

## Using higher taxa as surrogates of species richness: a study based on 3700 Coleoptera, Diptera, and Acari species in Central-Hungarian reserves

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### Abstract

The conservation of biodiversity needs to locate the most diverse sites. Species level is the most often considered taxonomic resolution. However, it is almost impossible to conduct a rapid species level survey of many hyperdiverse and difficult to identify taxa, mainly within arthropods, which are the main components of species richness. I tested whether higher taxa (genus and family) are good surrogates of species richness in three large and usually not surveyed groups in 16 reserves in Central-Hungary: Coleoptera (2415 spp), Diptera (1004 spp), and Acari (288 spp). Species richness of the reserves correlated strongly with both genus and family diversity for all groups. Species numbers also correlated between pairs of the three taxa, but not for genus and family numbers. Therefore, higher taxon diversity is a good surrogate of species diversity, but the diversity of one taxon can indicate the diversity of the other only at the species level.

Die Konservation der Biodiversität braucht die Lokalisation des vielfaltigsten Plätze. Der Artenstand ist die häufigst, bedachte Lösung. Jedoch ist es fast unmöglich, eine schnelle Vermessung auf dem Niveau der Arten bei vielen hyperdiversen und schweridentifizierenden Taxa zu machen, besonders bei Insekten, die die Hauptkomponente der Artenvielfalt sind. Ich untersuchte, ob die höheren Taxa (Genus und Familie) in drei großen und normalweise nicht ermessenen Gruppen auf 16 mittel-ungarischen Schutzgebieten gute Ersatz der Artenvielfalt sind: Coleoptera (2415 Spp), Diptera (1004 Spp), und Acari (288 Spp). Die Artenvielfalt der Schutzgebiete korrelierte stark mit beider Genus- und Familiendiversität für alle Gruppen. Die Nummer der Spezies korrelierte auch zwischen der Paaren der drei Taxa, aber die Nummer von Genera und Familien nicht. Also die höchste Taxondiversität ist ein guter Ersatz der Speziesdiversität, aber die Diversität von einem Taxon kann die Diversität von anderen Taxa nur auf Artenstand indizieren.

**Key words:** rapid biodiversity assessment – species number correlations – invertebrate surveys – nature reserves

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## Introduction

Conservation biology is a crisis discipline (Meffe & Carroll 1994), therefore methods, which give similar results to traditional, more resource consuming ecological methods are of high practical value. Many of conservation biology researches belong to biodiversity issues, for example to identify the most diverse sites. Species diversity is the most often targeted level. However, it is almost impossible to conduct a species level survey if species rich, and difficult to identify taxa are to be involved, like many invertebrate taxa (Stork 1994, Lawton et al. 1998, Báldi 1999). These groups require advanced trapping, handling and identification skills, thus a lot of resources (Nielsen & West 1994). In contrast, conservation needs rapid assessment of areas, for example to select the most diverse sites. There are at least two ways to overcome this problem. First, it is possible to use one or only a small number of species as surrogates (Caro & O'Doherty 1999). Second, which is investigated in the present paper, is to use lower taxonomic resolution (Vanderklift et al. 1998).

Higher-taxon richness as a surrogate for species richness is increasingly used for local scale applications (Andersen 1995, Blamford et al. 1996, Pik et al. 1999), however, terrestrial invertebrates received very little attention (Pik et al. 1999). This is a great lack in knowledge, due to the hyperdiverse and widespread nature of this group. There are very few exceptions, and even these considered limited taxonomic scope (e.g. ants), and/or used a morphospecies approach (Pik et al. 1999). Although the morphospecies approach can be beneficial for rapid surveys (Oliver & Beattie 1996), it is not the best way to use it as control for testing other correlations.

In the present paper I consider 3700 species of Coleoptera, Diptera, and Acari, which taxa belongs to hyperdiverse, unpopular and difficult to identify taxa. They are usually not, or only partly (e.g. Carabidae) involved into nature conservation considerations, while they provide a large proportion of species diver-

sity; in Hungary, for example, they represent ca 50 % of the total 43500 animal species (Korsós & Mészáros 1998). I used the results of the intensive faunistical studies in the late 1970's to explore the biodiversity of Central-Hungarian reserves (Mahunka 1986, 1987). I was interested in (i) whether higher taxon (family and/or genus) diversity is a good surrogate of species diversity; and (ii) whether the taxon numbers correlate among the three groups, i.e. diversity pattern of one taxon indicates that of the others.

## Materials and methods

The analysis was based on the inventories of 16 reserves in Central Hungary coordinated by the Hungarian Natural History Museum, and lasted from 1977 to 1980 (Mahunka 1986, 1987). One reserve (Lake Szelidi) was not sampled for Diptera and Acari, thus, for these groups 15 reserves were included. The reserves were surveyed by more than 70 collectors, and identification was based on ca 65 taxonomist experts from around the world. The surveys were based on search for new taxa by taxonomist experts. This method results in much faster accumulation of the species richness than during an ecologically designed sampling protocol, because experts continuously modify searching strategy and method. In addition, the rule of thumb is that even in the lack of sampling protocols, or design, sampling artefacts have played no role in determining the distribution of species richness in different areas (Rosenzweig 1995). The area, land use and isolation greatly varied across reserves (Tóth 1996). I included Coleoptera, Diptera, and Acari (Mesostigmata, Prostigmata, Tarsonemida, Oribatida) taxa in this analysis (Table 1).

All variables were  $\log_{10}$  transformed to normalise their distribution. The species number – genus number and species number – family number curves were constructed. Several researchers prefer to use sequential Bonferroni correction of the significance levels to correct for the table-wide statistical error (Rice 1989, Cabin & Mitchell 2000), therefore, I consider corrected P values, as well.

**Table 1.** Species, genus, family numbers, and literature sources of the studied invertebrate taxa in 16 Central-Hungarian reserves.

Taxon	Species number	Genus number	Family number	Sources – Author(s), volume and page numbers are given from Mahunka (1986 (I)) and 1987 (II))
Coleoptera	2415	882	101	Ádám & Merkl, I: 119–142; Ádám, I: 143–152; Rozner, I: 153–156; Ádám, I: 157–166; Somorjai, I: 167–174; Merkl, I: 175–178; Szalóki, I: 179–186; Wendt & Merkl, I: 187–190; Podlussány, I: 191–196; Endrődi, I: 197–218; Merkl, II: 111–119; Daffner, II: 122–123; Angelini, II: 124–125; Ádám, II: 126–168; Bellstedt & Merkl, II: 169–174; Szalóki, II: 175–179; Klausnitzer & Merkl, II: 180–181; Merkl, II: 182–188; Audisio, II: 189–192; Rucker & Merkl, II: 193–195; Merkl, I: 196–203; Horák & Merkl, II: 204–207; Ádám, II: 208–220; Merkl, II: 221–226; Gruev et al. II: 227–241.
Diptera	1004	377	40	Majer, II: 245–250; Wéber, II: 251–257; Tóth, II: 258–264; Wéber, II: 265–271; Soós, II: 272–276; Papp, II: 277–290; Dely-Draskovits, II: 291–302; Mihályi, II: 303–311; Polgár, II: 312–313.
Acari	288	132	67	Mahunka, I: 435–458; Komlowsky, II: 343–345; Mahunka, II: 346–397.

**Table 2.** Correlation of the same taxonomic levels between Coleoptera, Diptera, and Acari in Central-Hungarian Reserves (n = 15). Pearson's correlation and its P value is given in parenthesis, before sequential Bonferroni correction (therefore, it may be less than 0.05, but not significant after correction).

	Diptera	Acari
<b>Species by species</b>		
Coleoptera	0.637 (0.01) *	0.649 (0.008) *
Diptera		0.521 (0.042) *
<b>Genus by genus</b>		
Coleoptera	0.566 (0.028) ns	0.557 (0.03) ns
Diptera		0.443 (0.098) ns
<b>Family by family</b>		
Coleoptera	0.616 (0.14) ns	0.598 (0.018) ns
Diptera		0.511 (0.52) ns

ns: not significant; \*:  $p < 0.05$  after sequential Bonferroni correction

## Results

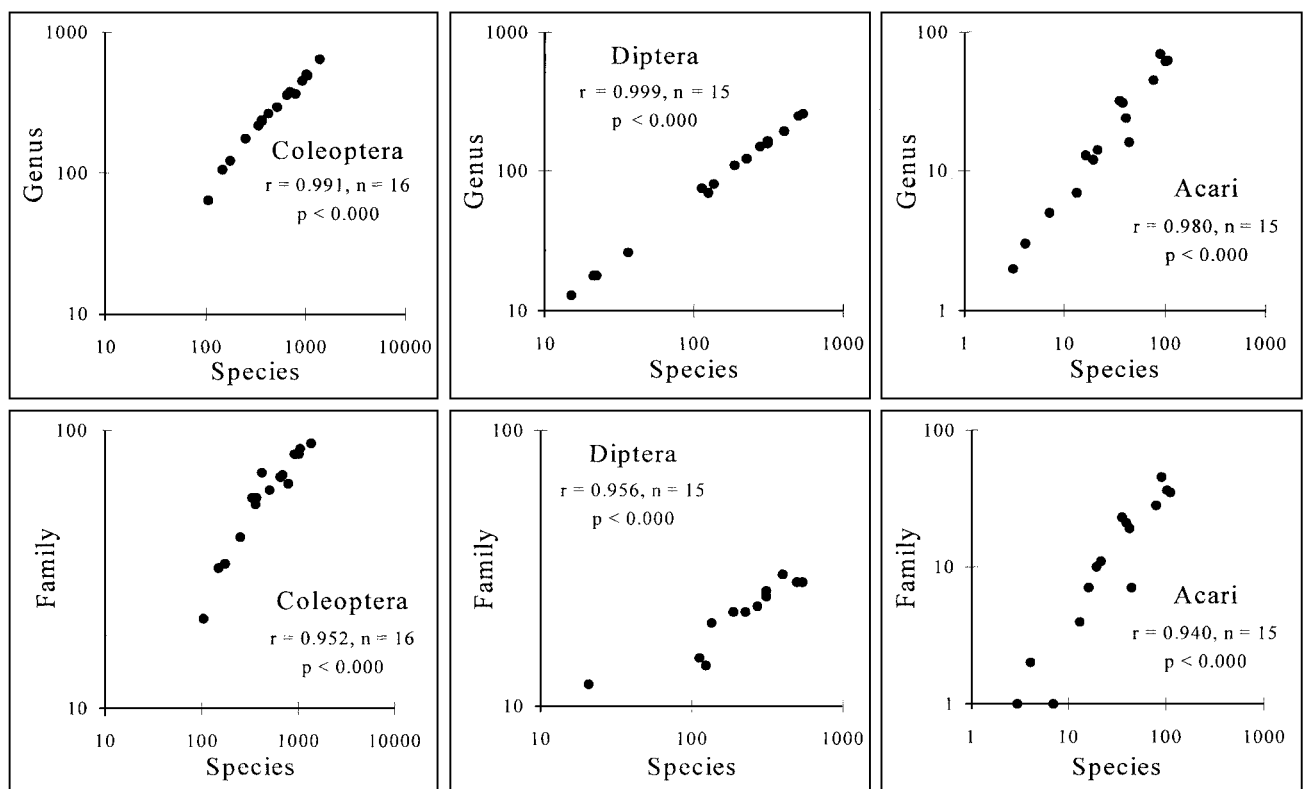
I found that both genus and family levels are good surrogates of species diversity in all the three studied taxa. Taxon richness patterns across the reserves are rather similar using species, genus, or family level data (Fig. 1). All relationships are highly significant after sequential Bonferroni correction. Therefore, to assess the relative diversity of reserves, family level identifica-

tion is sufficient, which means that only 208 taxa (families) should be identified instead of 3707 (species). In addition, family level differences are more obvious than that of at the species level.

The correlations of the same taxonomic level richness across reserves between the studied groups were not too strong (Table 2). After Bonferroni corrections within taxonomic levels, species numbers, but not genus or family numbers showed correlations between pairs of the three taxa.

## Discussion

The results found in this study are important, due to the large number of included species, and the unpopular and difficult to identify nature of the three taxa. Nevertheless, most other studies got similar results in a variety of taxa, including birds, ants, plants and several marine organisms (e.g., Williams & Gaston 1994, Andersen 1995, O'Brien et al. 1998, Vanderklift et al. 1998, Pik et al. 1999, Hodge & Frampton 2001, Enquist et al. 2002, Negi & Gadgil 2002, Ricotta et al. 2002). However, there are different results as well; Grelle (2002) found that only generic, and not family or order level is useful surrogate of species richness for



**Fig. 1.** Correlations between species-genus and species-family taxon richness values in three hyperdiverse arthropod taxa in Central-Hungarian reserves.

mammals. Prance (1995) argues that neotropical plant family richness is not an adequate predictor of species richness.

Taxon number correlation is of crucial interest in nature reserve design, because in the case of correlation, it is possible to predict species richness pattern of one taxon from the pattern of another, i.e. can be used as biodiversity indicator (McGeoch 1998). Although higher taxon richness is a good surrogate of species diversity, it can not be used to indicate diversity of other groups. The present results suggest that only species and not higher taxa levels can be used as indicator, a limitation not considered earlier (McGeoch 1998). However, even the cross-taxon congruence at the species level is controversial; significant congruence was found by some authors (e.g. Carroll & Pearson 1998, Crisp et al. 1998, Pearson & Carroll 1999, Lund & Rahbek 2002, this study), but not by others (e.g. Lawton et al. 1998, Ricketts et al. 2002, Vessby et al. 2002). Biodiversity indication seems to be less established than higher taxon surrogacy, an important point for balancing in the design of rapid biodiversity surveys.

I conclude that for the rapid assessment of species richness of three extremely species rich taxa (Coleoptera, Diptera, and Acari) family level inventories can provide useful data for conservational purposes. Therefore, rapid area inventories should concentrate the limited resources on surveying more high level taxonomic groups to lesser systematic resolution to get reliable species richness pattern for the studied areas. This strategy should get priority in many site assessments, even on the cost of leaving out vertebrates' surveys. First, vertebrates are usually not the best indicators of naturalness (Landres et al. 1988). Second, in highly fragmented areas, like in Central-Europe, the occurrences of vertebrates are probably more influenced by factors from the landscape matrix, and not the area of interest. Invertebrates, with much less mobility are probably more sensitive to fragmentation at the spatial scale of interest (e.g. Báldi & Kisbenedek 1994, Magura et al. 2001, Martin & Martin 2001).

Three additional notes: first, higher taxon surrogacy is probably spatial scale dependent (Vanderklift et al. 1998, Pik et al. 1999), which restricts the interpretation of these results to other scales. Second, for better established biodiversity studies species level identifications are inevitable necessary, because this taxonomic resolution is the most widely used level in biodiversity studies. Third, taxon richness (i.e. number of species, genera, etc.) is only one, and usually not the best measure of conservation value (e.g., Viro-lainen et al. 1999). Whether to use it, or not, depends on the aims and available resources of the given situation.

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