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# Reliability of a Higher-Taxon Approach to Richness, Rarity, and Composition Assessments at the Local Scale

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**Abstract:** *A promising shortcut for quantifying species patterns is to use genera and families as surrogates of species. At large spatial scales, concurrence between patterns of richness, rarity, and composition of species and higher taxa is generally high. Only a few researchers, however, have examined this relationship at the local scale, which is frequently the relevant scale in land-use conflicts. We investigated the reliability of the higher-taxon approach in assessing patterns of species richness, rarity, and composition at the local scale. We studied diversity patterns of three commonly used surrogate taxa: vascular plants, ground-dwelling beetles, and moths. We conducted year-round field surveys for these taxa in the Jerusalem Mountains and the Judean foothills, Israel. Richness and composition of species were highly correlated with richness and composition of genera for all taxa. At the family level, correlations with richness and composition of species were much lower. Excluding monotypic genera and families did not affect these relations. Rarity representation based on higher taxa varied considerably depending on the taxon, and rarity scale and was weaker compared with richness and composition representation. Cumulative richness curves of species and genera showed similar patterns, leveling off at equivalent sampling efforts. Genus-level assessments were a reliable surrogate for local patterns of species richness, rarity, and composition, but family-level assessments performed poorly. The advantage of using coarse taxonomic scales in local diversity surveys is that it may decrease identification time and the need for experts, but it will not reduce sampling effort.*

**Keywords:** conservation planning, Jerusalem Mountains, species diversity indicators, species richness, species composition, species rarity, surrogate taxa

Confiabilidad de un Enfoque de Taxón Superior para Evaluaciones de Riqueza, Rareza y Composición a Escala Local

**Resumen:** *La utilización de géneros y familias como sustitutos de especies es un atajo prometedor para la cuantificación de patrones de especies. En escalas espaciales grandes, la concurrencia entre patrones de riqueza, rareza y composición de especies y taxa mayores generalmente es alta. Sin embargo, pocos investigadores han examinado esta relación a escala local, que frecuentemente es la escala relevante en conflictos de uso de suelos. Investigamos la confiabilidad del enfoque de taxón superior en la evaluación de los patrones de riqueza, rareza y composición de especies a escala local. Estudiamos los patrones de diversidad de 3 taxa sustitutos utilizados comúnmente: plantas vasculares, escarabajos del suelo y mariposas nocturnas. Realizamos muestreos de estos taxa en las Montañas de Jerusalén y las colinas de Judean a lo largo de un año. La riqueza y composición de especies estuvieron altamente correlacionadas con la riqueza y composición de géneros de todos los taxa. A nivel de familia, las correlaciones con la riqueza y composición de especies fueron mucho menores. La exclusión de los géneros y familias monotípicas no afectó a esas relaciones. La representación de la rareza basada en taxa superiores varió considerablemente dependiendo del taxón, y la escala de rareza fue más débil en comparación con la representación de la riqueza y composición. Las curvas de acumulación de especies y*

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*géneros mostraron patrones similares, nivelándose en esfuerzos de muestreo equivalentes. Las evaluaciones a nivel de género fueron un sustituto confiable de los patrones de riqueza, rareza y composición de especies, pero las evaluaciones a nivel de familia funcionaron pobremente. La ventaja de la utilización de escalas taxonómicas gruesas es que puede reducir el tiempo de identificación y la necesidad de expertos, pero no reducirá el esfuerzo de muestreo.*

**Palabras Clave:** composición de especies, indicadores de diversidad, planificación de la conservación, Montañas de Jerusalén, rareza de especies, riqueza de especies, taxa sustitutos

## Introduction

A major challenge in conservation practice today is acquiring data on the distribution of species that can help guide planning and management. Because time, money, and taxonomic expertise are limited, it has been suggested that surrogates replace direct assessments of species richness, rarity, and composition if they can be measured cheaply and quickly and if their measurement is reliable scientifically (Lawton et al. 1998; Wilson 2000). Surrogates include environmental indicators, characteristics of the physical environment that affect the distribution of species, and taxonomic indicators, subsets of taxa expected to reflect wider patterns of diversity (Oliver et al. 2004). A third promising but less-studied tool is the surveying of higher taxa in which genera, families, and even orders are used as surrogates of species (Gaston & Williams 1993; Williams & Gaston 1994). This approach has gained empirical support (e.g., Balmford et al. 2000; Villasenor et al. 2005) and has the inherent advantage of studying the focal taxon itself, thus avoiding indirect measures.

Most of the research on species diversity indicators has focused on wide spatial scales, regional to global (Reid 1998; Lawton & Gaston 2001). This is particularly true for the use of higher taxa as surrogates of species (Balmford et al. 1996a, 2000). Nevertheless, conservation practitioners and planners are often faced with local-scale decision making, especially in densely populated areas, where only limited land is still available and habitat loss and fragmentation are dire. Many land-use conflicts are confined to an area of a few square kilometers. Tools developed for large spatial scales (in the magnitude of hundreds to thousands of square kilometers) may not be efficient for finer-scale diversity assessments because the patterns dealt with are more subtle and spatial autocorrelation may be high. We aimed to help bridge the gap between macroecological studies of biodiversity patterns and current needs in conservation practice. We focused on the higher-taxon approach and tested its efficacy as an indicator of local patterns of richness, rarity, and composition of species.

The higher-taxon approach is based on the assumption that the classification of specimens to genus and family is easier and faster than classification to species, making field surveys and data processing more efficient and

cost-effective (Balmford et al. 1996b). There are three underlying assumptions to this approach. First, there are fewer genera and families than species (i.e., monotypic genera and families do not have overriding effects on diversity patterns). Second, the sampling effort required to achieve a representative sample is lower for genera and families compared with species. Third, the distribution of species within genera and families is relatively homogeneous (i.e., there is little variation among genera and among families in the number of nested species within each). Although these assumptions rarely have been addressed directly (Balmford et al. 1996b; La Ferla et al. 2002), at large spatial scales the higher-taxon approach is generally very efficient in representing species richness; in most studies, 70–98% of the variation in patterns of species richness were represented by families and especially genera (e.g., Williams et al. 1994; Roy et al. 1996; Gaston 2000; Prinzing et al. 2003; Villasenor et al. 2005; but see Prance 1994; Andersen 1995; van Jaarsveld et al. 1998). Nevertheless, the efficacy of the higher-taxon approach decreases with increasing species richness and at coarser taxonomic resolutions (e.g., Balmford et al. 1996a, 2000; Cardoso et al. 2004).

At local scales, which are the most relevant for much conservation practice, little is known about the efficacy of the higher-taxon approach in terrestrial ecosystems (for aquatic ecosystems, see Heino and Soininen [2007]). Genus richness is usually a good predictor of species richness (e.g., Balmford et al. 1996b; Negi & Gadgil 2002; Ricotta et al. 2002), but the scarcity of studies in terrestrial ecosystems makes it hard to draw general conclusions. Direct inference from large scales (regional and global) may not be valid because it relies on the usually untested assumption that speciation and other community structuring processes act similarly across scales (Rapoport 1982; Mayr 1999). In fact, speciation rate and the reliability of the higher-taxon approach are scale-sensitive (Andersen 1995; Vanderklift et al. 1998; Jablonski 2007). Richness patterns and turnover rates expressed at local scales are usually much more subtle than those measured across a variety of ecosystems, making it harder to record them. Correlations evident at larger, macroecological scales are often diminished or even lost when narrowing the scale of observation because of the statistical constraint of lower variation in diversity (Grenyer et al. 2006).

Most researchers investigating the conservation applications of the higher-taxon approach have focused on its ability to reflect species numbers; aspects of species composition and rarity have been explored rarely (Pik et al. 1999; Balmford et al. 2000; Bergamini et al. 2005). Nevertheless, much of the biological variation at the local scale may lie in the composition of species rather than their numbers across closely related sites. Conservation planning and management should aim to protect areas with complementary sets of species rather than protecting only the richest sites (Margules & Pressey 2000). Tools used at the local scale should reflect subtle, yet ecologically meaningful, compositional differences. Taxa exhibiting significant variation in diversity patterns at local scales are mostly small-bodied and species-rich, with restricted dispersal ability. Many insect taxa fulfill these criteria and may thus be good indicators of diversity patterns and change in other taxa, mainly invertebrates (McGeoch 1998; Hilty & Merenlender 2000). The higher-taxon approach is expected to be most valuable for these taxa because of the high level of expertise and time required for identification of specimens to species. Nevertheless, many higher-taxon studies were performed on a narrow set of species-poor taxa such as mammals and birds (Gaston & Blackburn 1995; Balmford et al. 1996a; Williams et al. 1997; Grelle 2002), probably because they are well known taxonomically and are relatively easy to sample. Insect groups were seldom tested. Thus, in theory the higher-taxon approach is a promising tool for conservation planning and management, but its empirical efficacy at local scales is not well known.

We investigated three main underlying assumptions of the higher-taxon approach: (1) the distribution of species within genera and within families is relatively homogeneous (i.e., limited information on species diversity patterns is lost when applying coarser taxonomic resolution), (2) monotypic genera and families do not have overriding effects on diversity patterns, and (3) sampling effort required to achieve a representative sample of genera and families is lower than that of species. We investigated the relationship between richness, rarity, and composition patterns of species, genera, and families within three commonly used diversity and disturbance indicators: vascular plants, ground-dwelling beetles, and moths. The study was conducted in the Mediterranean region of Israel, where as in many other densely populated regions, critical land-use conflicts are confined to areas of a few square kilometers and adequate decision-making tools are urgently needed.

## Methods

### Study System

The research was conducted in the Jerusalem Mountains and the Judean Foothills, approximately 30 km south-

west of Jerusalem (Fig. 1). The area is characterized by Mediterranean-type vegetation, with long-term and intense human activity creating a mosaic of natural, semi-natural (e.g., abandoned agricultural fields in various successional stages), and human-dominated patches, typical of the Mediterranean basin (Weizel et al. 1978; Rundel et al. 1998). The area is among the last remnants of a unique transient ecosystem, at the interface of the humid Mediterranean ecosystem to its north and the arid ecosystem to its south (Weizel et al. 1978). It has high faunal and floral diversity and endemism and is of high conservation value (Yom-Tov & Tchernov 1988). The area is located in the central, most densely populated region of Israel, and faces intense development pressures (Feitelson 1995). In the last few years a great deal of effort was invested in promoting sustainable planning and management of this area (Kaplan et al. 2000), and to a large extent it is a model for modern planning in Israel. Nevertheless, little is known about the efficiency of diversity assessment tools in this ecosystem.

We used a stratified approach to select our sampling sites so that they would encompass the different levels of environmental variation in the region. We identified five landscape units that represented the major vegetation communities in the region (Kaplan et al. 2000). We used high-resolution aerial photographs (1:5000–7500) and ground truthing to identify the largest intact patches of natural vegetation within each unit and to categorize patches into habitat types (dwarf shrubland [batha], Mediterranean shrubland [garigue], and chaparral) on the basis of vegetation type and current state (height and density). We then estimated the proportion of the different habitat types in the region and located our sampling plots accordingly.

We sampled 40, 1000-m<sup>2</sup> plots, representing the typical habitat types of the region—natural vegetation at varying successional stages (circa 75% of the region) and disturbed habitats (circa 25% of the region). The 30 plots of natural vegetation were at a minimal distance of 500 m from physical disturbances (roads, settlements, agricultural fields) and included dwarf shrubland (circa 40% of the natural vegetation area; 12 plots), Mediterranean shrubland (circa 30% of the natural vegetation area; 9 plots), and chaparral (circa 30% of the natural vegetation area; 9 plots). Ten plots in disturbed area were located along the edges of a regional road that transected the area, a major development type in the region (Kaplan et al. 2000) (Fig. 1).

### Faunal and Floral Sampling

Sampling effort for the faunal and floral surveys was established in a preliminary study that determined the sampling effort at which diversity accumulation curves level off (Mandelik et al. 2002; Mandelik 2005).

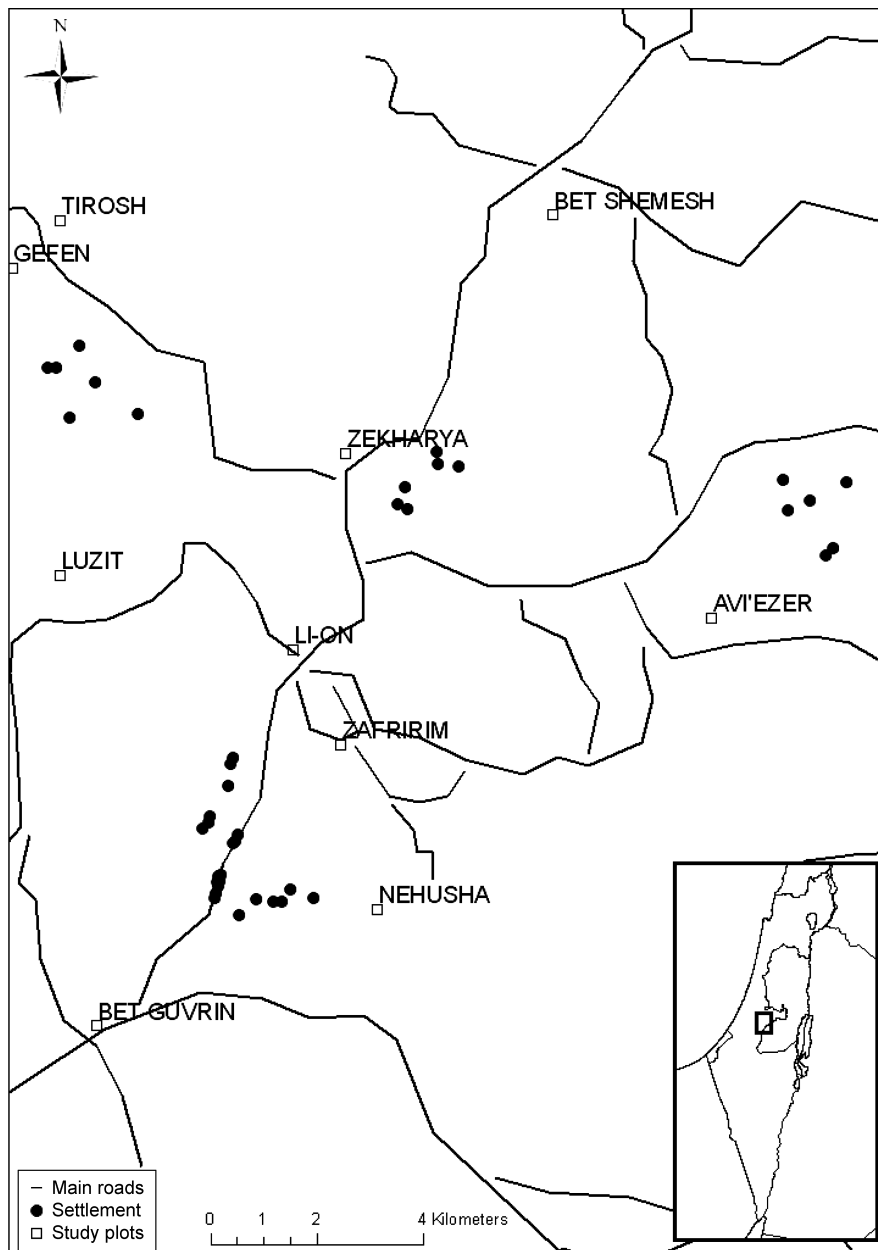


Figure 1. Study region and plots in the Jerusalem Mountains and the Judean foothills.

We sampled ground-dwelling beetles with pitfall traps, 10 cm in diameter and 10 cm in depth, filled with approximately 100 mL of ethylene glycol to prevent predation and decomposition of specimens. In each plot 12 pitfalls were buried flush with the ground surface in a  $10 \times 17$  m grid. To decrease potential biases in pitfalls catches due to microhabitat structure (Greenslade 1964; Mommertz et al. 1996), we matched (to the extent possible) ground-cover in a 2-m-diameter area around each trap and made sure no prominent obstacles were present (e.g., large rocks, trunks). We conducted five sampling rounds of 1 week each in the summer, autumn, winter, and early and late spring of 2001–2002. Specimens were identified by V.C. and deposited at the national entomological collections at Tel Aviv University.

Moths were sampled with 6V ultraviolet light traps with approximately 20-m attraction radii (average across species; V. K., unpublished data). A trap was placed at the center of each plot, in a relatively open patch, to standardize trap efficiency. Moths were sampled only in 25 plots, excluding the road plots and five adjacent plots in the nearby natural landscape to avoid potential bias in species distribution assessments due to light attraction (i.e., sampling individuals that were attracted to the light and not necessarily inhabiting the site). Moths were sampled in early and late autumn, winter, early and late spring and summer of 2001–2002. Sampling was conducted for 1 night each time, from dusk to dawn, during the first quarter of the moon cycle to standardize and increase trapping efficiency (Taylor 1986). Specimens were identified

by V.K. and deposited at the national entomological collections at Tel Aviv University.

Vascular plant species were recorded in each plot along four 50-m transects that were 5 m apart. Additional time was spent walking haphazardly in the plot recording new species encountered until no new species were found for 5 min (based on preliminary assessments, species accumulation curves level off after 5 min). We standardized additional sampling effort by species accumulation rate rather than constant time or area to avoid potential biases due to differences in the physical structure of the plots that affect the speed and facility of survey. Vascular plants were sampled twice, once in early and once in late spring of 2002. Specimens were identified by Y. M.

Our sampling design encompassed spatial heterogeneity and seasonal dynamics, the two major variation components in diversity patterns.

### Data Analysis

Some pitfall traps were damaged by, for example, animal trampling and falling branches. We therefore used a log-linear model to check the equivalency of the effective sampling effort (i.e., number of undamaged traps [response variable] in each plot in each sampling round [the explanatory variables]) (Sokal & Rohlf 1995).

Correlations between species, genus, and family richness and rarity within a taxon and across taxa were tested with Pearson correlations. To test for potential effects of monotypic genera and families, we compared the correlation coefficients obtained with and without monotypics with *t* tests on *z*-transformed coefficients (Sokal & Rohlf 1995). We used two rarity scales—a national/regional scale and a local scale. National/regional rarity was based on existing (external) databases and expert opinion to address potential biases in spatial representativeness of these collections (plants found in fewer than 100 sites in Israel were classified as rare, following Fragman et al. [1999]; beetle and moth species with fewer than 15 specimens in the national entomological collections at Tel Aviv University were classified as rare on the basis of the curators' expert opinion). Adjustments were made for a few species with large sampling biases (on the basis of the curators' judgment). We based local (relative) rarity scale on the relative abundances obtained in this study. We classified plant species that were found in 5% or fewer plots as rare and beetle and moth species represented by <1% of total specimens collected as rare. Because data on national/regional rarity were available only at the species level, we classified rare genera and families only at the local scale.

We used Mantel tests on similarity matrices to analyze correlations between species, genus, and family composition ( $\beta$  diversity, turnover rates) (Legendre & Legendre 1998). For beetles and moths, we used the Morisita similarity index because of its relative insensitivity to sam-

ple size and species richness (Wolda 1981; Krebs 1999). For plants, we had only presence/absence data and therefore used the Sorenson qualitative similarity index (Krebs 1999). We tested for plot independence (spatial autocorrelation between plots) with a Mantel test for the correlation between geographic (calculated with ArcGIS 9.0, Environmental Systems Research Institute, Redlands, California) and similarity distances.

We tested the differences in sampling effort required to achieve a representative sample of species, genera, and families by comparing the slopes of the cumulative richness curves. The slope shows the marginal contribution of increased sampling effort and is therefore more informative than the cumulative richness. Slope functions were calculated in 10,000 bootstrapping permutations.

### Results

The number of species, genera, and families varied by more than 50% between plots for all three taxa (except family richness of plants, Table 1). Spatial autocorrelations in species composition accounted for 9–16% of the variation and are thus of limited ecological significance (plants,  $r = -0.33$ ,  $p < 0.001$ ; beetles,  $r = -0.30$ ,  $p < 0.001$ ; moths,  $r = -0.40$ ,  $p < 0.001$ ). Significant differences in the number of undamaged traps were found between sampling periods but not between plots (plots,  $\chi^2 = 50.00$ ,  $df = 39$ ,  $p = 0.12$ ; sampling periods,  $\chi^2 = 19.96$ ,  $df = 4$ ,  $p < 0.001$ ). Thus, effective sampling effort was similar across sampling plots.

Correlations between species and genus richness in all taxa were significant (plants:  $r = 0.97$ ,  $n = 40$ ,  $p < 0.001$ ; beetles:  $r = 0.98$ ,  $n = 40$ ,  $p < 0.001$ ; moths:  $r = 0.97$ ,  $n = 25$ ,  $p < 0.001$ ) (Figs. 2a-c). At the family level, correlations with species richness were significant for plants ( $r = 0.49$ ,  $n = 40$ ,  $p < 0.001$ ) and beetles ( $r = 0.83$ ,  $n = 40$ ,  $p < 0.001$ ) but not for moths ( $r = 0.13$ ,  $n = 25$ ,  $p = 0.56$ ).

**Table 1.** Total and per-plot ranges of richness of species, genera, and families in taxa surveyed.

<i>Taxon</i>	<i>Total richness</i>	<i>Per-plot richness range</i>
Plants		
species	420	98–180
genus	236	84–143
family	58	28–40
Beetles		
species	424	34–99
genus	243	27–76
family	40	12–27
Moths		
species	111	34–69
genus	73	26–50
family	8	5–8

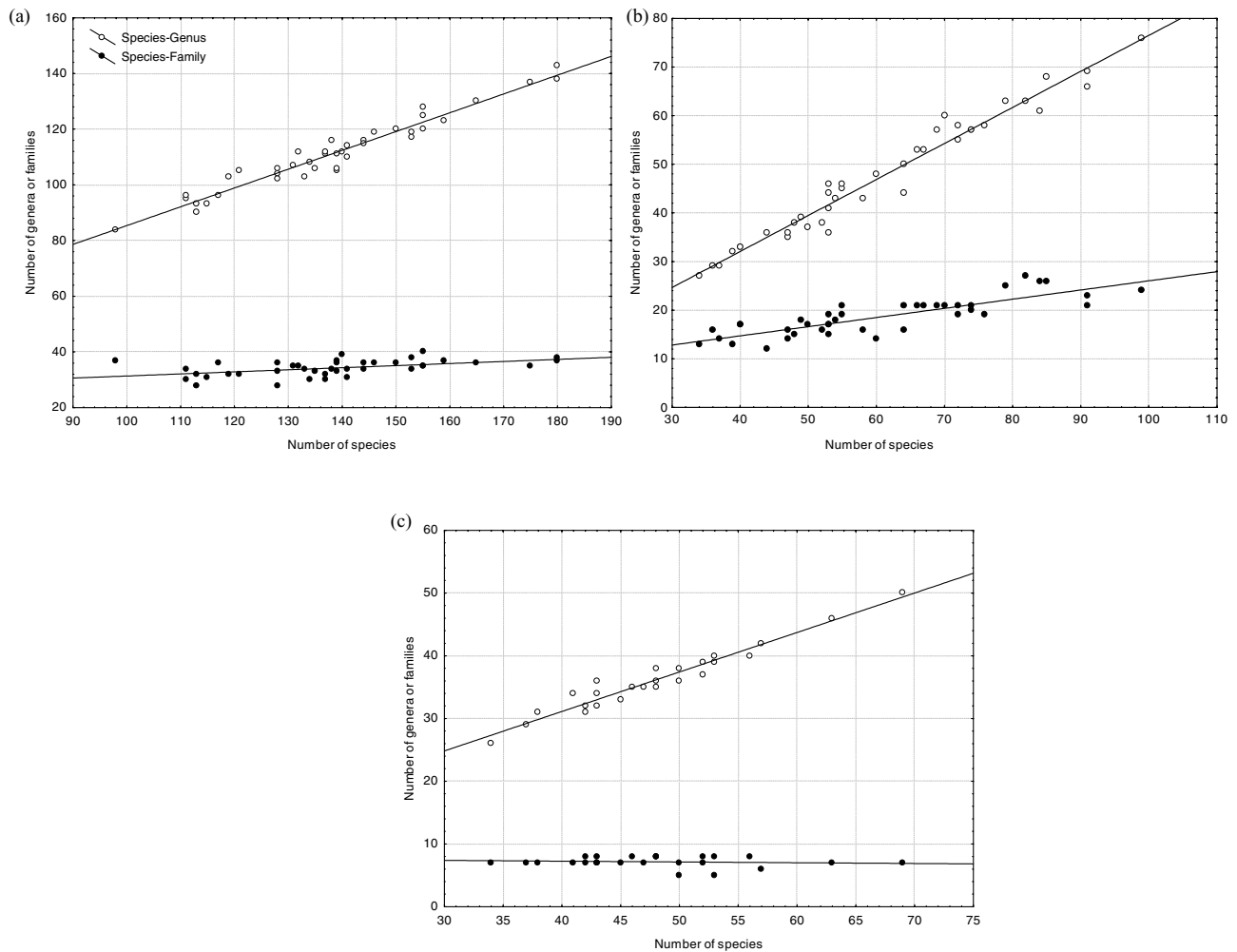


Figure 2. Correlation between richness of species and genera and between richness of species and families: (a) vascular plants, (b) ground-dwelling beetles, and (c) moths.

Correlation coefficients obtained with and without monotypic genera and families did not differ significantly, except marginally so for the species–family correlation of plants (plants: species–genus:  $t = 3.06$ ,  $p = 0.99$ ; species–family:  $t = 1.56$ ,  $p = 0.06$ ; beetles: species–genus:  $t = 1.25$ ,  $p = 0.89$ ; species–family:  $t = 0.88$ ,  $p = 0.19$ ; moths: species–genus:  $t = 4.62$ ,  $p = 0.99$ ; species–family:  $t = 0.5$ ,  $p = 0.31$ ).

The distribution of species between genera was similarly skewed for all three taxa: 64–70% of genera were monotypic and more than 91% of genera had one to three species (Fig. 3a). Variation between taxa in the number of species per family was higher than variation in the number of species per genus; 12–38% of the families were monotypic (Fig. 3b). Cross-taxon correlations in higher-taxon richness were significant between plants and beetles (genus:  $r = 0.49$ ,  $n = 40$ ,  $p = 0.001$ ; family:  $r = 0.31$ ,  $n = 40$ ,  $p = 0.049$ ), but not the moths.

Correlations between number of rare species and genera were significant, but the strength of significance var-

ied considerably between taxa and rarity scales (Table 2). We found a high correlation between rare genera and rare species (at the national scale) of beetles and moths that explained over 56% of the variation in their distribution. In plants, however, this relationship accounted for only 9% of the variation. Correlation coefficients were similar and high for local rarity patterns of species and genera for all taxa (88–98% of the variation in the number of locally rare species was reflected by rare genera). At the family level, significant correlations between locally rare species and families were found only for plants and beetles.

Species and genera composition were significantly correlated in all three taxa; 74–87% of the variation in species composition was reflected in genus composition (plants:  $r = 0.93$ ,  $p < 0.001$ ; beetles:  $r = 0.90$ ,  $p < 0.001$ ; moths:  $r = 0.86$ ,  $p < 0.001$ ). Correlations between species and family composition were lower and varied considerably between taxon. Family composition explained between 5% and 41% of the variation in species composition for moths and beetles, respectively (plants:  $r = 0.54$ ,

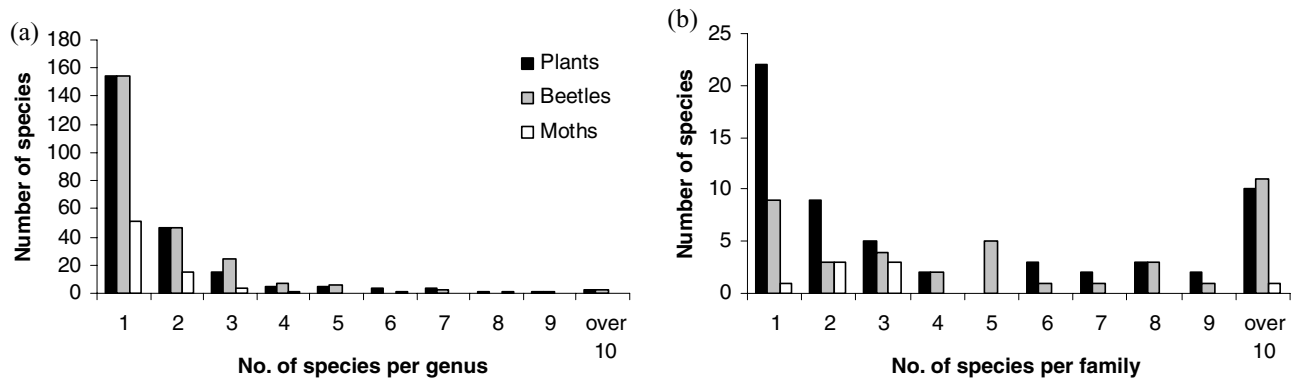


Figure 3. Distribution of species between (a) genera and (b) families.

$p < 0.001$ ; beetles:  $r = 0.64$ ,  $p < 0.001$ ; moths:  $r = 0.22$ ,  $p < 0.01$ ).

The slopes of cumulative richness curves were similar for the species and genus level for all three taxa, indicating that sampling effort required for achieving representative samples of species and genera were similar (Fig. 4). For both species and genus, the first approximately 2000 moth and beetle individuals sampled and the first approximately 5000 m<sup>2</sup> surveyed for plants accounted for the highest rate in the richness accumulation curve. After these points both curves decayed gradually and similarly. Family-level curves had steeper decay patterns, leveling off at a lower sampling effort of approximately 1000 moth and beetle individuals and approximately 3000 m<sup>2</sup> surveyed for plants.

## Discussion

In our study area genus-level assessments were a reliable surrogate for species diversity, but there was no significant reduction in the sampling effort required for genus relative to species assessments. To what extent do these findings support the application of the higher-taxon approach for local-scale conservation planning and manage-

ment? This will be determined largely by the trade-off between the reliability of the higher-taxon approach (i.e., the extent of information loss when applying coarse taxonomic resolution) and the reduction in time, money, and taxonomic expertise required to conduct surveys and process data.

The reliability of genus-level assessments as a surrogate for species-level assessments in the Mediterranean ecosystem we studied is indisputable; genus-level assessments represented over 80%, and often nearly 100%, of the variation in species richness, rarity, and composition. The linear relations between species and genera patterns further enhanced the predictive accuracy of this approach. Moreover, a comparative analysis of the performance of environmental, taxonomic, and higher-taxon indicators in representing species diversity patterns in this ecosystem demonstrated a clear superiority of the higher-taxon approach across all taxa and diversity components studied (Mandelik 2005). Similar results were obtained at larger spatial scales (Buckton & Ormerod 2002; Bergamini et al. 2005). The limited cross-taxon congruence in genera and families richness corresponded to a null hypothesis of higher correlation within the hierarchical taxonomic classification compared with intertaxa classification, where the major drivers for correlations may be ecological interactions. This limits the utility of the higher-taxon approach as an intertaxon assessment tool. It further demonstrates that intrataxon diversity relations were more consistent and predictable than cross-taxon relations and thus of higher applicative value. Interestingly, highly similar species-genus correlations were found among the three taxa, as well as in other studies (see Balmford et al. 1996b; Gaston 2000), indicating that these may reflect a generic pattern.

The efficacy of family-level data in representing species patterns varied considerably between taxa and diversity components. Although almost 70% of the variation in patterns of occurrence of beetle species were reflected in the family-level data, for plants and moths family-level data failed to reflect species patterns with what we view as reasonable accuracy for local conservation applications.

Table 2. Pearson correlation coefficients between number of rare species and number of rare genera and between rare species and rare families at national and local rarity scales.

Taxon	Rare species/ rare genera (p)	Rare species/ rare families (p)
Plants		
national	0.31 (<0.05)	0.27 (>0.05)
local	0.99 (<0.001)	0.89 (<0.001)
Beetles		
national	0.75 (<0.001)	0.66 (<0.001)
local	0.98 (<0.001)	0.87 (<0.001)
Moths		
national	0.92 (<0.001)	0.25 (>0.05)
local	0.94 (<0.001)	0.27 (>0.05)

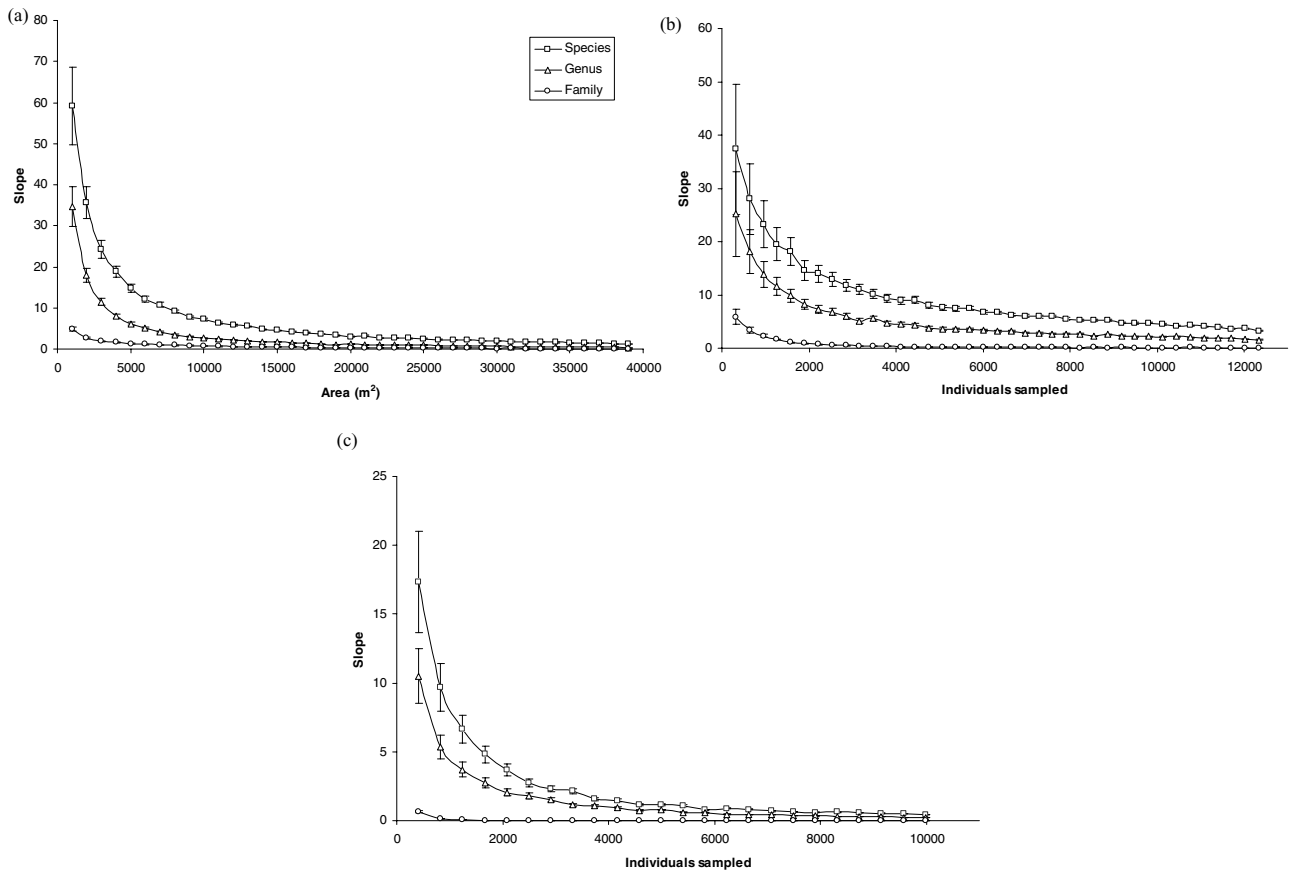


Figure 4. Slope of cumulative richness curves (with SD) for (a) plants, (b) ground-dwelling beetles, and (c) moths.

Similar patterns of reduced accuracy of family- compared with genus-level data have been found at both local (Balmford et al. 1996b, 2000; Baldi 2003) and larger spatial scales (e.g., Balmford et al. 1996a; Villasenor et al. 2005). Strong species–family correlations have been established on an exponential scale (Williams et al. 1994; Ricotta et al. 2002). Therefore, caution is required when interpreting family-level assessments at the local scale, and correlation with species patterns should be established first. This may make family-level assessments as a shortcut for direct species assessments at the local scale unprofitable. Nevertheless, once the pattern is established, for example, within the Mediterranean ecosystem in the central region of Israel, it can form the basis for numerous assessments in this region. Application of the higher-taxon approach for local-scale planning and management should be confined to genus-level assessments when no prior knowledge of the ecosystem and taxa is available.

Species rarity is not as well represented by genus-level data as are species richness and composition. Nevertheless, compared with other surrogates, the higher-taxon approach is also the most efficient at representing rarity (Mandelik 2005). Large differences occur between taxa and rarity scales, demonstrating the complexity of trans-

lating this diversity component into a practical conservation tool (Thomson et al. 2007). This difficulty may be augmented by the higher chances of an erroneous taxonomic identification of rare species compared with identification of a rare genus, which may bias rarity assessments across taxonomic levels. Local rarity, inherently dependent on total richness and thus showing parallel patterns, added limited information to total richness analysis. On the other hand, national (external) rarity scale is more independent of local richness (Gaston & Blackburn 1996) and showed vast differences between taxa in species–genus rarity correlations, making it hard to draw general conclusions. When reliable, high-resolution distributional data are available, national-scale rarity analysis should be preferred over local-scale analysis because it highlights different aspects of local diversity patterns.

In determining the reliability of the higher-taxon approach for local-scale applications, one must address not only the accuracy of the representation of species patterns but also the validity of the approach itself. By focusing on coarse taxonomic scales, there is an implicit underlying assumption of equivalency between taxa at the same taxonomic level, when in fact there are vast differences in taxonomic treatment among taxa (Ricotta et



al. 2002). Species diversity assessment is challenged by classical taxonomy and by the chances of missing cryptic species; thus, it relies on erroneous assessments of species numbers within higher taxa (e.g., Williams et al. 2006). Although this is problematic at all scales, local-scale diversity assessments might be less susceptible to such biases because the taxonomic set used is relatively less diverse (McGeoch 1998). Moreover, there is no reason to assume that there would be large differences in the relative abundance of cryptic species between closely related sites. The higher-taxon approach focuses exclusively on taxonomic diversity, whereas aspects of functionality, exceedingly used as main conservation target (Margules & Pressey 2000), are neglected. Nevertheless, the ultimate goal of conservation is to protect biodiversity, current evolutionary breadth, and future speciation potential (Jablonski & Chaloner 1994; Myers & Knoll 2001). Targeting higher taxa for conservation promotes this goal because higher taxa encompass a wider array of morphological and phylogenetic diversity than species (Roy et al. 1996).

Sampling effort required for a representative sample of diversity, a major component of field surveys costs, was surprisingly similar for species and genera. This probably stems from the high percentage of species-poor genera in the ecosystem we studied, which meant the spatial distributions of species and genera were highly overlapping. But even when the same sampling effort is applied, taxonomic resolution of field surveys and data processing may greatly affect time and expertise required. This will depend on taxon-specific characteristics used for taxonomic classification and on the number of taxonomic entities dealt with.

If the taxonomic classification is hierarchical (i.e., classification proceeds from coarse to fine taxonomic resolution), then a positive correlation is expected between taxonomic resolution and time and expertise required. Balmford et al. (1996b), surveying woody plants in Sri Lankan forests, found a 60–85% reduction in costs when applying coarse taxonomic resolution. It is hard to evaluate the generality of these findings across ecosystems and taxa. Because diversity patterns in this study did not differ on removal of monotypic genera, conducting genus- instead of species-level assessments may well be a useful shortcut in species diversity assessments. For more than half of the species (those belonging to the nonmonotypic genera), classification to genus reduced the numbers of taxonomic entities dealt with and consequently the expected time and expertise needed. In addition, field guides widely available for many taxa in large parts of the world can be readily used for genus but usually not for species identification.

Despite the local scale of this research, we found considerable variation in diversity across sampling plots. The majority of this variation was not attributable to spatial configuration (spatial autocorrelation), which highlights

the ecological significance of local-scale patterns and the factors that shape them. Research efforts have focused mostly on developing large-scale planning and management tools, although land-use conflicts are realized mostly at local scales. Cumulatively, local-scale development may encompass large areas and have cascading effects at the ecosystem level. There is a pressing need to further develop tools sensitive and accurate enough to reflect patterns at the local scale. Applying genus-level resolution to field and laboratory work may broaden the taxonomic and spatial scope of surveys and promote better-informed decision making.

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