HIGHER-TAXA SURROGACY AND EFFICIENCY IN SPIDER CONSERVATION: A CASE STUDY FROM TERAI CONSERVATION AREA, INDIA

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ABSTRACT

The establishment of a strong relationship between species richness and a surrogate index is a critical issue in conservation biology. Such a relationship could provide the basis for the establishment of cost-effective and easy-to-monitor methods for measuring biodiversity, providing an alternative for prioritization of sites for conservation. Both family and genus richness are tested for their ability to predict the number of spider (Araneae) species independent of sampling detection, spatial autocorrelation, area, geographical location and type of habitat. Data from two protected areas of Terai Conservation Area (TCA) were used as a test case. Genus richness is considered to be a good surrogate of species richness, despite some caution being needed regarding comparison of sites with considerably different sampling effort. Genus alone is found to be reliable indicator for ranking sites according to taxa richness or for determining near-minimum sets of sites for conservation. This study recommends surrogacy at this higher taxonomic level as a promising approach for prediction of spider species richness or evaluation and ranking of areas according to conservation importance.

INTRODUCTION

Biodiversity on Earth is rapidly diminishing, and conservation biologists are struggling to catalogue and preserve what remains of it. The rapid decline in biodiversity and practical challenges in describing and enumerating it rigorously enough, including the money, effort, expertise and time involved (May, 1994), have urged conservation biologists to rely on surrogates for explaining patterns in 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 at all such a goal is possible to achieve. Among the most popular of these approaches is the use of higher-taxa surrogates, as proposed by Gaston and Williams (1993; see also Williams, 1993; Williams and Gaston, 1994). Others include 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; MacNally *et al.*, 2003). Despite all the pros and cons that these have, the higher-taxon approach has several advantages, allowing information to be obtained on a large number of taxa with relatively little effort and use of resources. Another crucial advantage is the retention of broad biological information, which allows distribution patterns to be understood (Eggleton *et al*., 1994; Williams *et al*., 1994; Gaston *et al*., 1995) and conservation priority areas to be defined more efficiently (Williams, 1993; Williams *et al.*, 1994; Vanderklift *et al*., 1998), which is, after all, the ultimate goal of conservation biology. The higher-taxon approach has been used at both local and regional scales (Gaston *et al*., 1995; Larsen and Rahbek, 2005), and use of this approach could be highly demanding in terms of performing direct species measurements. Although most previous work points to reliability in the 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), caution should be exercised when applying the method and interpreting results since the method is subject to a series of limitations such as sampling effort, data quality, habitat type, geographic location and spatial autocorrelation (Gaston and Williams, 1993; Andersen, 1995; Grelle, 2002; Cardoso et al., 2004).

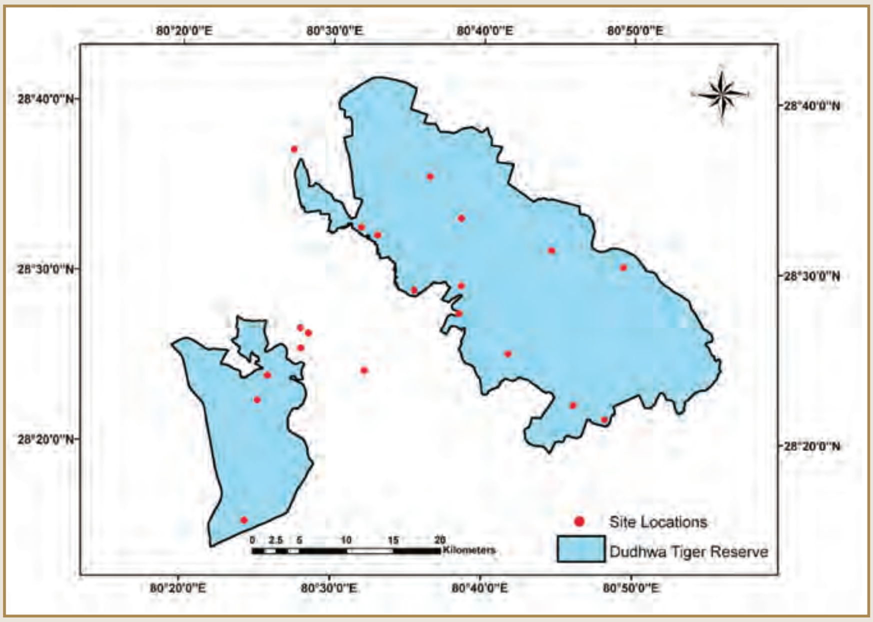
Nearly all studies of higher-taxa surrogates have simply looked at the extent of correspondence between the richness of areas measured at different taxonomic levels. But efficient reserve networks consist not just of rich sites but of sites that are rather different from one another biotically and that, therefore, exhibit high between-site complementarity (Pressey and Nicholls, 1989; Pressey *et al.*, 1993; Williams, 1998). Hence a full evaluation of the utility of the higher-taxon approach for reserve planning should include a consideration of the degree of cross-level correspondence in patterns of complementarity as well as richness and an assessment of how well entire reserve networks designed using information on genera or families manage to capture species-level diversity (Vane-Wright and Rahardja, 1993; Williams, 1993; Balmford *et al*., 1996a). One critical limitation is that even those tests that have addressed these other concerns have nearly always targeted relatively species-poor groups such as birds and mammals (Balmford *et al.*, 1996a). This is not surprising as very few good-quality, local-scale data sets of highly speciose groups such as insects and arachnids currently exist. Nevertheless, rapid assessment methods are obviously most needed for megadiverse groups, for which a shortage of expertise is compounded by the long time required to sort records down to the level of species (Bloemers *et al*., 1997; Lawton *et al*., 1998).

With this work, we intend to provide evidence of the possible usefulness of the higher-taxa surrogacy approach with spiders in the Terai, testing it as a species richness predictor. We also consider the effects of environmental and methodological factors on the validity of predictions. Finally, we test the use of this kind of surrogacy as a tool for reliable definition of conservation priority sites, either by ranking them according to taxa richness or by considering the complementarity of known taxa between sites to examine how well subsets of our sites capture species-level diversity when using information on species, genera, families and orders. The species richness of spiders and their respective spatial distributions are virtually unknown in India, with a certainly very low figure of 1520 species registered for the country (Sebastian and Peter, 2009). Although not even higher-taxa data are available for most of the country's territory, given the difficulty in identification of species, many remaining to be described or discovered, it seems advisable to test for future use such potential tools as different surrogates of biodiversity.

METHODS

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. Two protected areas of the Terai Conservation Area (TCA) under the jurisdiction of Dudhwa Tiger Reserve, one in the north—Dudhwa National Park—and the other in a nearby area in the south—Kishanpur Wildlife Sanctuary were sampled in 2006–2007 (Fig. 1).

Figure 1.



Map showing sampling sites in TCA

For simplicity, these two areas are simply referred to hitherto as belonging to northern and southern geographical regions. Ideally, all sites in all protected areas were sampled during the same year. We chose such areas because of their high habitat diversity. By comparing the two regions, the geographical effects on the surrogacy methods could be tested. In each area, we sampled several sites, a total of 10, trying to cover a majority of the most significant habitats represented. This way, we also considered the habitat effect by differentiating sites with arboreal cover from those without and those with "natural" vegetation from the ones dominated by introduced vegetation or under severe human influence or management. Ten major vegetation types were identified, and two sampling sites per vegetation type were selected for spider sampling. The size of the sampled sites ranged from 1.8 to 13.3 km^2. Spiders were sampled along 50 m transects using pitfall traps and semi-quantitative sampling. Ten transects were placed randomly within each vegetation type. Pitfall sampling was carried out for 64 weeks, and other semi-quantitative sampling methods were used on 64 occasions (once every week) at the same sampling sites. The pitfall traps consisted of cylindrical plastic bottles of diameter 10 cm and depth 11 cm (Churchill and Arthur, 1999). Six pitfall traps were laid along each transect line at intervals of 10 m. Traps were filled with preservative (69% water, 30% ethyl acetate, and 1% detergent). After seven days, the specimens were removed from the traps. This allowed us to maintain the spider specimens in a good condition before they were processed in the laboratory and identified. Semi-quantitative sampling involves aerial sampling; ground collection; beating; litter sampling; or sweep netting. Each sampling method involved 1 hour of active sampling, measured using a stopwatch.

ANALYSIS

To test if either family or genus richness can be reliably used to predict species richness, regression analysis was performed over all the 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 measures of adjustment, surrogacy reliability and predictive power. Searching for the possible influence of sampling detection, geographical location and habitat type on the surrogacy results, we also adjusted regression lines after separating the sites according to their characteristics, one factor at a time. Analysis of covariance (ANCOVA) was carried out to test for statistically significant differences between regression lines. If differences were found, the factor involved was considered to potentially influence the reliability of surrogacy. The SPSS 16.0 software package was used for statistical analysis. We estimated the relationship between study site areas. In order to test if the study site area affected the relationship between species richness and higher-order richness, we regressed the residuals of the relationship with the site area. The pattern of diversity is known to be spatially autocorrelated (Lennon *et al*., 2001). Autocorrelation distorts systematically the classical tests of association and can generate misleading results—correlation coefficients, regression slopes and the associated significance tests (Clifford *et al*., 1989; Lennon *et al*., 2001). To avoid this, we applied the modified correlation test of Clifford *et al.* (1989), which corrects the significance of the Pearson correlation coefficient for the spatial dependency within and between the two patterns examined. This correction uses the concept of "effective sample size". This is the equivalent sample size for the two patterns when the redundancy produced by spatial autocorrelation is removed. In the present study, the effective sampling size was always equal to or close to the real sample size, and thus the spatial autocorrelation did not affect the estimated level of statistical significance.

Two approaches were tested for prioritisation and ranking of sites for conservation. The first approach is scoring approach, which uses the raw number of taxa represented in each site as the sole value for ranking sites (Table 1). The Spearman rank correlation index was used 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. The second approach we tested a more efficient iterative approach of conservation priority ranking. For each of the considered taxonomic levels (family, genus and species), we first choose the site with the highest species richness and then calculate the complementarity richness by counting the species that are not already present. Subsequently we choose a site with the highest complementarity and repeat the procedure until all the species are represented in the data matrix. Finally we reorder the sites by complementarity richness and chose the richest site (combining the value of species richness and complementarity) 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 most species rich site in the respective taxa. By doing so, we tested the effect of using higher taxa for choosing a near-minimum set of sites that potentially preserves the maximum number of species.

RESULTS

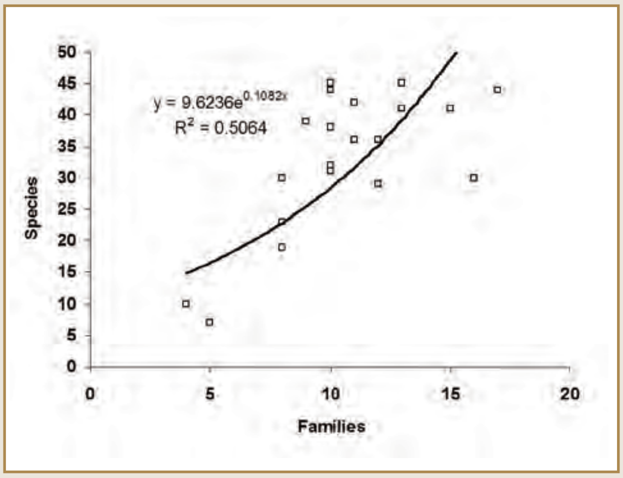
A total of 186 species belongs to 77 genera and 27 families were collected during the entire sampling period. Of these, 67 species (36% of all species) belong to morphospecies. The Terai spider assemblage represents 20% of all genera described from India, which is very rich. The nomenclature adopted consistently follows Platnick's (2008) world spider catalogue.

SPECIES RICHNESS PREDICTION

CHOOSING THE BEST SURROGATE

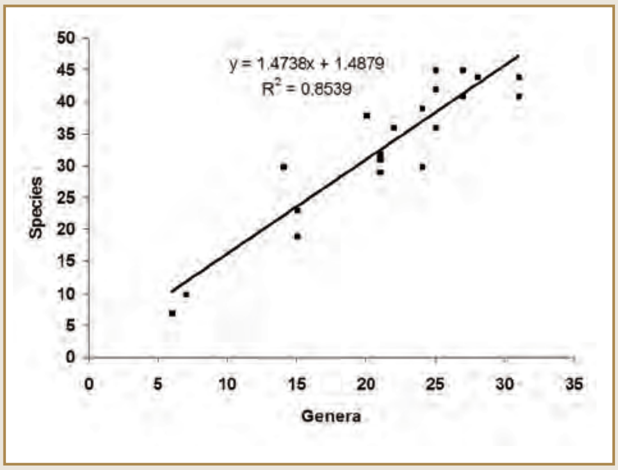
After fitting all previously defined regression types—linear, log-log and exponential—to family and genus taxonomic levels, we chose the ones with the highest regression coefficient value. A non-linear exponential relationship was found for the families and a linear relationship for the genera (Fig. 2). Both taxonomic levels present a highly significant relationship with the number of species ($n = 20$, $p < 0.001$); however, the genus richness seems to have a much better predictive power, with a high r^2 value.

Figure 2 a.



(a) Exponential relationship between family and species richness;

Figure 2 b.



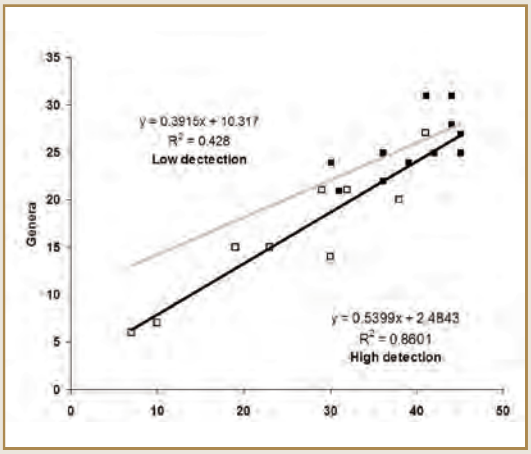
(b) linear relationship between genus and species richness in all 20 sites sampled for spiders in the study area

INFLUENCE OF FACTORS

Since genus richness was found to have high predictive power and has a linear relationship with species richness, in subsequent tests for influence of factors on taxonomic level, only genus-level data were considered. Comparing the regression lines of sites representing different detection (captured ratio for individuals per species) level for individual species was found significantly different ($n = 20$, $p < 0.05$) (Fig. 3a). This was to be expected as the heterogeneity in the detection probabilities of different species capture varies with local and regional species pools. The same did not happen with other factors, whose differences were not found to be statistically different.

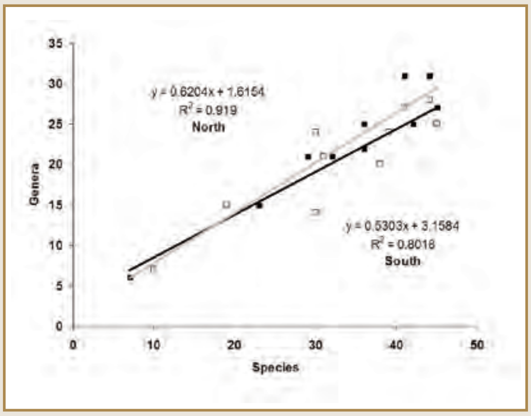
Regression-based analysis demonstrated only a weak correlation between area and different taxonomic levels for all classes ($r2 = 0.123$ and 0.204, respectively). The correlation between area and the residuals of the relationship between species richness and higher-taxonomic-level richness was not significant ($a = 0.001$).The spatial autocorrelation among sites seems to be not a significant effect since the effective sample size deviated only slightly from the real sample size without altering the results.

Figure 3 a.



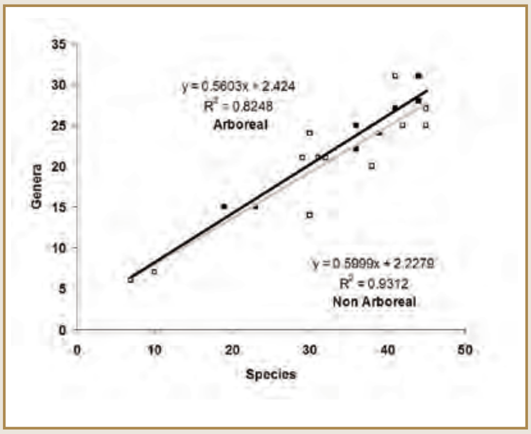
(a) Comparison of the relationship between genus richness and species richness between sites with high (open squares) and low (filled squares) detection;

Figure 3 b.



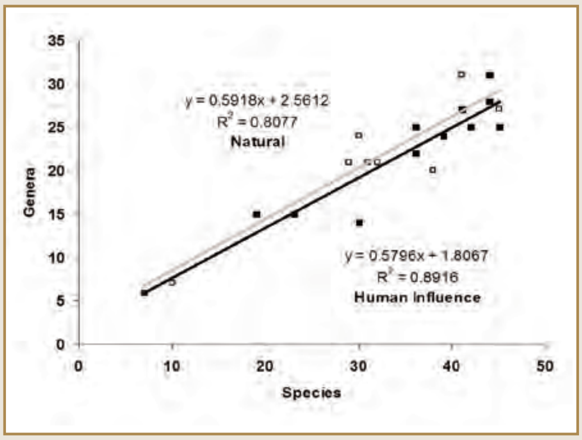
(b) comparison of sites in the northern (filled squares) and southern (open squares) regions;

Figure 3 c.



(c) comparison of sites with (filled squares) and without (open squares) arboreal cover;

Figure 3 d.

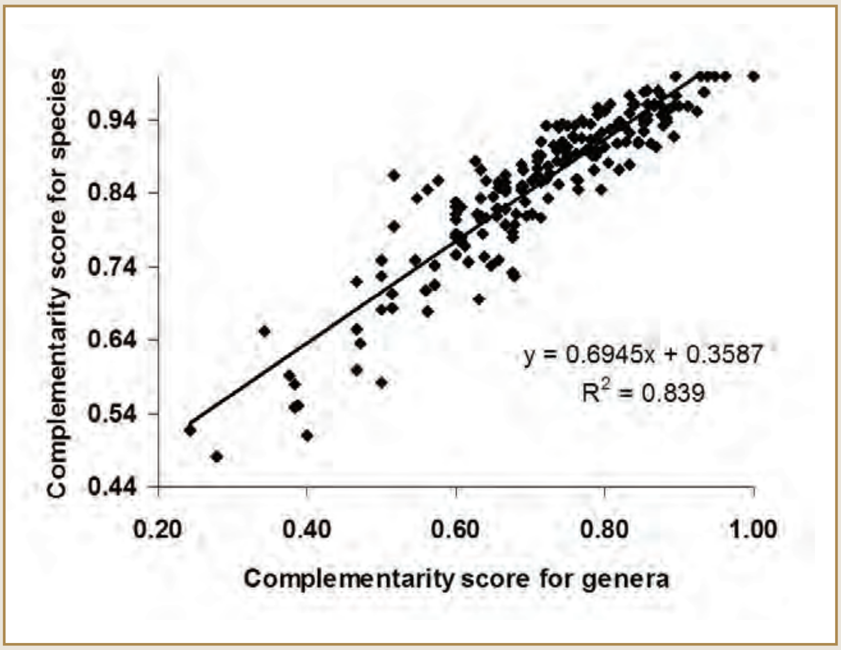


(d) comparison of "natural" areas (open squares) and those under intense human influence (filled squares).

CROSS-LEVEL CORRELATIONS IN COMPLEMENTARITY

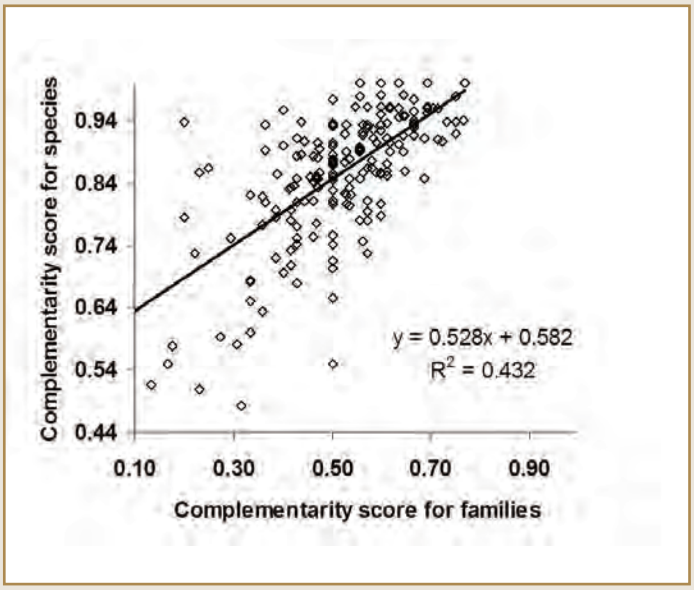
There was good congruence in the complementarity patterns measured in terms of species and genera but not across families (Fig. 4b). The between-site complementarity of species was quite closely related to the between-site complementarity of genera ($r^2 = 0.84$, $n = 0$ pairs of sites, $p < 0.001$); thus sites with very different spider species also had very different spider genera, and vice versa. However, the species-level complementarity could be far less closely predicted compared with the family-level complementarity (for species vs families, $r^2 = 0.44$, $n = 20$, $p < 0.10$). These results were apparently not confounded by variations in the difference in area of paired sites (since pairs are of widely differing size).Thus, it appears that the match in how well sites complement each other when assessed in terms of species and genera is real and, alongside congruence in richness, explains why sets of sites identified using spider genera do so well at representing spider species.

Figure 4 a.



Cross-level congruence in the complementarity of pairs of sites in the study area: a) species vs genera

Figure 4 b



(b) species vs families. Complementarity scores are calculated as the number of species or genera or families found at just one or the other site, divided by the combined total found at either or both (Colwell and Coddington, 1994).

Cross-level congruence in the complementarity of pairs of sites in the study area:

CONSERVATION PRIORITY

Scoring Approach

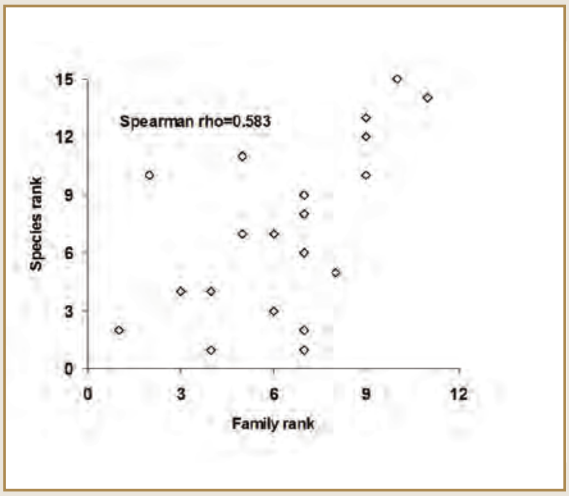
Using the rank of sites according to their taxa richness, families were found to have a low predictive power of species-based site ranking (Table 1), despite the high Spearman rank correlation value of 0.855. Examination of the rank scatter plot (Fig. 5b) also leads to conclusions about the low reliability of the family surrogacy approach. Genera, in contrast, seem to rank sites in much the same way as species do (Table 1) (Spearman rank correlation = 0.962). Predictive power is especially high at the highest and lowest ranked sites, not being as good at the middle ones (Fig. 5b).

Table 1. Taxa richness of sampled sites and respective ranking

Site	**Richness**			**Rank**		
	Species	**Genera**	**Families**	**Species**	**Genera**	**Families**
grsk2	45	27	13	1	3	4
pssk1	45	25	10	1	4	7
grsd2	44	31	17	2	1	1
rpsd2	44	28	10	2	2	7
pssd2	42	25	11	3	4	6
grsk1	41	31	15	4	1	3
mssd2	41	27	13	4	3	4
rpsk1	39	24	9	5	5	8
rpsd1	36	22	12	7	6	5

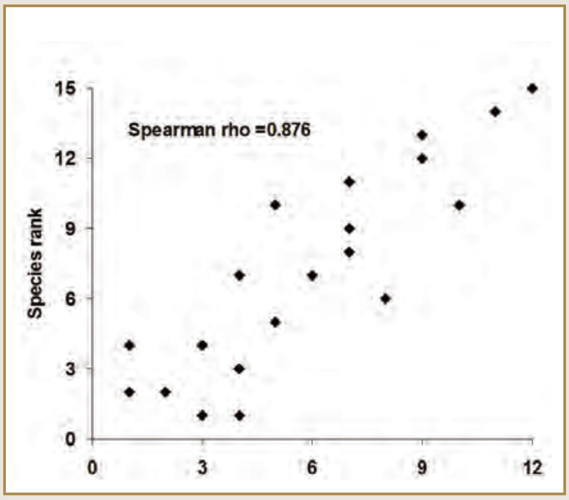
rpsk2	36	25	11	7	4	6
mssk1	32	21	10	8	7	7
pssd1	31	21	10	9	7	7
grsd1	30	24	16	10	5	2
mssd1	30	14	8	10	10	9
mssk2	29	21	12	11	7	5
plsd2	23	15	8	12	9	9
plsk1	19	15	8	13	9	9
plsk2	10	7	4	14	11	11
plsd1	7	6	5	15	12	10

Figure 5 a.



(a) Comparison of site ranking according to family and species richness;

Figure 5 b.

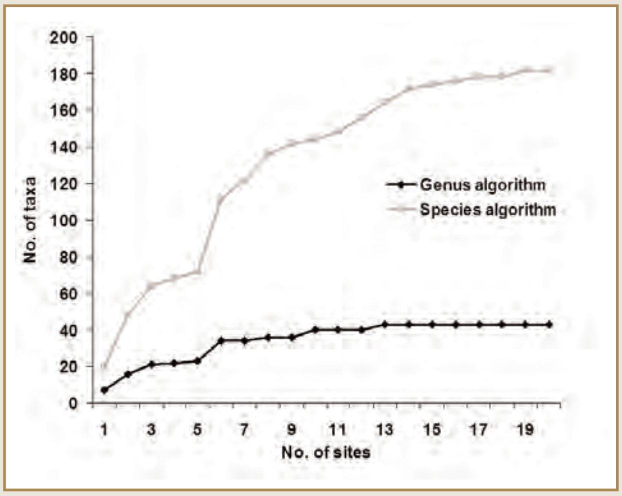


(b) comparison of site ranking according to genus and species richness

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. Thus, scoring of sites was not done simply according to their richness values but according to which ones will protect the maximum number of species not included in previously chosen sites. By using accumulation curves, the effects of adopting this approach for the different taxonomic levels can be carefully considered. The objective is to check what proportion of species can be protected by using the same number of sites that protects all considered higher taxa. Genus-level data were chosen for this analysis since it fitted best with the species algorithm. The number of sites (13 sites; 65% of all sites sampled) necessary to include all genera is enough to protect, at most, 90% of the species (Fig. 6).

Figure 6.



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

DISCUSSION

The results of the study suggest that only genus richness can be used as a significant and reliable surrogate of species richness, with a much higher regression coefficient value and predictive power compared with families. Its linear relationship is also simpler than the more complex, non-linear, exponential relationship that family richness has with species richness. Previous studies also recognize the same strong relationships between species and genera richness, while several studies highlight caveats on the use of family richness (Williams and Gaston, 1994; Gaston and Blackburn, 1995; Balmford *et al.*, 1996a, 1996b; Roy *et al.*, 1996; Grelle, 2002; Cardoso *et al.*, 2004; Bergamini *et al.*, 2005). However, there is evidence demonstrating family richness to be an equally good predictor of species richness (Williams *et al.*, 1994; Negi and Gadgil, 2002; Báldi, 2003). Given the findings of strong correlation and predictive power between higher-taxonomic-level richness and species richness, this study concluded that genus-level richness could be used in describing patterns of species diversity. However, caution should be exercised regarding the decision on the taxonomic level to be used in a similar analysis, which should be based on a preliminary analysis undertaken at the region of interest. This is mainly because the responses of organisms to environmental variability differ for the same group of species from region to region.

Species richness is known to increase as the sampling area and environmental variability (here measured as habitat diversity) increase. In the present study, the relationship between species richness and area or habitat diversity was found to be generally weak. Neither geographical location nor area nor habitat was found to have significant influence over the usefulness of higher-taxa surrogacy at the genus level. When the sampling effort is the same, the only factor found that may limit the use of higher-taxa surrogacy is imperfect detection of species in single or multiple sites.

Because species are detected imperfectly, some species that were not detected at the site may have in fact been present (*i.e.*, a false absence), while others could be genuinely absent from the site (*i.e.*, not part of the local community during that sampling period). Repeated surveys are needed to estimate the detection probability, and the assumptions that need to be fulfilled are (1) the occupancy status of the site for each species does not change during the season and (2) changes occur completely at random (*i.e.*, the members of the local species pool present at the site are constant during the sampling period) (MacKenzie *et al*., 2006).

The results also show that fine-scale variations in genus-level richness mirror variations in the species richness. This is also due to moderate cross-level correspondence in the extent to which different sites complement one another: sites that are highly complementary at the species level also tend to exhibit high complementarity at the genus level, and *vice versa*. In contrast, data on families and orders are much poorer predictors of patterns of species richness and species-level complementarity.

Attempts have been made recently to explore the performance of the higher-taxa approach in identifying priority areas for conservation (Balmford *et al.*, 2000; Fjeldså, 2002; Whiting *et al*., 2000). Accordingly, some encouraging results have been obtained, at a continental scale, but only for large grain sizes (Larsen and Rahbek, 2005). Such an analysis was performed at the regional scale in order to explore the ability of different taxonomic levels to encompass species diversity. The aim was to investigate the efficiency of different levels of information in prioritizing sites for conservation and to investigate the reliability of the higher-taxon approach. Analysis demonstrated that the higher-taxon approach performed as well as the species-level approach. Yet, its use in reserve selection should follow further analysis.

Genera, but not families, are also considered a good surrogate for choosing priority sites for conservation. Whether we choose to apply a simple scoring approach or a much more efficient iterative algorithm approach to the problem of sites ranking, genera can be used as a surrogate of species when no taxonomic data are 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 will guarantee that the proposed reserve network covers a large proportion of the species.

From a practical point of view, the method could be applied to monitoring and management proposes to frequently study and determine changes in biodiversity richness and distribution. The results show clearly that the higher-taxon approach could be used for performing rapid area inventories. Assuming, very conservatively, that there are no savings from higher-taxon surveys in terms of field time, that subsequent identification of spiders in the laboratory takes no longer than fieldwork, and that the identification time required for genera is fully half that for species, it follows that genus-level surveys will take at the most only 50% of the time required for sorting down to species. Perhaps more important than time savings, in most situations (e.g. the highly diverse tropics), the great majority of the work required for genus-level inventories of spiders could be carried out by well-trained parataxonomists or by nonspecialists using local or regionally based operational keys, rather than by expert scientists (Oliver and Beattie, 1996; Krell, 2004). Apart from spiders, the higher-taxon approach should continue to be encouraged for other, richer arthropod groups, and the cautious use of genus- level surveys represents a very promising route to setting priorities for megadiverse groups on the conservation map. The efficiency of the method to be used for prioritization of conservation areas needs to be demonstrated for different groups of taxa in different biomes and in different biogeographical areas (Balmford *et al*., 2000).

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