

# Higher taxa surrogates of spider (*Araneae*) diversity and their efficiency in conservation

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## Abstract

A number of alternative approaches have been suggested during recent years to predict species richness of a given taxa, while retaining information on the identities of the observed individuals. Such information can be extremely useful for choosing conservation priority areas, either by using simple richness values or, preferentially, by considering the complementarity of potential sites. Among the most popular approaches is the use of higher taxa surrogates. Both family and genus richness are here tested in their ability to predict the number of spider (*Araneae*) species independently of sampling effort, geographical location and type of habitat. We use data from three Portuguese protected areas as a test case. Genus richness is considered a good surrogate of species richness, despite some caution being needed regarding the comparison of sites with considerably different sampling effort, the same not happening with families. Only genera are also found to be reliable either for ranking sites according to taxa richness or for determining near-minimum sets of sites for conservation. We therefore recommend surrogacy at this taxonomic level as a promising approach for the prediction of spider species richness or evaluation and ranking of areas according to their conservation importance. The reached conclusions should uphold for Portugal and the entire Mediterranean region.

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## 1. Introduction

A number of alternative approaches have been suggested during recent years to predict the species richness of any given taxa when not all species are known and to conclude on the spatial and temporal distribution of biodiversity. Such approaches try to overcome the problem of the enormous amount of resources (e.g. time, money, taxonomists) required to reach close to complete inventories, if such a goal is possible to achieve. Among the most popular is the use of higher taxa surrogates, as proposed by Gaston and Williams (1993; Williams 1993; Williams and Gaston 1994). Others are the use of indicator (or surrogate) groups of overall richness (e.g. Pearson and Cassola, 1992; Beccaloni and Gaston, 1995; Prendergast and Eversham, 1997) and the

inference of diversity from available information on environmental variables (e.g. Braithwaite et al., 1989; McNally et al., 2003).

Despite all the pros and cons all these have, the higher taxon approach has several advantages, namely by allowing information to be obtained on a large number of taxa with relatively low effort and resource use. Another crucial advantage is the retention of broad biological information that allows the understanding of distribution patterns (Eggleton et al., 1994; Williams et al., 1994; Gaston et al., 1995) and more efficiency in the definition of conservation priority areas (Williams, 1993; Williams et al., 1994; Vanderklift et al., 1998; Balmford et al., 2000), after all, the ultimate goal of conservation biology. Although most previous work points to a reliable use of higher taxa surrogacy in many different kinds of organisms (Williams and Gaston, 1994; Williams et al., 1994; Gaston and Blackburn, 1995; Vanderklift et al., 1998; Balmford et al., 2000; Martín-Piera, 2000; Borges et al., 2002; Cardoso et al.,

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in press), caution is mandatory, given that several factors may influence the relationship between species richness and higher taxa richness (Gaston and Williams, 1993; Andersen, 1995). Some of these factors are sampling effort, geographical location and habitat type.

Spider species richness and respective spatial distribution are virtually unknown in Portugal with a certainly very low figure of 693 species registered for the country (Cardoso, 2000, 2003). Although not even higher taxa data is available for most of the country's territory, given the difficulty in the identification of species, many remaining to be described or discovered, it seems advisable to test for future use such potential tools as are different surrogates of biodiversity.

With this work, we intend to provide evidence of the possible usefulness of the higher taxa surrogacy approach with spiders in Portugal and the entire Mediterranean region, testing it as a species richness predictor. We also consider the effects of geographical, environmental and methodological factors in the validity of predictions. Finally, we test the use of this kind of surrogacy as a tool for a reliable definition of conservation priority sites, either by ranking them according to taxa richness or by considering complementarity of known taxa between sites.

## 2. Methods

### 2.1. Fieldwork

Fieldwork design was implemented to test for several effects that can influence the higher taxa surrogates approach—geographical location, type of habitat and sampling effort. Three Portuguese protected areas were chosen, one in the north—Douro Internacional Natural Park—sampled during 2001, and two nearby areas closer to the south of the country—Serras de Aire e Candeeiros Natural Park and Paúl do Boquilobo Nature Reserve—sampled during 2002 (Fig. 1). For a question of simplicity, these three areas are simply referenced from now on as belonging to north and south geographical regions since the latter two are very close to each other. Ideally, all sites in all protected areas should have been sampled during the same year, but the distance between them and the large number of sites involved made it logistically unfeasible. We chose such areas due to high habitat diversity and, by comparing the two regions, allowing the study of geographical effects on the surrogacy methods to be tested (Table 1). In each area, we sampled several sites, summing 27, trying to cover the majority of the most significant habitats represented. This way, we could also consider habitat effect by differentiating sites with and without arboreal cover and those with

“natural”, autochthonous vegetation, from the ones dominated by introduced vegetation or under severe human influence or management. To test for sampling effort influence over surrogacy results, some of the sites were subjected to high effort, others to low effort sampling. High effort consisted in a 10-month continuous sampling, from February to November. A row of eight 33 cl capacity pitfall traps, each 5 m apart from the next in line was set up for each site. We used beer cups with 8 cm diameter and 12 cm depth during the all 10-month period, with fortnightly collecting. Sweep netting sessions with the duration of 1 h were performed only once, in the end of May or beginning of June, at each site with a standard 40 cm diameter sweep net. Low effort sites were sampled in the same way as high effort, except for the sampling period duration, as we made one single month pitfall trapping during May and June, with one sweep netting session during the middle of that period. One of the sites (PBM) suffered from a very intensive collecting effort, with 10 month continuous pitfall trapping with 32 traps and sweep netting sessions of 1 h every 2 weeks during the total period.

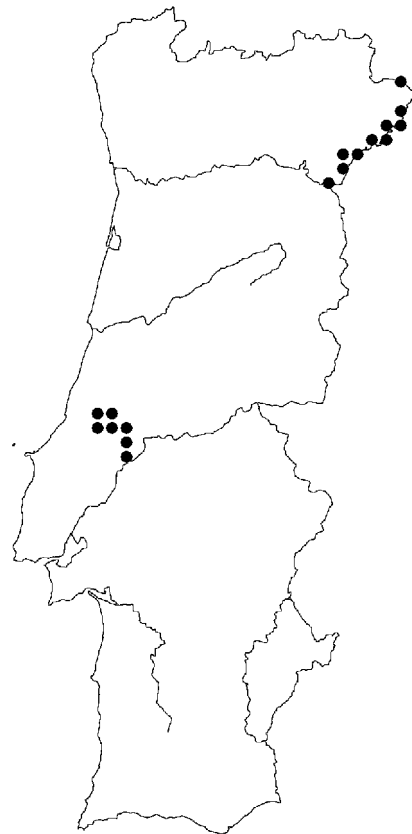


Fig. 1. Location of sampled sites in Portugal according to UTM squares (10×10 km). A single circle can refer to different sites if they are located at the same square.

Table 1

Sampled sites with respective code, Universal Transverse Mercator square (10×10 km) and characteristics: sampling effort (High or Low), location in the country (North or South), presence of arboreal vegetation (Yes or No) and “naturalness” of the habitat (Natural or Human influenced)

Site	Code	UTM	Effort	Location	Arboreal	Natural
Paúl Boquilobo (montado)	PBM	29SND36	H <sup>a</sup>	S	Y	H
Fonte d’Aldeia	FAM	29TQF18	H	N	Y	H
Palão	PAE	29TPF85	H	N	Y	H
Mazouco	MAG	29TPF85	H	N	N	N
Algozinho	ALR	29TQF07	H	N	Y	N
Tó	TOC	29TQF07	H	N	Y	N
Vila Chã da Braciosa	VCP	29TQF28	H	N	N	H
Picotino	PIP	29TPF86	H	N	Y	H
Vale Garcia	VGM	29SND37	H	S	N	N
Serro Ventoso	SVC	29SND17	H	S	Y	N
Barrenta	BAE	29SND28	H	S	Y	H
Picote	PIM	29TQF28	L	N	Y	N
Bruçó	BRP	29TPF96	H	N	Y	H
Bairro	BAP	29SND37	H	S	Y	H
Picote (arribas)	PIR	29TQF28	H	N	N	N
Mira d’Aire	MIP	29SND27	H	S	N	H
Freixiosa	FRA	29TQF29	L	N	Y	N
Constantim	COC	29TQG21	L	N	Y	N
Paúl Boquilobo (valas)	PBV	29SND36	L	S	Y	N
Paúl Boquilobo (choupal)	PBC	29SND36	L	S	Y	H
Paúl Boquilobo (salgueiral)	PBS	29SND35	H	S	Y	N
Bemposta	BEZ	29TQF17	L	N	Y	N
Barca d’Alva	BAM	29TPF74	L	N	N	N
Lagoaça	LAC	29TPF96	L	N	Y	N
Santo António	SAO	29SND27	L	S	N	H
Lamoso	LAR	29TQF07	L	N	Y	N
São Mamede	SMM	29SND18	L	S	N	N

<sup>a</sup> Very high effort, not comparable to other sites.

## 2.2. Statistical procedures

To test if either family or genus richness can be reliably used to predict species richness we performed regression analysis over all available data. Linear, log–log and exponential regression were tested. We used both the percentage of variance explained by the independent variable and visual evaluation of the scatter plots as a measure of adjustment, surrogacy reliability and predictive power. In search for the possible influence of sampling effort, geographical location and habitat type over surrogacy results, we also adjusted regression lines after separating sites according to their characteristics, one factor at a time. We used analysis of covariance (ANCOVA) in order to test for statistically significant differences between regression lines. If differences were found, the factor involved was considered as potentially influencing the reliability of surrogacy. Statistica 5.1 software was used for statistical analysis (Statsoft Inc., 1998). For allowing a reliable analysis of covariance, we had to exclude PBM, since it can be considered as an outlier, not possible to compare with other sites, all of them having a much lower sampling effort. Its inclusion would only change regression and covariance in artificial and unpredictable ways.

Two approaches were tested for prioritisation and ranking of sites for conservation. A scoring approach, which uses the raw number of taxa represented in each site as the sole value for ranking. We used Spearman rank correlation index to test for surrogacy reliability in the scoring of sites. In addition, scatter plots of family and genus richness versus species richness ranking of sites were used for visual inspection of reliability. We furthermore tested a more efficient iterative approach of conservation priority ranking. For each of the considered taxonomic levels (family, genus or species), we first chose the richest site and from it, in a stepwise manner, the one site that would further raise the number of represented taxa was added to the set of sites to be considered for protection. In case of ties, we chose the richest site in the respective taxa. By doing so, we could test the effect of using higher taxa for choosing a near-minimum set of sites that potentially preserves the maximum number of species.

## 3. Results

About 30,000 spiders belonging to 412 species or morphospecies were captured during the entire two

years fieldwork. Of the whole, 374 were identified at least to genus level, the only species considered here, since genus identification is required for most calculations (Table 2). These species belong to 162 genera and 39 families. All numbers are considerably high when compared to the 693 species, 250 genera and 45 families currently registered for Portugal (Cardoso, 2000, 2003). It's remarkable that we captured almost half the species in a single site, PBM, but that site suffered a very high sampling effort during 1 year, not comparable to others. Adopted systematics consistently follows Platnick's world spider catalogue (2003).

3.1. Species richness prediction

3.1.1. Choosing the best surrogate

After fitting all previously defined regression types—linear, log–log and exponential—to family and genus taxonomic levels, we choose the ones with the highest regression coefficient value. A non-linear exponential relationship is found for the former and a linear relationship for the latter (Fig. 2). Both taxonomic levels present a highly significant relationship with the number of species ( $n = 27$ ,  $P < 0.001$ ) with a high  $r^2$  value. How-

ever, a highly significant relationship does not equal high predictive power (Andersen 1995; Cardoso et al., in press). We verify that some sites with a similar number of families have very different numbers of species. Correspondently, sites with similar numbers of species present very different numbers of families (Table 2, Fig. 2a). Genus richness seems to have much better predictive power, no major discrepancies like those described for family richness are found (Table 2, Fig. 2b).

3.1.2. Influence of factors

Since we only find genus richness to have high predictive power and presenting a simpler linear relationship with species richness, we only test the influence of several factors for this taxonomic level. Comparing regression lines of sites presenting different sampling effort (Fig. 3a), we find them to be significantly different ( $n = 26$ ,  $P < 0.05$ ). This was to be expected since the more we collect, the more species will appear, many of them belonging to genera previously represented. The same doesn't happen with all other tested effects (Fig. 3b–d), whose differences are not found to be statistically meaningful ( $n = 26$ , n.s.).

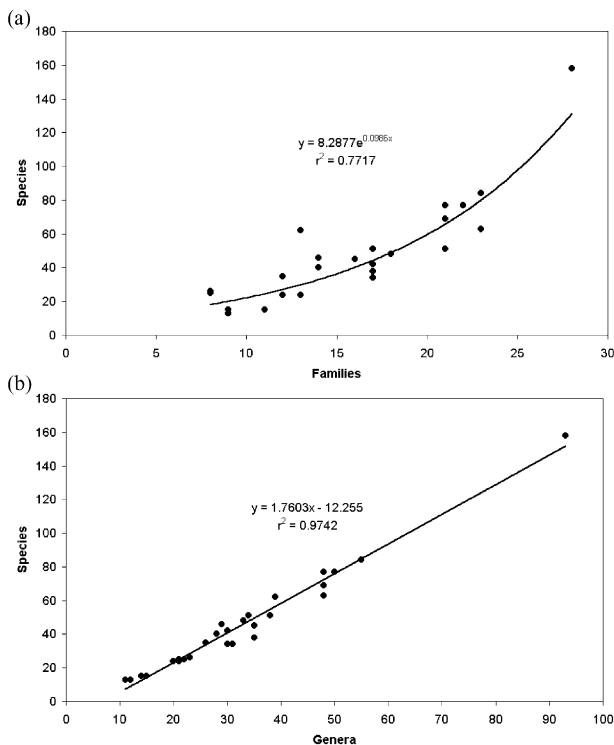


Fig. 2. (a) Exponential relationship between family and species richness in all 27 sampled sites; (b) linear relationship between genus and species richness in all 27 sampled sites (some of the circles are overlapping).

Table 2  
Taxa richness of sampled sites and respective ranking

Site	Richness			Rank		
	Species	Genera	Families	Species	Genera	Families
PBM	158	93	28	1	1	1
FAM	84	55	23	2	2	2
PAE	77	50	21	3	3	5
MAG	77	48	22	3	4	4
ALR	69	48	21	5	4	5
TOC	63	48	23	6	4	2
VCP	62	39	13	7	7	17
PIP	51	38	21	8	8	5
VGM	51	34	17	8	11	9
SVC	48	33	18	10	12	8
BAE	46	29	14	11	16	15
PIM	45	35	16	12	9	14
BRP	42	30	17	13	14	9
BAP	40	28	14	14	17	15
PIR	38	35	17	15	9	9
MIP	35	26	12	16	18	19
FRA	34	31	17	17	13	9
COC	34	30	17	17	14	9
PBV	26	23	8	19	19	25
PBC	25	22	8	20	20	25
PBS	25	21	8	20	21	25
BEZ	24	21	12	22	21	19
BAM	24	20	13	22	23	17
LAC	15	15	11	24	24	21
SÃO	15	14	9	24	25	22
LAR	13	12	9	26	26	22
SMM	13	11	9	26	27	22

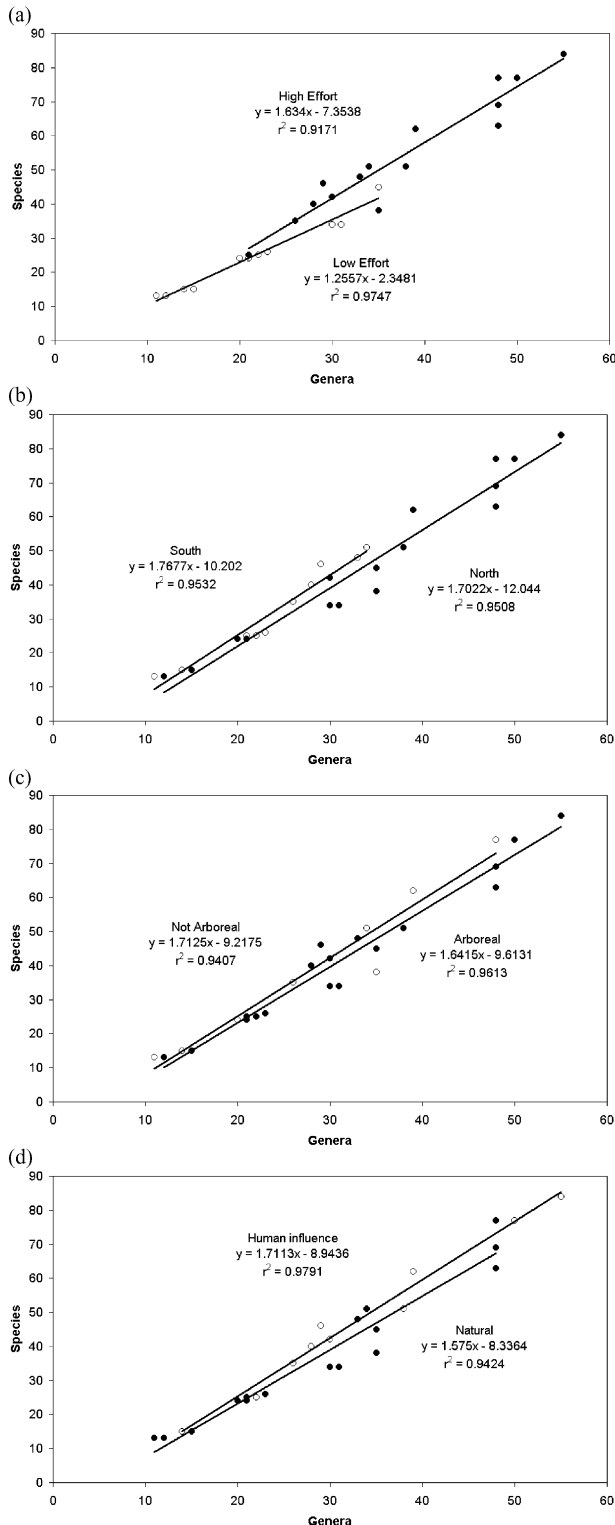


Fig. 3. (a) Comparison of genus richness and species richness relationship between high (filled circles) and low (open circles) effort sites; (b) comparison of genus richness and species richness relationship between northern (filled circles) and southern (open circles) sites; (c) comparison of genus richness and species richness relationship between sites with (filled circles) and without (open circles) arboreal cover; (d) comparison of genus richness and species richness relationship between sites considered as “natural” (filled circles) and those with high human influence (open circles).

### 3.2. Conservation priority

#### 3.2.1. Scoring approach

Using the rank of sites according to their taxa richness, we find families to have low predictive power of species-based site ranking (Table 2), despite the high Spearman rank correlation value of 0.855. Examination of the rank scatter plot (Fig. 4a) also leads us to conclude about the low reliability of the family surrogacy approach. Genera, on the contrary, seem to rank sites in much the same way as species do (Table 2) (Spearman rank correlation = 0.962). Predictive power is especially high at the highest and lowest ranked sites, being not as good at the middle ones (Fig. 4b).

#### 3.2.2. Iterative approach

Although a scoring approach to site ranking can be evaluated for future use, it is not the most efficient method for establishing conservation networks of sites. Complementarity is a fundamental issue to be taken into account. This way, we should score sites not simply according to their richness values, but according to which ones will allow the protection of the maximum number of species not included in previously chosen sites. By using accumulation curves, we can see the effects of adopting this approach for the different taxonomic levels (Fig. 5). The objective is to check what proportion of species can be protected by using the

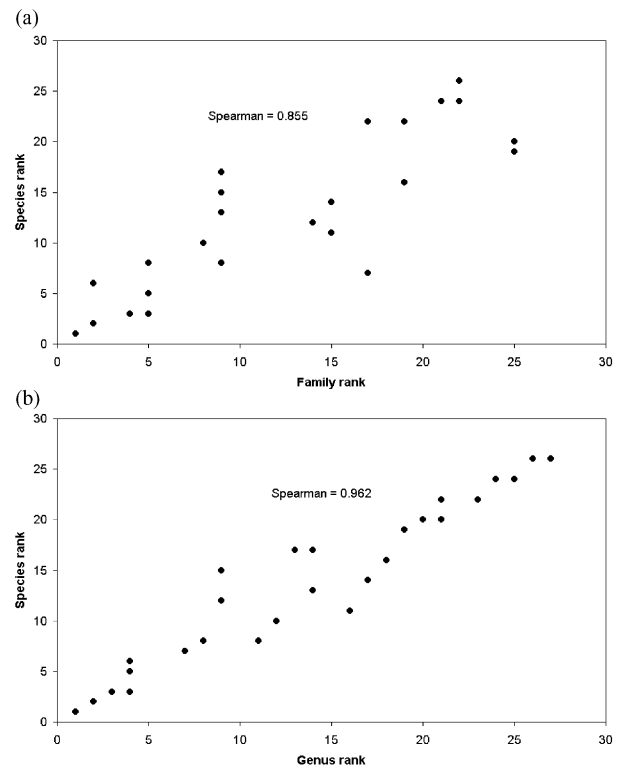


Fig. 4. (a) Comparison of site ranking according to family and species richness; (b) comparison of site ranking according to genus and species richness.



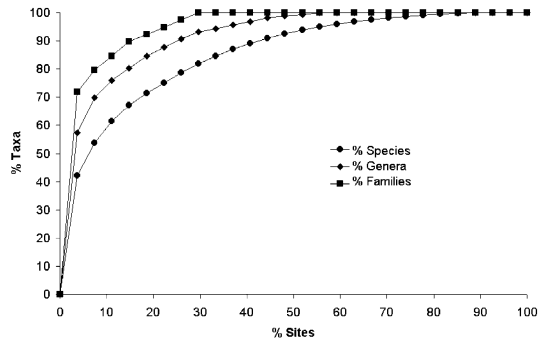


Fig. 5. Accumulation curves of the number of taxa represented by the adding of sites in a stepwise manner, considering complementarity.

same number of sites that protects all considered higher taxa. Twenty-four (89%) sites are necessary to include all species but only 15 (56%) for genera and 8 (30%) for families. The number of sites necessary to include all families is enough to protect, at most, 82% of species. If genus level is used, 95% of species can be protected.

#### 4. Discussion

All data points to the fact that only genus richness can be used as a significant and reliable surrogate of species richness, with much higher regression coefficient value and predictive power than families. Its linear relationship is also simpler than the more complex, non-linear, exponential relationship that family richness has with species richness. The only factor that we should be careful about is sampling effort, which can influence the reliability of predictions. Neither geographical location or habitat type are found to have significant influence over the usefulness of higher taxa surrogacy at genus level, at least in Portugal. The use of this taxonomic level as surrogate may even provide more precise estimates of species richness of spiders, with less potentially influencing factors, than another recently tested surrogacy approach with the same dataset, the use of indicator groups (Cardoso et al., submitted for publication).

Genera, but not families, are also considered a good surrogate for choosing priority sites for conservation. Either if we choose to apply a simple scoring approach or a much more efficient iterative approach to the problem of sites ranking, genera can be used as a surrogate of species, when no data is available on these. The use of caution is suggested, and in case of doubt, a conservative approach should be taken, by trying to protect more sites than those expected to be necessary to represent all genera. This way we should be able to guarantee that the proposed reserve network covers a large proportion of species. Contrary to what happens with species richness estimates, indicator groups used

for choosing conservation priority sites are more efficient than genera surrogacy with the same dataset (Cardoso et al., submitted for publication), if an iterative prioritisation is used.

However, two questions may refrain our enthusiasm regarding the use of genera as surrogate of species. The first one is that systematics of all invertebrates, particularly spiders, is constantly changing. Many species move from one genus or even family to other in a constant basis, as taxa revisions are permanently being published (Platnick, 2003). The second question, probably most important and being related to this, regards the difficulty of identifying many individuals even to genus level. In some cases, it's just easier to identify the species and only afterwards check the current higher taxon where the species belongs. Both these theoretical problems can be override by another possible and demonstrated approach with spiders, the use of indicator or surrogate groups (Cardoso et al., submitted for publication). Nonetheless, this last methodology has its own problems, like the possible loss of more information than with the higher taxa surrogacy and the required identification of all species belonging to the indicator group.

Despite some problems inherent to the higher taxa approach, our work concludes that not only it is a reliable but an extremely useful method both for species richness prediction and definition of a conservation priority sites network, both in Portugal or the entire Mediterranean region. Surrogacy can be seen both as a preliminary approach, if not possible to have all species identified in a reasonable amount of time for conservation purposes, or as an end in itself, in regions where most species are unknown, or when no resources are available to go further in identification.

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