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Rapid biodiversity assessment of spiders (Araneae) using semi-quantitative sampling: a case study in a Mediterranean forest

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Abstract. 1. A thorough inventory of a Mediterranean oak forest spider fauna carried out during 2 weeks is presented. It used a semi-quantitative sampling protocol to collect comparable data in a rigorous, rapid and efficient way. Four hundred and eighty samples of one person-hour of work each were collected, mostly inside a delimited 1-ha plot.

2. Sampling yielded 10 808 adult spiders representing 204 species. The number of species present at the site was estimated using five different richness estimators (Chao1, Chao2, Jackknife1, Jackknife2 and Michaelis–Menten). The estimates ranged from 232 to 260. The most reliable estimates were provided by the Chao estimators and the least reliable was obtained with the Michaelis–Menten. However, the behavior of the Michaelis–Menten accumulation curves supports the use of this estimator as a stopping or reliability rule.

3. Nineteen per cent of the species were represented by a single specimen (singletons) and 12% by just two specimens (doubletons). The presence of locally rare species in this exhaustive inventory is discussed.

4. The effects of day, time of day, collector experience and sampling method on the number of adults, number of species and taxonomic composition of the samples are assessed. Sampling method is the single most important factor influencing the results and all methods generate unique species. Time of day is also important, in such way that each combination of method and time of day may be considered as a different method in itself. There are insignificant differences between the collectors in terms of species and number of adult spiders collected. Despite the high collecting effort, the species richness and abundance of spiders remained constant throughout the sampling period.

Key words. Arthropods, Iberian Peninsula, inventory, oak forest, Portugal, rare species, richness estimation, sampling intensity, sampling methods, semi-quantitative sampling.

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Introduction

Despite their fundamental roles in natural ecosystems, ecosystem services and potential use in identifying conservation priority areas, arthropods have largely been ignored in conservation studies (Franklin, 1993; Kremen *et al*., 1993; New, 1999a, b). This is due to their small size, great diversity and lack of identification guides or even specialists of many groups. When corrected for knowledge bias, data on arthropods show that risk of extinction is as real as for vertebrates (Thomas & Morris, 1994; McKinney, 1999; Dunn, 2005). Because of the lack of reliable data for arthropods, decisions on conservation and natural resource management are often based on vertebrate or plant data, or simply on the uniqueness of the habitats. Rigorous, feasible, rapid and efficient sampling protocols are needed to collect comparable data for arthropods that can be used to estimate local species richness and/or complementarity between sites.

Among arthropods, spiders probably are one of the best target groups. They are hyperdiverse yet can be easily sampled and sorted to morphospecies and they probably are the most abundant representatives of the top-predators guild in many habitat types. Coddington *et al*. (1991) suggested a sampling strategy for spiders that has subsequently been tested and refined in a number of spider studies, mainly in tropical and temperate forests (Coddington *et al*., 1991, 1996; Silva & Coddington, 1996; Dobyns, 1997; Toti *et al*., 2000; Sørensen *et al*., 2002; Scharff *et al*., 2003). All sampling protocols used in these studies have changed in various ways, depending on habitats (complex or simple), time (long or short, in terms of days, and thereby number of samples), human resources (number of collectors, experienced versus inexperienced) and methods (different number of methods). Thus, none of the protocols are exactly the same and they have never been standardised, which obviously has to be taken into consideration when comparing results from the various studies. Except for Coddington *et al*. (1996), all sampling designs have been unbalanced, in the sense that they used different number of samples between methods and times of day. Scharff *et al*. (2003) explained why they used unbalanced designs but this leads to unbalanced statistical designs for the analysis of variance and thereby the statistical tests of significance.

Although shortcuts for the rapid assessment of spider richness in the Mediterranean have already been proposed by using higher taxa surrogates (Cardoso *et al*., 2004a) or indicator taxa (Cardoso *et al*., 2004b), no standardised and optimised field protocol has been proposed for the habitats in the region. The inventory here presented is the second (chronologically) of three planned intensive inventories on the spider fauna of Portugal, the example of which will allow the creation of a protocol in the near future (Cardoso *et al*., 2007a, b). They are to be carried out in three different, yet typical, Mediterranean habitats, and build on the previous spider sampling protocols mentioned above, but differ in the number of samples included (more samples) and the sampling design (fully balanced). The fully balanced sampling design used (i.e. same number of samples per day, per time of day, per collector and per method) will enable to study the spider species richness and species composition and to test whether different factors (day, time of day, collectors, methods) may affect the overall results. All the gathered data are also an important contribution for the increased knowledge on the Portuguese, Iberian and Mediterranean fauna.

Materials and methods

Study site

The study was carried in a mixed English oak (*Quercus robur* L.) and pyrenean oak (*Quercus pyrenaica* Willd.) woodland, located in Mata da Albergaria, Peneda-Gerês National Park (PNPG), in northern Portugal, at an altitude of 600 to 700 m (41º47.700′N, 008º08.200′W) from June 1 to 15 of 2005. The canopy was dense, 10 to 20 m high, and with an equally dense understorey dominated by ferns [mainly *Pteridium aquilinum* (L.)] and heather (*Erica* spp.). The leaf litter of much of the sampled area was relatively deep. The habitat is considered typical for the northern areas of the Iberian Peninsula. Average minimum temperature of the area in January is 2 ºC and average maximum temperature in August is 24 ºC. Annual mean temperature is 11 ºC and precipitation is 1500 mm, distributed over most of the year.

Sampling procedures

A 1-ha (100 × 100 m) sampling area was defined and delimited (hereafter called 'sampling plot' or just 'plot') within a rather uniform part of an old primary oak woodland area. Gaps and streams etc., were avoided in order to reduce 'habitat edge effects' (Scharff *et al*., 2003) caused by species that prefer habitats not present in the plot. Most of the sampling took place within this sampling plot, but additional plotless sampling also took place outside the plot, using identical sampling methods (see below). The plotless sampling took place up to 100 m away from the sampling plot and collectors thereby covered an area of approx. 10 ha. Contrary to the plot-based sampling, plotless sampling took place in a much more heterogeneous habitat, including areas adjacent to a river that runs through the area.

Sampling followed the semi-quantitative sampling design of Coddington *et al*. (1991), with modifications (Sørensen *et al*., 2002; Scharff *et al*., 2003). Each sample represented one method applied for 1 h of active, continuous collecting (i.e. including time required to transfer the specimens to a vial, but excluding interruptions).

A total of 480 samples were taken inside and outside the plot. Of these, 80 were pitfall and bark trap samples placed in the periphery of the plot, and the remaining 400 samples were taken by collectors in the following way: eight collectors concentrating on spiders collected 256 samples inside the plot and 64 outside the plot (for a total of 320 samples). Two collectors sampled all arthropods, not only spiders, in order to provide data that could be used to test how many spiders are missed if the focal taxon was broadened from spiders to all arthropods and collected 64 samples inside the plot and 16 outside the plot (for a total of 80 samples). Four different collecting methods ('aerial', 'ground', 'beat' and 'sweep'; see descriptions below) were used and the collectors worked both day and night. Sampling followed a

balanced design, so that each collector made the same number of samples per method, day and time of day.

Sampling day, time of day, collector experience, and sampling method were used to test the effects of inventory design parameters on the richness, abundance and composition of the samples.

Sampling day. Most of the samples were taken during the period of June 4 to 11 (hereafter called days 1 to 8). This is considered the most productive time frame of the year (in terms of spider species richness) in the Mediterranean area (Cardoso *et al*., 2007). Such intensive collecting within a limited area can theoretically lead to the depletion of fauna, so the possible depletion and/or change in species composition along days caused by the collecting scheme was tested. In some comparisons, days 1 to 4 were defined as the first 'week' and days 5 to 8 as the second 'week'.

Time of day. Tests were made to verify whether night collecting would be more productive than day collecting in terms of species richness and abundance, and whether species composition would differ between day and night. Every day, each collector made two samples during the day and two samples during the night inside the plot. Headlamps were used for the night collecting.

Collectors. Ten collectors worked for 8 days. Six were considered experienced collectors, since they had previous experience with semi-quantitative spider sampling protocols, whereas the remaining four collectors had no such experience. However, all collectors had some previous experience with spider collecting. As mentioned above, two of the experienced collectors sampled all arthropods and not just spiders.

Methods. Six sampling methods, considered to cover all microhabitats except for the high canopy layer, were used. Five of the methods (aerial, beat, ground, sweep and pitfall) have been extensively used in similar protocols, and worked well, so effort was concentrated on these. Bark traps were tested for their ability to add new species to the former methods.

Aerial. Hand collection with pooter, vial, forceps or brush from knee level to as high as the collector can reach. Specimens were transferred directly to 70% ethanol. A total of 100 samples were made, 64 of which within the plot.

Beat. Branches of trees and other vegetation were tapped with a wooden stick while holding a 1-m square beating tray underneath to catch the falling specimens. The stopwatch was running while the collector beat, searched for falling specimens and transferred specimens to the sample vial. A total of 100 samples were made, 64 of which within the plot.

Ground. Hand collecting from ground level to knee height. In this study, this method included the cryptic fauna found under logs and stones or even in litter, which was sampled by a separate method in other studies (Scharff *et al*., 2003). A total of 100 samples were made, 64 of which within the plot.

Sweep. A round sweep net, with a diameter of 40 cm, was used to sweep low herbaceous or shrubby vegetation. The net was emptied after a few sweeps to avoid damage to the specimens. The stopwatch was running while the collector swept, searched for specimens in the sweep bag, and transferred specimens to a sample vial, thus counting only effective sampling time. A total of 100 samples were made, 64 of which within the plot.

Pitfall. Pitfall traps were 8 cm wide, 12 cm deep, and two-thirds filled with a solution containing 50% ethylene glycol (anti-freeze fluid). Traps were sheltered by wooden lids on stilts 2–3 cm above trap level. A total of 256 pitfall traps were set up in the periphery of the plot in a square design with 16×16 traps. Each trap was 5 m apart from the nearest and a sample was defined as four pooled traps. Pooling of traps was carried out to reduce stochastic heterogeneity among samples and to homogenise the sampling effort, making it more comparable with the effort of time-based methods (the effort necessary to dig down four traps and collect the content was considered equivalent to approximately one person-hour of work). Pooling the 256 pitfall traps generated 64 samples. The traps were set just outside the plot to avoid interference with the collectors. Pitfall traps were left in the field for 2 weeks (June 1 to 15).

Bark traps. Bark traps were made from pieces of cardboard paper (50×50 cm) wrapped around tree trunks to act as shelter, thus trapping cryptic species. A total of 64 traps were mounted on trees, and worked for 2 weeks (June 1 to 15). A sample was defined as four pooled traps, for the same reasons as explained for the pitfall traps.

Sorting and identification was carried out by the first author. Whenever possible, identifications were made to species level; otherwise, morphospecies were defined. Only adult specimens were considered for statistical analyses, as juveniles cannot usually be assigned to species and very few studies even attempt to identify juveniles. In many of the analyses, only the plot-based samples, which fully complied with a balanced design, have been considered. Pitfall traps were also considered part of the plot, since they complement the other four 'main' sampling methods.

Statistical analysis

The software package ESTIMATES 7.5 (Colwell, 2005) was used to calculate randomised species accumulation curves for the observed species richness (using the Mao Tau procedure), singleton and doubleton curves and various richness estimates (Chao1, Chao2, first and second order Jackknife and Michaelis–Menten), using 1000 randomizations in all calculations. All curves were sample-based and rescaled to individuals, as suggested by Gotelli and Colwell (2001). In order to statistically determine whether the randomised curves were approaching the asymptote, still increasing or even decreasing at the end of the sampling process, the slope of the final segment of the curve was calculated as: Slope = $1/(n_S - n_{S\pm1})$ where n_S = final number of individuals for each curve (corresponding to the total richness value S) and $n_{S\pm1}$ = number of individuals corresponding to the point in the curve where the final single species was added or

Table 1. Summary table of results and species richness estimates for all data (total plot-based and plotless sampling data).

	Plot-based samples		
	Pitfall trap samples excluded	Pitfall trap samples included	Total (plot-based and plotless samples)
Samples	256	320	480
Individuals (inc. juv.)	6000 (12 852)	7516 (14 956)	10 808 (21 748)
Individuals/sample	23.4	23.5	22.5
Species	150	185	204
Species/sample	12.1	11.9	11.2
Sampling intensity	40	41	53
Singletons	33 (22%)	38 (21%)	39 (19%)
Doubletons	17 (11%)	24 (13%)	25 (12%)
Estimates			
Chao1 ± SD	179 ± 12	213 ± 11	232 ± 11
Chao2 ± SD	179 ± 12	215 ± 11	234 ± 11
Jackknife 1 ± SD	183 ± 6	225 ± 7	245 ± 7
Jackknife 2	199	240	260
Michaelis–Menten	145	178	194
Completeness	84%	87%	88%

subtracted to S (corresponding to a richness value of S ± 1). If S ± 1 was larger than S, the result was given a negative sign, reflecting a negative slope.

Inventory completeness (*sensu* Sørensen *et al*., 2002; Scharff *et al*., 2003) was calculated as the ratio of the observed species richness to the Chao1 richness estimate. This estimator was chosen because it was found to be very accurate in previous studies and so that values of completeness could be compared to such studies (e.g. Sørensen *et al*., 2002; Scharff *et al*., 2003; Cardoso *et al*., 2007a, b). Sampling intensity (Coddington *et al*., 1996) is the ratio of specimens to species, and was here used as a crude measure of sampling effort (but see Gotelli & Colwell, 2001 for pitfalls).

Most of the statistical analyses were carried out with the software package STATISTICA 6 (Statsoft Inc., 2001). To test if there were differences in abundance or species richness per sample (dependent variables) between days, time of day, collectors and methods (independent factors), three four-way ANOVA's were made for each dependent variable. The first and second ANOVAS were carried out without taking any interactions into account. In the second ANOVA, the days of sampling (1–8) were grouped into 2 'weeks' of 4 days each, sampling hours were grouped into day or night periods, collectors were grouped into 'experienced' and 'inexperienced' and methods into 'active search' (aerial and ground) versus 'tool-based methods' (beat and sweep). The third ANOVA was dealing with interactions, with sampling hours grouped into day and night periods and collectors grouped according to experience. All data on abundance were log10 (n + 1) transformed to successfully control the heterogeneity of variance (Zar, 1984). In all cases, post-hoc Tukey honestly significant difference (HSD) tests were used to determine which treatments were responsible for significantly different results.

An analysis of similarity was used (ANOSIM by Clarke, 1993; implemented at Seaby & Henderson, 2004) and the Spearman rank correlation index to compare sample composition of days, times of day, collectors and methods. Data on the abundance of species per sample were log10 (n + 1) transformed for the ANOSIM analyses, so that the most common species did not disproportionably influence the results.

All material is deposited in the Natural History Museum of Denmark, Zoological Museum, University of Copenhagen (ZMUC).

Results

A total of 21 748 spiders were collected in 480 samples (inside and outside the plot), including 10 808 adults (50%) representing 29 families, 119 genera, and 204 species (Appendix 1). The most abundant species, *Dipoena melanogaster* (C. L. Koch, 1837) (Theridiidae) accounted for only 8% of the specimens. The material included 26 new species for the country (see Cardoso, 2007 for the current Portuguese checklist), some of which were also new species or even genera for the Iberian Peninsula (Appendix 1; see Morano, 2005 for the current Iberian checklist).

Richness estimates

The overall sampling intensity was 53 specimens per species, and the estimated number of spider species present in the whole area sampled (inside and outside the plot), at the time of the inventory and available for the collecting methods used, was 232 to 260 species (Table 1). The estimate based on Michaelis–Menten was lower (194) than the observed (204) number of species and was therefore not useful as an estimate. The observed species accumulation curve (Fig. 1) had a final slope of 0.004 and the singleton and doubleton curves approached each other, but did not cross. Among the non-parametric estimators, the accumulation curves of both Chao1 and Chao2 reached an asymptote, with slope values less than 0.001 (Fig. 1). With an estimate of 232 species, Chao1 generated the lowest estimate. The estimates of Jackknife1 (245 species) and Jackknife2 (260 species) were higher, but the accumulation curves did not reach an asymptote. Chao1 was used to calculate a 'sampling completeness' of 88% (Table 1),

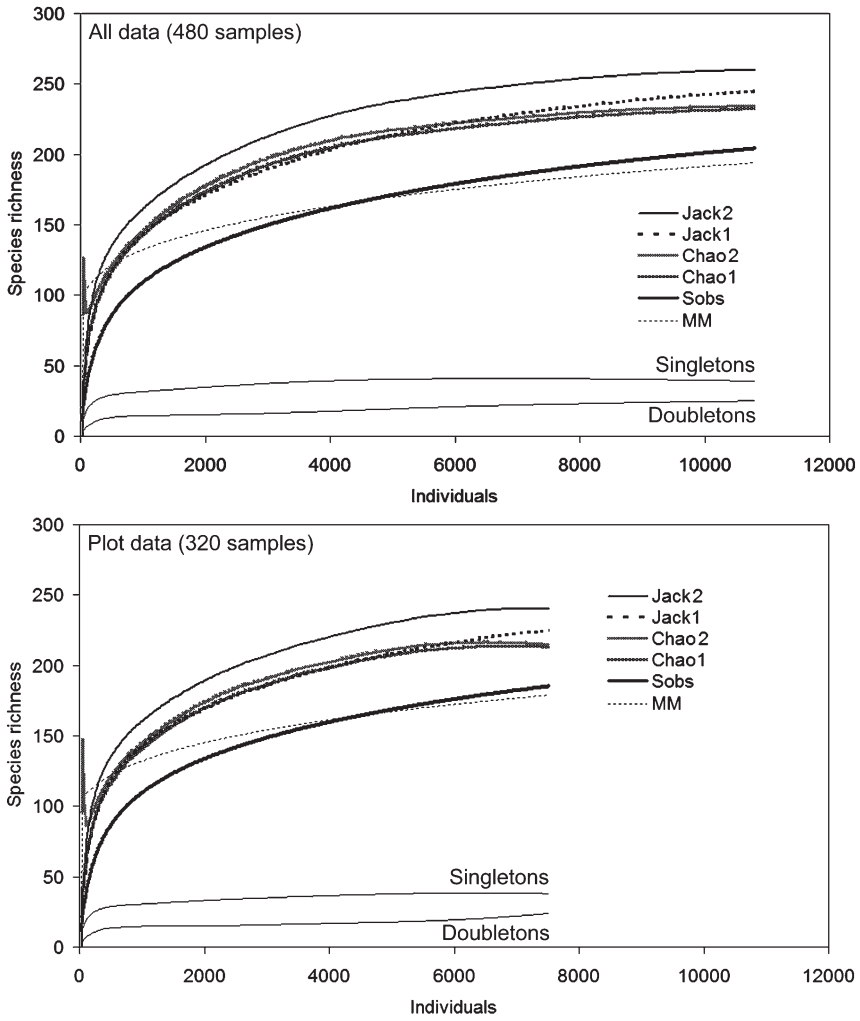

Fig. 1. Randomised accumulation curves for observed species richness, singletons, doubletons and richness estimators for total and plot-based data.

meaning that 88% of the estimated number of species in the area was collected.

Out of the 480 samples, 256 were taken within the plot by collectors focusing on spiders only. Adding to these the 64 pitfall samples, 320 samples were defined as plot-based (Table 1). These samples generated 14,956 spiders of which 7516 were adults (50%) and represented 185 species (Table 1). Plot-based sampling intensity was 41 individuals per species, but ranged from 8 to 26 depending on the method. Thirty-eight species (21%) were singletons and 24 (13%) doubletons. The estimated spider species richness within the plot ranged from 213 to 240. Again, the Michaelis–Menten estimate was lower (178) than the observed (185) number of species. It crossed the observed species curve (Fig. 1) at 4557 individuals, equivalent to 194 samples, or 61% of the total number of individuals collected. From that point, the Michaelis–Menten estimator was lower than the observed richness. Also, at this point, the Chao1 and Chao2 estimators have reached the asymptote, although by the end of the curves the Chao2 decreased (slope = –0.003) (Fig. 1). The Jackknife1 was still rising (slope = 0.004) while the Jackknife2 seemed to have reached an asymptote by the end of the curve (slope < 0.001). With an estimate of 213 species, Chao1 generated the lowest estimate and this value was used to calculate a 'sampling completeness' of 87% (Table 1). The singleton and doubleton curves approached each other, but did not cross (Fig. 1).

Effects of sampling day, time of day, collectors and methods

The ANOVA results revealed that all tested factors, except the sampling day, influenced both richness and abundance per sample significantly (Tables 2 to 5). All the other factors had a very strong influence on the dependent variables, especially the methods (Table 5), followed by time of day (Table 3). When the collectors were grouped by level of experience, the differences were much reduced (Table 4), thereby indicating relatively strong differences between collectors that were grouped together. The ANOVA results taking interactions into account revealed a strong interaction between method and period, that is different methods behaved differently when comparing day and night productivity (for individuals $F_{3,128} = 19.629$, $P < 0.001$; for species $F_{3,128} = 7.373$, $P < 0.001$).

Table 2. Summary table with results for individual days and consecutive 'weeks' in chronological order. Based on 256 samples from within the plot.

	Day (ANOVA individuals/sample $P = 0.829$; species/sample $P = 0.296$)								Week (days) (ANOVA individuals/sample $P = 0.931$; species/sample $P = 0.044$)	
	1	2	3	4	5	6	7	8	1–4	5–8
No. of samples	32	32	32	32	32	32	32	32	128	128
No. of individuals	781	713	802	653	793	747	784	727	2949	3051
Individuals/sample	24.4	22.3	25.1	20.4	24.8	23.3	24.5	22.7	23.0	23.8
No. of species	88	84	86	84	88	86	87	87	125	131
Unique species	4	4	4	5	4	4	9	2	19	25
Species/sample	12.2	11.2	11.9	11.3	13.1	12.5	12.7	12.1	11.7	12.6
Sampling intensity	9	8	9	8	9	9	9	8	24	23

Table 3. Summary table of results based on the 256 night and day samples from within the plot (D1, D2, N1, N2 refer to the first and second day and night samples in sequence). The different groups revealed by the Tukey HSD test results are indicated for individuals and species per sample (a, b).

	Time of day (ANOVA individuals/sample $P < 0.001$; species/sample $P < 0.001$)				Whole period (ANOVA individuals/sample $P < 0.001$; species/sample $P < 0.001$)	
	D1	D2	N1	N2	Day	Night
No. of samples	64	64	64	64	128	128
No. of individuals	1297	1280	1778	1645	2577	3423
Individuals/sample	20.3^{a}	20.0^{a}	27.8^{b}	25.7^{b}	20.1	26.7
No. of species	103	101	106	104	126	124
No. of unique species	13	10	8	6	26	24
Species/sample	10.4^{a}	10.1^{a}	14.5^{b}	13.6^{b}	10.2	14.0
Sampling intensity	13	13	17	16	20	28

Table 4. Summary table with results for each collector, based on all samples from within the plot. Collectors 1 through 4 were considered experienced, collectors 5 through 8 were considered inexperienced and collectors A and B were capturing all arthropods, not only spiders, and are treated separately. The different groups revealed by the Tukey HSD test results are indicated for individuals and species per sample (a, b, c, d, e).

	Collector (ANOVA individuals/sample $P < 0.001$; species/sample $P < 0.001$)										Experience (ANOVA individuals/sample $P = 0.033$; species/sample $P = 0.017$)	
	1	2	3	4	5	6	7	8	A	B	Experienced	Inexperienced
No. of samples	32	32	32	32	32	32	32	32	32	32	128	128
No. of Individuals	970	921	583	730	669	837	800	490	468	703	3204	2796
Individuals/sample	30.3^{a}	28.8^{a}	18.2^{c}	$22.8^{a,b,c}$	$20.9^{b,c}$	$26.2^{a,b}$	$25.0^{a,b,c}$	15.3^{c}	14.6	22.0	25.0	21.8
No. of species	83	104	75	78	85	83	80	70	70	83	130	120
No. of unique species	5	11	3	6	7	5	1	1	—	—	30	20
Species/sample	$13.5^{a,b}$	15.2^{a}	$10.0^{d,e}$	$12.0^{b,c,d,e}$	$10.6^{c,d,e}$	$13.3^{a,b}$	$12.5^{b,c,d}$	9.9^{e}	8.4	11.2	12.7	11.6
Sampling intensity	12	9	8	9	8	10	10	7	7	8	25	23

Sampling day. A non-randomised collecting curve gives a graphic illustration of the accumulation of species over time (Fig. 2). The curve was very steep in the beginning (first day) when many new species were found and then gradually levelled off during the next days, as it became more difficult to find additional species and eventually the curve became almost horizontal as very few new species were added to the species pool. Only two new species were found during the last day of collecting and the last 16 samples (two night samples of eight collectors) did not add any new species at all.

The abundance and species richness per sample were almost constant throughout the sampling days (Table 2). The species richness per sample even increased from the first to the second 'weeks', although only by marginally significant values. Species composition as revealed by ANOSIM and Spearman correlation results was similar for all the days (ANOSIM $P > 0.05$ in most paired comparisons, full data $R = 0.002$, $P = 0.255$; $r_s > 0.648$, $P < 0.001$ in all paired comparisons). The only exception was day 1, which had a species composition that differed significantly from days 4, 6 and 7 ($0.040 < R < 0.046$, $P < 0.05$).

Table 5. Summary table with results for individual methods and based on the 256 samples from within the plot and 64 pitfall samples. Search methods: aerial, ground; tool methods: beat, sweep.

	Method (ANOVA individuals/sample $P < 0.001$; species/sample $P < 0.001$)					Method type (ANOVA individuals/sample $P < 0.001$; species/sample $P < 0.001$)	
	Aerial	Ground	Beat	Sweep	Pitfall	Search	Tool
No. of samples	64	64	64	64	64	128	128
No. of individuals	872	803	2117	2208	1516	1675	4325
Individuals/sample	13.6	12.5	33.1	34.5	23.7	13.1	33.8
No. of species	79	98	81	93	83	121	105
Unique species	8	6	7	9	35	45	29
Species/sample	8.3	7.9	15.7	16.5	11.5	8.1	16.1
Sampling intensity	11	8	26	24	18	14	41
Singletons	25	32	23	27	27	30	21
Doubletons	9	14	7	7	12	14	17
Estimates							
Chao1 ± SD	109 ± 14	131 ± 13	113 ± 15	137 ± 19	110 ± 12		
Chao2 ± SD	115 ± 16	131 ± 13	109 ± 13	140 ± 19	110 ± 11		
Jackknife1 ± SD	105 ± 5	130 ± 6	104 ± 4	121 ± 6	112 ± 6		
Jackknife2	122	147	118	141	126		
Michaelis–Menten	87	116	80	93	85		
Completeness	72%	75%	72%	68%	75%		

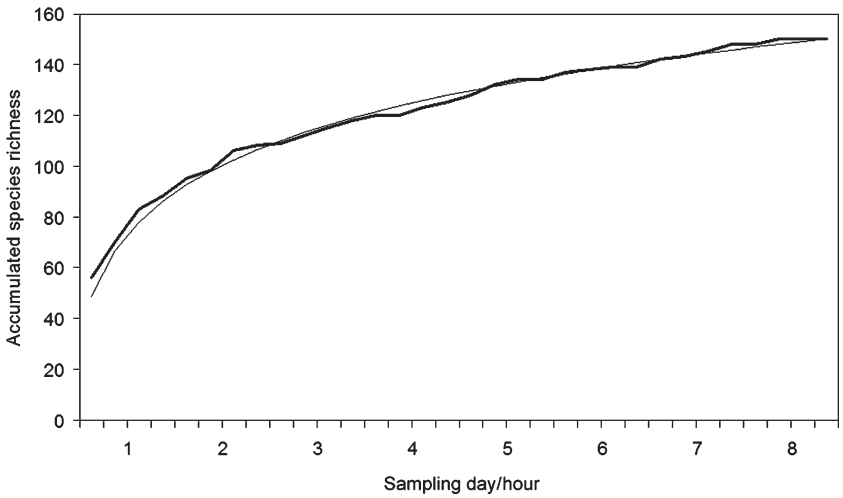

Fig. 2. Chronological accumulation curve (thick curve) of species richness inside the plot, and randomised accumulation curve based on the same data (thin curve). Subdivisions on the x-axis represent one 'collecting hour', each representing eight samples taken simultaneously by eight collectors.

Time of day. Night samples revealed more species and specimens than day samples (Table 3). The Tukey HSD tests revealed highly significant differences between day and night samples ($P < 0.001$ in all paired comparisons) but no difference between similar periods (D1 versus D2 and N1 versus N2; $P > 0.433$ in all cases). The observed number of individuals was also higher at night. The observed species richness though, was almost the same day and night and the number of unique species per sample was higher during the day (Table 3). The Spearman correlation index did not detect any differences in species composition ($r_s > 0.672$, $P < 0.001$ in all paired comparisons) but the analysis of similarity revealed very significant differences between day and night samples, in all cases with P-values below 0.001 (full data $R = 0.069$, $P < 0.001$).

Collectors. The relatively low significance of the ANOVA results for collectors (Table 4) was reflected in the few cases where collectors differ in abundance or richness per sample. If collectors were grouped into experienced and inexperienced, there were only marginal differences (in number of species and individuals) between the two groups. The experienced collectors were the most productive (Table 4) and the most experienced collector (collector 2) captured more species than the rest. The species composition in most of the samples was mostly correlated for all collectors ($r_s > 0.583$, $P < 0.001$ in all paired comparisons), although the ANOSIM results indicate that collectors 2 and 6 collected in different ways and thereby produced samples with a species composition significantly different from some other collectors ($P > 0.05$ in most paired comparisons but full data

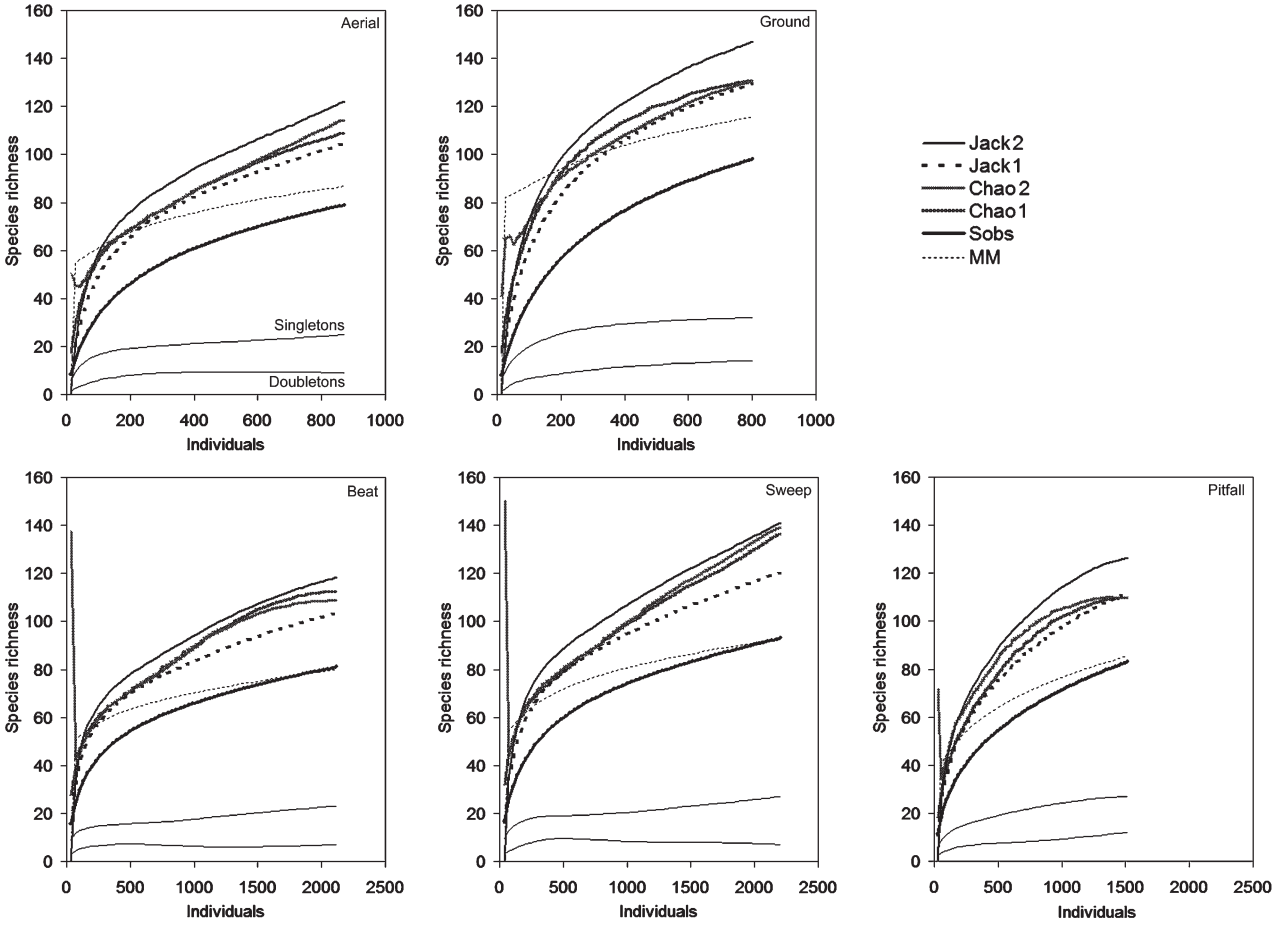

Fig. 3. Randomised accumulation curves for observed species richness, singletons, doubletons and richness estimators for all methods, inside the sampling plot.

$R = 0.015$, $P < 0.001$). The two collectors that were sampling all arthropods, including spiders, must be analysed separately, but they produced spider samples that were comparable in numbers to those of collectors concentrating on spiders only (Table 4).

Methods. Methods that employed some kind of tool to capture spiders (like beat and sweep) were the most productive in terms of number of species or individuals per sample (Table 5). Despite such differences between samples, the total number of species sampled by each method was relatively similar. Each sampling method captured approximately half of the observed species (Table 5).

As already seen, richness estimators based on all data (gathering all methods) stabilised and some even reached an asymptote (Fig. 1). This was not the case for estimates based on individual methods. All curves for aerial collecting (Fig. 3) revealed a very steep final slope between 0.034 (Chao1) and 0.059 (Jackknife2) with no asymptote. The same with ground collecting [Fig. 3; all slopes between 0.02 (Chao1) and 0.053 (Jackknife2)] and sweep netting [Fig. 3; all slopes between 0.017 (Jackknife2) and 0.026 (Chao1)]. The Chao estimators for beating (Fig. 3; Chao1 slope = 0.005, Chao2 slope = 0.003) and pitfall trapping (Fig. 3; Chao1 slope = 0.006, Chao2 slope = 0.003), on the contrary, presented curves that were closer to the asymptote.

The ANOSIM results suggested that each method sampled a different part of the spider community ($P < 0.001$ in all paired comparisons; full data $R = 0.639$, $P < 0.001$). The pitfall traps collected more unique species than any other method and the species composition of those samples were also more distinct. In fact, pitfall samples presented a strong negative correlation with all other methods ($r_s < -0.386$, $P < 0.001$ in all paired comparisons), except ground collecting, with which there was no correlation, positive or negative ($r_s = 0.112$, $P > 0.05$).

Methods and time of day interaction. Different methods generated quite different results, in terms of collected individuals and species per period (Table 6). Aerial collecting was much more productive at night ($P < 0.001$). Ground collecting at night was more productive than day collecting, but only in terms of individuals per sample ($P = 0.028$), not species per sample ($P = 0.112$),

Table 6. Summary table showing results for each collecting method and time of day, based on the 256 samples from the plot.

	Aerial		Ground		Beat		Sweep	
	Day	Night	Day	Night	Day	Night	Day	Night
Samples	32	32	32	32	32	32	32	32
Individuals	207	665	331	472	982	1135	1057	1151
Individuals/sample	6.5	20.8	10.3	14.8	30.7	35.5	33.0	36.0
Species	46	66	65	77	67	64	67	83
Unique species	2	5	13	3	4	2	6	3
Species/sample	4.6	12.1	6.7	9.2	14.7	16.8	15.0	17.9
Sampling intensity	5	10	5	6	15	18	16	14
Singletons	22	21	26	27	19	15	17	25
Doubletons	5	4	8	15	4	7	8	12
Estimates								
Chao1 ± SD	84 ± 18	108 ± 20	101 ± 16	99 ± 10	101 ± 17	77 ± 8	82 ± 9	106 ± 11
Chao2 ± SD	91 ± 20	100 ± 16	94 ± 13	97 ± 9	91 ± 12	79 ± 9	86 ± 10	116 ± 14
Jackknife1 ± SD	69 ± 5	86 ± 3	90 ± 6	103 ± 6	85 ± 4	80 ± 5	84 ± 5	110 ± 6
Jackknife2	87	101	105	114	98	88	95	127
Michaelis–Menten	63	74	88	99	72	67	72	88
Completeness	55	61	64	78	66	83	82	78

and the observed number of species collected at night was higher than those collected during the day (Table 6). Collecting based on beating presented no significant differences in abundance or richness per sample between day and night ($P > 0.330$) but the total number of collected individuals was higher at night whereas the total number of species was higher in the day samples (Table 6). Sweeping was more productive at night ($P = 0.04$) which was also obvious from the observed values (Table 6).

For all methods, although day and night abundances of species were always correlated ($r_s > 0.463$, $P < 0.001$), they presented highly significant differences in composition (ANOSIM $P < 0.001$ in all paired comparisons; full data $R = 0.479$, $P < 0.001$). Such differences were higher for aerial and sweep ($R = 0.478$ and 0.388 respectively) than for ground and beat ($R = 0.144$ and 0.169).

Discussion

The results of this inventory suggest that the species richness of spring adult spiders living in the Mediterranean oak forest at Peneda-Gerês National Park is somewhere between 213 and 260, depending on whether data from the plotless sampling are included. If so, estimated numbers in the higher end of the range are obtained, certainly because the plotless sampling included a larger area and other habitats (riverine oak forest), besides the higher sampling effort. These are estimates of the 'instantaneous' species richness (*sensu* Coddington *et al*., 1996) being without doubt an underestimate of the 'true' total richness of the area. Since species that may be adult at another time of the year are missed, as are species not accessible to the methods applied, the true total species richness of the area investigated is expected to be somewhat higher, probably well above 300 species (see also Cardoso *et al*., 2007). Most other semi-quantitative studies have been carried out in tropical or temperate forests. Of the temperate sites, the mixed oak-pine forest at the Ellicott Rock site in Georgia, USA (Coddington *et al*., 1996) was nearly comparable in latitude and altitude to our sampling area. Surprisingly, the oak forest in Peneda-Gerês has approximately twice as many observed species as the oak-pine forest in Ellicot Rock. Of the tropical sites, the Rio Tigre site in Bolivia at 500 m (Coddington *et al*., 1991, 1996) and the Pakitza site in Peru at 350 m (Silva & Coddington, 1996) are most nearly comparable in elevation, but are tropical forests, and thereby represent a completely different vegetation type. Pakitza & Rio Tigre have approximately 1.6 and 2.4 times more observed species than our site in Peneda-Gerês. In terms of species diversity, our Mediterranean habitat is therefore intermediate.

A total of 50% of the specimens collected in this study are adults. This is a very high fraction, compared to the figures reported from other studies in both tropical and temperate areas, where the fraction are typically 25–30% (Coddington *et al*., 1991; Coddington *et al*., 1996; Scharff *et al*., 2003). The high fraction of adults could perhaps be explained by the vegetation structure of the sampling area. The dense arboreal vegetation allows more species to co-exist as adults during any given season of the year, and especially during the peak richness season of May and June (Cardoso *et al*., 2007).

The inventory added 26 new species to the Portuguese national checklist of 730 species (Cardoso, 2007) and revealed 27 specimens of the newly described linyphiid species *Labulla machadoi* Hormiga & Scharff, 2005, which was otherwise only known from a few old specimens in museum collections. This clearly reveals how little is known about the Portuguese/Iberian/Mediterranean spider fauna and how much there still is to be found.

Richness estimation

The Michaelis–Menten estimator constantly produced estimates that were lower than the observed values (Fig. 1) and this study thereby supports other findings (Soberón & Llorente, 1993; Colwell & Coddington, 1994) that have concluded that the

Table 7. Summary table with results and estimated spider species richness for a selected number of studies following a semi-quantitative sampling inventory.

Reference	Coddington *et al*. 1996	Dobyns 1997	Sørensen *et al*. 2002 (plot)	Sørensen *et al*. 2002 (total)	Scharff *et al*. 2003	Gerês (plot)	Gerês (total)
Site	USA	USA	Tanzania	Tanzania	Denmark	Portugal	Portugal
No. of samples	133	157	200	370	149	320	480
No. of individuals	1629	2842	4708	9096	8710	7516	10 808
No. of species	89	92	148	170	66	185	204
Sampling intensity	18	31	32	53	132	41	53
Singletons	29%	20%	24%	19%	29%	21%	19%
Estimated richness (Chao1)	123	112	176	197	81	213	232
Completeness	72%	82%	84%	86%	81%	87%	88%

Michaelis–Menten estimator is not an adequate species richness estimator for very intensive protocols with many samples and high completeness values. However, the behaviour of the Michaelis–Menten curve (Fig. 1) for the plot data supports its use as a stopping rule (Magurran, 2004). Both Chao1 and Chao2 estimators reach an asymptote at approximately the same number of collected specimens as where the Michaelis–Menten curve crosses the observed species accumulation curve (Fig. 1). Beyond this point, the Chao estimates only increase by 4%, despite 65% more individuals collected.

Both Chao estimators are doing well, reaching an asymptote with both plot and plotless data (Fig. 1), with very low final slope values. Chao1 delivers the lowest estimates, and Chao2 is the same or very close (Table 1), which also agrees well with other studies where these estimators have been applied. Based on the present study, the use of the two Chao estimators is recommended for short-term semi-quantitative sampling programs in delimited and relatively uniform areas. They provided the lowest and most conservative estimate and perhaps also the most realistic, given the high effort employed during this inventory and the fact that only two new species were added in the last day of inventory. They also reached the asymptote with low slope values more often than the Jackknife estimators did. The possible use of the Michaelis–Menten curve as a stop-rule is suggested, the non-parametric estimator values seem to reach the asymptote at about the same time when that curve crosses the observed species accumulation curve.

Rare species

Rare species in this kind of inventories may be true rare or just apparently rare. The high number of locally rare species is often explained as a result of undersampling and/or various kinds of edge effects (Scharff *et al*., 2003). The edge effects include phenological edge effects (individuals that are mature outside the normal breeding season), methodological edge effects (individuals that inhabit microhabitats not adequately accessed with the sampling methods used) and spatial edge effects (individuals that prefer habitats not present in the study area) and all of these problems could very well have affected the present inventory. However, since little is known about the phenology of spiders in the sampled habitat and very little about the habitat preference of Mediterranean spiders, it is difficult to evaluate the potential edge effects intervening in this case. For instance, it is known that *Hyptiotes paradoxus* is closely associated with evergreen trees and shrubs in northern Europe, and that the presence of *H. paradoxus* therefore could be considered an example of a spatial edge effect. But the species is often found in deciduous forests in Portugal (P. Cardoso, pers. obs.) and one should therefore be careful with such conclusions. The same is true for *Atypus affinis*, but the habitat preference of this species is indeed different in southern and northern Europe. In northern Europe, *A. affinis* is always found in open habitats (like heathlands) where the characteristic silken tubes are exposed on the ground. In southern Europe, the silken tubes of *A. affinis* are found under deep leaf litter in oak forests.

Singletons represented 22% of the species found within the plot (320 samples) (Table 1), but when the remaining 160 samples are added, the percentage of singletons falls to 19%. This suggests that in this particular case, enlarging the area (and habitat types) investigated improved the quality of the inventory. The same pattern was shown when comparing the inventory completeness of the plot (87%) and total pooled samples (88%). Most probably, the increase in effort was enough to compensate the increase in area and heterogeneity of the habitats sampled. The high degree of completeness and the relatively low (compared to other similar studies) percentage of singletons suggest that this inventory was exhaustive. Given the sampling effort and the results that point towards an adequate inventory, it is surprising to see that 64 out of 204 observed species are only represented by one or two specimens (Table 1).

Effects of fauna depletion, time of day, collector and method

This inventory represents one of the most comprehensive inventories carried out to date (Table 7) based on the semi-quantitative sampling outlined by Coddington *et al*. (1991) both in terms of number of samples and adult specimens. During the inventory, 6000 adult spiders were removed from the sampling plot (Table 1), and one could think that the intensive collecting had a negative effect on the overall spider fauna so that the species richness and abundance would decrease over the sampling days. However, the species richness and abundance of spiders remained constant throughout the sampling (Table 2). This result agrees with

previous studies in both temperate and tropical areas (Sørensen *et al*., 2002; Scharff *et al*., 2003), confirming that irrespectively of the sampled habitat, the abundance of spiders in forests is so high that it is almost impossible to cause the depletion of fauna.

Several previous tropical studies have shown that both species richness and abundance of spiders are higher at night (Green, 1999; Sørensen *et al*., 2002) and this is also supported in this study. This is different from results obtained in temperate areas, where Scharff *et al*. (2003) found higher abundance of species but not higher species richness during the night, in a beech forest in Denmark. In another temperate study, Coddington *et al*. (1996) and Dobyns (1997) found no difference at all between night and day collecting in Georgia, USA.

Although differences were found between the most and least productive collectors, most of the paired comparisons revealed none, probably because of the simplicity in learning the techniques even for inexperienced persons. Moreover, the total number of specimens and species and the number of unique species sampled by each collector were ranked slightly differently than the respective species per sample. This means that, in the future, sampling performed by different collectors will be perfectly comparable, which is encouraging as a start for the definition of a standardised and optimised protocol.

More surprising was the fact that the two collectors sampling all arthropods were not statistically distinguishable from all other collectors. This could be due to various reasons, such as an unconscious preference for collecting spiders (having experience with this type of sampling) or due to the use of methods biased towards spiders. Although more studies would have to be conducted with more collectors focussing on all arthropods, these results suggest that it may be possible to collect taxonomically broader and still get usable data. Even more encouraging, it may be feasible by simply expanding the number of methods employed to some complementary 'passive' methods (e.g. Malaise traps, pan traps, Berlese funnels), to build all-arthropod sampling protocols without a considerable increase in the amount of required field resources (material, time or collectors).

As expected, and in accordance with all previous studies (Coddington *et al*., 1991, 1996; Dobyns, 1997; Sørensen *et al*., 2002; Scharff *et al*., 2003; Cardoso *et al*., 2007a, b), 'methods' is the single most important factor influencing the results. Methods differ greatly in the number of species and individuals per sample and also in the composition of spiders in samples. Preferably, methods that sample all microhabitats should be selected and overlap as little as possible. All methods generate unique species and are therefore worthwhile, and should not have been left out of the sampling protocol. With 35 unique species, pitfall trapping is by far the most productive method for unique species (Table 5). Obviously, pitfall trapping is an essential method to include in spider inventories. Bark traps were tested as a new method in this inventory. They catch cryptic species that hide beneath bark etc., but even though they worked for 2 weeks, each trap only generated an average of one adult spider per trap and only two species [*Segestria senoculata* (Linnaeus, 1758) and *Poecilochroa albomaculata* (Lucas, 1846)] were unique to the method. The bark trap method is therefore considered inefficient and it is suggested that the effort would rather be directed towards other methods.

Looking at the estimates provided by each method (Fig. 3), beating and pitfall trapping present more robust Chao1 estimates than sweeping, ground and aerial. This is clearly seen in the species accumulation curves, where the Chao1 curves for beating and pitfall trapping approach the asymptote, whereas sweeping, ground and aerial show typical signs of undersampling, with a species accumulation curve that show no signs of asymptotic behaviour. In other words, more effort (collected individuals) was probably needed for aerial, ground and sweeping and more species could have been found with these methods. Almost all methods performed better at night and each method provided unique species both day and night. These results emphasise the importance of collecting in both periods. They also suggest that, in the future, each individual combination of method and period should probably be regarded as a different method in itself.

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Appendix 1. List of species and number of adult spiders collected in Peneda-Gerês National Park in northern Portugal; †genus new to the Iberian Peninsula; ‡species new to the Iberian Peninsula; §genus new to Portugal; ¶species new to Portugal. Nomenclature following Platnick (2007).

Agelenidae (9 spp.)	379
Malthonica lusitanica Simon, 1898	187
Tegenaria aff. *ramblae*	1
Tegenaria duellica Simon, 1875	1
Tegenaria feminea Simon, 1870	2
Tegenaria montigena Simon, 1937	92
Tegenaria picta Simon, 1870	6
Tegenaria ramblae Barrientos, 1978	40
Tegenaria sp.	6
Textrix pinicola Simon, 1875	44
Amaurobiidae (1 sp.)	16
†*Callobius* sp.	16
Anyphaenidae (1 sp.)	35
Anyphaena accentuata (Walckenaer, 1802)	35
Araneidae (14 spp.)	1514
Agalenatea redii (Scopoli, 1763)	1
Araneus sturmi (Hahn, 1831)	42
Araneus triguttatus (Fabricius, 1793)	4
Araniella cucurbitina (Clerck, 1757)	248
Araniella opisthographa (Kulczyński, 1905)	37
Cercidia prominens (Westring, 1851)	50
Cyclosa conica (Pallas, 1772)	10
Gibbaranea bituberculata (Walckenaer, 1802)	31
Gibbaranea gibbosa (Walckenaer, 1802)	4
Hypsosinga albovittata (Westring, 1851)	3
Hypsosinga sanguinea (C. L. Koch, 1844)	4
Mangora acalypha (Walckenaer, 1802)	719
Nuctenea umbratica (Clerck, 1757)	1
Zilla dioidia (Walckenaer, 1802)	360
Atypidae (1 sp.)	2
Atypus affinis Eichwald, 1830	2
Clubionidae (6 spp.)	397
Clubiona brevipes Blackwall, 1841	82
Clubiona comta C. L. Koch, 1839	195
Clubiona corticalis (Walckenaer, 1802)	3
Clubiona diniensis Simon, 1878	2
Clubiona leucaspis Simon, 1932	3
Clubiona terrestris Westring, 1851	112
Corinnidae (4 spp.)	107
§*Cetonana* sp.	1
Phrurolithus cf. *festivus* (C. L. Koch, 1835)	5
Phrurolithus minimus C. L. Koch, 1839	99
Trachelas validus Simon, 1884	2
Dictynidae (5 spp.)	558
Dictyna arundinacea (Linnaeus, 1758)	1
Lathys humilis (Blackwall, 1855)	276
Lathys sp.	14
Mastigusa arietina (Thorell, 1871)	2
Nigma puella (Simon, 1870)	265
Dysderidae (11 spp.)	335
Dysdera falciformis Barrientos & Ferrández, 1982	3
Dysdera fuscipes Simon, 1882	13
Dysdera lusitanica Kulczyński, 1915	14
Dysdera machadoi Ferrández, 1996	97

Appendix 1. *Continued*

Dysdera sp. 1	1
Dysdera sp. 2	1
Harpactea fageli Brignoli, 1980	5
Harpactea hombergi (Scopoli, 1763)	15
Harpactea sp.	2
§*Harpactocrates* sp.	1
Rhode scutiventris Simon, 1882	183
Gnaphosidae (15 spp.)	139
Callilepis concolor Simon, 1914	13
Callilepis nocturna (Linnaeus, 1758)	3
‡*Callilepis schuszteri* (Herman, 1879)	5
Drassodes fugax (Simon, 1878)	17
Drassodes sp.	6
Drassyllus sp.	1
†*Echemus angustifrons* (Westring, 1861)	11
Micaria dives (Lucas, 1846)	2
Nomisia excerpta (O. P.-Cambridge, 1872)	2
Poecilochroa albomaculata (Lucas, 1846)	2
Scotophaeus blackwalli (Thorell, 1871)	1
Setaphis parvula (Lucas, 1846)	1
Zelotes aff. *flagellans* (L. Koch, 1882)	8
¶*Zelotes gallicus* Simon, 1914	36
Zelotes sp.	31
Hahniidae (2 spp.)	8
Hahnia candida Simon, 1875	7
¶*Hahnia montana* (Blackwall, 1841)	1
Linyphiidae (32 spp.)	806
Centromerus dilutus (O. P.-Cambridge, 1875)	2
Centromerus sp.	1
Erigone dentipalpis (Wider, 1834)	3
Erigone promiscua (O. P.-Cambridge, 1873)	48
Labulla machadoi Hormiga & Scharff, 2005	29
Lepthyphantes minutus (Blackwall, 1833)	8
Linyphia maura Thorell, 1875	2
Linyphiidae sp. 1	1
Linyphiidae sp. 2	6
Linyphiidae sp. 3	1
Linyphiidae sp. 4	1
Linyphiidae sp. 5	3
Linyphiidae sp. 6	2
Meioneta fuscipalpa (C. L. Koch, 1836)	10
§*Microneta viaria* (Blackwall, 1841)	16
Neriene furtiva (O. P.-Cambridge, 1871)	10
¶*Neriene peltata* (Wider, 1834)	76
Neriene radiata (Walckenaer, 1842)	155
§*Obscuriphantes obscurus* (Blackwall, 1841)	2
Palliduphantes stygius (Simon, 1884)	2
†*Peponocranium ludicrum* (O. P.-Cambridge, 1861)	1
Pocadicnemis pumila (Blackwall, 1841)	18
Prinerigone vagans (Audouin, 1826)	3
Sintula sp.	281
§*Tapinocyba* sp.	1
Tenuiphantes tenuis (Blackwall, 1852)	24
Tenuiphantes zimmermanni (Bertkau, 1890)	5
Tiso vagans (Blackwall, 1834)	1
Trichoncus similipes Denis, 1965	68
Trichoncus trifidus Denis, 1965	20
Walckenaeria dalmasi (Simon, 1914)	5
¶*Walckenaeria* cf. *dysderoides* (Wider, 1834)	
Liocranidae (3 spp.)	22
Agroeca inopina O. P.-Cambridge, 1886	18
Liocranum rupicola (Walckenaer, 1830)	2
Scotina celans (Blackwall, 1841)	2
Lycosidae (5 spp.)	103
Alopecosa pulverulenta (Clerck, 1757)	2
¶*Arctosa leopardus* (Sundevall, 1833)	1
Pardosa hortensis (Thorell, 1872)	80
Pardosa pullata (Clerck, 1757)	1
Lycosidae sp.	19
Mimetidae (2 spp.)	20
Ero aphana (Walckenaer, 1802)	18
Ero tuberculata (De Geer, 1778)	2
Miturgidae (2 spp.)	68
¶*Cheiracanthium elegans* Thorell, 1875	60
Cheiracanthium striolatum Simon, 1878	8
Nemesiidae (1 sp.)	3
Nemesia ungoliant Decae, Cardoso & Selden, 2007	3
Oonopidae (1 sp.)	31
Oonops sp.	31
Philodromidae (10 spp.)	485
Philodromus albidus Kulczyński, 1911	3
Philodromus aureolus (Clerck, 1757)	81
Philodromus buxi Simon, 1884	2
¶*Philodromus cespitum* (Walckenaer, 1802)	1
Philodromus dispar Walckenaer, 1826	96
Philodromus margaritatus (Clerck, 1757)	1
Philodromus pulchellus Lucas, 1846	1
Philodromus rufus Walckenaer, 1826	47
Philodromus sp.	18
Tibellus oblongus (Walckenaer, 1802)	235
Pisauridae (1 sp.)	100
Pisaura mirabilis (Clerck, 1757)	100
Salticidae (16 spp.)	1264
Aelurillus v-insignitus (Clerck, 1757)	1
Ballus chalybeius (Walckenaer, 1802)	200
Chalcoscirtus infimus (Simon, 1868)	3
Euophrys frontalis (Walckenaer, 1802)	24
Euophrys sulphurea (L. Koch, 1867)	2
Evarcha jucunda (Lucas, 1846)	3
Evarcha laetabunda (C. L. Koch, 1846)	352
Heliophanus cupreus (Walckenaer, 1802)	552
Neon levis (Simon, 1871)	41
Pseudicius encarpatus (Walckenaer, 1802)	4
Salticus mutabilis Lucas, 1846	1
Salticus scenicus (Clerck, 1757)	31
Salticus zebraneus (C. L. Koch, 1837)	5
Synageles venator (Lucas, 1836)	8
Talavera petrensis (C. L. Koch, 1837)	1
Salticidae sp.	36
Segestridae (1 sp.)	1
Segestria senoculata (Linnaeus, 1758)	1
Sparassidae (2 spp.)	32
Micrommata virescens (Clerck, 1757)	31
Olios argelasius (Walckenaer, 1805)	1
Tetragnathidae (3 spp.)	512
Metellina mengei (Blackwall, 1870)	44
Metellina merianae (Scopoli, 1763)	54
Tetragnatha extensa (Linnaeus, 1758)	414
Theridiidae (35 spp.)	3303
Achaearanea lunata (Clerck, 1757)	84
¶*Achaearanea riparia* (Blackwall, 1834)	1
Anelosimus pulchellus (Walckenaer, 1802)	69

Appendix 1. *Continued*

Anelosimus vittatus (C. L. Koch, 1836)	124
Crustulina guttata (Wider, 1834)	3
‡*Dipoena erythropus* (Simon, 1881)	64
Dipoena melanogaster (C. L. Koch, 1837)	863
‡*Dipoena nigroreticulata* (Simon, 1879)	9
‡*Dipoena torva* (Thorell, 1875)	3
Dipoena sp.	20
¶*Enoplognatha latimana* Hippa & Oksala, 1982	3
Enoplognatha ovata (Clerck, 1757)	2
Episinus angulatus (Blackwall, 1836)	6
Episinus maculipes Cavanna, 1876	10
Episinus truncatus Latreille, 1809	79
Keijia tincta (Walckenaer, 1802)	221
Kochiura aulica (C. L. Koch, 1838)	13
¶*Lasaeola tristis* (Hahn, 1833)	614
Neottiura bimaculata (Linnaeus, 1767)	6
Neottiura curvimana (Simon, 1914)	2
Paidiscura pallens (Blackwall, 1834)	199
Pholcomma gibbum (Westring, 1851)	18
Phoroncidia paradoxa (Lucas, 1846)	52
Rhomphaea rostrata (Simon, 1873)	6
Simitidion simile (C. L. Koch, 1836)	243
Steatoda bipunctata (Linnaeus, 1758)	5
Theridion blackwalli O. P.-Cambridge, 1871	3
Theridion hannoniae Denis, 1944	1
Theridion hemerobium Simon, 1914	1
Theridion impressum L. Koch, 1881	1
Theridion mystaceum L. Koch, 1870	405
Theridion pinastri L. Koch, 1872	4
Theridion sisyphium (Clerck, 1757)	45
Theridion varians Hahn, 1833	120
Theridion sp.	2
Thomisidae (17 spp.)	323
†*Bassaniana versicolor* (Keyserling, 1880)	2
Diaea dorsata (Fabricius, 1777)	16
Ebrechtella tricuspidata (Fabricius, 1775)	2
Heriaeus melloteei Simon, 1886	1
Misumena vatia (Clerck, 1757)	26
Ozyptila atomaria (Panzer, 1801)	16
Pistius truncatus (Pallas, 1772)	4
Synema globosum (Fabricius, 1775)	27
Thomisus onustus Walckenaer, 1805	1
¶*Tmarus stellio* Simon, 1875	67
Tmarus sp.	20
Xysticus acerbus Thorell, 1872	1
Xysticus cristatus (Clerck, 1757)	16
Xysticus erraticus (Blackwall, 1834)	50
Xysticus ferrugineus Menge, 1876	6
Xysticus lanio C. L. Koch, 1835	55
Xysticus tortuosus Simon, 1932	13
Uloboridae (2 spp.)	6
Hyptiotes paradoxus (C. L. Koch, 1834)	1
Uloborus walckenaerius Latreille, 1806	5
Zodariidae (1 sp.)	121
Zodarion machadoi Denis, 1939	121
Zoridae (1 sp.)	118
Zora spinimana (Sundevall, 1833)	118
Total number of adult specimens	10 808