

Original Articles

A framework to identify indicator species for ecosystem services in agricultural landscapes



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ABSTRACT

Improving our understanding of the relationships between biodiversity and the delivery of ecosystem services is crucial for the development of sustainable agriculture. We introduce a novel framework that is based on the identification of indicator species for single or multiple ecosystem services across taxonomic groups based on indicator species analyses. We utilize multi-species community data (unlike previous single species approaches) without giving up information about the identity of species in our framework (unlike previous species richness approaches). We compiled a comprehensive community dataset including abundances of 683 invertebrate, vertebrate and plant species to identify indicator species that were either positively or negatively related to biological control, diversity of red-listed species or crop yield in agricultural landscapes in southern Sweden. Our results demonstrate that some taxonomic groups include significantly higher percentages of indicator species for these ecosystem services. Spider communities for example included a higher percentage of significant positive indicator species for biological control than ground or rove beetle communities. Bundles of indicator species for the analysed ecosystem service potentials usually included species that could be linked to the respective ecosystem service based on their functional role in local communities. Several of these species are conspicuous enough to be monitored by trained amateurs and could be used in bundles that are either crucial for the provision of individual ecosystem services or indicate agricultural landscapes with high value for red-listed species or crop yields. The use of bundles of characteristic indicator species for the simultaneous assessment of ecosystem services may reduce the amount of labour, time and cost in future assessments. In addition, future analysis using our framework in other ecosystems or with other subsets of ecosystem services and taxonomic groups will improve our understanding of service-providing species in local communities. In any case, expert knowledge is needed to select species from the identified subsets of significant indicator species and these species should be validated by existing data or additional sampling prior to being used for ecosystem service monitoring.

1. Introduction

Intensified use of mineral fertilisers, pesticides and fossil fuels in agriculture to meet increasing demands for food and fibre undermines the sustainability of agriculture by harming biodiversity-based

Ecosystem Services (ES) (Power, 2010). A proposed solution to this dilemma is ecological intensification of agricultural production, i.e. increasing yield by promoting biodiversity-based ES (Doré et al., 2011). Understanding the relationship between biodiversity and ES is therefore crucial for the development of sustainable agriculture (Duru et al.,

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Table 1
Major characteristics for ecosystem service potentials and biotic communities that were analysed in this study.

	Unit	Scale	Range	Study landscapes	References
<i>a) ES potentials</i>					
Biological control potential	aphid biocontrol index	Field	0.12–0.86	31	Rusch et al. (2013)
Red-list biodiversity potential	weighted # red-listed species	Both	4–12	23	This study
Yield potential	t/ha ^a	Field	2.80–8.20	40	This study
<i>b) Biotic communities</i>					
Spiders (Araneae)	NA	Field	NA	41	Rusch et al. (2014)
Ground beetles (Carabidae)	NA	Field	NA	41	Rusch et al. (2014)
Rove beetles (Staphylinidae)	NA	Field	NA	41	Rusch et al. (2014)
Hoverflies (Syrphidae)	NA	Farm	NA	41	Jönsson et al. (2015)
Birds (Aves)	NA	Farm	NA	24	This study
Plants (Tracheophyta)	NA	Farm	NA	39	Rader et al. (2014)

* Yield values were corrected for differences in farming systems by using residuals after fitting farming system (conventional or organic) to yield quantities in t ha⁻¹ (Birkhofer et al., 2016).

2015). Although species richness can be a predictor for the levels of some ES (Balvanera et al., 2006; Harrison et al., 2014; Tilman et al., 2014), these relationships are not always strong (Lyashevskaya and Farnsworth, 2012; Gagic et al., 2015). Instead, ES are in many cases provided by abundant and functionally important species (Winfrey et al., 2015) that indicate the provision of ES (Bastian, 2013). Considering the relationship between individual species and their abundances in local communities on one side, and ES levels on the other, might therefore facilitate the management of ES through species conservation and may provide better predictions of ES levels (Mokany et al., 2008).

Indicator species analysis was originally developed to identify species that indicate different environmental conditions and anthropogenic stress levels in local habitats (Dufrière and Legendre, 1997; Baker and King, 2010; Siddig et al., 2016). Ground beetles, for example, have been used as bio-indicators for environmental gradients (Rainio and Niemelä, 2003) and arable weed species can act as indicators of overall biodiversity in agroecosystems (Albrecht, 2003). There is a growing awareness that only multi-taxon studies allow us to address the complex relationships between community changes and related functions (Allan et al., 2014). From an ecosystem service perspective, multi-taxon bundles would consist of species that are positively or negatively related to levels ES potentials (“potential” defined as the ability of landscapes to deliver an ES) (Haines-Young et al., 2012). Such approaches could also contribute to the identification of landscapes with a high overall potential for multifunctionality (sensu “ecosystem service multifunctionality” in Manning et al., 2018; e.g. Birkhofer et al., 2018) by monitoring bundles of species that act as indicators for sets of multiple ES. Previous studies addressed the indicator-based assessment of ES potentials by monitoring single species (species approach, Luck et al., 2003) or species richness patterns in local communities (species richness approach, Cardinale et al., 2012). There is, however, no empirical knowledge on how bundles of individual species across taxonomic groups can be utilized to indicate levels of ES (Harrison et al., 2014). In addition, our framework allows for the simultaneous analysis of all species in local communities (with the exception of very rare species) which reflects the fact that species are not independent entities in local communities, but instead interact with each other.

Here, we introduce a novel framework to identify indicator species from communities across taxa for a) predaceous arthropod taxa (Araenae, Carabidae and Staphylinidae) and levels of aphid biological control and for b) a large range of taxonomic groups (Araenae, Carabidae, Staphylinidae, Syrphidae, Aves and plants) and levels of overall biodiversity and yield potential in agricultural landscapes. The first analysis is motivated by the fact that communities of generalist predators contribute to biological control services (Symondson et al., 2002). This approach therefore holds particular potential for the future improvement of biological control strategies through conservation

practices that target bundles of predator species. The second set of analyses is motivated by previous results that suggest that species in communities of individual taxa can act as indicators for biodiversity or yield (Wolters et al., 2006; Ekroos et al., 2013). This approach holds particular potential for the future assessment of biodiversity and yield potentials by monitoring a selected range of species that could be simultaneously utilized as indicators for overall biodiversity and yield in agricultural landscapes.

For the indicator analyses, we used a comprehensive community dataset of 683 invertebrate, vertebrate and plant species and altered the traditional concept (assessing indicators of changing environmental conditions) to a novel framework (assessing indicators of high or low ES levels). We hypothesize that the identified positive indicator species in the predator species vs. biological control analysis (a) can be causally linked to aphid biological control. We further hypothesize that indicator species in the second set of analyses (multi-taxon species list vs. biodiversity of red-listed species and crop yield) (b) are characteristic for agricultural landscapes with different levels of trade-offs between biodiversity and yield. In addition, our multi-taxon analyses highlight the suitability of individual taxonomic groups as indicators for different ES. Identifying multi-species indicator bundles for ES fills important knowledge gaps as it will help to improve our understanding of the linkage between biodiversity and ES (Maes et al., 2016). The proposed framework can be utilized in future studies focusing on community data to identify service-providing species or to utilize sets of species as simultaneous indicators of levels of ES in agricultural landscapes.

2. Material and methods

2.1. Study sites

Communities and ES potentials (Table 1) were quantified within 1 km radius landscapes centred around 41 farms in the province of Scania in southern Sweden in spring and summer 2011 (Fig. 1; hereafter referred to as “study landscapes”). This scale was chosen to facilitate the selection of study landscapes because several of the studied taxonomic groups are known to relate to landscape characteristics at this scale (e.g. beetles & spiders: Rusch et al., 2014, plants: Rader et al., 2014). This study only used landscapes with farms that cultivated spring barley (*Hordeum vulgare* L.). Barley is a common crop in agricultural production areas of Scania and therefore allows for selection of non-overlapping radii and a wide distribution of study landscapes in Scania. The majority of barley fields in the study landscapes was ploughed or treated with a cultivator (31 out of 41), but only about half of the fields were treated with herbicides (21). Note that plant communities were not assessed inside barley fields, but in field margins in this study. The selection of landscapes with a focus on barley production across Southern Sweden allows for some generalizations regarding

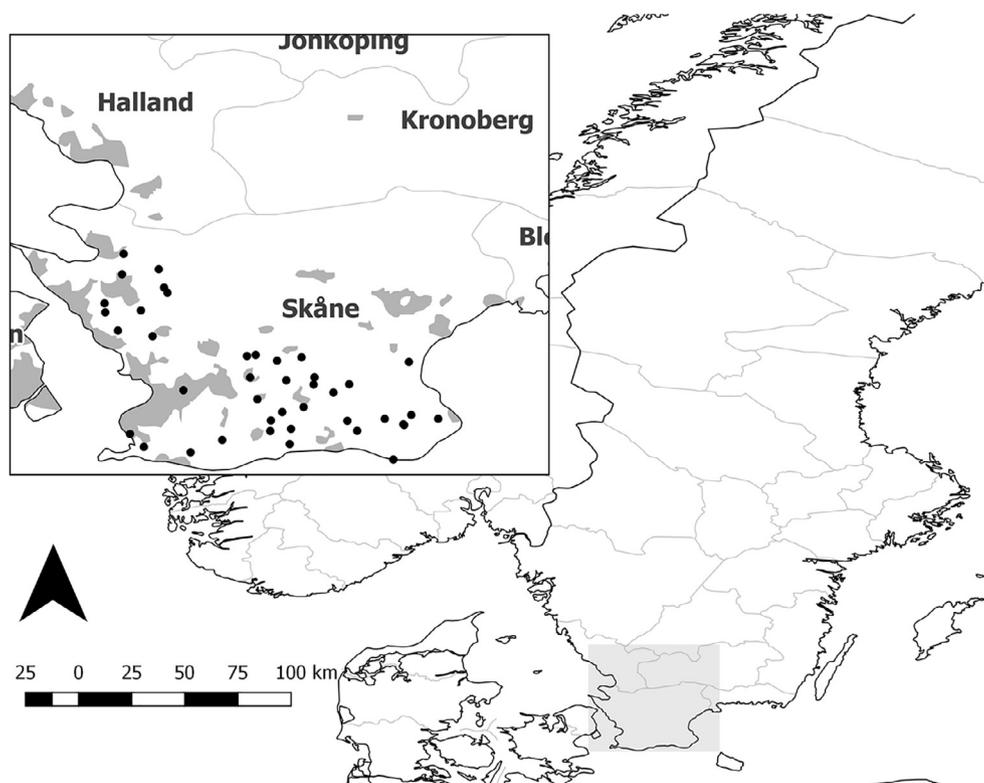


Fig. 1. Map of Sweden with the detailed map (top left corner) marked as grey box. Study landscapes are marked in the detailed map (●), grey areas in the detailed map represent urban areas.

relationships between biodiversity and ES provision across larger areas. However, other crop systems (e.g. oilseed crops) may not share the observed relationships. For each landscape, the centre was the midpoint of a field that the farmers had defined as their farming centre, i.e. typically close to the farmstead. Taxonomic groups and ES were studied at scales and locations in these landscapes based on results of previous studies and practical constraints (Ekroos et al., 2016; Birkhofer et al., 2018). Some taxonomic groups and ES potentials were sampled within a focal spring barley field in each landscape (field scale, Table 1) whereas others were sampled in replicated locations within the 1 km landscape radius (farm scale, Table 1). The map of study locations was created in QGIS 2.14.22 using free vector and raster map data @ naturalearthdata.com.

2.2. Taxonomic groups

Taxonomic groups included 266 invertebrate (spiders, ground beetles, rove beetles, and hoverflies), 95 vertebrate (birds) and 322 plant species that reflect major trophic groups (predators, herbivores, autotrophs).

Spiders (Araneae), ground beetles (Carabidae) and rove beetles (Staphylinidae) were sampled in a 20 × 100 m area located at the edge of a spring barley field in each study landscape that was not treated with insecticides. Three pitfall traps (diameter 12 cm; depth 12 cm) were placed in this area with 10 m distance from each other and the field edge. Pitfall traps were kept open for two periods of 7 days that coincide with periods of populations build-up in cereal aphids (first period: from 30 May to 10 June; second period: from 20 June to 1 July). All collected specimen were stored in 70% ethanol and samples from both periods were pooled prior to further analyses (see Rusch et al. (2014) for more details).

Birds were surveyed using standard point counts. A grid of 16 points (4 × 4, 400 m apart) was centred to each study landscape and numbered row wise from west to east, starting with the southernmost row.

Points with odd numbers were moved to the closest field border. At each survey point, the identity and location of all birds observed during 5 min were recorded on orthophoto maps (scale 1:2500). Two visits (approx. 2 weeks apart) were made to each landscape within the period 11 May to 14 June under appropriate weather conditions (no strong winds or heavy rain). Based on expert opinion on reasonable observation distances for most species, only observations made within 150 m from the observation point were included. Bird counts in the present analysis were summarized for each landscape as the mean over visits of the mean over survey points.

The presence of all vascular plant species was recorded within field margins in each landscape. Border points numbered 3, 5, 7, 9, 11 and 15 from the grid for the bird surveys were used for plant surveys conducted between 1 June and 31 August along 100 m transects at each survey point. Plant species identity and frequency were recorded within six 1 × 1 m quadrats spaced equally along each transect (see Rader et al. (2014) for more details).

2.3. Ecosystem service potentials

Ecosystem service potentials provide proxy values for the provision of biological control, biodiversity of red-listed species and yield ES (Table 1).

Biological control potential of cereal aphids that are crop pests was quantified using an exclusion experiment in a spring barley field in each landscape during the milk ripening stage (between 18 and 27 July). Four replicated pairs of two treatments were established along a transect in the middle of each insecticide-free strip (see sampling of spiders and beetles): (i) an open treatment where all natural enemies had access to the prey and (ii) a cage treatment where all ground-dwelling and flying natural enemies were excluded (mesh size: 0.5 cm; diameter: 0.3 m, height: 1 m and covered with a sticky glue). For each pair, the two treatment plots were randomly allocated along the transect and separated by 2 m. Pairs were separated by 5 m. Twenty-

four late instar bird cherry-oat aphids (*Rhopalosiphum padi*, L.) distributed on eight barley plants in pots were introduced in each replicate. The number of remaining aphids was counted after 5 days. For each field, suppression of aphids due to natural enemies was quantified as the average proportion of aphids observed in the open treatment in relation to aphid numbers in the cage treatment and values were standardized to a maximum value of 1 (see Rusch et al. (2013) for more details).

The biodiversity potential for red-listed species of a landscape was defined based on the number of red-listed species across all sampled taxonomic groups in each landscape, weighted by the respective IUCN category in the Swedish national red list (ArtDatabanken, 2015), multipliers for species: near threatened \times 1 (8 species); vulnerable \times 2 (9 species); endangered \times 3 (1 species); regionally extinct \times 4 (1 species). The resulting index ranged from 0 (no red-listed species in the landscape) to a maximum observed value of 12. This index characterizes the biodiversity value of each study landscape based on the number of red-listed species and the category of threat to each species. Data included two ground beetle, eight plant and nine bird species on the Swedish red list. Note that red-lists exist in Sweden for all taxonomic groups in this study, but that no red-listed spider, rove beetle or hoverfly species were observed.

For crop yield potential, 40 out of 41 participating farmers responded to a questionnaire asking to provide quantitative data on barley yields for their fields. The dataset includes conventionally and organically managed barley fields; yields were only used after partialling out the effect of farming system for all indicator analyses (residuals of crop yield were used in all consecutive analyses, e.g. Birkhofer et al., 2016).

2.4. Statistical analysis

Indicator species analysis has traditionally been used to identify species that are characteristics for specific environmental conditions. Here we alter this framework to identify indicator species for particularly low or high levels of ES potentials. Threshold indicator analysis (TITAN, Baker and King, 2010) was used to calculate indicator values (IndVal) for each species in local communities. We related species from a) Araneae, Carabidae and Staphylinidae communities to biological control indices and b) species ($N = 31$ independent landscapes) from all taxonomic groups to biodiversity of red-listed species ($N = 23$ landscapes) and yield potentials ($N = 40$ landscapes, with the exception of $N = 23$ landscapes for birds and $N = 39$ landscapes for plants). Indicator values for individual species from these analyses range from 0 (no indication) to 1 (maximum indication) and describe each species' quality as an indicator of individual ES potentials. TITAN calculates indicator values for species in a local community at all values along a continuous gradient of ES values. Indicator species were then selected in this study based on the significance of the IndVal assessed by permutation tests ($P < 0.05$ for significant indicator species, $P < 0.01$ for significant high potential indicator species). This classification of two indicator species groups based on P-value is justified as a lower P-value from permutation tests suggests that the IndVal of a particular species deviates even more frequently from the results of permutations and therefore is an even more reliable indicator species.

Positive indicator species have a positive relationship to an ES potential (e.g. Fig. 2c), negative indicator species have a negative relationship to an ES potential (e.g. Fig. 2d). Species that were observed in four or fewer landscapes were excluded from indicator analyses (375 species) as rare species generally cannot be used as indicators. All species data was $\log(x + 1)$ -transformed prior to indicator analyses to reduce the role of outliers as recommended (Baker and King, 2010). Indicator analyses were performed in R using the code provided by Baker and King (2010). Chi-squared tests for 2×2 contingency tables were used to test if the percentage of positive and negative indicator species for biological control, biodiversity and yield potentials within

each taxonomic group differed from the number of indicator species in all other taxonomic groups (Bortz, 2000, all tests $df = 1$). P-values for these tests were adjusted for multiple testing by applying Bonferroni corrections. Bundles of indicator species across taxa were identified by TITAN as those species that were significant indicators for both ES (biodiversity and yield potential). This subset of species was then plotted in a two-dimensional scatterplot showing z-score for biodiversity (axis 1) and yield (axis 2) potential and species in the same quadrant of this scatterplot then formed a bundle.

3. Results

3.1. Indicators of ES

Among the analysed communities of predaceous arthropod taxa, 8 Araneae (32% of all analysed Araneae species), 2 Carabidae (7%) and 4 Staphylinidae (17%) species were significant positive indicators for aphid biological control (IndVal $P < 0.05$; Fig. 3a). Only 1 Araneae (4%), 4 Carabidae (15%) and 3 Staphylinidae (13%) species were significant negative indicators of aphid biological control. The percentage of significant positive and negative indicator species for aphid biological control differed significantly between Araneae and Carabidae and between Araneae and Staphylinidae, but not between Carabidae and Staphylinidae (Fig. 4a; at a Bonferroni-corrected $\alpha = 0.017$).

Significant positive indicators for the red-list biodiversity potential of agricultural landscapes included 2 Araneae (10%), 2 Carabidae (10%), 7 Staphylinidae (33%), 0 Syrphidae (0%), 7 Aves (11%) and 8 plant (8%) species (Fig. 3b). Significant negative indicators for this ES potential included 4 Araneae (20%), 0 Carabidae (0%), 0 Staphylinidae (0%), 1 Syrphidae (10%), 7 Aves (11%) and 5 plant (5%) species. The percentage of significant positive and negative indicator species for the red-list biodiversity potential differed significantly between Araneae and Carabidae, Araneae and Staphylinidae, Syrphidae and Carabidae, Syrphidae and Staphylinidae, Syrphidae and plants, Staphylinidae and Aves and between Staphylinidae and plants, but not between other pairs (Fig. 4b; at a Bonferroni-corrected $\alpha = 0.003$).

Significant positive indicators for the yield potential of agricultural landscapes included 6 Araneae (19%), 6 Carabidae (19%), 1 Staphylinidae (4%), 1 Syrphidae (9%), 5 Aves (8%) and 29 plant (21%) species (Fig. 3c). Significant negative indicators for this ES potential included 4 Araneae (13%), 7 Carabidae (23%), 3 Staphylinidae (13%), 6 Syrphidae (55%), 12 Aves (19%) and 23 plant (16%) species. The percentage of significant positive and negative indicator species for the crop yield potential differed significantly between Syrphidae and Araneae, Syrphidae and Carabidae and between Syrphidae and plants, but not between other pairs (Fig. 4c; at a Bonferroni-corrected $\alpha = 0.003$).

The bundle of significant positive high potential indicator species for biological control (IndVal $P < 0.01$) included *Drassyllus pussillus*, *Pachygnatha degeeri* (both Araneae) and *Philonthus cognatus* (Fig. 2a; Staphylinidae). High potential indicator species for low biological control values were *Robertus lividus* (Araneae) and *Aleochara bipustulata* (Staphylinidae, Fig. 2b).

High potential indicator species for landscapes with high red-list biodiversity potential were *Agyreta rurestris*, *Oedothorax fuscus* (both Araneae), *Anotylus tetracarlinatus*, *Tachyporus chrysomelinus* (both Staphylinidae), *Motacilla flava*, *Numenius arquata*, *Pica pica* (all Aves, Fig. 2c) and *Agrostis gigantea* (plants). High potential indicator species for landscape with low red-list biodiversity potential were *Melanostoma mellinum* (Syrphidae), *Phasianus colchicus* (Aves, Fig. 2d), *Prunus spinosa* and *Convolvulus arvensis* (both plants).

The bundle of high potential indicator species for landscapes with high yield potential included *Pardosa amentata* (Araneae), *Bembidion obtusum*, *Pterostichus melanarius* (both Carabidae), *Passer montanus*, *Sylvia curruca* (both Aves), *Heracleum sphondylium*, *Lapsana communis*, *Fraxinus excelsior*, *Fumaria officinalis*, *Persicaria lapathifolia* and *Prunus avium* (all plants, Fig. 2e). High potential indicator species for

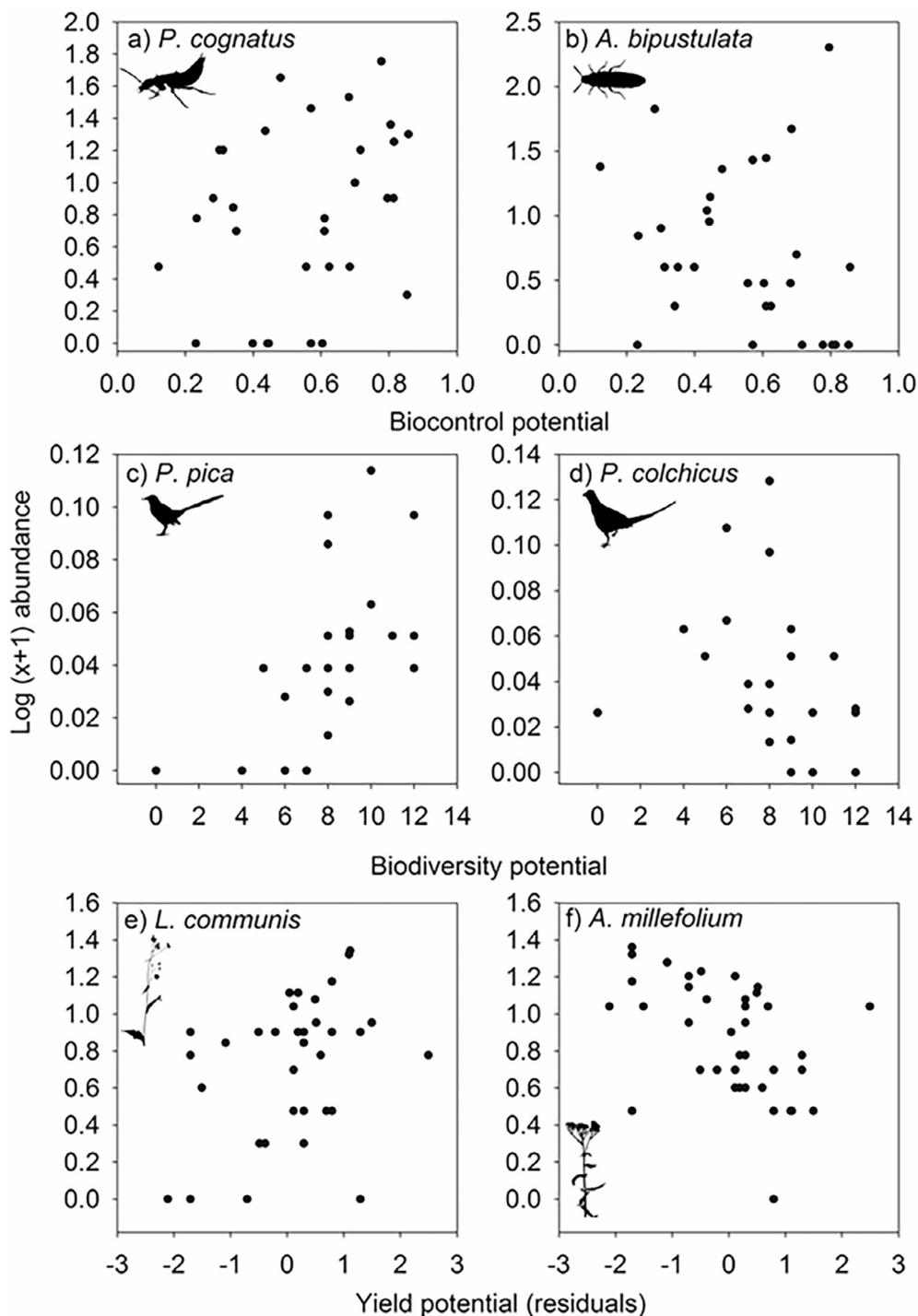


Fig. 2. Examples for significant positive (a, c & e) and negative (b, d & f) indicator species for biological control (a & b, Staphylinidae), red-list biodiversity (c & d, Aves) and yield (e & f, plants) potentials according to threshold indicator analysis (Baker and King, 2010). Plotted is the log (x + 1)-transformed abundance of each species against the ES potential for which the species was identified as significant indicator species.

landscapes with low yield potential were *Oedothorax agrestis* (Araneae), *Amischa analis* (Staphylinidae), *Sphaerophoria scripta* (Syrphidae), *Erithacus rubecula*, *Ficedula hypoleuca*, *Parus palustris* (all Aves), *Achillea millefolium*, *Artemisia vulgaris*, *Dactylis glomerata*, *Hypericum maculatum*, *Medicago falcata*, *Rumex acetosa*, *Stellaria graminea* and *Trifolium medium* (all plants, Fig. 2f).

3.2. Cross-taxon bundles of indicators for ES

The cross-taxon bundle of significant indicator species (IndVal

$P < 0.05$) for landscapes with high yield, but low red-list biodiversity potential included 1 Araneae (*Pardosa amenata*) and 1 Aves species (*Turdus philomelos*) (Fig. 5a). Two plant (*Poa trivialis* & *Euphorbia helioscopia*) and 1 bird species (*Corvus frugilegus*) were simultaneous indicators for landscapes with high biodiversity and high yield potential (Fig. 5b). One Staphylinidae (*Atheta fungi*) and 1 plant species (*Hypericum perforatum*) were indicators for landscapes with high biodiversity, but low yield potential (Fig. 5c). One Araneae (*Oedothorax agrestis*), 1 Syrphidae (*Melanostoma mellinum*), 1 Aves (*Fringilla coelebs*) and 1 plant species (*Rumex crispus*) formed the bundle that indicated landscapes

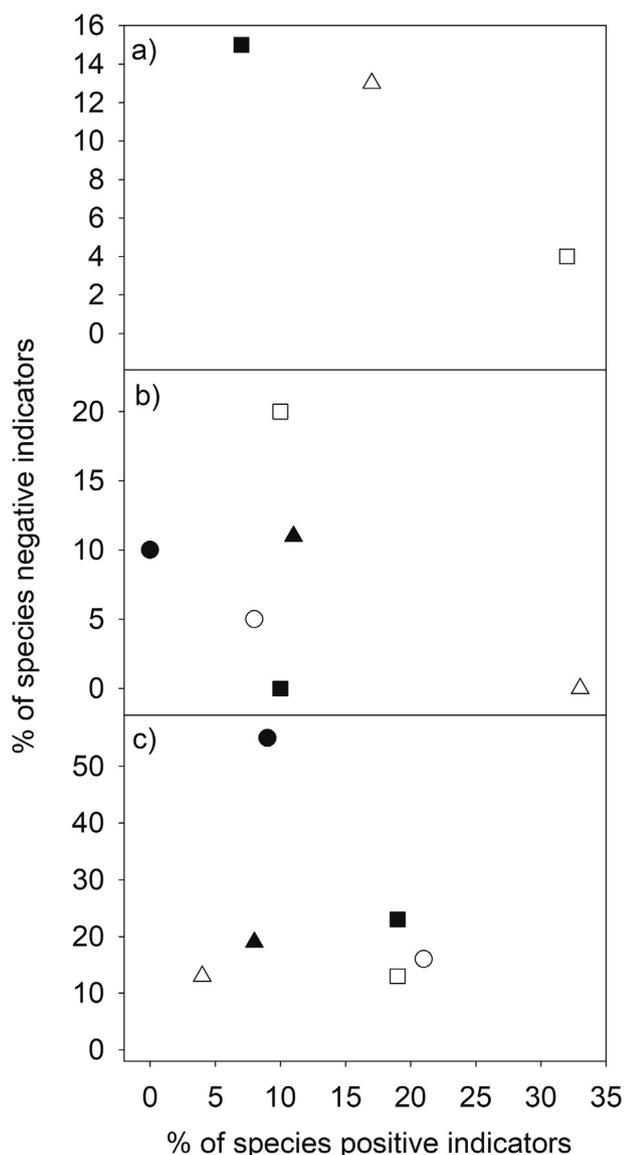


Fig. 3. Percentage of significant positive (x-axis) and negative (y-axis) indicator species according to the threshold indicator species analyses for ES potentials: a) biological control, b) red-list biodiversity and c) yield with symbols representing different taxonomic groups: Araneae (□), Carabidae (■), Staphylinidae (Δ), Syrphidae (●), Aves (▲) and plants (○).

with low red-list biodiversity and low yield potential (Fig. 5d)

4. Discussion

Our framework illustrates how indicator species for ES can be identified from community data. Previous assessments of ES potentials were based on single or few pre-selected species often within the same taxonomic group (species approach, reviewed in Luck et al., 2003), or related the overall species richness in local communities to ES potentials (species richness approach, reviewed in Cardinale et al., 2012; Stork et al., 2017). Departing from these approaches our framework is based on the identification of potential indicator species across taxonomic groups based on indicator analyses utilizing community data (unlike the species approach) without giving up information about the identity of species (unlike in the species richness approach). Our results highlight the potential of some taxonomic groups to include larger percentages of indicator species for individual ES potentials, but also suggest an added value of a multi-taxon approaches in indicator species

analyses for ES potentials. The discussion exemplifies, based on the results of our comprehensive dataset, how existing expert knowledge should be used to process the results of the proposed statistical framework.

4.1. Indicators of ES

Spider communities in our study included a higher percentage and overall number of positive indicator species for aphid biological control compared to predaceous beetle taxa. This is in line with the generally acknowledged importance of spiders for aphid biological control in cereal fields (e.g. Nyffeler, 1999; Birkhofer et al., 2016). The identified high potential indicator species *Pachygnatha degeeri* has been previously documented as a dominant aphid predator in arable fields using DNA-based gut content analysis (Harwood et al., 2005). The high potential rove beetle indicator species *Philonthus cognatus* does not actively climb up plants to feed on aphids. However, the species is a major predator of aphids on the soil surface, with single individuals consuming up to 30 aphids per day under laboratory conditions (Kollat-Palenga and Basedow, 2000). Aphids are frequently dislodged from cereal tillers (e.g. by rainfall, Von Berg et al., 2008) and then become available as prey to ground running predators like *Philonthus cognatus* or *Drassyllus pussillus*. The two negative indicator species are not known to feed on aphids. Based on the identified indicator species and their feeding ecology, we conclude that our framework can be used to identify indicators for ES across communities of different taxonomic groups that include potential ES providing units. The presented framework therefore provides a tool to actively select species with high potential for the provision of ES (e.g. biological control). Combined with a detailed understanding of species responses to agricultural management practices and their ecology and behaviour (e.g. trait-based studies), such framework will help to develop future conservation programs that aim for the provision of ES. Flower fields, as national agri-environmental scheme, for example increase the mean body size of web building spider communities compared to arable fields (Mader et al., 2017). Such differences in body size distributions in predator communities directly affect the provision of biological control services (Rusch et al., 2015).

The second set of analyses provides examples for explorative applications of our framework, by testing if species can be linked to ES without obvious assumptions about the functional role of species in a given taxonomic group. This approach is closer to the original purpose of indicator analyses, in which information about species is used as proxy for local environmental conditions (Dufrêne and Legendre, 1997). A high percentage of rove beetles acted as positive indicators for the red-list biodiversity potential of agricultural landscapes. There were no red-listed rove beetle species in our data and the observed high proportion is therefore not biased by the conservation status of rove beetles itself. Identified rove beetle indicator species included rather small and often cryptic species that are either detritivorous, fungivorous, parasitic or predaceous and often utilize habitats of decaying organic material (Clough et al., 2007, high potential indicators: *Anotylius tetracarinus*, *Tachyporus chrysomelinus*). These high potential indicator species are not well suited for practical use as indicators of ES due to the difficulties with their taxonomic identification. However, invertebrates contribute to important ES in agricultural landscapes (e.g. biological control, organic matter decomposition) and may even include the dominant ES providing species. For these sets of ES, it may be unavoidable to focus on more cryptic or taxonomically challenging species groups. If this is the case, our framework is only relevant if monitoring and identification would be more cost efficient and reliable than assessing ES directly. The high percentage of negative indicator species for the red-list biodiversity potential of agricultural landscapes among spiders is caused by four spider species that are characteristic for intensively managed agricultural habitats (called “agrobiont” species, *Oedothorax agrestis*, *Pardosa amentata*, *Pardosa prativaga*, *Pardosa pulata*; Hänggi et al., 1995; Birkhofer et al., 2013). These species are cursorial

a) Biocontrol						
	Araneae	Carabidae	Staphylinidae			
Araneae		<0.001	0.003			
Carabidae	20.19		0.076			
Staphylinidae	8.88	3.15				

b) Biodiversity						
	Araneae	Carabidae	Staphylinidae	Syrphidae	Aves	Plants
Araneae		<0.001	<0.001	0.035	0.226	0.085
Carabidae	13.33		na	<0.001	0.006	0.027
Staphylinidae	32.23	na		<0.001	<0.001	<0.001
Syrphidae	4.44	20.00	43.00		0.006	0.002
Aves	1.46	7.62	20.63	7.62		0.508
Plants	2.96	4.91	14.24	9.44	0.44	

c) Yield						
	Araneae	Carabidae	Staphylinidae	Syrphidae	Aves	Plants
Araneae		0.228	0.017	<0.001	0.022	0.826
Carabidae	1.45		0.122	<0.001	0.195	0.307
Staphylinidae	5.73	2.40		0.345	0.658	0.023
Syrphidae	21.2	12.68	0.89		0.082	<0.001
Aves	5.22	1.68	0.20	3.03		0.031
Plants	0.05	1.04	5.17	20.47	4.64	

Fig. 4. Chi² values (lower triangle) and respective P-values (upper triangle) for pairwise comparisons of the percentage of significant positive and negative indicator species for a) aphid biological control potential, b) biodiversity potential for red-listed species and c) crop yield potential between different taxonomic groups. Bold P-values indicate significant pairwise differences after Bonferroni correction for multiple testing. “na” stands for a single pairwise test which had 0% negative indicators for both taxonomic groups.

hunters and do not rely on a web to capture prey. Such hunting mode makes these species less dependent on structural complexity, as they do not require web attachment structure that is temporally stable. Such structural, persistent vegetation elements are often more common in less intensively managed arable fields or semi-natural habitats (Diehl et al., 2013).

High potential indicator species from more conspicuous taxonomic groups may be more suitable for red-list biodiversity monitoring. Bird species with preferences for humid habitats and agricultural landscapes with water bodies (*Motacilla flava*, *Numenius arquata*) and plant species that share these habitat preferences (*Agrostis gigantea*) for example, were positive high potential indicators of landscapes with high red-list

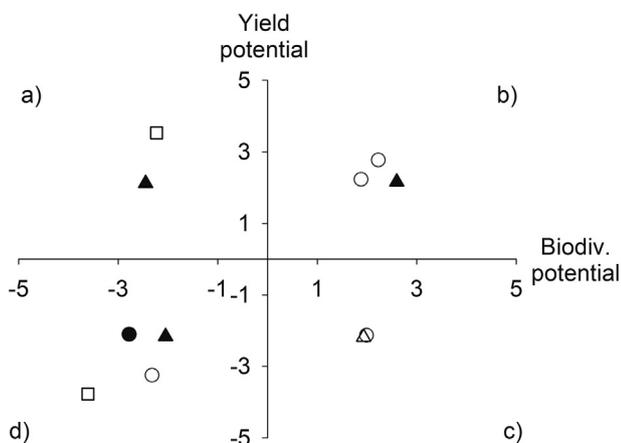


Fig. 5. Scatterplot showing the z-scores as standardized measure of the strength of positive or negative relationships between significant indicator species and yield and red-list biodiversity potential from threshold indicator analyses for Araneae (□), Staphylinidae (Δ), Syrphidae (●), Aves (▲) and plant (○) species. Negative z-scores reflect indicators for low ES values, positive z-scores reflect indicators for high ES values. Significant indicator species are named in the results section.

biodiversity potential in our study area. A joint monitoring program for these species together with species that are high potential indicators of landscapes with low red-list biodiversity potential amongst bird (*Phasianus colchicum*) and plant (*Convolvulus arvensis*) communities provides a powerful framework to assess the overall biodiversity of agricultural landscapes based on a subset of characteristic species. Monitoring agricultural landscapes for selected, conspicuous bird and plant species will save time and resources compared to monitoring for all red-listed species across the studied taxonomic groups.

All spider, ground beetle and bird species that were identified as positive indicators of yield potential are known to feed on agricultural pests (Field et al., 2008; Kromp, 1999; Laursen, 1978; Nyffeler and Benz, 1988) and include characteristic species of agricultural landscapes (e.g. Carabidae: *Pterostichus melanarius*, Aves: *Sylvia curruca*). The non-woody plant species that were positive indicators for crop yields all prefer habitats with high nutrient levels and some are common weeds in arable fields in Sweden (*Fumaria officinalis*, *Lapsana communis* and *Persicaria lapathifolia*, Rydberg and Milberg, 2000). The joint use of these positive indicator species with negative indicator species for yield potential from the same taxonomic groups (Aves: *Ficedula hypoleuca*, *Poecile palustris* as primarily forest inhabiting bird species or plants that are low abundance perennials that benefit from extensification: *Achillea millefolium*, *Artemisia vulgaris*, *Rumex acetosa* and *Stellaria graminea*, Rydberg & Milberg, 2000) provides a promising framework to estimate the yield potential of agricultural landscapes from animal community data in our study region. However, farmers assess yields of individual fields anyway so a post-harvest evaluation based on species indicators is useless. This particular approach may still have an applied value, as predictions of crop yields during the growing season based on indicator assessment may be an option. To become operational this approach would need further in-depth analyses in the future.

4.2. Cross-taxon bundles of indicators for ES

A small number of the 683 species in our study formed cross-taxon indicator bundles for both, red-list biodiversity and yield ES potentials. In terms of practical use for the simultaneous assessment of these two ES with indicator species, two bundles seem particularly promising in our study. Landscapes with high red-list biodiversity and high yield potential were indicated by higher abundances of the bird species *Corvus frugilegus* and high frequencies of the plant species *Poa trivialis*

and *Euphorbia helioscopia*. All three species are fairly common (occurrence in at least 18 landscapes per species in our study) and can be identified by amateurs with some training. The cross-taxon bundle of species that indicated landscapes with low red-list biodiversity and low yield potential included equally common and charismatic species with the bird species *Fringilla coelebs* and the plant species *Rumex crispus* (occurrence in at least 17 landscapes per species in our study). The two invertebrate species in that bundle (Araneae: *Oedothorax agrestis*; Syrphidae: *Melanostoma mellinum*) are only identifiable by trained experts. This limitation is also true for the invertebrate species in the other cross taxon bundles (Araneae: *Pardosa amentata*, Staphylinidae: *Atheta fungi*), rendering those bundles impractical for application in our study region. It is notable that in agricultural fields, crop plant communities have been intentionally assembled to provide multiple ecosystem services before (Storkey et al., 2015) and our framework may be used in this context to help designing the most efficient crop plant communities.

5. Conclusions

Our framework documents the potential of indicator analyses to identify individual, but also sets of high potential indicator species and cross-taxon bundles for ES. However, it also highlights that ecological knowledge on how to link the identified indicator species to ES and how to select species that are “easy” enough to identify as indicators is crucial to operationalize such approaches. We also emphasize that the use of any set of indicator species that is identified with our framework is most likely only valid for the given study region (context dependency) and that a follow-up study should test the suitability of candidate indicator species for future community monitoring programs that focus on ES assessment (validation of indicators). The latter step could be replaced by the use of existing community data from the same region to validate indicator species. Finally, some ES may be easier to directly assess instead of using indicator analysis, this may for example be true for the yield potential in our study. However, both the biodiversity and pest control potential are very laborious to assess directly by large cross-taxon sampling campaigns (biodiversity) or complex ecological field experiments (biocontrol). The proposed framework can provide shortcuts for both ES, by running a sampling campaign or experiment once and by then testing the validity and suitability of the candidate species in follow-up analyses. Following this protocol will then allow monitoring selected conspicuous indicator species in consecutive years with no need for additional cross-taxon sampling campaigns or field experiments. The proposed framework thereby provides a novel tool to develop regional, multi-taxon indicator bundles for the simultaneous assessment of multiple ES that will contribute to a reduction of costs in future assessments. The bundling of indicator species with comparable relationships to single or several ES potentials across taxonomic groups will further safeguard the use of indicators for ES against unexpected fluctuations in abundances of single taxa.

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