

Methodological approach to assess biodiversity in agro ecosystems – A case study

Abordagem metodológica para a avaliação da biodiversidade em ecossistemas agrários - estudo de caso

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ABSTRACT

In agroecosystems, the evaluation of biodiversity is extremely important given its relation with their sustainability, however it is a difficult and expensive task. The use of the higher taxa surrogacy has been proposed as an effective and less expensive way to assess biodiversity, but is still being used mainly in natural, more stable, ecosystems. In this study, we tested the use of the higher taxa surrogacy approach for spiders in pear orchards, under different production systems, in the “Oeste” region of Portugal. Spiders were chosen for this case study, since they are important predators, acting as biological control agents in agroecosystems. We concluded that genus can be used as a higher *taxa* surrogate of species richness with a good accuracy.

Key-Words: Higher *taxa* surrogacy, pear orchards, spiders.

RESUMO

Em ecossistemas agrícolas, a avaliação da biodiversidade é extremamente importante dada a sua relação com a sustentabilidade, sendo contudo uma tarefa difícil e dispendiosa. O uso da relação entre o número de espécies e o número de táxones de alto nível, tem sido proposto como uma alternativa eficaz e económica para a avaliação da biodiversidade, contudo a sua utilização tem estado praticamente restringida aos ecossistemas naturais, mais estáveis. Neste estudo, testou-se o uso da relação entre o número de espécies e o número de táxones de alto nível em aranhas, em pomares de pêra sob diferentes modos de produção, na região Oeste de Portugal. As aranhas foram seleccionadas para este estudo de caso por serem importantes predadores, actuando como agentes de luta biológica contra pragas. Concluiu-se que o género pode ser usado na avaliação da riqueza de espécies, com um elevado grau de precisão.

Palavras-chave: Aranhas, pomares de pêra, relação entre táxones

Introduction

In the last few years, the interest in associating nature conservation to agriculture has increased enormously in Europe and several measures have been taken for the implementation of a sustainable agriculture (Amaro, 2003).

One way of measuring the sustainability of an agroecosystem is through the evaluation of its biodiver-

sity (Moonen and Barberi, 2008; Paoletti, 1999). Biodiversity is often measured by the number of species sampled in an ecosystem (Primack, 2002), which is a rather difficult and expensive task, especially when considering invertebrate taxa (Duelli *et al.*, 1999; Martín-Piera, 2000). However, since invertebrates account for more than 90% of the genetic variability in agroecosystems, it seems necessary to use them as the closest correlates to the overall biodiversity (Duelli, 1997).

The use of the higher *taxa* surrogacy approach (order, family, genus) has been proposed by several authors as a way of measuring diversity, based on the existence of a strong relationship between higher *taxa* richness and species richness (Andersen, 1995; Gaston and Williams, 1993; Wilkie *et al.*, 2003; Groc *et al.*, 2010). Therefore with a lower effort and using fewer resources, a large amount of information from several *taxa* can be obtained without identification to the species level (Gaston and Williams, 1993). In fact, the higher *taxa* approach has already been used for several different organisms (e.g. Gaston and Williams, 1993; Andersen, 1995; Gaston and Blackburn, 1995; Martín-Piera, 2000; Ricotta *et al.*, 2002; Biaggini *et al.*, 2007; Cotes *et al.*, 2010; Groc *et al.*, 2010), including spiders (Borges *et al.*, 2002; Cardoso *et al.*, 2004; Gouveia, 2004).

However, some limitations must be considered when using this approach, because several factors can influence the relationship between species richness and higher *taxa* richness, namely, genealogy and status of higher *taxa*, choice of higher *taxa* rank, spatial scale at which the assessment occurs, areas with unusual patterns of speciation, and sampling period (Gaston and Williams, 1993; Andersen, 1995). Spiders, as predators, are beneficial arthropods in agroecosystems, helping in pest control, and so their monitoring is important (Duelli, 1997; Marc *et al.*, 1999; Tavares *et al.*, 2011).

Very few studies using higher *taxa* surrogacy have been conducted in agroecosystems (Duelli, 1997; Cotes *et al.*, 2010); and most of them deal with natural ecosystems conservation. The higher *taxa* approach has already been used on spider's priority conservation areas in Portugal (Borges *et al.*, 2002; Cardoso *et al.*, 2004; Gouveia, 2004), but not yet in agroecosystems.

In this work, the use of the higher *taxa* surrogacy approach was tested for spiders in pear orchards in the "Oeste" region of Portugal.

Material and Methods

The study took place in six pear orchards, in the Oeste region of Portugal (Figure 1), from June to November 2006 and from April to June 2007, every two weeks. Two orchards of each type of production system were sampled: Organic Agriculture (OA1 and OA2), Integrated Pest Management (IPM1 and IPM2) and Conventional Agriculture (CA1 and CA2). Conventional Agriculture (CA) uses broad-spectrum pesticides applied rigidly at certain established periods; Integrated Pest Management

(IPM), uses chemical control (selective pesticides) together with other control measures when considered necessary after previous monitoring procedures; and Organic Agriculture (OA), does not use synthetic pesticides. OA1 orchard (0.6 ha), in Vilar village, was situated at a house's backyard, surrounded by a non-cultivated field, pear orchards, a vineyard and vegetable plots. It was bordered by wildflower strips and by a stone wall covered with weeds. Vegetation covered the orchard's inter-rows. OA2 (1 ha), in Freiria village, was also situated at a house's backyard. It was bordered by a road and shrub hedges, surrounded by a vineyard, pear orchards and a non-cultivated field. It had wildflower strips along the field edge, inter-rows covered with vegetation and botanically rich alleyways. IPM1 (3.5 ha), near Caldas da Rainha city, was at a valley, surrounded by pine trees, eucalyptus and riparian vegetation, and bordered by other orchards (pear and apple). It had wildflower strips along the orchard edges, botanically rich alleyways and vegetation covering the inter-rows. IPM2 (3 ha), in Peral village was bordered by a road, a small brook with riparian vegetation, wildflowers strips, hedges with trees and shrubs, and was surrounded by orchards and non-cultivated fields. Vegetation covered the inter-rows. CA1 (0.1 ha), also in Peral village, was above a valley, bordered by vegetable crops, apple trees, weeds and piles of dried plants (reeds). On one side was a wooden wall with nearby grassland. Inter-rows were covered with vegetation. CA2 (4 ha), in Vermelha village, was at a valley, bordered by other pear orchards, riparian vegetation near a small brook, wildflowers strips, shrubs and tree hedges and surrounded by pine trees and eucalyptus. Inter-rows were covered with vegetation. Spiders were collected by ten pit-fall traps (10 cm diameter opening) in each orchard, placed along the intertree - strips, separated by 5 meters from each other. Plywood square was placed as a roof over the traps, allowing spiders to crawl under it, but avoiding the accumulation of debris or rain. Pitfall trapping was chosen, as it is a method directed at epigeous spiders that requires the less experience, effort and cost to employ (Cardoso, 2004; Cardoso *et al.*, 2007). Additionally, it can capture almost half of the spider species living in a typical Mediterranean habitat and can capture a great number of individuals (Cardoso *et al.*, 2009), which is important for the statistical robustness of the data.

Pit-falls had 30% ethylene glycol inside. The liquid content was filtered with a filter paper and the solid content was stored in 75% alcohol. Spiders were later separated from the remaining material in labora-

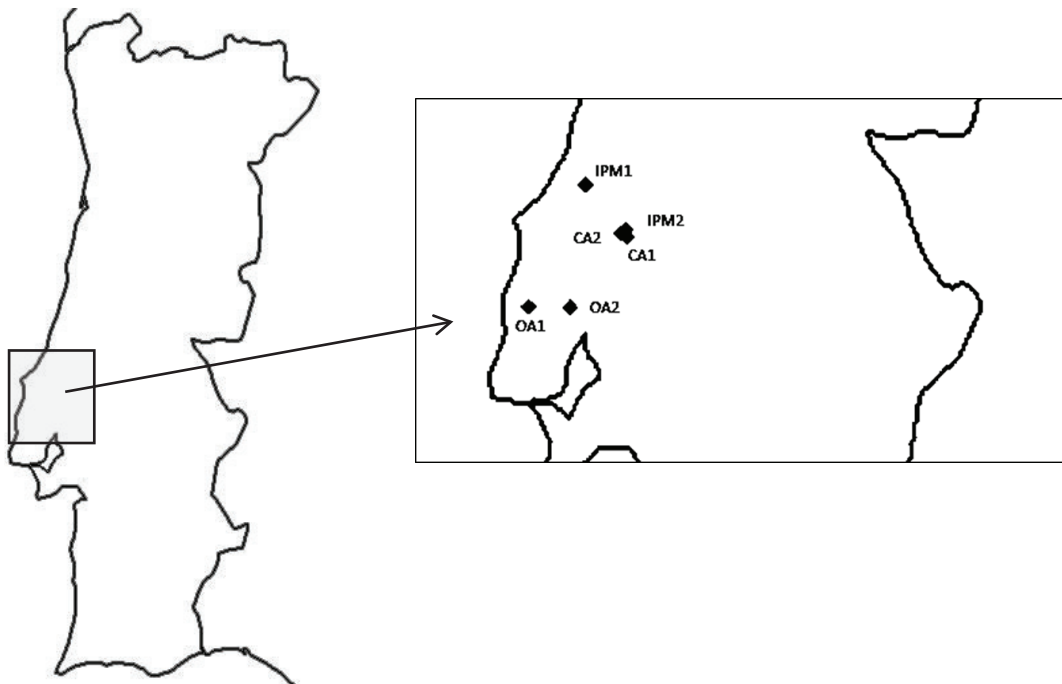


Figure 1 – Map of Portugal: the Oeste region, where the orchards were sampled is indicated by the square. Orchards are indicated by the dark shapes: OA1, OA2, IPM1, IPM2, CA1, CA2.

tory and stored in 70% alcohol and glycerine. Adult specimens were identified to species level or morph species.

For the evaluation of the potential use of family and genus as higher *taxa* surrogates, we used the regression analysis for each orchard and for all of them together. Three regression models were tested: a linear model ($y=a+bx$), an exponential model ($y =a \cdot e^{bx}$) and a log-log model ($\log y=a+b \cdot \log x$). Species were tested as the dependent variable and the higher taxonomic categories as the independent variable. Statistical analysis was performed with STATISTICA 7.0 and SPSS softwares.

Results

In this study, 1288 adult's spiders were collected with the pit-fall traps. Fifteen families, 49 genera and 64 species and morphospecies were identified (Table 1).

All 42 regressions (Table 2) performed were highly significant ($p<0.001$), except the exponential model for the family-species relationship in CA2 ($p=0.004$) (Table 2right). Both higher *taxa* tested (family and genus) presented good relationships with species, independently of the regression models applied, being the genus-species relationships stronger than

the family-species ones. When all orchards were analysed together, r^2 was strong ($r^2>0.80$) for both higher *taxa*-species relationships. When orchards were analysed separately, no model predominated over the others, in terms of fitness. When analysing all orchards together, the linear model was the strongest one (highest r^2) for the relationship genus-species and the exponential model for the relationship family-species.

Discussion

The relationship between family-species and genus-species was statistically significant. According to Martín-Piera (2000), an increase in higher *taxa* implies an increase in the number of species.

Three regression models were tested, as proposed by Borges *et al.* (2002). According to those authors, the log-log model is usually the most liable model, because it normalizes residuals distribution and consequently has a more powerful statistical prediction. However, in the present study, when orchards were analysed separately, no model revealed itself stronger than the other, and when all orchards were analysed together, the linear model was the most adequate for the relationship genus-species and the exponential one for the relationship family-species.

Table 1 – Spiders species sampled in the six orchards (total number of adults) of Organic Agriculture (OA), Integrated Pest Management (IPM) and Conventional Agriculture (CA).

Family	Species	OA1	OA2	IPM1	IPM2	CA1	CA2
Agelenidae	<i>Malthonica lusitanica</i>	2	0	1	0	9	0
	<i>Tegenaria atrica</i>	1	0	0	0	0	0
	<i>Tegenaria feminea</i>	13	2	15	4	6	0
	<i>Tegenaria montigena</i>	0	1	3	0	1	0
	<i>Tegenaria</i> spp.	0	0	0	0	0	1
Corinnidae	<i>Phrurolithus minimus</i>	0	0	1	0	0	0
	<i>Liophrurillus flavitarsis</i>	0	0	0	0	2	0
Dyctinidae	<i>Dictyna civica</i>	1	0	0	1	1	0
	<i>Altella</i> sp.	0	0	0	0	1	0
Dysderidae	<i>Dysdera crocata</i>	3	2	0	1	4	0
	<i>Dysdera fuscipes</i>	5	0	0	2	2	0
	<i>Dysdera lusitanica</i>	0	0	2	1	0	0
	<i>Harpactea</i> spp.	0	0	6	1	8	0
	<i>Rhode scutiventris</i>	0	0	0	0	0	2
Gnaphosidae	<i>Drassodes lapidosus</i>	0	0	0	1	2	0
	<i>Drassodes luteomicans</i>	0	0	1	2	2	0
	<i>Gnaphosa alacris</i>	1	1	0	0	2	0
	<i>Haplodrassus dalmatensis</i>	0	2	1	1	1	0
	<i>Haplodrassus macellinus</i>	2	0	3	0	2	0
	<i>Micaria pallipes</i>	0	2	3	0	2	1
	<i>Trachyzelotes fuscipes</i>	3	12	18	1	4	13
	<i>Setaphis carmeli</i>	0	1	2	1	1	0
	<i>Zelotes aeneus</i>	18	13	163	18	34	166
	<i>Zelotes civicus</i>	0	0	1	0	1	0
	<i>Zelotes electus</i>	0	0	1	0	0	0
	<i>Zelotes tenuis</i>	7	12	29	11	22	6
	<i>Zelotes ruscinensis</i>	0	1	0	1	2	0
Linyphiidae	<i>Canariphantes zonatus</i>	0	0	0	0	1	0
	<i>Gongylidiellum vivum</i>	0	0	0	1	0	0
	<i>Lessertia denticHELIS</i>	0	0	0	5	0	0
	<i>Microctenonyx subitaneus</i>	0	0	0	5	0	0
	<i>Prinerigone vagans</i>	0	0	0	1	0	0
	<i>Palliduphantes stygius</i>	32	2	5	5	18	0
	<i>Pelecopsis inedita</i>	0	0	1	0	0	0
	<i>Tenuiphantes tenuis</i>	19	21	27	6	22	16
	<i>Linyph</i> spp.1	1	0	0	0	0	0
	<i>Linyph</i> spp.2	0	0	2	0	0	0
	<i>Meioneta</i> spp.	1	0	1	0	0	0
	Liocranidae	<i>Agraecina lineata</i>	1	3	5	1	0
<i>Agroeca brunnea</i>		0	0	1	0	0	0
Lycosidae	<i>Alopecosa albofasciata</i>	41	34	22	8	60	7
	<i>Arctosa excellens</i>	0	0	0	3	0	0
	<i>Hogna radiata</i>	0	1	0	0	4	0
	<i>Pardosa proxima</i>	3	10	30	2	1	4
	<i>Pardosa hortensis</i>	1	3	0	0	0	0
	<i>Pardosa pullata</i>	0	0	0	0	1	0
	<i>Trochosa ruricola</i>	0	1	0	0	0	0
Nemesiidae	<i>Nemesia bacelerei</i>	0	0	0	0	41	0
Pisauridae	<i>Pisaura mirabilis</i>	4	0	0	0	0	0
Salticidae	<i>Euophrys herbigrada</i>	1	0	0	0	1	0
	<i>Euophrys sulphurea</i>	1	0	1	0	0	0
	<i>Evarcha jucunda</i>	0	0	1	0	0	0
	<i>Phlegra fasciata</i>	1	0	1	0	1	0
	<i>Pseudeuophrys erratica</i>	0	0	0	1	0	0
	<i>Talavera aequipes</i>	0	0	0	0	1	0
Titanoecidae	<i>Nurscia albomaculata</i>	0	1	4	1	1	1
Theridiidae	<i>Robertus arundineti</i>	1	0	0	0	0	2
	<i>Robertus</i> spp.	0	0	0	1	0	0
	<i>Theridion</i> spp.	0	0	0	0	1	0
Thomisidae	<i>Ozyptila bicuspis</i>	1	0	1	3	3	20
	<i>Ozyptila pauxilla</i>	7	2	5	0	13	10
	<i>Xysticus kochi</i>	0	0	0	1	0	0
	<i>Xysticus nubilus</i>	1	0	0	0	0	0
Zodariidae	<i>Zodarion atlanticum</i>	0	1	10	0	2	1
Total number of individuals		172	128	367	90	280	251
Number of families		12	9	12	12	14	10
Total number of species		27	22	32	29	37	15

Table 2 – LEFT: Regression analysis between the number of species (dependent variable) and the number of genera (independent variable); and RIGHT: Regression analysis between the number of species (dependent variable) and the number of families (independent variable); Orchards: Organic Agriculture (OA1, OA2), Integrated Pest Management (IPM1, IPM2) and Conventional Agriculture (CA1, CA2)

Orchard	Model	slope	Adjusted r ²	p-value
OA1	Linear	0.9600	0.9566	<0.001
	Exponencial	0.2508	0.8389	<0.001
	Log-Log	0.0256	0.9672	<0.001
OA2	Linear	1.0278	0.9280	<0.001
	Exponencial	0.2322	0.8755	<0.001
	Log-Log	1.0052	0.9518	<0.001
IPM1	Linear	1.2450	0.9582	<0.001
	Exponencial	0.1467	0.9564	<0.001
	Log-Log	1.1389	0.9287	<0.001
IPM2	Linear	1.0694	0.9000	<0.001
	Exponencial	0.2159	0.8493	<0.001
	Log-Log	0.9486	0.9169	<0.001
CA1	Linear	1.0659	0.9280	<0.001
	Exponencial	0.1598	0.9641	<0.001
	Log-Log	0.9486	0.9169	<0.001
CA2	Linear	0.9458	0.8540	<0.001
	Exponencial	0.2992	0.9577	<0.001
	Log-Log	0.9680	0.8355	<0.001
All together	Linear	1.1006	0.9019	<0.001
	Exponencial	0.0399	0.8598	<0.001
	Log-Log	1.0513	0.8818	<0.001

Model	slope	Ajusted r ²	p-value
Linear	1.2779	0.7990	<0.001
Exponencial	0.3322	0.6842	<0.001
Log-Log	1.115	0.8637	<0.001
Linear	1.3492	0.6780	<0.001
Exponencial	0.3025	0.5739	<0.001
Log-Log	1.0606	0.6966	<0.001
Linear	2.0711	0.8050	<0.001
Exponencial	0.2440	0.7540	<0.001
Log-Log	1.2259	0.7186	<0.001
Linear	1.2799	0.6440	<0.001
Exponencial	0.2696	0.9479	<0.001
Log-Log	0.9816	0.7145	<0.001
Linear	1.5818	0.8238	<0.001
Exponencial	0.2383	0.8217	<0.001
Log-Log	1.0327	0.7688	<0.001
Linear	1.1548	0.8860	<0.001
Exponencial	0.3904	0.6200	= 0.004
Log-Log	1.0452	0.8480	<0.001
Linear	1.5663	0.8397	<0.001
Exponencial	0.058	0.8623	<0.001
Log-Log	1.1465	0.8475	<0.001

The same conclusion was reached by Cardoso *et al.* (2004) and Gouveia (2004). In the case of the CA2 orchard the exponential model for the family-species relationship was not adequate. This is due to the fact that although the number of families is relatively high in this plot and close to the number of families found for all the orchards, the number of species is much lower than the one found for the other orchards (Table 1). Thus, the exponential model will not be adequate, since in this particular case, as long as we increase the number of families, the number of species will not increase exponentially. CA2 revealed a very low diversity of species, being overall dominated by a single species *Zelotes egregioides*. Abundance of a single species is characteristic of very disturbed habitats (Samu, Sunderland and Szinetár, 1999).

The taxon that best predicted species richness was the genus, as also concluded in other studies, namely Borges *et al.* (2002), Cardoso *et al.* (2004), Gouveia (2004) and Groc *et al.* (2010), conducted in different ecosystems. According to Martín-Piera (2000), the genus explains a higher percentage of variance than the family. Additionally, when analysing the different

orchards separately, the relationship family-species presented r² values of a wider range, while those of the relationship genus-species were less variable.

Attention must be made to the fact that Andersen (1995), applying the higher *taxa* surrogacy approach for species of ants in different regions of Australia, found that the relationship genus-species was very strong within regions, but varied substantially between regions. However, in Portugal this has not been observed: studies conducted in different regions presented similar results (Borges *et al.*, 2002; Cardoso *et al.*, 2004; Gouveia, 2004). According to Cardoso *et al.* (2004), neither geographical location nor habitat type appears to have a strong influence in the higher *taxa* approach of spiders in Portugal.

Conclusions

This study presents additional evidence that higher *taxa* can be used to predict species richness in a given area with reasonable accuracy, being the genus the best surrogate for species as proposed by Cardo-

so *et al.* 2004. Identification to genus level and posterior extrapolation through a linear model revealed to be a good methodology to be used for spider's species. The relationship family-species revealed a lower correlation, and is not adequate for all situations such as the orchard CA2. It may be possible that disturbed habitats present a different family-species relationship.

The higher *taxa* surrogacy approach for spiders seems to be an interesting method for a less expensive and time consuming biodiversity assessment in agro ecosystems.

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