed. The curves were compared after linearisation by means of a log–log transformation. The slope and intercept values of the resulting lines were then compared. Possible differences between the curves obtained for the focal species and those obtained for all species were tested by a null model; i.e., a number of species corresponding to that of the focal species was randomly extracted from the total data set and their presence used to build analogous rarefaction curves. This was repeated 10,000 times to build a null model distribution to test the significance of the observed values for the focal species.

The contribution of each spatial component (subplot, plot, SCI) to the network species diversity was quantified by the diversity partitioning system shown in Fig. 1 (Gering et al., 2003; Crist and Veech, 2006). Inventory diversity is the α-diversity, i.e. the number of species found in a given unit (subplot, plot, SCI or network), while differentiation diversity (β-diversity) is the mean number of species of the upper level that are, on average, absent from the sampling units of the given level (Crist and Veech, 2006). The total diversity of the network may be considered both the network α-diversity, and the γ-diversity according to the Whittaker (1972, 1977) notations. According to Crist and Veech (2006), species richness in the network was partitioned into the inventory diversity at subplot scale ($\alpha_{\mathrm{Subplot}}$), that summed to the differentiation diversity within each plot (β_{Plot}) to give the inventory diversity at plot scale (α_{Plot}); this value summed to the differentiation diversity across the plots within each SCI (β_{SCI}) to give the inventory diversity at the SCI scale (α_{SCI}). Lastly, this latter summed to the differentiation diversity across the SCIs (β_{Network}) to give the inventory diversity of the network scale ($\gamma_{\mathrm{Network}}$). The software Partition was used to test for departure from random expectations of the richness values obtained at the different hierarchical levels for all species, using a sample-based randomisation test (Veech and Crist, 2007b).

By using the Arrhenius species–area models it was possible to calculate how much of the β_{Network} was due to the differences in size of the different SCIs and how much to the compositional differences among them. In fact, for a hypothetically perfect nested flora the smaller SCIs would contain only a fraction of the species contained in the largest SCI, and the flora of this latter would correspond to the total flora of the network. By calculating the differences between the total flora and the flora of the largest SCI, the amount of the β_{Network} due to the area variation across SCIs (β_{Area}) and to the replacement in species composition across SCIs ($\beta_{\mathrm{Replacement}}$) were quantified (Crist and Veech, 2006). These analyses were performed for all species and for the set of focal species. A null model corresponding to that described above, with 10,000 random groups of species of the same size of the focal species set, was used to test the significance of the species diversity partitioning.

4. Results

4.1. *General floristic patterns*

A pooled list of 783 species was obtained from the 219 sampled plots. Five annual crop species were excluded from analyses, resulting in a pooled species richness of 778 species. The total number of focal species was 65 (8.4%). Species richness per plot averaged 28.2 and ranged from 0 to 119; focal species richness per plot averaged 1.3 and ranged from 0 to 6. At the plot scale the eight SCIs differed widely in species richness (Table 1), with the Kruskal–Wallis statistic indicating significant differences among the eight SCIs for both all species (K–W = 20.54; $p = 0.005$) and focal species (K–W = 15.4, $p = 0.031$). Important differences were also found with respect to the pooled species richness recorded at the SCI scale (Table 1), with AVM being the richest site (499 species), followed by BVM (394) and FAR (316); AMI was the least species rich SCI

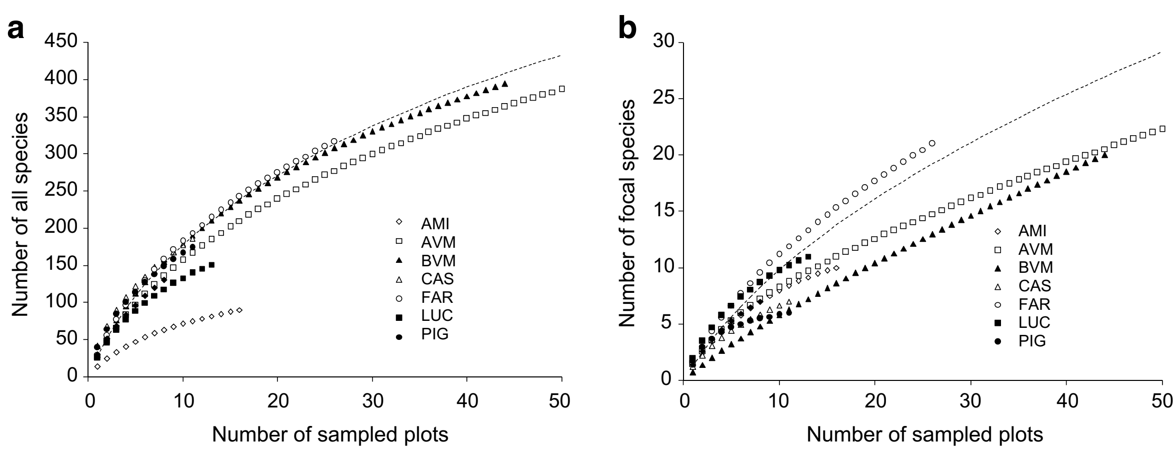

Fig. 2 – Plot-based rarefaction curves for all species (a) and focal species (b) in the eight sampled SCIs. The plot-based rarefaction curve for the pooled sample of all 219 plots is also shown (dashed line) in both graphs. Note that only the first part of the x-axis is reported and that the AVM SCI and the pooled sample would continue till 90 plots and till 219 plots, respectively. The name of the SCIs are coded as in Table 1.

with 90 species. A similar pattern was observed for the number of focal species recorded in each SCI (Table 1), with this number well correlated to the number of all species per SCI ($r = 0.9922$, $p = 0.0009$).

4.2. *Rarefaction curves of the eight SCIs*

The plot-based rarefaction curves for all species (Fig. 2a) showed rather similar patterns for most of the SCIs, at least for their low a number of sampled plots, but differences appeared as the number of plots sampled increased, with FAR, CAS and BVM showing the highest values of species richness. The lack of any asymptotic trend characterized the eight curves, even though AMI showed a lightly flattening pattern. The curves of FAR and CAS were slightly higher than the curve obtained for the composite sample, indicating a high species richness and compositional heterogeneity for these two sites.

The plot-based rarefaction curves of the eight SCIs for the focal species (Fig. 2b) showed different patterns, with FAR still having the steepest curve, much higher, in relative terms, than those of the other SCIs. In this case, the most flattening curve was that of PIG. The most different pattern, with respect to the rarefaction curves calculated for all species, was that by BVM; this SCI had one of the highest curves for all species but one of the lowest for the focal species.

The proportion of focal species *versus* all species was not constant across spatial scales or across SCIs (Fig. 3). In general, this ratio slightly increased as the number of sampled plots increased, but there were exceptions with decreasing (LUC and especially PIG), horizontal (AVM), or unimodal (AMI) patterns. Notably the ratio of focal species versus all species was highest in AMI, which had the lowest pattern for all species but an intermediate pattern for focal species.

4.3. *SCI scale species richness*

In general, the number of all species recorded in each SCI was well predicted by the number of plots located within it and, thus, from its area, and the same was true for focal species. The power function model explained 71.4% of the variance in the number of all species (Fig. 4a) and 88.9% of the variance in the number of focal species (Fig 4b). The most important outliers were AMI, with a negative deviation for all species, and FAR with a positive deviation for the focal species.

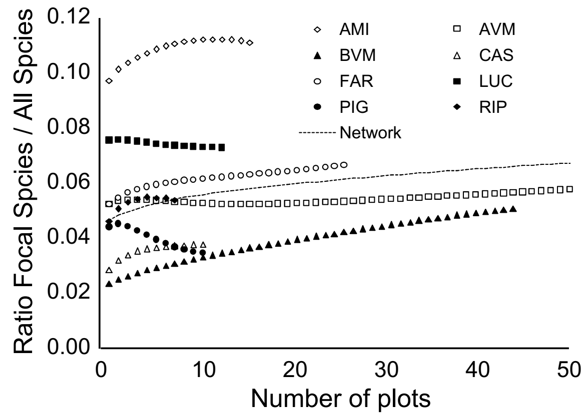

Fig. 3 – Ratio between the plot-based rarefaction curves calculated for the focal species and all species in the eight sampled SCIs. The same curve for the pooled sample of all 219 plots is also shown (dashed line). Note that only the first part of the *x*-axis is reported and that the AVM SCI and the pooled sample would continue till 90 plots and a ratio of 0.064 species and till 219 and a ratio of 0.084, respectively. The name of the SCIs are coded as in Table 1.

4.4. *General rarefaction curves*

The plot-based rarefaction curves for all species and for focal species were both higher than the corresponding SCI-based rarefaction curves (Fig. 5a and b), indicating a degree of compositional differences among the SCIs and a deviation from a purely random distribution of species.

The curves obtained for the focal species were steeper than the corresponding curves calculated for all species. In fact, once submitted to a log–log transformation, the plot-based and SCI-based (scaled in terms of number of plots) rarefaction curves of focal species both showed higher

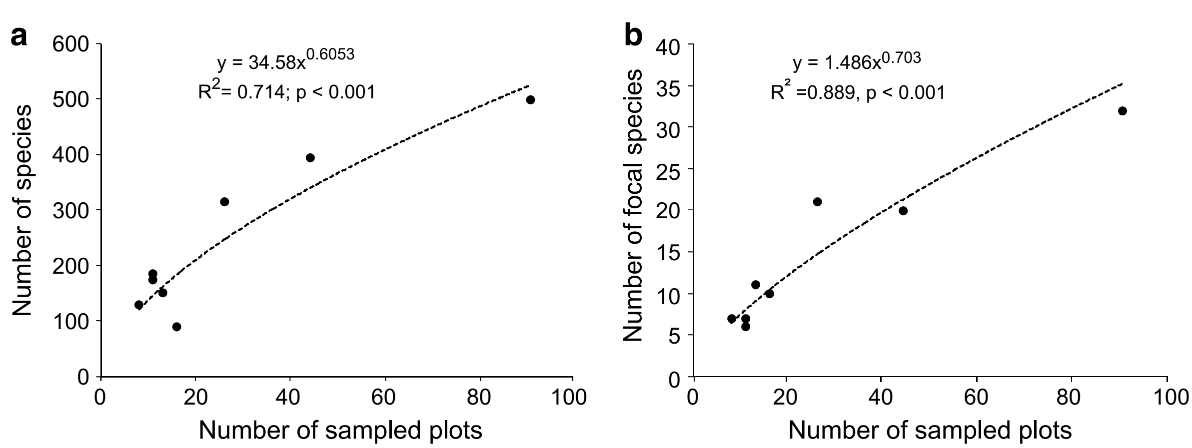

Fig. 4 – Species–area curves for the pooled list of species collected in the eight SCIs by the performed sample: (a) SCI's species richness for all species; (b) SCI's species richness for focal species only.

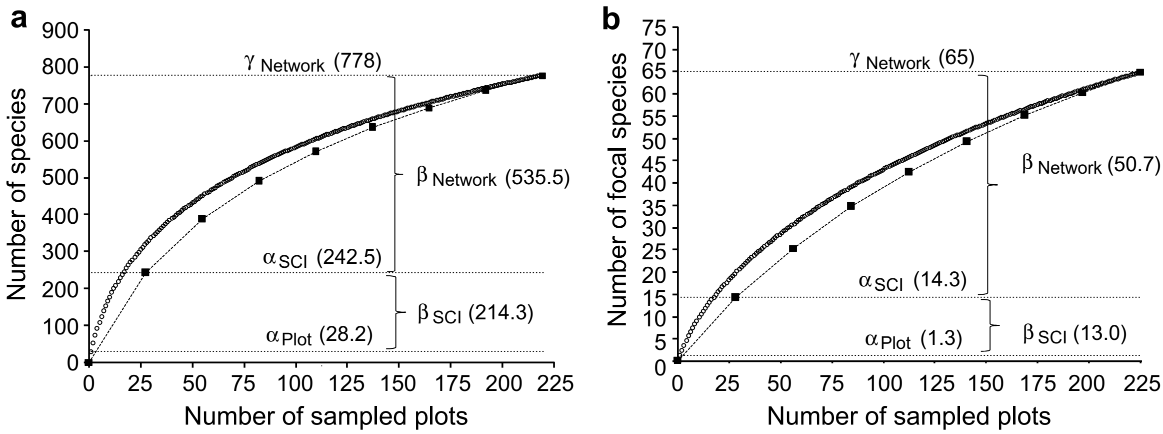

Fig. 5 – Plot-based and SCI-based rarefaction curves for all species (a) and for focal species in the eight sampled SCIs. An indication (in terms of number of species) of the different components of the species richness partitioning is also reported on the two graphs.

Table 2 – Parameters and model fitting for the log–log linear fit of the sample-based and SCI-based rarefaction curves for the data set of all species and focal species

Rarefaction curve	All species		Focal species	
	Slope	Intercept	Slope	Intercept
Plot-based	0.507 (R^2 = 0.973; p < 0.001)	1.739	0.638 (R^2 = 0.988; p < 0.001)	0.351
mSCI-based	0.555 (R^2 = 0.991; p < 0.01)	1.609	0.728 (R^2 = 0.995; p < 0.01)	0.129

For calculation and comparative purposes the x-axis of the SCI-based rarefaction curves were scaled according to the corresponding number of plots.

slopes and lower intercepts than the corresponding curves calculated for all species (Table 2). This was not an artefact due to the lower number of species involved in the calculation. In fact, the plot-based and SCI-based rarefaction curves of focal species were significantly higher than the corresponding null models calculated for groups of 65 species (10,000 repetitions): for the plot-based rarefaction curve, the probability of getting a curve higher than that of focal species from a null combination of 65 species (Fig. 6a) did not exceed a value of $p = 0.005$ for most of the curve and reached a value of $p = 0.01$ at the end of the curve. For the SCI-based rarefaction curve, the probability of getting a curve higher than that of focal species from a null combination of 65 species (Fig. 5b) was constantly very low and reached a value of $p = 0.005$ only at the end of the curve, for a number of seven SCIs.

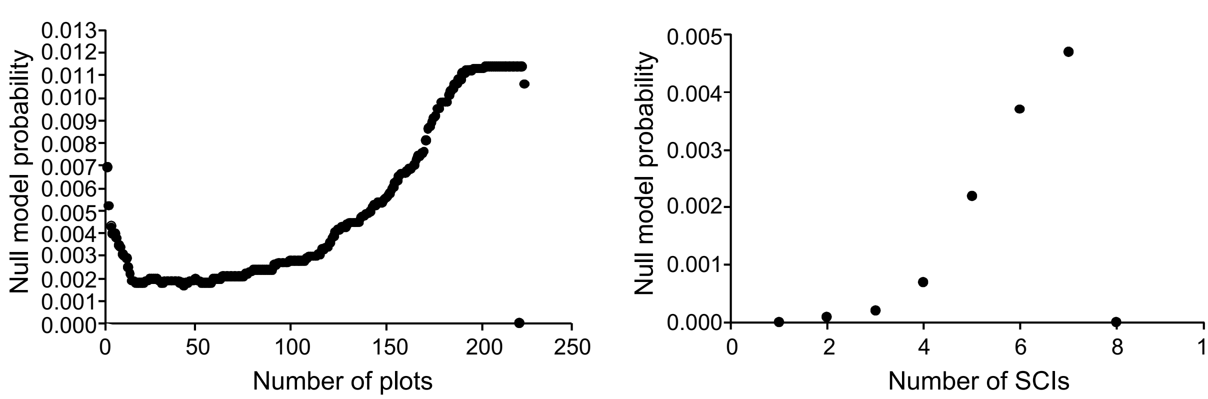

Fig. 6 – Probability, under a null model, that the plot-based rarefaction (a) and SCI-based (b) rarefaction curves of focal species fall below an analogous curve calculated for random combinations of 65 species, as a function of number of plot or SCI sampled.

Table 3 – Additive partitioning of species richness between α_{SCI}, β_{Area} and $\beta_{Replacement}$ for all the species and the focal species groups

Spatial component	All species		Focal species	
	No. of species	%	No. of species	%
α_{SCI}	243	31.1	14.1	21.7
β_{Area}	283	36.3	15.2	23.4
$\beta_{Replacement}$	255	32.6	35.7	54.9
$\gamma_{Network}$	780	100.0	65.0	100.0

4.5. *Species diversity partitioning*

According to an additive partitioning picture, the pooled list of 778 species found in the network, was 1.4% due to the subplot $\alpha_{Subplot}$, 2.2% due to the β_{Plot} (giving an α_{Plot} of 3.6%), 27.5% due to the β_{SCI} (giving an α_{SCI} of 31.2%) and 68.8% due to the $\beta_{Network}$ (Fig. 5a); this suggests a major role of the differentiation among plots of the same SCI and, on a larger extent, among the different SCIs of the network. The randomisation tests showed that the species richness at the plot and the SCI scale were both was significantly lower than expected ($p < 0.001$). When calculated for the focal species the pooled list of 65 species found in the network, was 0.7% due to the subplot $\alpha_{Subplot}$, 1.3% due to the β_{Plot} (giving an α_{Plot} of 2.0%), 19.9% due to the β_{SCI} (giving an α_{SCI} of 21.9%) and 78.1% due to the $\beta_{Network}$ (Fig. 5b), indicating that the species richness of this group was more dependent on the differences across the different SCIs of the network. The randomisation tests showed that the focal species richness at the plot and the SCI scales were both significantly lower than expected ($p < 0.001$).

The additive portioning of species richness performed across SCIs and using Arrhenius' like species–area curves, showed a markedly different partitioning of the larger-scale components of diversity between all species and focal species. In particular, the α_{SCI} and β_{Area} components were higher for all species than for the focal species (Table 3), while the higher $\beta_{Network}$ component of the focal species was almost exclusively due to the $\beta_{Replacement}$. The null models, based on 10,000 random combination of 65 species each, confirmed the value of the α_{SCI} and β_{Area} components of focal species were lower than expected, while their $\beta_{Replacement}$ component was significantly higher than expected.

5. Discussion

5.1. *Partitioning species diversity across scales within the Natura 2000 network*

The eight investigated SCIs differed in species richness at both the plot and whole-site spatial scales. The plot-based rarefaction curves also differed across SCIs, with the highest curve (FAR) being, in its first part, as high as the curve obtained by the pooled sample of 219 plots, indicating an extremely high species richness of this SCI. The pooled data set was expected to have the highest curve, because of its higher heterogeneity with respect to each single SCI. In fact, rarefaction curves grow more steeply with higher species richness per sampling unit, but also with higher complementarity among them (Gotelli and Colwell, 2001; Ugland et al. 2003, 2005; Chiarucci and Bonini, 2005; Rocchini et al., 2005). A quasi-asymptotic pattern was observed only in the case of one SCI (AMI), suggesting an adequate sampling intensity for this site (Chiarucci et al., 2001b; Gotelli and Colwell, 2001; Fattorini, 2007). It should be noted that this SCI is largely covered by homogeneous *Fagus sylvatica* forest, that is characterized by low species diversity and a high floristic homogeneity (Selvi, 1996; Chiarucci et al., 2001a).

The rarefaction curve calculated for the 219 plots of the network did not show any asymptotic pattern, suggesting that the total species richness of this set of SCIs is much higher than that obtained by our sample. As a consequence, a much higher sampling density would be needed to get a complete species list, but this would almost certainly result in prohibitive costs. As a possible reference, the design adopted by the Swiss biodiversity monitoring program (Koellner et al., 2004; Bühler, 2006) uses a density of points that is only 1/25 of that here adopted. Basically, even a very high density of sampling points, as adopted here, cannot provide a reliable estimation of plant species richness over a large area. This is likely to be an important problem for biodiversity estimation, also given the problems associated with the use of species richness estimators (Chiarucci et al., 2003; Lam and Kleinn, 2008).

For the whole network, the plant species diversity was largely due to the β-diversity component within each SCI and, especially, across SCIs. In relative terms, the β-diversity within each SCI accounted for 36.3% and the β-diversity across SCIs for 32.6% of the total species richness recorded in the network. This observed pattern was certainly dependent on the variety of vegetation and habitat types within this area, due to the complex geological, topographical and land-use types, as well as the extremely long history of its human exploitation (De Dominicis, 1993). The millennial use of these areas for agricultural, pastoral and sylvicultural use produced a complex mosaic, composed of few natural remnants, mixed to several semi-natural habitats and a rich variety of secondary vegetation types (see De Dominicis, 1993). The major role of the compositional complementarity in determining larger-scale diversity was reported by other studies. For example, in bird communities of USA, Veech and Crist (2007a) reported that landscape-level β-diversity typically accounted for more than half of the γ-diversity and was significantly and positively related to habitat and climate heterogeneity. In the same way, Gering et al. (2003) found that broad-scale β-diversity of arboreal beetles in the eastern deciduous forest of Ohio and Indiana (USA), analyzed at four different spatial scales (from the individual tree to the ecoregion), accounted for most of the variation and supported the hypothesis that ecoregions largely structured the richness and composition of beetle communities. This pattern was largely due to the high environmental heterogeneity involved with this larger spatial scale.

In the investigated network, more than half of the β-diversity was due to the variation in area across sites (β_{Area}). One of the most frequently debated theories in conservation biology has been whether the best strategy for species survival is to have a single large or several small remnant refuge patches as nature reserves (see e.g. Fahrig, 2001; Zhou and Wang, 2006). The partitioning of species richness observed in the *Natura 2000* network of the Siena Province was likely to indicate the choice of larger areas is better. However, the compositional complementarity among sites was responsible for a comparable amount of β-diversity. Consequently, the conclusion that a single large area should be preferred should be taken with caution, given the dependence of species richness and complementarity on factors other than the area, e.g. the distance among sites (Nekola and White, 1999) or the total extension of the network (Scheiner, 2003). Additive partitioning may be integrated in the future as a tool for the selection of networks of protected areas based on complementarity. However, Rodrigues and Gaston (2002) noted that representation differs with respect to the conservation aims, and in order to guarantee the role of reserves in maintaining biodiversity over time, the size of the chosen units must be that at which the populations of species are likely to persist. These latter observations are in agreement with the need to include large sites within a network of protected areas. In fact, because of the well known species–area relationships (Arrhenius, 1921; Scheiner, 2003), adding a new largest area to the network will produce a steeper slope of the species–area curve characterizing the network (that is, an increase in β-diversity, Ricotta et al., 2002). In addition, the quality of the surrounding matrix is also very important for the conservation capacity of a network of protected areas (see e.g. Briers, 2002).

Finally, the complex landscape structure of southern Tuscany and its *Natura 2000* network is likely to strongly change in the near future. The recent process of abandonment of hilly areas is causing a reduction of the semi-natural open habitats, such as the pastures and grasslands linked to the traditional management practices, and as a consequence forest cover increases and the landscape becomes more homogeneous (Vos et al., 2001; Rocchini et al., 2006). This will certainly affect both the species richness hosted in the *Natura 2000* network and its partitioning across the spatial components.

In summary, the combined use of rarefaction curves (and/or species–area curves) and additive partitioning of species diversity can be used to unify the different approaches for quantifying species diversity and composition used until now (Crist et al., 2003). Recently, Olszewski (2004) applied the additive partitioning concept proposed by Lande (1996) to rarefaction curves, in order to compare diversity components among areas sampled with different sampling efforts. Even if this latter method appeared formally correct from a mathematical point of view, problems occur when sampling effort is expressed as area units (rather than as number of individuals, see Olszewski, 2004 for details). To date, the additive partitioning method proposed by Gering et al. (2003) represents a straightforward manner to split species diversity into its spatial components. Moreover, the autocorrelative structure in community composition is explicitly quantified by using such an approach. The increase in composition similarity with decreasing distance is a well know pattern in ecology (see e.g. Nekola and White, 1999, and requires to be considered in the analysis of species distribution. The autocorrelation structure can determine a lower species richness when aggregating closer plots with respect to the expectations obtained by using all the plots. The use of rarefaction curves implemented with additive partition techniques can help to quantify these departures from random expectation and may represent an way to look at the autocorrelative structure of the investigated plant communities.

5.2. *Diversity of diversity pattern: behaviour of focal species*

Although the sampling design adopted in this study was based on a probabilistic design and was consequently more suited for finding common rather than focal species, some phytogeographycally important species were recorded. Among these, *Viola etrusca* was the species with the most restricted range size, being endemic of southern Tuscany (Selvi et al., 1995). Overall, more than 8% of the species found in the sample were listed as “focal species” and, although many of these species were fairly common in the area, this proportion seems very high.

The rarefaction curves obtained for the focal species showed a relative ordering of sites that was quite different from that obtained for all the species, suggesting that the species richness patterns of focal (rare, endemic or threatened) species could differ largely from those of all species. The ratio of the “number of focal species” with respect to the “number of all species” was in agreement with this observation. This ratio showed a slight increasing pattern as a function of the number of sampled plots, suggesting that the proportion of focal species with respect to all species changes with the number of species sampled. This pattern was expected, since the focal species are mostly rare species and thus needing larger or a specifically designed sampling strategy to be detected (Newmaster et al., 2005; Ringvall and Kruys, 2005; Guisan et al., 2006; Hedgren and Weslien, 2008). However, this pattern was not constant among the eight sites that showed markedly different patterns, with constant, decreasing, increasing or even unimodal-like patterns. These differences show how difficult it is to get a reliable estimate of the number of rare, or focal, species from a probabilistic sample. Some authors (e.g. Jiguet and Julliard, 2006; Pearman and Weber, 2007) reported that the species richness patterns of common species reflected those of all species and, consequently, data about common species can be used to make inference for the species richness patterns of all species. On the contrary, rare or endemic species are not related to the general patterns of total species richness, because of the more peculiar distributional patterns. This result has already been reported by Lennon et al. (2004); using South African and British birds, these authors showed that common species were more responsible for richness patterns than rare species were. In a similar way, Bacaro and Ricotta (2007), pointed out that rare species scarcely contribute to increase plot-to-plot semi-variance based β-diversity with respect to common species. Basically, the ratio between rarefaction curves of focal species versus all species provided useful insights on the proportion of important species on the total flora. This proportion changed across spatial scales, or completeness of the list of species, but the ratio could be used as an indicator of the richness of this groups of plants in the same way suggested to calculate taxon–subtaxon ratios (Gotelli and Colwell, 2001) or cross-taxon congruency (Chiarucci et al., 2007).

Focal species showed a more evident pattern of species diversity partitioning between spatial scales, with their diversity being more dependent on the complementarity across sites ($\beta_{\text{Replacement}}$). In general, it is known that most of the spatial pattern of species diversity is due to relatively few, more common, species (Bonn et al., 2002; Pearman and Weber, 2007; Gaston, 2008). As previously stated, the data collection system adopted in this study could be considered more adequate for getting a picture about the species diversity patterns of common and all species, than that of rare or focal species. However, some interesting data on focal species emerged and they could be profitably used for conservation purposes. The differences in floristic composition of focal species across SCIs ($\beta_{\text{Replacement}}$) were more important than expected by the randomisation tests. In fact, the SCIs showed a focal species richness (α_{SCI}) lower than that expected by chance but they were more complementary ($\beta_{\text{Replacement}}$) than expected by chance.

In theory, a species can be rare because of many reasons, such as declining population (unsuccessful reproductive or high death rate), recent immigration, or a small proportion of suitable habitat (see, for example, the classical descriptions of rarity by Rabinowitz et al. (1986). Hubbell and Foster (1983) found that most rare species are specialists in habitat utilisation (e.g. topography or edaphic conditions) or in regeneration niche (relatively ephemeral or regenerative conditions in gap openings) and, for these reasons, they are spatially segregated. The mechanism suggested by Hubbell and Foster (1983) appeared to be crucial in explaining the high complementarity observed in the data set of focal species. In fact, this *Natura 2000* network is composed by heterogeneous, human-managed and ecologically differentiated natural and semi-natural areas. In particular, these SCIs host extremely differentiated ecological features, such as serpentine (Chiarucci, 1994) or pliocenic clay substrates (Chiarucci et al., 1995), that determine the presence of specific, and thus high complementary, floras. For conservation purposes, the patterns of focal species richness highly dependent on the larger scale complementarity suggests that for this group of plants a strategy based on several small nature reserves could work better than a strategy based on a few larger ones. This makes evident that the strategies to preserve plant species should combine larger sites, with large populations of many species, but also small sites with peculiar features of topography, soils, or any other ecological parameter. The importance of small patches in a larger-scale conservation strategy has been evidenced by many other authors (e.g. Fischer and Lindenmayer, 2002).

In summary, the high level of complementarity in ecological conditions, coupled with the variety of land-use management, is responsible of the high levels of β-diversity in the observed patterns of focal species more than of all species. This is a rather obvious conclusion when remembering that the focal species were selected as those most important or characterising rare habitat types but provided indications about the strategies to be adopted for selecting or prioritising protected areas. These results confirmed previous findings suggesting that the selection of protected areas on the basis of threatened and endemic species performed considerably better than a random selection (Bonn et al., 2002; Lennon et al., 2004); however, such a selection did not guarantee the representation of overall species diversity, suggesting a separation between the species diversity patterns of threatened and endemic species with respect to that of all species, as also confirmed by the present results. On the other hand, Jiguet and Julliard (2006) observed that a good strategy to select conservation areas for protecting most bird species in continental France was based on the selection of the sites hosting the most peculiar community composition and not the sites hosting the rare species. However, Fontaine et al. (2007) evidenced the need to focus the European conservation strategies and reserve selection on rare species that are the most threatened.

6. Conclusion

Natura 2000 network is certainly the most important conservation network in Europe. Starting from this existent evidence, it is now time for a step forward in the direction of assessing its effectiveness in space and time. Quantifying and monitoring species diversity within the network is certainly the right way to achieve this aim. The use of a spatially restricted random sample for assessing and monitoring plant species diversity could provide different quantitative results, based on robust but straightforward statistics, such as rarefaction curves. These are nowadays a standard approach that can be profitably used for evaluating the temporal shifts in species diversity. Moreover, other modern techniques, such as the additive partitioning of species diversity, can be applied to data collected by random sampling strategies to quantify the contribution of the different spatial components to the species diversity of the whole system, and these tools could be used for both assessment and monitoring purposes.

The use of such analytical tools allowed us to observe how the species richness patterns and partitioning of all species were not representative of those of focal species, for which the set of protected areas was set up. Basically, the focal species richness was more influenced by larger-scale patterns, such as the regional altitudinal and or geological gradients and this supports the view that including a high number of ecologically different areas in the conservation network is essential. On the other hand, the species diversity pattern of all species was more dependent on the size of each protected area, supporting the view that protected areas should be as large as possible in order to preserve a high number of total species, that should better ensure long-term insurance of the ecosystem functioning processes.

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