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Surrogate taxa for biodiversity in agricultural landscapes of eastern Austria

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Abstract

In an agricultural landscape in eastern Austria eight terrestrial organism groups were investigated as potential biodiversity indicators. We present a cross-taxon congruence assessment obtained at the landscape scale using two groups of plants (bryophytes and vascular plants), five groups of invertebrates (gastropods, spiders, orthopterans, carabid beetles and ants) and one vertebrate taxon (birds). We tested four different approaches: correlated species counts, surrogate measures of the overall species richness that was assessed, a multi-taxa (or shopping basket) approach and a simple complementarity algorithm. With few exceptions, pairwise correlations between taxa, correlations between one taxon and the species richness of the remaining groups, and correlations between a combination of the richness of two taxa and the remaining species richness were highly positive. Complementarity-derived priority sets of sampling sites using one taxon as a surrogate for the pooled species richness of all other taxa captured significantly more species than selecting areas randomly. As an essential first step in selecting useful biodiversity indicators, we demonstrate that species richness of vascular plants and birds showed the highest correlations with the overall species richness. In a multi-taxa approach and in complementarity site selection, each of the eight investigated taxa had the capability to capture a high percentage of the overall species richness.
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1. Introduction

Limited financial resources and taxonomic expertise hinder detailed assessments, mapping and monitoring of biodiversity, so that conservation strategies and biodiversity management will benefit greatly if the species richness of one organism group could efficiently indicate the richness of other taxa (Flather et al., 1997; Reid, 1998; Howard et al., 1998; Ricketts et al., 1999). The use of such an organism group—frequently termed surrogate or indicator taxon for biodiversity (Pearson and Cassola, 1992; McGeoch, 1998; Gladstone, 2002; Negi and Gadgil, 2002)—would facilitate, for instance, the selection of representative nature reserve networks (Howard et al., 1998) or an efficient biodiversity monitoring programme (Noss, 1990). An ideal biodiversity indicator should possess a set of properties (Noss, 1990; McGeoch, 1998) like cost-efficiency or applicability at different spatial scales, but basically it needs to show a

high correlation to the quantity to be indicated (Markert et al., 2003). However, applied ecology is far from clear on how species richness of particular taxonomic groups are correlated with each other. Some much-cited studies found no or limited evidence for an efficient biodiversity indicator taxon (e.g. Kremen, 1992; Prendergast et al., 1993a; Lawton et al., 1998, van Jaarsveld et al., 1998; but see also Howard et al., 1998 or Lund and Rahbek, 2002).

Nevertheless, several biodiversity indicator measures have been proposed. The simplest biodiversity indicator approach is one where species richness counts for an indicator taxon are correlated with species richness counts of another taxon (Pearson and Cassola, 1992; Abensperg-Traun et al., 1996; Flather et al., 1997). The published results are contradictory, with mostly limited predictive power at the local scale (<10 ha) (Abensperg-Traun et al., 1996; Pharo and Beattie, 1997), but often yielding good results at coarser spatial scales (> 100 km²) (Murphy and Wilcox, 1986; Ricketts et al., 1999; Heino, 2002). Studies performed at intermediate spatial scales (landscape scale, ca 0.1–100 km²) are scarce (e.g. Murphy and Wilcox, 1986; Prendergast et al., 1993a; Howard et al., 1998).

A central question of the biodiversity indicator approach is "how effectively does one taxon predict the pooled species richness of a wide array of other taxa?" (Ricketts et al., 1999). With exceptions (e.g. Abensperg-Traun et al., 1996; Duelli and Obrist, 1998; Ricketts et al., 1999; Gladstone, 2002), few studies have attempted to answer this essential question, perhaps because of the lack of comprehensive data.

Another method is the so-called multi-taxa or "shopping basket" approach (Vane-Wright et al., 1994; Kotze and Samways, 1999). While single groups may fail to serve as biodiversity surrogates, we probably can select a set of taxa with different ecological requirements to circumvent this problem (Ricketts et al., 1999).

Besides these three simple correlation methods described above, the principle of complementarity has been implicitly (e.g. Kirkpatrick, 1983) and explicitly (Vane-Wright et al., 1991; Csuti et al., 1997) applied in area selection for conservation purposes (for a review see Justus and Sakar, 2002). Complementarity can provide an efficient answer about where to concentrate conservation efforts (Brooks et al., 2001a), because it ensures maximum representation of the selected attributes (e.g. all species, rare species, endangered species etc.). It has been demonstrated that indicator taxa can act as surrogates in complementarity-derived area sets (Howard et al., 1998; Lund and Rahbek, 2002). However, simple scoring methods are less robust than the use of complementarity algorithms (Pressey and Nicholls, 1989; Prendergast et al., 1993a, b; Howard et al., 1998; Reyers and van Jaarsveld, 2000; Hopkinson et al., 2001; Lund and Rahbek, 2002).

The present study tests the quality of eight potential indicator taxa in the agricultural landscape of eastern Austria. This landscape is structurally diverse, used for multiple purposes and is typical of many areas in central Europe. We selected a variety of taxa with different ecofunctional characters: bryophytes, vascular plants, gastropods, spiders, orthopterans, carabid beetles, ants and birds. (1) We ask whether there are significant pairwise correlations between the species richness of individual taxa. (2) We test each taxon for its correlation with overall species richness. (3) We investigate the usefulness of combinations of two taxa as surrogates for the combined richness of the remaining taxa. And, finally, (4) we ask if complementary sets of sites based on each of the eight potential surrogate taxa capture species richness of the other seven taxa significantly more effectively than random site selection.

2. Methods

2.1. Site description

The study area (Fig. 1) is rectangular (ca. 94×44 km) and ranges from the Pannonic lowlands around Lake Neusiedl in the east (117 m a.s.l.) to the mountainous region of the easternmost Alps in the southwest (720 m a.s.l.). The area has a Pannonic (continental) to Central European climate with an average ambient temperature of 13–16 °C during the summer vegetation growth period and a range in mean annual precipitation of 550–1000 mm. Geologically, the area is dominated by sediments from the quaternary and tertiary periods (basins of Lake Neusiedl and Vienna) and by limestone and flysch (Alps, Leithagebirge). The sampling area contains a large variety of typical central European land-use types such as crop fields, meadows, pastures and vineyards, but also some area-specific habitats (i.e. inland salt pans). Natural and seminatural elements such as dry grasslands, hedges, ditches, rocks and forest-grooves are mostly restricted to small remnant patches.

2.2. Sampling design

We randomly selected 38 sampling sites, each ca. 600×600 m. This geographic scale was chosen because it directly matches the national recording scheme for plants and animals. To limit the sample areas to agriculturally transformed land, sampling sites dominated by forest and human settlements were excluded prior to selection. Within the final set forest cover ranged from <1 to 56% with a mean of 12.5% and the area of arable fields ranged from 0 to 97% with a mean of 55%. Within each of the 38 sites we investigated 10 sampling points, using an identical scheme for all sites (Fig. 1).

2.3. Sample collection

2.3.1. Plants

Within a radius of 10 m (bryophytes) or 20 m (vascular plants) around the sampling point, all species were recorded. Bryophytes were sampled once during the winter season (which is known to be optimal for bryophyte growth in the investigated area), and vascular plants twice between April and September 1998 and 1999.

2.3.2. Gastropods

All gastropods within a radius of 10 m around the sampling point were censused by hand searches in April to September 1998 and 1999 for 15 min. Within the 10 m radius, we also collected four randomly located soil samples ($10 \times 10 \times 5$ cm depth). These were washed in a 0.5 mm sieve, dried, and the remaining material was searched for gastropods. Only live animals were recorded. Gastropods caught by pitfall trapping (see surface-active arthropods) were also identified.

2.3.3. Surface-active arthropods

Spiders, carabid beetles and ants were obtained by pitfall trapping. One pitfall (ø 4.5 cm, covered with a transparent roof, with ethylene glycol as preservative) per sampling point was exposed for three 14-day periods (September 1998, May 1999, June/July 1999).

2.3.4. Orthopterans

Within a radius of 20 m around the sampling point, all orthopterans (Ensifera and Caelifera) were recorded once for 10 min during July and August 1999. The species were identified in the field based on morphological and acoustic characteristics. Bat detectors were used to record species with ultrasound songs.

2.3.5. Birds

Bird species numbers were assessed by means of point counts with infinite counting range (Bibby et al., 1992a). During the 2001 breeding season (April–June), birds were counted twice between 0600 to 1200 for 5 min respectively at each sampling point, and were identified using acoustic and morphological characteristics (Bibby et al., 1992a). Thus, in each study site, a total of 100 min were spent recording species.

2.4. Data analysis

The species identified across the 10 sampling points per site were pooled for respective taxa.
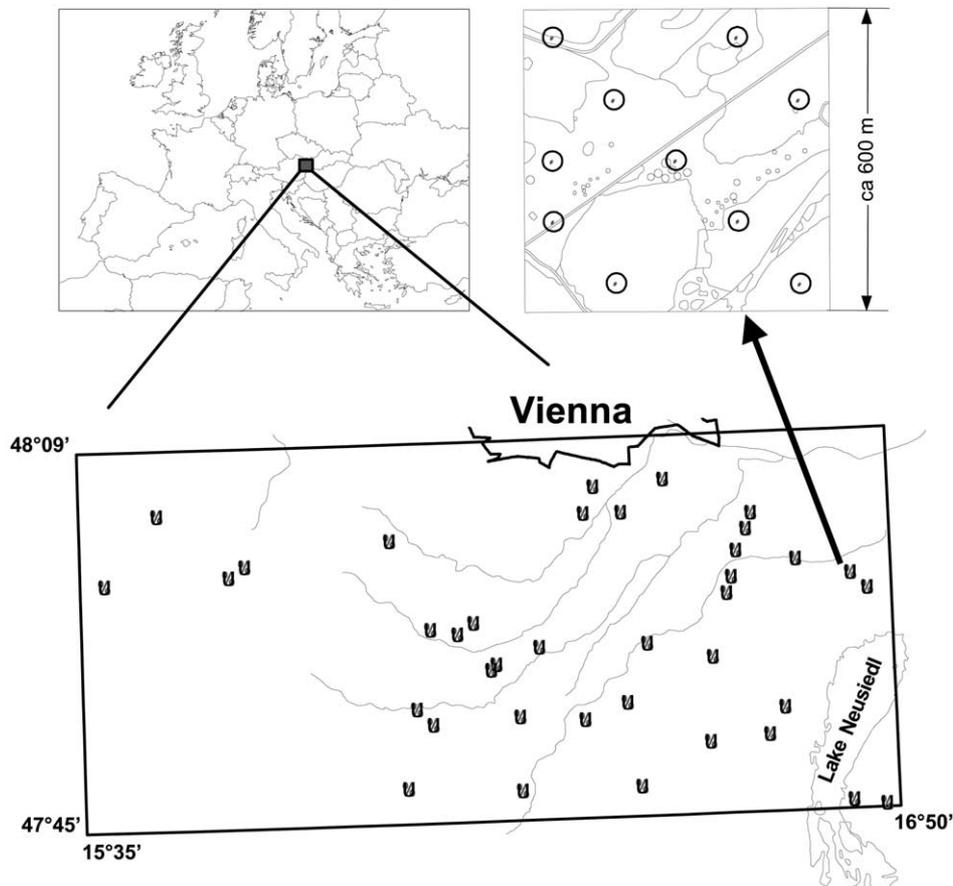

Fig. 1. Sampling area and sampling scheme.

2.4.1. Species richness correlations

To adjust for large differences between taxa in total species richness values, species numbers for individual taxa and sampling site were calculated as percentages of a taxon's total number of species recorded across all study sites (cf Ricketts et al., 1999). Original species richness values are shown only in Fig. 3. Pearson's correlation coefficient was used to determine cross-taxon congruence. Since the assumption of data normality was not satisfied in some of the groups (bryophytes, vascular plants and birds), 95% confidence intervals of correlation coefficients were constructed by bootstrapping (Efron and Tibshirani, 1993). We calculated accelerated bias-corrected percentile limits (ABC) following the protocol in Manly (1997).

The significance was determined using a randomization test (Manly, 1997) with 50,000 randomizations. The significance level was Bonferroni-adjusted (Sokal and Rohlf, 1995) to $0.05/77 = 0.00065$ owing to the large number (77) of correlations tested.

To evaluate the importance of how different methods of counting species numbers affect the correlations, rarefaction was applied in pairwise correlation analyses to data of spiders and carabids for which numbers of individuals were available. We calculated expected species numbers using formula (2.1) in Gotelli and Graves (1995), which is based on sampling without replacement from some parent distribution. All calculations were done using a spreadsheet programme with macros programmed in Visual Basic for Applications.

2.4.2. Complementarity

Using the principle of complementarity in area selection for conservation purposes, a simple richness-based algorithm termed "greedy" (Csuti et al., 1997; Brooks et al., 2001b) was used. The greedy algorithm provides only a "near-optimal" solution, in contrast to optimal solutions based on linear integer programming algorithms (Underhill, 1994; Csuti et al., 1997; Hopkinson et al., 2001). Nevertheless, the greedy algorithm is
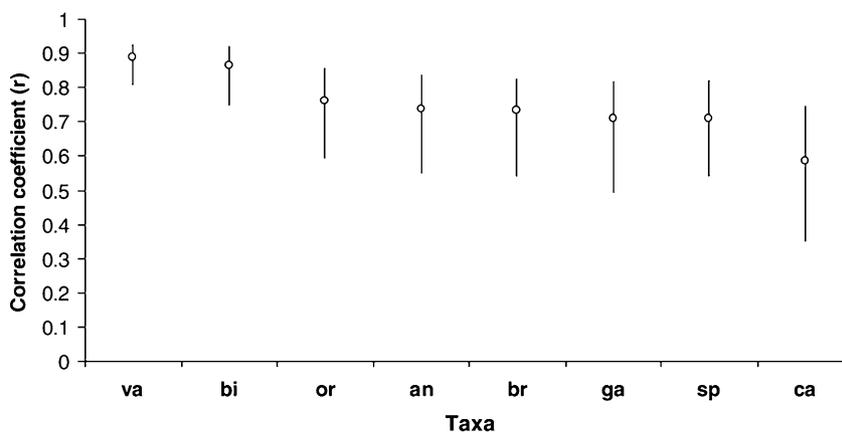

Fig. 2. Ability of one taxon to act as a biodiversity surrogate for overall species richness (total species richness minus species richness of the predicting taxon). Ninety-five percent confidence intervals of correlation coefficients (accelerated bias-corrected percentile limits) are shown. All values are significant at $P < 0.00002$ testwise significance levels except for the carabid-rest correlation which is significant at $P < 0.00008$ (50,000 randomizations). Taxa are ordered by descending Pearson correlation coefficient (an, ants; bi, birds; br, bryophytes; ca, carabids; ga, gastropods; or, orthopterans; sp, spiders; va, vascular plants).

Table 1
Cross-taxon species richness correlations[a] expressed as Pearson correlation coefficients (50,000 randomizations)[b]

Taxa	Bryophytes	Vasc. Plants	Gastropods	Spiders	Orthopterans	Carabid Beetles	Ants	Birds
Bryophytes	1	0.76***	0.78***	0.39	0.56*	0.27	0.59**	0.64***
Vasc. plants		1	0.69***	0.64**	0.77***	0.50	0.74***	0.80***
Gastropods			1	0.42	0.53*	0.47	0.43	0.73***
Spiders	0.54*	0.73***	0.43	1	0.62***	0.70***	0.73***	0.71***
Orthopterans				0.65***	1	0.56*	0.67***	0.71***
Carabid beetles	0.30	0.57**	0.41	0.70**	0.54**	1	0.47	0.58***
Ants				0.80***		0.58**	1	0.70***
Birds				0.69***		0.72***		1

[a] Results without rarefaction above diagonal, results with rarefaction of spiders and carabids below diagonal.
[b] Bonferroni-adjusted testwise error: *$P < 0.05/77$ ($= 0.00065$); **$P < 0.01/77$ ($= 0.00013$); ***$P < 0.00002$ (smallest error resolution with 50,000 randomizations).

advocated here because of its speed of calculation, its simplicity and the fact that the outcome closely approximates an optimal solution (Csuti et al., 1997).

The greedy algorithm starts with the sampling site containing the most species and sequentially selects sites based on the degree to which they add unrepresented species to the whole selection (Vane-Wright et al., 1991; Kershaw et al., 1994). Thus, for every taxon, a minimum set of sampling sites representing all species at least once is generated. If all species of the potential surrogate taxon are represented (e.g. 23 sites are needed to represent all bryophytes, 11 sites for orthopterans, and 36 sites for vascular plants), the remaining sampling sites were ordered according to declining species richness of the potential surrogate taxon. The pooled richness of the other taxa was ordered in the respective
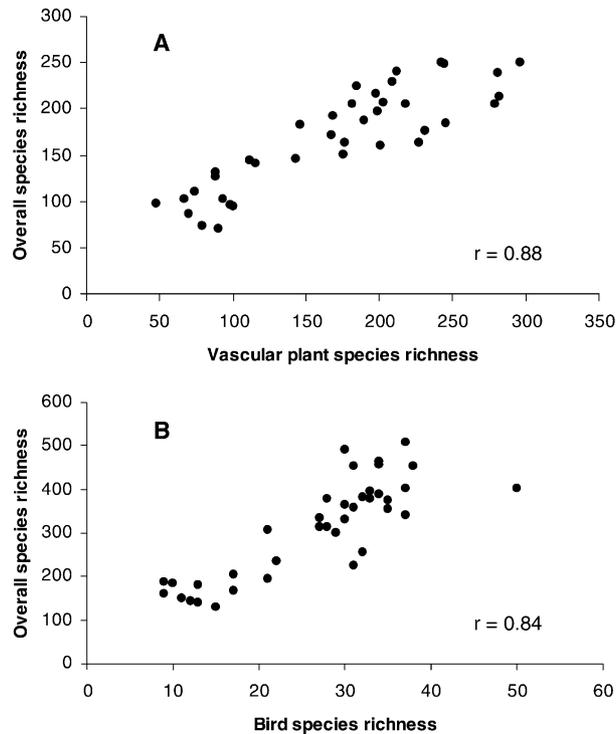

Fig. 3. (A) Scatterplot of overall species richness (total species richness minus species richness of vascular plants) plotted against the number of vascular plants; $n = 38$, $P < 0.001$. (B) Scatterplot of overall species richness (total species richness minus species richness of birds) plotted against the number of birds; $n = 38$, $P < 0.001$.
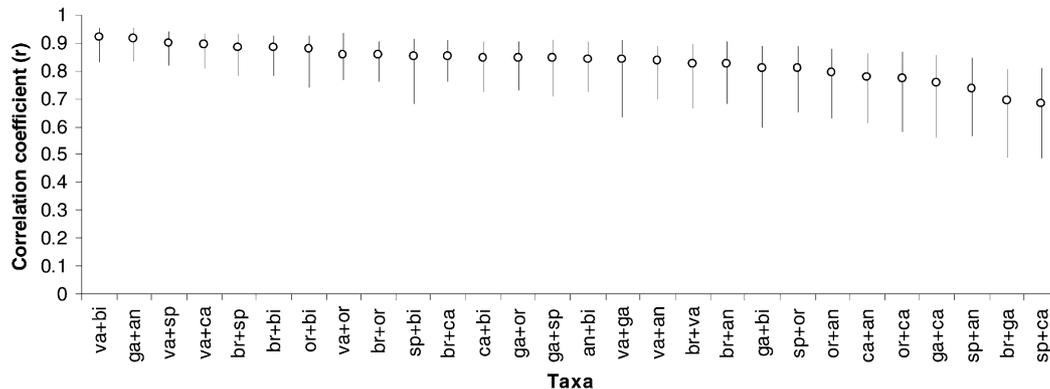

Fig. 4. Multi-taxa approach: Ability of a combination of two taxa to act as biodiversity surrogate for overall species richness (total species richness minus species richness of the predicting taxa). Ninety-five percent confidence intervals of correlation coefficients (accelerated bias-corrected percentile limits) are shown. All values are significant at $P < 0.00002$ testwise significance levels (50,000 randomizations). Taxa combinations are ordered by descending Pearson correlation coefficient. Abbreviations as in Fig. 2.

site sequence of the potential surrogate taxon and was plotted against a random selection of sampling sites (1000 simulations without replacement).

3. Results

In total we found 1871 species: 215 bryophytes, 960 vascular plants, 96 gastropods, 215 spiders, 46 orthopterans, 181 carabid beetles, 40 ants and 118 birds.

3.1. Pairwise correlations

Without rarefaction, 21 out of 28 correlations between the species richness of individual groups were both significant and positive (Table 1). High cross-taxon congruence ($r > 0.7$) existed between vascular plants and four other taxa (birds, orthopterans, bryophytes and ants), between birds and three additional taxa (gastropods, spiders and orthopterans), between bryophytes and gastropods, and between spiders and ants. In contrast, the most idiosyncratic taxa were the carabid beetles and to a lesser degree the gastropods. With rarefaction, three more correlations were significant (vascular plants and carabids, spiders and bryophytes, carabids and ants).

3.2. Overall species richness

Each taxon was significantly correlated with the combined species richness of all other groups (Fig. 2). Vascular plants and birds showed the highest correlations with overall species richness ($r = 0.89$ and 0.87, respectively), followed by orthopterans, ants, bryophytes, gastropods and spiders ($r = 0.76$ to 0.71). Only carabid beetles showed a comparably weak relationship with the overall species richness ($r = 0.58$). When species numbers were not adjusted, the magnitude of correlations of vascular plants and birds with overall richness changed only marginally (Fig. 3).

3.3. Multi-taxa approach

All 28 combinations of two taxa as surrogates for the remaining groups were significant at the $P < 0.00002$ testwise significance level (Fig. 4). "Shopping baskets" of vascular plants + birds or gastropods + ants were most highly correlated with the pooled species richness of the other six taxa (both $r = 0.92$). Only two combinations (bryophytes plus gastropods and spiders plus carabids) were comparatively weakly correlated ($r = 0.69$ and 0.68, respectively).

3.4. Complementarity

Complementarity-based site sets of six taxa (vascular plants, gastropods, spiders, orthopterans, carabid beetles and birds) were more effective throughout the selection procedure in representing overall species richness than sets selected at random (Fig. 5). Bryophytes gave a better result than random after taking four samples and ants after 10 samples (Fig. 5).

4. Discussion

4.1. Pairwise correlations

Our results suggest that the use of surrogate groups at the landscape scale is a workable concept for biodiversity assessment in agricultural landscapes. This contradicts some of the published opinion on the usefulness of surrogate taxa (Pimm and Lawton, 1998; Lawton and Gaston, 2001; Vessby et al., 2002). Despite the considerable quantity of studies on surrogate taxa, there is little comparable work with regard to spatial scale and habitat context.

The search for surrogate taxa reaches from scales of 0.1 m^2 study plots to > 100.000 km^2 sized quadrats - from local to continental scale. Scale is an important issue in ecology (Shmida and Wilson, 1985; Wiens, 1989; Pimm, 1991) and scale dependency is well documented for species richness patterns (Lomolino and Davis, 1997; Rahbek and Graves, 2000; Crawley and Harral, 2001; Whittaker et al., 2001). Thus, the degree of covariance of species richness patterns varies across different spatial scales (Pearson and Carroll, 1999).

We may have chosen an optimal spatial scale ($\sim$36 ha) to detect species richness correlations in these kinds of agricultural landscapes. One sampling site is about twice the size of an average Austrian farm and is shaped by different farming styles (Zechmeister et al., 2003). A substantial part and variety of different typical landscape elements could be found in each site. Hedgerows, field margins, roadsides, small channels, remnant woods and grasslands are nested with varying quantity and quality in a field, field-meadow or meadow matrix. Thus our study appears to be unique in that it examined a wide range of taxa, and used a landscape-scale approach that incorporates a considerable variety of different habitats. Studies performed at a comparable scale (>1 ha to 1000 ha) are scarce and mostly constrained to single habitats. Vessby et al. (2002) and Panzer and Schwartz (1998) worked in grasslands, Howard et al. (1998) in tropical forests. Murphy and Wilcox (1986) detected positive correlations between butterflies, birds and vascular plants in canyons with multiple habitats, but the species–area effect was not evened out, as in our case.

4.2. Overall species richness

Our findings are in broad accordance with the few studies that have tested the use of individual taxa as
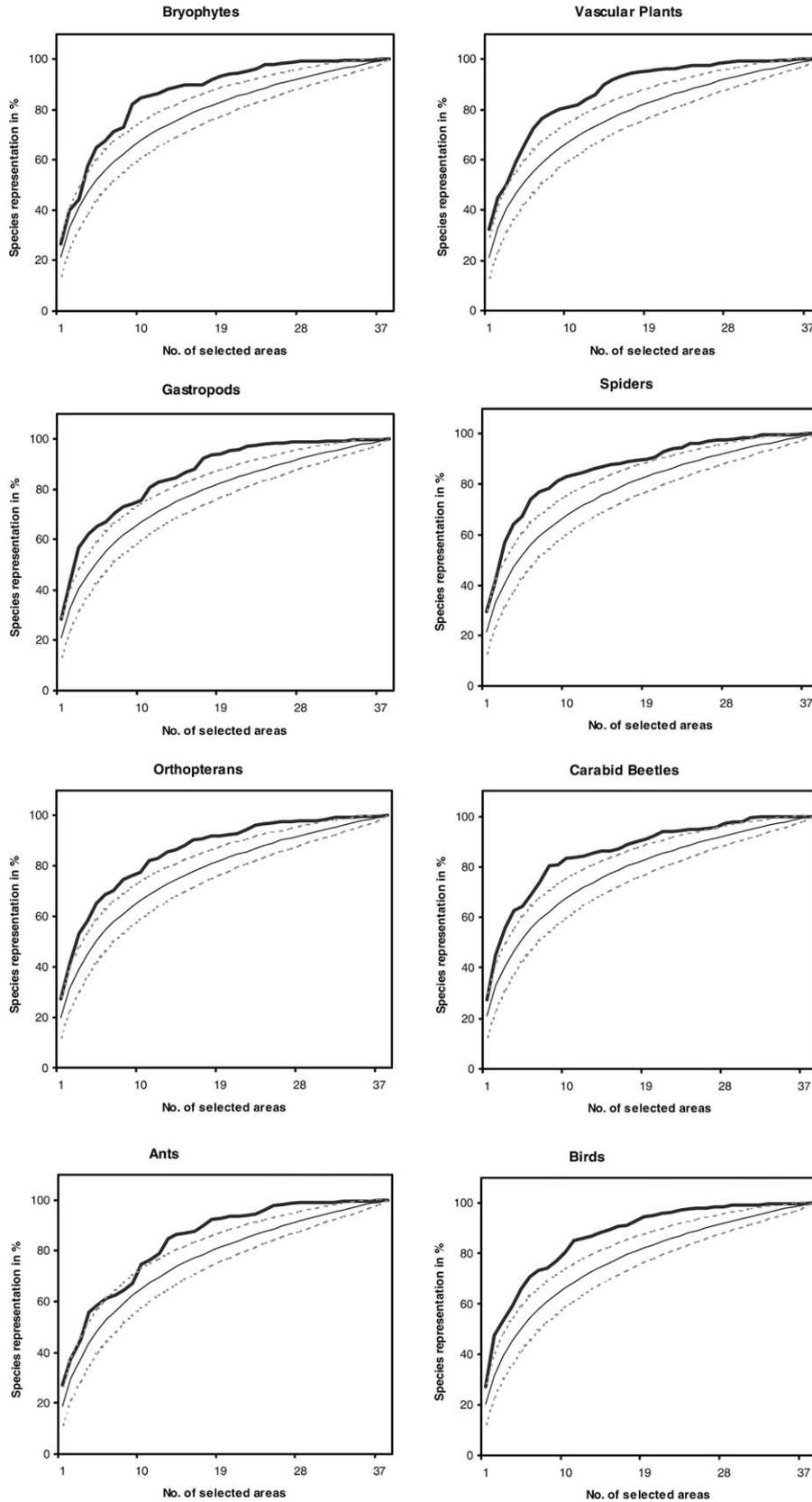
Fig. 5. Cumulative representation of species when sampling sites are selected using the greedy algorithm. Bold solid lines represent the effectiveness of the surrogate taxon in representing the pooled species richness of the other taxa; thin solid lines are the corresponding random selection with confidence limits (dotted lines).

indicators for overall species richness. Only the work of Duelli and Obrist (1998) is somewhat comparable to our study. They searched for the best correlates within a dataset of more than 20 different taxa (mainly insects) in an agricultural landscape and detected high positive correlations between several taxa (e.g. Hymenoptera, vascular plants) and overall species richness. As in our study, they found that the carabid beetles correlated weakly with total species number. Our best performing groups, birds and vascular plants, have often been suggested as useful indicator taxa for overall species richness, but few studies exist at a comparable scale (Panzer and Schwartz, 1998).

Ricketts et al. (1999) tested the utility of nine taxonomic groups as indicator taxa at the continental scale (North America north of Mexico) with existing distribution data. They constructed an overall richness index and found that every investigated taxon is strongly correlated with this index. In a marine ecosystem, Gladstone (2002) found a significant relationship between the richness of molluscs and the richness of all investigated taxa.

4.3. Multi-taxa approach

In a multi-taxa approach the best results were achieved with combinations of taxa with widely differing ecofunctional characters (e.g. gastropods and ants), possibly because they cover an array of organism responses to landscape scale characteristics. Whereas the multi-taxa approach has been frequently recommended (Vane-Wright et al., 1991), it has rarely been applied (Kotze and Samways, 1999; Ricketts et al., 1999). This approach requires a better theoretical and empirical basis and needs to be evaluated in different landscapes and with different groups of organisms (Allen et al., 2001).

4.4. Complementarity

We showed that minimum sets of complementary areas based on six of the eight taxa represent significantly more species than areas selected at random. This is true also for taxa such as carabid beetles that show weak relationships with the overall species richness in the other analyses. It means, in our case, that every group (except bryophytes and ants at the first selection steps) can be used as surrogates in priority area selection when using a simple complementarity algorithm. The efficiency of complementarity-derived minimum area sets has repeatedly been demonstrated (Howard et al., 1998; Reyers et al., 2000; Lund and Rahbek, 2002; Sætersdal et al., in press) and our results provide additional support for that approach.

4.5. Possible causes for the strength of the detected correlations

Greater agricultural disturbance leads most often to landscape simplification and decreasing species richness (Zechmeister and Moser, 2001; Moser et al., 2002). In highly modified landscapes, the impact of agricultural disturbance is thus probably superimposed upon idiosyncratic preference patterns of different taxa (Dobson et al., 1997; Blair, 1999). However, some of our investigated taxa respond more negatively to increasing disturbance (gastropods, bryophytes), than others (carabid beetles, spiders) (Zulka et al., unpublished).

An important, but often undervalued aspect is, how the sampling scheme affects correlation patterns. While in our study all taxa were assessed during a comparably short time span at identical sites, other studies used data that were not originally designed to obtain cross-taxon congruence data (Reyers and van Jaarsveld, 2000) and thus were not as stringently matched as ours. Data from published distribution maps or unpublished collections are strongly influenced by recording bias (Conroy and Noon, 1996; Dennis et al., 1999). Sometimes hotspot-maps for species richness are little more than the main centres of activity of the observers and collectors (Funk and Richardson, 2002).

4.6. Conservation aspects

We conclude that the use of biodiversity surrogate taxa at the landscape scale is of considerable value in agricultural landscapes without special conservation designation that form large part of Europe and other temperate regions. Species richness of vascular plants and birds proved to be especially efficient short-cuts for covering overall species richness. For both groups, the sampling protocols are well known and identification is reliable in Europe. The utility of both taxa as a first coarse-filter surrogate for other organism groups has been argued (Bibby et al., 1992b; Panzer and Schwartz, 1998) and a recent study has highlighted the use of vascular plants as a surrogate species group in small scale site selection in forests (Sætersdal et al., in press).

In a typical central European landscape, biodiversity must be managed in multiple-use areas, mostly dominated by agriculture. The main conservation goal in these landscapes must be the general maintenance and restoration of biodiversity. The re-organisation of the "Common Agricultural Policy" of the European Union (nearly half of the European Union's budget is spent on agricultural subsidies!) towards more environmentally friendly agriculture has led to the development of agro-environment schemes in many European countries. These schemes need to be assessed to ensure that the money is effectively spent (Bignal, 1998; Kleijn et al., 2001; Zechmeister et al., 2003). So, what is required is

not only a "wise use" of landscapes (Davis, 1993) but also a "wise use" of financial incentives. Given that we have demonstrated that there are possible short-cuts to assess biodiversity in these landscapes, the first step for the development of reliable indicators can thus be taken. Further studies need to test whether our results are region-specific or whether they are of generic nature with regard to agricultural landscapes and different taxa.

Finally, biodiversity monitoring schemes are being developed in some countries (Delbaere, 2002; Hintermann et al., 2002). Our results can support such attempts because the existence of strong positive correlations of a surrogate taxon with overall diversity is a prerequisite for the development of useful biodiversity indicators for monitoring programmes. The political will to establish such programmes will increase if scientists can develop reliable and cost-efficient short-cut measures for biodiversity assessment.

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