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Higher taxa surrogates versus surrogate groups of spider biodiversity

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Abstract
A possible alternative solution to the enormous effort required to do a biodiversity assessment of mega diverse taxa like spiders is to use surrogates, either higher taxa or surrogate groups, whose biodiversity values reflect the overall values of the group. Both these options are here evaluated and compared in their effectiveness and feasibility in the Mediterranean region, using spiders of a north-eastern Portuguese protected natural area – Parque Natural do Douro Internacional – as a test case. High regression values with total species richness and good predictive power were found in both strategies, but if effort is also taken into account, the best approach is to use a surrogate group of families. In this test case, the species richness of four families (Gnaphosidae, Lycosidae, Theridiidae and Agelenidae) shows evidence of high relationship with the overall species richness of spiders. The use of these families as surrogates, through the sampling and identification of their species, in any given site/habitat, make it possible to estimate the total number of spider species present, in a fast and reliable way.

Key words: species richness, diversity, Araneae, Mediterranean, Portugal

INTRODUCTION

Concern for the conservation of biodiversity hotspots is growing as areas and habitats are permanently lost or reduced in size. The first step in fighting such threats is to identify biodiversity hotspots through inventories of a wide range of taxa and areas, followed by a ranking of the areas according to their biodiversity values. Only then will it be possible to select priority areas for conservation. The most commonly used diversity measure is the number of species present in a given area, but when it comes to biodiversity assessment of mega diverse and mostly unknown taxa like spiders (and other arthropods), a difficult question remains to be answered: how can we efficiently evaluate and compare species richness between sites/ habitats? The ideal approach would be to make a complete assessment of all existing species in each unit to be evaluated. But how feasible and onerous is this? A possible solution for this problem is the use of surrogates, either higher taxa surrogates (e.g. Gaston & Williams 1993; Williams & Gaston 1994) or surrogate (indicator) groups (e.g. Pearson & Cassola 1992; Beccaloni & Gaston 1995), whose richness values reflect and allow prediction of the overall values of the group being investigated. The effectiveness and applicability of both these strategies have already been tested for a wide range of taxa (e. g. Williams & Gaston 1994; Williams et al. 1994; Beccaloni & Gaston 1995; Gaston & Blackburn 1995; Vanderklift et al. 1998; Balmford et al. 2000; Martín-Piera 2000; Borges et al. 2002).

In the higher taxa surrogacy approach, all collected specimens are identified to a level higher than species, assuming that richness values obtained for such level will have a strong relationship to and allow prediction of species richness in any given area. This approach has proven successful (Williams & Gaston 1994; Williams et al. 1994; Gaston & Blackburn 1995; Vanderklift et al. 1998; Balmford et al. 2000; Martín-Piera 2000; Borges et al. 2002) but may fail in certain cases (Andersen 1995) due to different sampling effort between areas, great heterogeneity of habitats or too broad spatial scale considered. Another factor can be a different interpretation of similar results. Researchers may have different opinions about what level of relationship and predictive power must be reached in order to consider any approach as useful (e.g. Williams & Gaston 1994; Andersen 1995).

The surrogate, or indicator groups approach, having the same objective as the higher taxa surrogacy, uses a different methodology. Some specimens, within certain more narrowly defined taxa (like orders or families), are identified to species level and their richness values should reflect the overall richness of the studied group (total biodiversity or a single filum, class or even order). As with the former strategy, this approach has proven successful in some studies (Pearson & Cassola 1992; Beccaloni & Gaston 1995; Duelli & Obrist 1998; Reyers et al. 2000) but failed in others (Prendergast et al. 1993; Prendergast & Eversham 1997; Lawton et al. 1998; Van Jaarsveld et al. 1998). The failures are mainly caused by the use of many unrelated and ecologically divergent taxa, which do not behave synchronously with habitat or geographical change.

Spiders (Araneae) are often used in ecological studies, but not yet in Portugal, where little is known about their overall distribution and diversity (Cardoso 2000). Studies in other parts of the world have shown that spiders may be useful indicators of the overall species richness and health of biotic communities (Kremen et al. 1993; Norris 1999; Toti et al. 2000) and they may therefore be potentially interesting targets for biodiversity research in Portugal. Due to the richness and abundance of this group in the country, simply counting all species and specimens in any given area will not be possible, and hence we need to develop simple measures to identify high diversity areas in a reliable way, in order to set conservation priorities based on sound scientific data. This paper evaluates how effective higher taxa surrogacy and group surrogacy are in predicting the number of spider species present at a given site, at a given time, in the Iberian Peninsula and possibly the Mediterranean region.

MATERIAL AND METHODS

Field methodology

This study is based on fieldwork carried out in a protected area in north-eastern Portugal – Parque Natural do Douro Internacional (Fig. 1) from February to December 2001. With more than 85000 km², it is one of the largest protected areas in the country and one with great variety of habitats. Most of the major contrasting habitats have been included in this study in order to compare and evaluate the different surrogacy approaches across a wide range of habitats and geography (Tab. 1). Two

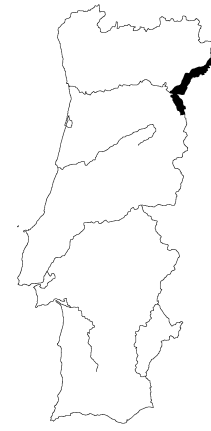

Fig. 1. The study area in Portugal – Parque Natural do Douro Internacional.

sampling procedures were used in different sites, long and short-term sampling. For each, several techniques were employed.

Long-term sampling sites:
- Two lines of 8 pitfall traps, 8 cm diameter, 5 m apart from each other, with fortnightly collecting, traps remaining open only during the second week of each two weeks period, during 10 months (22 collecting periods) from February to December 2001;
- One series of 5 arboreal pitfall traps, 8 cm diameter, in a wooden base hanging from branches of trees about 2/6 m high, at sites where arboreal vegetation was present. Same periods as above;
- Ten series of 20 sweeps with a standard 40 cm diameter sweeping net, a single time during the last week of May or first week of June.

Short-term sampling sites:
- One series of 8 pitfall traps with fortnightly collecting, continuously acting, during one month (two collecting periods) from May to June 2001;
- Ten series of 20 sweeps as in long–term sampling.

Besides these, all spiders caught during the study period with non-standardized techniques, like aerial and ground active search and looking under stones or logs, have been considered. These techniques were employed with low effort, made in a casual manner, not adding much to the number of collected species at either site.

Statistical procedures

Both higher taxa surrogates and surrogate groups were tested for their regression values and predictive power for overall species richness. In both cases, two approaches were tested: families and genera as higher taxa surrogates and one or several families as a surrogate group. In the latter, a stepwise adding of families was used. For each step, the family that would increase regression value (R^2) the most was added to the surrogate group. This was done up to 9 times, thereby establishing a final group of 10 families. The inclusion of more families is possible, but it would require more effort with the

Table 1. Sampling sites with habitat type, Universal Transverse Mercator square (10x10 km) and sampling procedure (Long or Short-term sampling).

Site	Habitat	UTM	Sampling
Algozinho	Riverside (mainly *Fraxinus angustifolia, Salix salvifolius*)	29TQF07	L
Barca d'Alva	*Cystus ladanifer* bush area	29TPF74	S
Bemposta	*Juniperus oxycedrus* wood	29TQF17	S
Bruçó	*Pseudotsuga menziesii* plantation	29TPF96	L
Constantim	Oak forest (*Quercus pyrenaica*)	29TQG21	S
Fonte d'Aldeia	Cork oak plantation (*Quercus suber*)	29TQF18	L
Freixiosa	Mixed woods (*Quercus ilex, Juniperus oxycedrus*)	29TQF29	S
Lagoaça	*Castanea sativa* wood	29TPF96	S
Lamoso	Riverside (mainly *Fraxinus angustifolia, Salix salvifolius*)	29TQF07	S
Mazouco	*Cytisus scoparius* bush area	29TPF85	L
Palão	Recent eucalyptus plantation (*Eucalyptus* sp.)	29TPF85	L
Picote	Mixed woods (*Quercus ilex, Juniperus oxycedrus*)	29TQF28	S
Picote – arribas	High rocky cliffs bordering river	29TQF28	L
Picotino	Pine wood (*Pinus pinaster*)	29TPF86	L
Tó	Oak forest (*Quercus pyrenaica*)	29TQF07	L
Vila Chã da Braciosa	Resting wheat field	29TQF28	L

consequence of decreasing the utility of surrogacy.

To reach the best relationship possible, both linear and non-linear (logarithmic, exponential and power) relationships were tested and the one with the highest value was chosen. Linear relationship was expected for surrogate groups whereas a non-linear relationship was expected for higher taxa surrogacy. This is due to collecting effort. At low collecting effort, each new species being found will most likely belong to a previously not collected higher taxon (family or genus), but at some point the majority of species being added will belong to higher taxa already represented in the sample.

More important than regression values per se is the predictive power of each approach. That is to say, it's the accuracy of the estimate that counts. Accuracy can be tested with an analysis of the scatter plots and standard deviation of the estimates. Scatter plots were analysed for the approaches mentioned above. Standard deviations could not be obtained for non-linear relationships. The effort required to identify taxa for each surrogate approach is also an important measure to consider. Microsoft Excel 2000 and SPSS 10.0 (SPSS Inc. 1999) were used for all statistical analysis.

RESULTS AND DISCUSSION

Two hundred forty eight species were identified at least to genus level. These belong to 117 genera and 37 families. Whenever it was not possible to reach species level, morphospecies were established (87 cases in all 248 species). Many times it was only possible to reach family level. When this was the case, such morphospecies were not considered, only this way it was viable to use the same dataset for all regression analysis. Observed richness was used to make the regression and predict accuracy values. Each approach was considered separately and compared a posteriori.

Families as higher taxa surrogates

As expected, a non-linear relationship was found between family and species richness. Despite a highly significant relationship with species richness, the number of families present at each site reveals poor predictive power (Fig. 2A). For example, despite having almost the same number of families, "Vila Chã da Braciosa" holds close to three times more species than "Barca d'Alva".

Genera as higher taxa surrogates

Like for family surrogacy, a non-linear and highly significant relationship was found between number of genera and species richness (Fig. 2B). In this case, however, also a high predictive power could be related to it, allowing us to reach a good estimate of the total number of species based on the number of genera at each site. Unfortunately, the identification of the 117 genera may require a large effort, perhaps not so different from the one required to identify all 248 species. As a

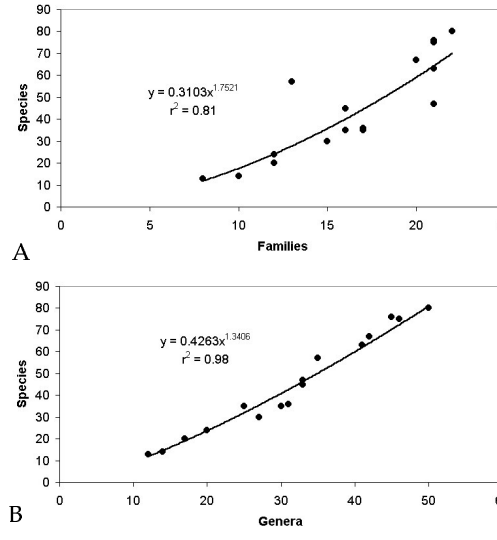

Fig. 2. Higher taxa surrogacy, both approaches present a power relationship (both cases: N=16; P<0.001). (**A**) Relationship between number of families and total number of species. (**B**) Relationship between number of genera and total number of species.

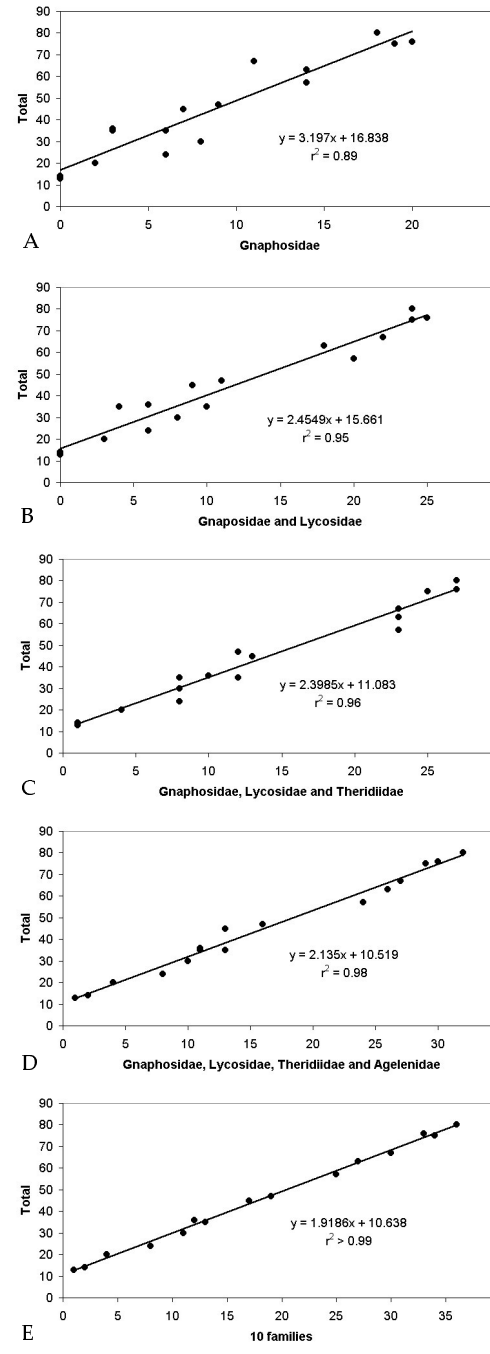

Fig. 3. Surrogate groups, all approaches present a linear relationship (all cases: N=16; P<0.001). (**A**) Relationship between the number of Gnaphosidae species and total species richness. (**B**) Relationship between the number of Gnaphosidae and Lycosidae species and total species richness. (**C**) Relationship between the number of Gnaphosidae, Lycosidae and Theridiidae species and total species richness. (**D**) Relationship between the number of Gnaphosidae, Lycosidae, Theridiidae and Agelenidae species and total species richness. (**E**) Relationship between the number of Gnaphosidae, Lycosidae, Theridiidae, Agelenidae, Uloboridae, Zoridae, Oonopidae, Hersiliidae, Hahniidae and Anyphaenidae species and total species richness.

consequence, this approach should be considered carefully before being applied.

A single family as surrogate

The use of just one family, Gnaphosidae (Fig. 3A), as a surrogate, resulted in a highly significant linear relationship with overall species richness, much higher than with any other family tested. It's noteworthy that gnaphosids are almost exclusively captured with one single method (pitfall traps) and that it is the most species rich family in this survey (with 53 species). However, two sites with only 3 species of Gnaphosidae ("Bruçó" and "Freixiosa") are more diverse than a site with 13 species of the same family ("Picote – arribas"). In this case, using only one family as a surrogate group leads to a low predictive power.

Several families as surrogate group

The minimum number of families necessary to include in the surrogate group in order to obtain a good predictive power appears to be 4 – Gnaphosidae, Lycosidae, Theridiidae and Agelenidae (Fig. 3). Scatter plots were drawn for up to 10 families but only the last is presented (Fig. 3E), showing that there is no notorious change if more than 4 families are used. The addition of more families slightly increases the regression values and decreases the standard deviation of the estimate, but the additional effort required to include 10 families is considered unnecessary, since it does not result in a proportional increase in predictive power. The four families mentioned

above include 88 species, or approximately 35% of the overall species richness.

Comparison of approaches

Close relationship was found between total (overall) species richness and the taxa richness found with all different surrogate approaches. However, high predictive power was only found when genera were used as surrogates or when four families were used as a surrogate group. Comparing these two approaches, the latter seems to be preferable, with an almost identical R^2 value, a simpler linear relationship with species richness and, most importantly, a smaller effort in identification of specimens. We therefore recommend the use of a surrogate group consisting of the families Gnaphosidae, Lycosidae, Theridiidae and Agelenidae.

In spite of the uncertainties, the use of few families as a surrogate resulted in a quick and reliable estimate of the total number of spider species present at the time of collecting, at any given site. Due to the high variability of habitats here considered, we think that this approach can be very useful for the Iberian Peninsula and probably the Mediterranean region. Since this work was developed in a Mediterranean ecosystem, our concrete conclusions are not likely to be valid for other major biogeographical areas. The general approach however, can be tested for such areas by the methodology we describe.

Results are only preliminary since not all morphospecies were identified to at least corresponding genera, which excluded much material. Subsequent identification of all individuals to named species could change the values for the obtained species richness. Moreover, the use of other methods, or applying different effort, may provide different results. Further work is currently being carried out to test whether sampling intensity, geography or habitat type may influence predictive power, regression and significance values, thereby altering conclusions presented here.

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