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The conservation value of secondary forests in the southern Brazilian Mata Atlântica from a spider perspective

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Abstract. In many tropical areas of the world, pristine forests have become rare. Nevertheless, due to shifts in the human population the area covered by secondary forests is increasing. These forests may harbor a rich flora and fauna and are considered to be main refuges for species of primary forests. However, this issue is far from clear. To assess the conservation value of secondary forests in the Atlantic Forest of Brazil, we compared the diversity of spiders in differently aged secondary forests with old-growth forests. Within a larger project treating several invertebrate taxa, we sampled spiders using a standard protocol in 24 sites of three successional stages (5–8, 15–20, 30–50 years old) and old-growth forests (> 100 years untouched) in two nature reserves. We describe the diversity and structure of the assemblages using morphospecies and genera and analyze richness at the genus level. Generic richness and diversity showed no differences between successional stages; i.e., did not increase from the youngest to older forests, but guild diversity did increase. The youngest stage showed the highest variability in generic composition, and the turnover of genera and species was strong between the younger forests (5–20 years old) and forests older than 30 years. High alpha diversity, high turnover among sites and the lack of differences in richness between stages support the value of secondary forests for species conservation in the region studied.

Keywords: Araneae, diversity, guild structure, Atlantic Forests, Brazil

The Brazilian Atlantic forest (Mata Atlântica) is one of the ''hottest hotspots'' of biodiversity (Laurance 2009), due to its exceptional species richness and high number of endemic taxa in the various forest types (Forzza et al. 2012). However, the coastal region of Brazil has experienced an exceptionally high degree of forest conversion and deforestation (Myers et al. 2000; Ribeiro et al. 2009) for more than 500 years. In contrast to the more strongly deforested areas of the Atlantic coast, in the state of Paraná in southern Brazil large remnants of Atlantic forests still exist, forming a mosaic of patches of old-growth forests (sensu Clark 1996; also see Wirth et al. 2009) and secondary forests in various stages of succession. These secondary forests originate mainly from abandoned buffalo pastures. Recently the issue of the importance of these secondary forests for the conservation of biodiversity initiated a controversial discussion (see Bihn et al. 2008b).

Conservation strategies and management in the tropics are often based on large, exotic and beautiful or rare, endangered vertebrate species. However, the overwhelming part of biodiversity consists of invertebrates. Furthermore, invertebrates are involved in numerous important ecosystem functions (e.g., nutrient cycling or pollination). The analyses of invertebrate diversity for conservation are usually restricted to species numbers or lists of species of selected taxa. Although the number of species is not a quality measure per se, richness and diversity measures, which include the relative abundance of species, are valuable approximations to biodiversity and the conservation value of a habitat (Gaston 1996; Gotelli & Colwell 2001; Brose et al. 2003; Magurran 2004). This is especially true when autecological data are lacking; i.e., when knowledge of the distribution, natural history traits and habitat preferences for most of the species is sparse. However, to evaluate the richness of an assemblage a reference is needed. Comparing species numbers of assemblages in secondary vegetation with the original (primary) vegetation seems to be a meaningful approach to estimate degradation, to recognize the loss of functional diversity (Bihn et al. 2008b, 2010) and to classify areas with regard to their conservation value (Dunn 2004), although there is some evidence of functional redundancy (Lawton et al. 1998; Loreau et al. 2001).

The Brazilian-German cooperative project SOLOBIOMA (Höfer et al. 2007, 2011) studied the biogeochemistry and, in a multi-taxon approach, the diversity of earthworms (Römbke et al. 2009), enchytraeids (Schmelz et al. 2009, 2011), ants (Bihn et al. 2008a,b), beetles (Hopp et al. 2010, 2011; Ottermanns et al. 2011) and spiders in order to evaluate the conservation value of secondary forests in the Mata Atlântica. The overall aim of this project was to check the possibility of classifying secondary forest stages by their soil fauna and comparing that with the ''traditional'' classification by age and vegetation. In the absence of true primary vegetation in this region, we had to rely on ''old-growth'' forests as a reference.

Spiders are a species-rich taxon in the tropics. In Brazil the taxonomy is comparatively well studied (Brescovit et al. 2011), and meaningful faunistic inventories are available (Höfer 1990, 1997; Silva 1996; Silva & Coddington 1996; Höfer & Brescovit 2001; Rego et al. 2007; Venticinque et al. 2008; Bonaldo et al. 2009). However, in these studies there is a strong bias toward the Amazonian region. During the most recent years and based on taxonomic advances and faunistic knowledge, several studies in the Mata Atlântica, focusing on spiders, have approached ecological questions (effects of disturbance, fragmentation and vegetation type: Benati et al. 2005; Candiani et al. 2005; Oliveira-Alves et al. 2005; Podgaiski et al. 2007). However, studies with well-replicated designs are still rare (Dias et al. 2005; Bonaldo et al. 2007; Lo-Man-Hung et al. 2008; Pinto-Leite et al. 2008; Ricetti & Bonaldo 2008). To assess the conservation value of secondary forests, we sampled spiders on

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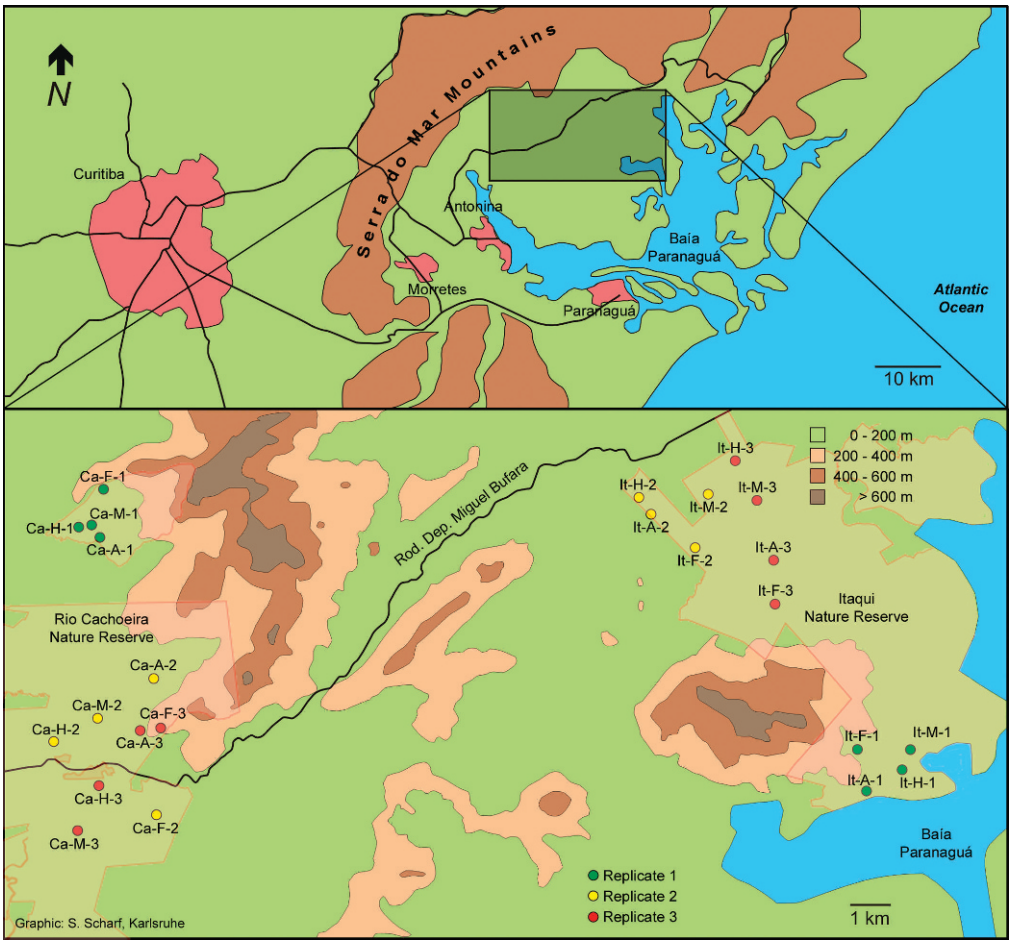

Figure 1.—Location of the study region in Paraná state, Brazil and the sampling sites in the two Nature Reserves Rio Cachoeira (Ca) and Itaqui (It); successional stages: H – herbaceous, A – arboreal, M – medium, F – old-growth forest.

the ground and in the lower vegetation in three different stages of secondary and old-growth forests, appraising the changes in richness and composition of genera across the successional gradient.

METHODS

Study area.—This study was conducted in the coastal region of Paraná State in southeastern Brazil. Originally the region was covered by dense ombrophilous lowland and submontane forests (IBGE 1992), but these ecosystems suffered massive exploitation and were largely converted to buffalo pastures (IPARDES 1995). Today, the landscape is characterized by a mosaic of open land, secondary forests and few relatively large patches of old-growth forests. The regional climate is humid subtropical (Köppen's Cfa: Strahler & Strahler 2005), with mean temperatures between 16.2 °C in July and 24.5 °C in February (IPARDES 2001). Average precipitation ranges between 2000 and 3000 mm year^{-1} (Roderjan & Kunyoshi 1988). Rainfall is more or less evenly distributed throughout the year, although with some seasonality (low rainfall from April to August).

The areas studied are part of an ecological restoration program (Feretti & Britez 2006). Sampled sites were located in two private nature reserves (RPPN) "Reserva Natural do Rio Cachoeira" and "Reserva Natural Serra do Itaqui" (Fig. 1). Both are owned and managed by the Brazilian NGO "Society for wildlife research and environmental education" (SPVS) and are part of the Environmental Protection Area (EPA) of Guaraqueçaba and also the Mata Atlântica Biosphere Reserve. Within their areas of 12,000 and 6,700 ha, respectively, ranging from sea level to elevations of 700 m a.s.l., different successional stages from pasture to forest were categorized a priori by the SPVS using age and vegetational structure, based on orthophotos from 1952, 1980 and 2002 and knowledge of the residents on historical use.

Study design.—In both reserves (subsequently called localities), which are located approximately 25 km apart (Cachoeira: 25.3142°S, 48.6958°W; Itaqui: 25.2733°S, 48.4872°W), we sampled spiders along a chronosequence of four forest stages: 5–8 years old (H – herbaceous stage), 10–15 years old (A – arboreal stage), 35–50 years old (M – medium stage) and > 100 years old (F – old-growth); the latter was used as a reference stage. In each stage we sampled three spatially separated replicate sites of 30 × 50 m^2 each. In total, 12 sites (3 replicates × 4 stages) were studied in both localities (Fig. 1) during several days of sampling (see below) in springtime (October/November) of 2005 (Cachoeira) and 2007 (Itaqui). The springtime period provides a high degree of sampling completeness without the necessity of resampling throughout the year (Baldissera et al. 2003; Rodrigues 2005; Podgaiski et al. 2007).

Table 1.—Absolute and relative abundance and richness of the spider families captured on lower vegetation (by beating and looking up). N = number of individuals, G = number of genera, S = number of morphospecies.

Family	N	% N	G	% G	S	% S
Theridiidae	1010	37.4	29	19.6	96	30.2
Linyphiidae	374	13.8	9	6.1	23	7.2
Salticidae	370	13.7	29	19.6	52	16.4
Araneidae	234	8.7	21	14.2	53	16.7
Anyphaenidae	148	5.5	8	5.4	10	3.1
Thomisidae	119	4.4	7	4.7	10	3.1
Pholcidae	98	3.6	3	2.0	12	3.8
Uloboridae	69	2.6	3	2.0	5	1.6
Tetragnathidae	60	2.2	5	3.4	9	2.8
Dictynidae	58	2.2	1	0.7	1	0.3
Mimetidae	33	1.2	3	2.0	4	1.3
Scytodidae	32	1.2	1	0.7	2	0.6
Oonopidae	24	0.9	5	3.4	5	1.6
Theridiosomatidae	24	0.9	5	3.4	12	3.8
Corinnidae	10	0.4	4	2.7	7	2.2
Oxyopidae	9	0.3	3	2.0	4	1.3
Hahniidae	8	0.3	1	0.7	1	0.3
Zoridae	5	0.2	1	0.7	2	0.6
Miturgidae	4	0.2	2	1.4	2	0.6
Lycosidae	3	0.1	1	0.7	1	0.3
Deinopidae	2	0.1	1	0.7	1	0.3
Hersiliidae	2	0.1	1	0.7	1	0.3
Sparassidae	2	0.1	1	0.7	1	0.3
Amaurobiidae	1	0.0	1	0.7	1	0.3
Ctenidae	1	0.0	1	0.7	1	0.3
Philodromidae	1	0.0	1	0.7	1	0.3
Synotaxidae	1	0.0	1	0.7	1	0.3
Sum: 27	2702		148		318	

Sampling methods and identification.—A structured sampling, following a widely accepted standard protocol (Coddington et al. 1991), was applied to sample spider diversity in these forests:

a) Ground hand sampling (''looking down'' of Coddington et al. 1991): two experienced persons sampled for one hour at night with headlights, exploring all structures below knee level, resulting in one sample per person, two samples per site.
b) Aerial hand sampling (''looking up'' of Coddington et al. 1991): one person sampled for one hour at night, exploring all structures from knee height upwards to overhead arm's reach; i.e., lower vegetation, resulting in 1 sample per site.
c) Beating: Three persons striking vegetation at any reachable level (i.e., lower vegetation) with a stick, collecting the spiders falling on a 50 × 50-cm tray held below, for one hour. Twenty beating points made one sample. Depending on the person sampling, a different number of samples per site (3–9) resulted.
d) Pitfall trapping: Ten traps per site were installed to capture active ground spiders for one week, usually resulting in 10 samples per site, with a few failures. Traps were 330 ml PE cups with an opening diameter of 7.5 cm, filled with 100 ml of 4% formaldehyde solution and protected against rain by transparent plastic plates.

The spiders sampled were stored in 75% ethanol. All adult spiders were determined to morphospecies or to morphogenera if possible, using a conservative approach to delimit morphospecies and morphogenera. All analyses are based on adult spiders. Notwithstanding the progress in spider taxonomy in the Neotropics, severe shortcomings in the analyses of the diversity of tropical faunas remains a prime difficulty in identifying specimens to the species level or to sort all adult specimens to the level of morphospecies. This is due to the high number of inadequately described species and the lack of identification keys (Uehara-Prado et al. 2009). We therefore used genera as a surrogate for the comparison of species richness and diversity, which has been shown to be a successful strategy even at local scales (Andersen & Hauge 1995; Balmford et al. 1996; Baldissera et al. 2008; Bihn et al. 2008b).

Identifications were made by the first and third authors, with help from Brazilian experts at Butantan Institute, São Paulo (IBSP) and Museu de Ciências Naturais da Fundação Zoobotânica, Porto Alegre (MCN). Morphospecies numbers (in the appendix) were assigned according to IBSP and MCN numeration to assure future comparability. Voucher material is deposited at the entomological department of Universidade Federal do Paraná in Curitiba (UFPR), at IBSP and MCN.

Data analysis.—We pooled the complementary captures from the different methods and strata for all analyses. Richness and diversity of the spider assemblages per site (alpha diversity) were described by the numbers of genera (G) observed, the ratio of genera/individuals (G/N), the Shannon index (H), the Shannon evenness measure (E) and log series α (Magurran 2004). We used rarefaction (Hurlbert 1971; Coleman 1982; Gotelli & Entsminger 2004; Magurran 2004) for the

Table 2.—Absolute and relative abundance and richness of the spider families captured on the ground (by pitfall traps and looking down). N = number of individuals, G = number of genera, S = number of morphospecies.

Family	N	% N	G	% G	S	% S
Zoridae	855	47.7	1	0.9	8	3.6
Theridiidae	210	11.7	25	21.6	48	21.6
Linyphiidae	126	7.0	12	10.3	29	13.1
Ctenidae	121	6.8	2	1.7	6	2.7
Pholcidae	69	3.9	5	4.3	13	5.9
Lycosidae	62	3.5	5	4.3	9	4.1
Pisauridae	54	3.0	1	0.9	2	0.9
Araneidae	49	2.7	10	8.6	22	9.9
Mysmenidae	40	2.2	3	2.6	4	1.8
Hahniidae	26	1.5	1	0.9	7	3.2
Salticidae	25	1.4	8	6.9	14	6.3
Corinnidae	18	1.0	3	2.6	6	2.7
Amaurobiidae	17	1.0	1	0.9	3	1.4
Oonopidae	16	0.9	4	3.5	5	2.3
Ochyroceratidae	14	0.8	1	0.9	3	1.4
Theridiosomatidae	12	0.7	2	1.7	4	1.8
Tetragnathidae	11	0.6	5	4.3	7	3.2
Thomisidae	11	0.6	3	2.6	6	2.7
Anyphaenidae	10	0.6	3	2.6	3	1.4
Scytodidae	10	0.6	1	0.9	2	0.9
Nemesiidae	8	0.5	2	1.7	2	0.9
Titanoecidae	7	0.4	1	0.9	1	0.5
Mimetidae	4	0.2	1	0.9	2	0.9
Gnaphosidae	2	0.1	1	0.9	1	0.5
Palpimanidae	2	0.1	2	1.7	2	0.9
Prodidomidae	2	0.1	1	0.9	1	0.5
Anapidae	1	0.1	1	0.9	1	0.5
Caponiidae	1	0.1	1	0.9	1	0.5
Deinopidae	1	0.1	1	0.9	1	0.5
Dipluridae	1	0.1	1	0.9	1	0.5
Liocranidae	1	0.1	1	0.9	1	0.5
Miturgidae	1	0.1	1	0.9	1	0.5
Nesticidae	1	0.1	1	0.9	1	0.5
Symphytognathidae	1	0.1	1	0.9	1	0.5
Synotaxidae	1	0.1	1	0.9	1	0.5
Trechaleidae	1	0.1	1	0.9	1	0.5
Uloboridae	1	0.1	1	0.9	1	0.5
Zodariidae	1	0.1	1	0.9	1	0.5
Sum: 38	1793		116		222	

direct comparison of generic richness between the single sites. It was calculated with R version 2.10.2 (R Development Core Team 2009), using the rarefy function of the package VEGAN 1.17-2 (Oksanen et al. 2009). To evaluate the proportion of rare genera at the single site, we calculated the relative abundance of singletons (proportion of genera with one individual from the total genera number per site: Magurran 2004). We calculated the nonparametric sample-based estimators Chao 2 and ICE (Magurran 2004) with EstimateS 8.0 (Colwell 2005). A coverage measure was calculated for each site using the number of observed genera as a percent of the estimated richness.

Similarity across stages (beta diversity) was analyzed with qualitative presence/absence (Sørensen index) and quantitative (abundance) data for assemblage structure (NESS = Normalized Expected Species Shared: Grassle & Smith 1976). In contrast to the Sørensen Index, NESS is a quantitative similarity measure, which accounts for the individual numbers of shared species in the sites compared or assemblages (as in the Renkonen or Bray-Curtis qualitative index), but weights the rare species with ascending values for the sample size. Therefore it seems to be a good measure for tropical communities, where rare species account for a considerable part of the recorded species (Chazdon et al. 1998; Novotny & Basset 2000). We calculated NESS with the program BIODIV 97 for Excel.

To visualize differences in spider assemblages of the forest stages and localities, we used a three-dimensional ordination based on a non-metric multidimensional scaling (nMDS) analysis, calculated on Bray-Curtis similarities of square-root transformed abundances of genera using Winkyst 1.0 (100 random perturbations) and Canoco for Windows 4.53 (Ter Braak 2002). The similarity matrix was tested for spatial autocorrelation using the mantel function of the R package ECODIST. The spatial distribution of the study sites had no effect on the patterns of beta diversity ($P = 0.98$).

To complete the comparison of the forest stages, we used available guild classifications for the Neotropical spider fauna

Table 3.—Alpha diversity of spiders in the Cachoeira sites (genus based, samples from all methods pooled). Site codes: Ca H1–3 = Cachoeira sites of herbaceous stage, Ca A1–3 of arboreal stage, Ca M1–3 of medium stage, Ca F1–3 of old-growth. N = number of individuals, G = number of genera, H = Shannon Index, E = evenness, α = Fishers's alpha index, Ra = rarefied genera number, Sg = portion of singletons, Chao 2 = estimated generic richness, ICE = sample-based richness estimate, Coverage = number of observed genera as a percentage of Chao 2-estimated richness, SD = standard deviation, CV = coefficient of variation.

Site	N	G	G/N	H	E	A	Ra (SD)	Sg	Chao 2 (SD)	ICE	Coverage
Ca H1	165	51	0.31	3.5	0.66	25.3	44.0 (2.1)	0.39	61.6 (6.2)	73.5	82.8
Ca H2	139	40	0.29	3.1	0.57	18.8	36.4 (1.6)	0.55	69.0 (16.1)	86.8	58
Ca H3	194	51	0.26	3.3	0.52	22.5	40.5 (2.4)	0.45	79.0 (14.8)	83.0	64.6
Ca A1	169	37	0.22	2.6	0.36	14.6	30.7 (2.0)	0.49	53.3 (10.2)	62.1	69.4
Ca A2	134	50	0.37	3.4	0.59	28.9	46.4 (1.6)	0.54	94.4 (22.0)	119.7	53
Ca A3	185	52	0.28	3.4	0.58	24.0	41.5 (2.4)	0.46	100.6 (25.4)	103.7	51.7
Ca M1	137	49	0.36	3.2	0.51	27.3	44.5 (1.7)	0.61	86.9 (18.8)	115.0	56.4
Ca M2	155	46	0.30	3.4	0.56	22.1	39.8 (2.0)	0.52	94.1 (26.2)	93.1	48.9
Ca M3	169	44	0.26	3.0	0.45	19.3	36.4 (2.1)	0.50	70.3 (14.5)	78.1	62.6
Ca F1	216	54	0.25	3.3	0.50	23.1	40.6 (2.5)	0.46	95.7 (22.5)	88.4	56.4
Ca F2	212	49	0.23	3.2	0.51	20.0	36.7 (2.5)	0.47	83.7 (18.6)	89.5	58.5
Ca F3	241	57	0.24	3.3	0.48	23.6	39.9 (2.7)	0.46	79.6 (11.3)	92.8	71.6
Total	2116	157							220.4 (25.2)	200.0	71.3
Mean	176.3	49.3	0.28	3.2	0.52	22.5	39.8	0.49	80.7	90.5	61.2
CV	19%	12%	17%	8%	15%	17%	11%	12%	18%	18%	16%

(Höfer & Brescovit 2001; Dias et al. 2010). We assigned the specimens to 16 distinct guilds. The assignment of a species to a guild is usually based on the family, in some cases on the genus, which was possible for almost all specimens in our samples. In a few cases we had to apply personal knowledge of the biology of a taxon based on our own observations in the field, the sampling method and information in the literature (Silva & Coddington 1996; Álvares et al. 2004). Only the Amaurobiidae (18 individuals) were not assigned to a guild due to the unclear taxonomic status and lack of ecological information for Neotropical species. For the comparison of guild structure in the different stages, data from the two localities were pooled.

The rarefied genera numbers, the estimated richness and the alpha diversity values were tested for significant effects of the stage (four levels) and the locality (two levels) with two-way ANOVAs using Statistica 8.0 (StatSoft 2007). Permutational multivariate analysis of variance (Permanova, Version 1.6: Anderson 2001, 2005) was used to analyze the generic turnover in the spider assemblage of different forest stages and to underpin the ordination with a statistical analysis. We tested the main factors of the residuals and their interaction terms with 9999 permutations using Bray-Curtis dissimilarities between the study sites.

Indicator analysis was done with R, version 2.10.1 (R Development Core Team 2009) and the packages MASS (Venables & Ripley 2002) and labdsv (Roberts 2007). Because indicators of single stages were weak, we pooled the beating tray data of the two younger and the two older stages to one group each [stages H and A = young (Y), stages M and F = old (O)] in order to achieve a distinctive separation with indicator genera of high indicator values for younger and older forests, respectively.

Table 4.—Alpha diversity of spiders in the Itaqui sites (genera based, samples from all methods pooled). Site codes: It H1–3 = Itaqui sites of herbaceous stage, It A1–3 of arboreal stage, It M1–3 of medium stage, It F1–3 of old growth. N = number of individuals, G = number of genera, H = Shannon index, E = evenness, α = Fishers's alpha index, Ra = rarefied genera number, Sg = portion of singletons, Chao 2 = estimated generic richness, ICE = sample-based richness estimate, Coverage = number of observed genera as a percentage of Chao 2-estimated richness, SD = standard deviation, CV = coefficient of variation.

Site	N	G	G/N	H	E	α	Ra (SD)	Sg	Chao2 (SD)	ICE	Coverage
It H1	121	38	0.31	3.2	0.64	19.0	37.5 (0.7)	0.42	51.6 (8.3)	64.7	73.6
It H2	253	54	0.21	3.2	0.45	21.0	37.1 (2.7)	0.48	97.2 (22.2)	103.3	55.6
It H3	125	34	0.28	2.4	0.31	15.4	32.5 (1.1)	0.68	71.7 (21.4)	128.6	47.4
It A1	150	44	0.29	3.2	0.53	21.0	38.6 (1.9)	0.52	75.7 (17.3)	90.6	58.1
It A2	230	50	0.22	2.5	0.26	18.5	32.7 (2.6)	0.54	117.3 (37.4)	101.8	42.6
It A3	160	42	0.26	3.1	0.54	17.8	35.4 (1.9)	0.46	61.1 (12.0)	71.1	68.7
It M1	205	43	0.21	3.0	0.49	16.6	33.4 (2.3)	0.44	70.7 (16.1)	79.7	60.8
It M2	277	54	0.20	3.2	0.46	20.0	37.3 (2.7)	0.37	78.2 (13.6)	77.3	69.1
It M3	281	57	0.20	3.3	0.46	21.6	38.7 (2.8)	0.37	73.5 (8.9)	85.2	77.6
It F1	123	33	0.27	3.1	0.69	14.8	32.4 (0.7)	0.36	47.3 (9.9)	51.3	69.8
It F2	274	60	0.22	3.4	0.47	23.7	39.4 (2.9)	0.45	109.2 (24.7)	105.5	54.9
It F3	180	44	0.24	3.2	0.58	18.6	37.2 (2.0)	0.36	60.4 (9.7)	67.0	72.8
Total	2379	154							196.8 (17.3)	191.5	78.3
Mean	198.3	46.1	0.24	3.1	0.49	19.0	36.0	0.45	76.2	85.5	62.6
CV	32%	19%	16%	10%	25%	14%	7%	21%	29%	25%	18%

Table 5.—Sampling effort, generic richness (observed and estimated) and diversity per stage (means and standard deviations from three replicates, all samples pooled). N = number of individuals, G = number of genera, α = Fishers's alpha index, Ra = rarefied genera number, Sg = portion of singletons (pooled data for the three replicates), Chao 2 = estimated generic richness, ICE = sample-based richness estimate, Coverage = number of observed genera as a percentage of Chao 2-estimated richness. SD = standard deviation. Abbreviations for stage as in Tables 3 and 4.

Stage	Samples	Total N	Mean N (SD)	Total G	Ra (SD)	Sg	α (SD)	Chao 2 (SD)	ICE	Coverage
Ca H	60	498	166 (28)	89	47.6 (3.4)	0.34	31.6 (2.3)	116.6 (12.5)	125.2	76.3
Ca A	69	488	163 (26)	85	43.7 (3.4)	0.34	29.8 (2.2)	111.3 (11.9)	126.2	76.3
Ca M	70	461	153 (16)	83	42.9 (3.3)	0.41	29.5 (2.3)	115.8 (14.3)	135.5	71.7
Ca F	72	669	223 (16)	84	40.9 (3.2)	0.36	25.4 (1.7)	119.3 (17.0)	113.6	70.4
It H	69	499	166 (75)	86	44.9 (3.4)	0.34	30.0 (2.2)	102.5 (8.0)	115.8	83.9
It A	65	540	180 (44)	82	39.3 (3.3)	0.43	26.9 (2.0)	116.5 (15.2)	132.2	70.4
It M	72	763	254 (43)	89	40.6 (3.3)	0.33	26.1 (1.7)	117.6 (13.9)	118.6	75.7
It F	62	577	192 (76)	81	41.4 (3.2)	0.40	25.7 (1.8)	123.5 (19.7)	127.4	65.6
Total	539	4495	187 (51)	192	49.8 (3.8)	0.23	40.7 (1.4)	248.8 (22.3)	229.3	77.2

RESULTS

A total of 11,293 individuals were collected from 539 samples, of which only the 4,495 (39.8%) adults were identified and sorted to 43 families, 192 genera and 440 morphospecies (Appendix 1). We were able to identify and name 155 species according to the available literature. Although the two localities were sampled in different years, similar numbers of spiders were collected: 2,116 individuals of 33 families and 157 genera in Cachoeira (2005) and 2,379 individuals of 37 families and 154 genera in Itaqui (2007). The ratios of females/males (0.941, 0.948) and adults/juveniles (0.673, 0.669) were also similar.

Overall, Theridiidae ranked first in abundance, accounting for 27% of all adults, and also in species richness with 117 morphospecies in 34 genera. The theridiid genera *Dipoena* (19 morphospecies), *Theridion* (16), *Cryptachaea* (13) and *Thymoites* (10) showed the highest species richness. Only the araneid genus *Mangora* was represented by a comparably high number of morphospecies (10). Zoridae ranked second with 19% of the individuals, but only eight morphospecies. The spider assemblages in Cachoeira and Itaqui showed a similar ranking (Spearman $r = 0.36$) of family abundance values, but Theridiidae and Linyphiidae were nearly twice as abundant in Itaqui as in Cachoeira. The Araneidae (58 morphospecies/21 genera), Salticidae (55/29) and Linyphiidae (43/15) accounted together for more than 35% of all species and 34% of all genera collected.

As expected, sampling in different strata (ground/vegetation) yielded strongly complementary sets of lineages. In the vegetation 74% of all spiders captured were web-builders. Theridiidae and Linyphiidae alone accounted for more than 50% (Table 1), with more than 100 species. The only abundant hunting spiders in the vegetation were Salticidae (55 morphospecies) and Anyphaenidae (10 species). There was no dominant (10% criterion) species or genus in the vegetation, and the 316 morphospecies (148 genera) collected showed that this stratum houses a large part of the total diversity. In strong contrast, half of all spiders captured on the ground belong to one genus of small hunting zorids, and 70% of all were hunting spiders (Table 2). All abundant hunting-spider families (Zoridae, Ctenidae, Lycosidae, Pisauridae) were represented by few genera and species and thus overall richness (216 morphospecies, 116 genera) was lower than in the vegetation. Very few mygalomorphs (i.e., Nemesiidae, Dipluridae) were collected.

Alpha diversity.—The number of individuals ranged from 134 to 241, representing 37 to 57 genera, in Cachoeira and from 121 to 277, representing 33 to 60 genera, in Itaqui. Means of all generic richness values were very close, and the coefficient of variation rarely exceeded 20% (Tables 3, 4). The same applied to the diversity indices. Typical for nonrecurring sampling of tropical habitats, nearly half of the morphospecies or genera were represented by only one adult specimen per site of a stage (singletons: Tables 3, 4, Appendix 1). Both estimators produced very similar values (mean of 81 genera in Cachoeira, 76 in Itaqui), corresponding to a coverage of over 60%. The richness of genera (total, mean rarefied, estimated) was very similar across the stages of forest succession (see means in Table 5).

After correcting for the sampling effort (number of samples, individuals), no differences between the stages were found. None of the statistical tests (two-way ANOVAs with stage and locality as factors and rarefied and estimated generic richness and the two diversity indices as dependent variables) showed a significant effect of stage or locality. The spider assemblages in younger stages were as rich in genera and as diverse as in the old-growth forests. At the stage level the portion of singletons was 33% or higher, the estimated number of genera, based on the Chao 2 and ICE estimators, was mostly less than twice the number of observed genera and, consequently, coverage was higher than 66% (Table 5). At the morphospecies level the portion of singletons in the stages was even higher.

Beta diversity.—Qualitative similarity (Sørensen index) of the different stages at each locality ranged from 0.53 (youngest stage with older) to around 0.7 (between older stages) (Tables 6, 7), reflecting a turnover of genera (and species)

Table 6.—Qualitative (Sørensen index, upper right) and quantitative (NESS index, lower left, m = 228) similarities between the forest stages in Cachoeira reserve, based on genera data, all methods pooled. Abbreviations for stage as in Table 3.

	Ca H	Ca A	Ca M	Ca F
Ca H		0.58	0.56	0.53
Ca A	0.76		0.70	0.67
Ca M	0.72	0.93		0.71
Ca F	0.70	0.92	0.92	

Table 7.—Qualitative (Sørensen index, upper right) and quantitative (NESS index, lower left, m = 248) similarities between the forest stages in Itaqui reserve, based on genera data, all methods pooled. Abbreviations for stage as in Table 4.

	It H	It A	It M	It F
It H		0.59	0.54	0.53
It A	0.82		0.65	0.58
It M	0.72	0.85		0.66
It F	0.67	0.76	0.91	

along the successional gradient. Furthermore, within-stage similarities were not higher, ranging from 0.4 (stage H) to 0.7 (stage F) in Cachoeira and from 0.3 (H) to 0.6 (M) in Itaqui. Similarities of the same stages from the two reserves were usually higher (Tables 8, 9) than of the different stages within the same locality (Tables 6, 7). Similarities between stage H and other stages were always lowest; the spider assemblage of the herbaceous stage differed strongly from the older stages.

Quantitative similarity (NESS) is generally higher than qualitative similarity (Tables 6–9), indicating that the dominant genera (respectively, species) were abundant in all stages. This is also obvious in the list of the ten most abundant genera (respectively, species) of the two localities, representing 49% and 50%, respectively, of all adults (Tables 10, 11). One zorid genus clearly dominated in all stages, and the positions of many abundant genera in the list are also very similar. Abundant spider species reflecting the turnover between younger (H, A) and older forests (M, F) are the linyphiids of the genus *Anodoration* and several theriidid genera (*Spintharus*, *Theridion*, *Thwaitesia*) in Itaqui and the dictynid *Thallumetus* and pholcids of the genus *Mesabolivar* in Cachoeira. In Itaqui the latter was also found exclusively in the two older stages, but was not among the ten most abundant genera (see also indicator analysis).

Multivariate analysis.—The ordination (Stress = 0.12: Fig. 2) shows the stages of both localities arranged along the first axis. The younger stages (H, A) are especially well separated from each other and from the older stages, with the exception of one herbaceous site in Cachoeira. A much higher variability of the youngest (H) stage is obvious. Sites of the two older stages (M, F) ordinate close to each other. Sites at Itaqui and Cachoeira separate along the second and third axes. Although the nMDS is based on Bray-Curtis distances, which are more biased to dominant species than the NESS measures, the ordination visualizes the same differences between sites as the NESS values (Tables 6, 7, 9). Several genera (mainly orb- and sheet-weavers, some anyphaenids) characterized the youngest herbaceous stage, whereas the older stages grouped apart from the younger by pholcids (*Mesabolivar* spp.), the anyphaenid genus *Patrera*, the uloborid genus *Miagrammopes* and the theridiid genus *Spintharus*. The nMDS ordination was confirmed by a Permanova analysis. The four stages showed highly significant differences concerning their composition of spider assemblages ($F = 2.34$; $P = 0.0007$).

Table 8.—Qualitative similarity (Sørensen) between the forest stages in both reserves, based on genera data, all methods pooled. Abbreviations for stage as in Tables 3 and 4.

	It H	It A	It M	It F
Ca H	0.65	0.56	0.49	0.51
Ca A	0.58	0.62	0.65	0.66
Ca M	0.56	0.66	0.69	0.69
Ca F	0.50	0.64	0.68	0.68

Table 9.—Quantitative similarity (NESS, m = 228) between the forest stages in both reserves, based on genera data, all methods pooled. Abbreviations for stage as in Tables 3 and 4.

	It H	It A	It M	It F
Ca H	0.82	0.75	0.65	0.65
Ca A	0.76	0.85	0.91	0.85
Ca M	0.68	0.80	0.89	0.86
Ca F	0.57	0.80	0.91	0.92

Functional diversity.—Weavers were more abundant than hunting spiders in all stages (62/38%–56/44%), with the exception of the young arboreal stage (49/51%). Most spiders (40%) belonged to the diurnal space-web weavers, and these were more abundant in the herbaceous stage than in the older ones. Twenty-one percent were ground runners, most abundant in the young arboreal stage and less in the herbaceous. Spiders known to be diurnal dominated the collections with 44% of all individuals, while nocturnal spiders accounted for 20%. The portion of diurnal spiders decreased with the age of the stages from 53% to 41%. In older forests distinctly more orb weavers (e.g., near the ground), sedentary sheet-web weavers and nocturnal ground ambushers (i.e., ctenids) were caught than in the younger stages. Ground runners were most abundant in the more open young arboreal stage (due to a higher proportion of lycosids). The number of guilds in the stages was nearly equal, but the diversity of guilds appeared to increase from the young herbaceous to the old forest stages (Table 12).

Indicator analysis.—Indicators of single stages were weak, so the two younger (H + A) and the two older (M + F) stages were pooled to show a clear separation by genera (Table 13). *Spintharus* and *Miagrammopes* showed high indicator values for the older forest stages, whereas *Anodoration* and *Titidius* were indicatory taxa for the younger forests. The same genera fitted best to the nMDS ordination space, but species arrows are not shown in Fig. 2 to maintain legibility.

DISCUSSION

Given the project's approach, we put time and effort into the use of replicates to allow for a statistical analysis of biodiversity patterns of spiders in secondary forests, rather than to attempt to inventory the entire spider assemblage. We therefore did not undertake a special effort to sample cryptic, specialized or rare species, but rather used an accepted and widely used protocol to sample the spider assemblage on the ground and lower vegetation. By doing so we also made our samples per site comparable within our study and to other studies in the Neotropics. Due to difficulties in identifying the species and to avoid a biased result by wrong morphospecification of the partly undescribed tropical species, we based our richness measures and estimates on genera. According to other studies, genera serve as a reliable base for evaluating species richness (Baldissera et al. 2008; Bihn et al. 2010).

Table 10.—Assemblage structure (relative abundance of the ten most abundant genera) and total number of individuals (Ind.) in the four forest stages in Cachoeira reserve, pooled from all methods in all sites Abbreviations for stage as in Table 3.

Family	Genus	Ca H %	Ca A %	Ca M %	Ca F %	Ca total %	Ca Ind.
Zoridae	gen. 1	15.0	16.1	22.3	29.7	20.3	429
Salticidae	*Tariona*	5.1	6.7	3.8	4.1	5.1	108
Theridiidae	*Dipoena*	5.3	3.9	5.6	5.4	5.0	105
Linyphiidae	*Sphecozone*	6.4	3.3	0.4	7.6	4.3	90
Theridiidae	*Theridion*	3.1	2.4	0.8	6.7	3.1	66
Pholcidae	*Mesabolivar*	0.2	1.8	1.2	9.1	2.9	61
Araneidae	*Mangora*	2.0	0.9	2.8	6.5	2.8	60
Anyphaenidae	*Patrera*	0.0	1.5	3.8	3.9	2.2	47
Dictynidae	*Thallumetus*	0.0	0.0	4.0	5.4	2.1	45
Theridiidae	*Spintharus*	0.4	1.5	1.6	5.4	2.1	45

The temporal distant sampling of the two localities had no effect on any of the analyzed variables (total number of individuals, genera, families; ratios of female/male and adult/juvenile). The absence of autocorrelation in the dataset indicates that neither the temporal distance of the two sampling campaigns nor the spatial distance between the two localities had significant effects on the sampled spider assemblages.

Shortcomings in the methods, sampling protocol and identification could have masked differences in richness between the stages. Probably old-growth forests offer more specific microhabitats (e.g., in bromeliads or dead wood) for specialized, cryptically living or rare (less abundant, not widely distributed, not active during the whole year) species. These species cannot be assessed by either strongly vision-based sampling or by beating the easily accessible lower vegetation (Dias et al. 2000; Rinaldi et al. 2002). Thus, to assess and evaluate the diversity of complex habitats such as an old-growth forest in an unbiased way, more effort might be necessary, using special sampling techniques for specialized species. It is even questionable whether the old-growth sites studied, although not strongly altered by humans, were suitable as a reference in place of primary forests. They could have obscured differences between stages or a directed succession, being ''old-growth successional states'' in themselves. The lack of any native earthworm species in the investigated sites and the high dominance of the invasive species *Pontoscolex corethrurus* in all, even the oldest, forest sites (Römbke et al. 2009) shed some light on the long history of anthropogenic influence in the region.

Notwithstanding these possible constraints, our survey of spiders revealed a high richness at the genus and species level when compared to other studies in the realm of the Atlantic Forests. Some of them, however, sampled in urban parks, plantations or small forest fragments (Rinaldi & Ruiz 2002; Benati et al. 2005; Candiani et al. 2005; Oliveira-Alves et al. 2005). Comparably high richness values were recorded by Brescovit et al. (2004), Podgaiski et al. (2007) and Baldissera et al. (2008) for Atlantic forests and Ricetti & Bonaldo (2008) for Amazonian forests. The differences in both sampled and estimated alpha-diversity values between sites (of all types) and also between the two sampled reserves of our study were low and not significant. Even the youngest successional stages in the study area house a considerable diversity of spiders. This is not unusual, because such habitats often show high structural heterogeneity, prey availability and ecotone characteristics, which increase species numbers (Kotze & Samways 1999; Baldissera et al. 2003; Platen 2006; Pétillon & Garbutt 2008).

The high turnover of species between all sites, independent of the stage, was interesting. Stages differ in their species composition, not in richness. Variability within the a priori defined stages originates from the heterogeneity of structural and microclimatic conditions (openness, plant density), which in all stages is based on physical and pedological heterogeneity (exposition, inclination, soil type, groundwater level). The higher variability within the youngest stage (visible in the ordination) is probably caused by differences in historical (largely unknown) land use (e.g., the use of machines, fertilizers or pesticides), which mainly influences early

Table 11.—Assemblage structure (relative abundance of the ten most abundant genera) and total number of individuals (Ind.) in the four forest stages in Itaqui reserve, pooled from all methods in all sites. Abbreviations for stage as in Table 4.

Family	Genus	It H %	It A %	It M %	It F %	It total %	It Ind.
Zoridae	gen. 1	7.4	30.9	18.3	15.1	18.1	431
Theridiidae	*Dipoena*	2.4	6.1	7.9	3.6	5.3	126
Linyphiidae	*Sphecozone*	5.0	2.8	6.0	5.4	4.9	117
Theridiidae	*Spintharus*	0.2	1.9	9.7	5.2	4.8	115
Linyphiidae	*Anodoration*	16.2	2.8	0.0	0.0	4.0	96
Salticidae	*Tariona*	0.4	1.5	4.3	4.9	3.0	71
Theridiidae	*Thwaitesia*	0.4	1.3	1.6	7.1	2.6	62
Ctenidae	*Isoctenus*	0.8	2.4	2.9	3.8	2.6	61
Theridiidae	*Episinus*	6.4	1.3	2.2	0.9	2.6	61
Theridiidae	*Theridion*	9.2	0.2	0.1	1.9	2.5	59

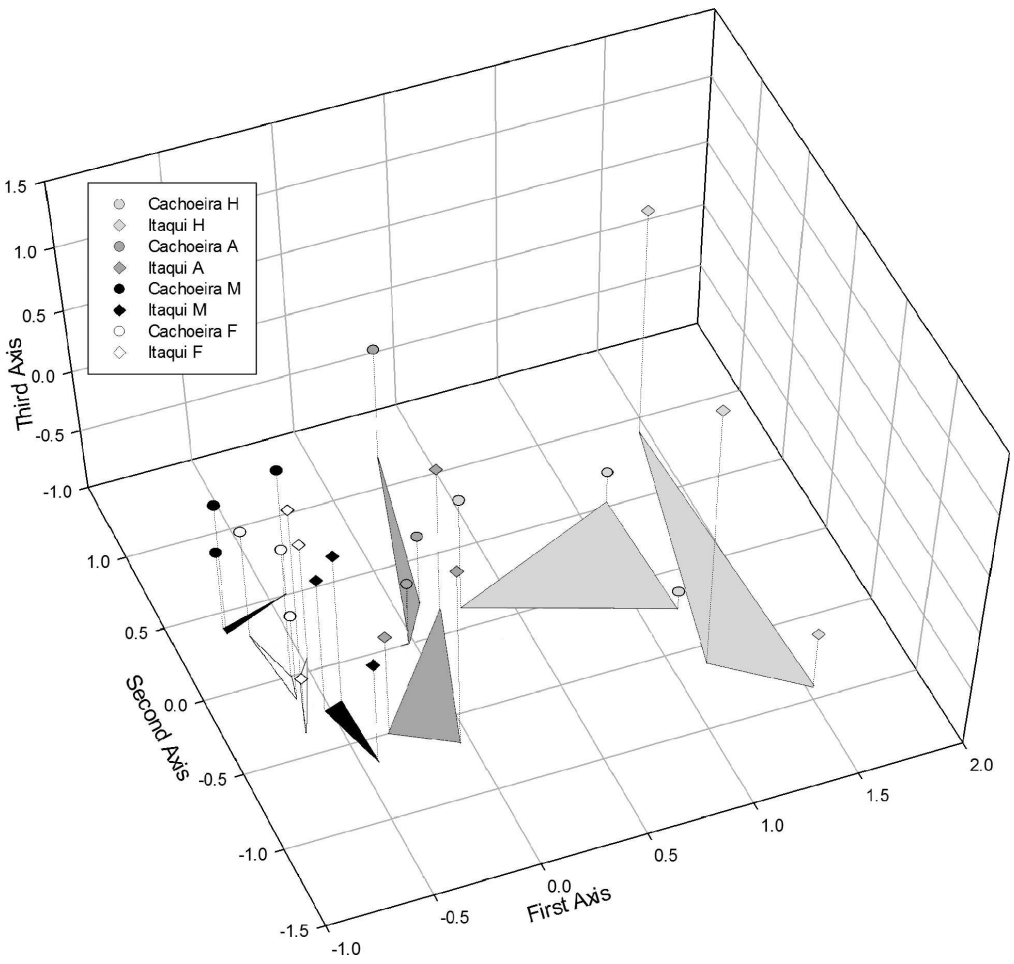

Figure 2.—Three-dimensional representation of a non-metric multidimensional scaling analysis (nMDS), based on Bray-Curtis distances; generic data pooled from all methods and sites in Cachoeira and Itaqui and square-root transformed (stress = 0.12).

Table 12.—Guild structure of the spider assemblage in the four stages, data of both localities and all methods pooled. Taxa assigned to guilds following Dias (2010) or Höfer and Brescovit (2001)[1]. H – herbaceous, A – arboreal, M – medium, F – old-growth forest.

Guild	Stages				Assigned families (genera)
	H	A	M	F	
Diurnal aerial ambushers	32	46	34	19	Thomisidae, Philodromidae
Diurnal aerial hunters	5	4	2	1	Miturgidae 2 (*Radulphius*), Oxyopidae
Diurnal ground runners	1	0	0	0	Liocranidae
Nocturnal aerial ambushers	2	2	0	1	Hersiliidae, Sparassidae,Trechaleidae
Nocturnal aerial hunters	77	37	68	46	Anyphaenidae, Scytodidae, Corinnidae
Aerial runners	91	101	121	110	Salticidae, Mimetidae
Nocturnal ground ambushers	13	29	39	49	Ctenidae, Nemesiidae
Nocturnal ground hunters	10	15	20	12	Salticidae 2 (*Asaphobelis*), Oonopidae, Palpimanidae, Caponiidae, Zodariidae, Prodidomidae
Ground runners/Nocturnal ground hunters	34	13	0	20	Lycosidae 1, Gnaphosidae
Ground runners	111	276	251	224	Miturgidae 1 (*Teminius, Strotarchis*), Zoridae
Diurnal ground orb weavers[1]	3	8	5	25	Mysmenidae, Symphytognathidae
Diurnal space-web weavers	487	374	460	459	Dictynidae, Linyphiidae, Synotaxidae, Theridiidae, Nesticidae
Nocturnal ground weavers[1]	12	2	20	12	Deinopidae, Dipluridae, Titanoecidae Anapidae, Hahniidae
Nocturnal space web weavers	1	2	4	7	Ochyroceratidae
Sedentary sheet weavers[1]	16	54	58	97	Pholcidae and Pisauridae 2 (*Architis*)
Orb weavers	103	65	138	154	Araneidae, Tetragnathidae, Theridiosomatidae, Uloboridae
Shannon Index H	1.75	1.83	1.87	1.94	
Evenness E	0.64	0.68	0.69	0.72	

Table 13.—Indicator analysis of the vegetation-bound spiders (beating tray data): O = older stages (M & F); Y = younger stages (H & A).

	Cluster	Indicator value	Probability
Spintharus	O	0.82	0.003
Miagrammopes	O	0.82	0.003
Patrera	O	0.76	0.002
Mangora	O	0.69	0.007
Thallumetus	O	0.67	0.003
Mesabolivar	O	0.63	0.041
Faiditus	O	0.50	0.013
Chrosiothes	O	0.42	0.043
Onoculus	O	0.42	0.043
Anodoration	Y	0.92	0.001
Titidius	Y	0.77	0.003
Hetschkia	Y	0.59	0.027

succession. During further succession, differences in biotic (prey availability, structure) and abiotic (climate) habitat parameters within and between the stages appear to decrease. An experimental manipulation of food and structure in one arboreal stage and the old-growth forest suggested food limitation of the decomposer fauna, but also revealed no effect of food or structure or any influence of stage on the spiders (Raub et al. 2014). Spiders are mostly generalist predators and seem to adapt easily to different food conditions and prey types (Uetz 1992), as long as suitable habitat structures and climate are provided. Baldissera et al. (2008) also found no differences in family, generic and species composition of the spider assemblages of natural *Araucaria* forest fragments and *Eucalyptus* monocultures, when appropriate habitat structures where provided.

The richness of our sites is comparable to other studies in Atlantic forests (see above), but some studies showed a different (family level) composition of assemblages (Rinaldi et al. 2002; Rinaldi & Ruiz 2002) and also significant differences in richness between young secondary and old-growth forest sites (Pinto-Leite et al. 2008; Uehara-Prado et al. 2009). We assume such differences to be caused by different uses of the sampled areas; for example, the use of pesticides or heavy machinery, and by the influence of the matrix of a forest fragment (see above).

Studies from tropical forest regions in the Brazilian Amazon revealed distinctly lower species richness of spiders in anthropogenic altered landscapes with forest patches than in a continuous forest cover (Lo-Man-Hung et al. 2011). However, as shown by Rego et al. (2005), taxa-specific responses can also lead to opposite responses in Neotropical forest fragments. High spider richness in the younger secondary sites should be regarded carefully in the context of conservation issues and not be taken as an absolute measure of habitat quality. Other invertebrate groups investigated in the same area showed an increase in richness along the successional gradient (Bihn et al. 2008b; Hopp et al. 2010).

The use of indicator taxa is becoming more and more important in the context of the growing anthropogenic pressure on highly diverse and threatened tropical ecosystems. For the evaluation of the conservation potential and state of secondary and old-growth tropical forests, precise but quick and cheap tools such as indicators are needed (Uehara-Prado et al. 2009). However, the use of indicator taxa in the evaluation of ecosystems is a controversial topic, especially because of the indirect effects in food webs (Abrams et al. 1996), together with the lack of knowledge of the interrelations between the taxa. Therefore a multi-taxon approach with a carefully selected set of organisms (Kotze & Samways 1999; Cabra-García et al. 2012) should be used. Nonetheless, the results of our indicator analysis can be used for evaluations of secondary forest areas in the southern Mata Atlântica region. The identified genera can serve as indicator taxa for the evaluation of priority areas for forest conservation. For future evaluations they should be combined with the outcomes of other arthropod studies (Bihn et al. 2008b; Hopp et al. 2011; Ottermanns et al. 2011), and ecological traits should also be included to establish a reliable multi-taxon approach for the implementation of conservation strategies (Kotze & Samways 1999; Uehara-Prado et al. 2009).

Recovery of (species) richness can be relatively fast. Dunn (2004) reported a time span of 20–40 years for ant and bird richness recovery, which is comparable to the age of our medium-aged secondary forests. However, the regeneration of the original forest community often needs much more time (Dunn 2004; Bihn et al. 2008b). Among spiders, some forest-dwelling Lycosidae still do not seem to find adequate habitat in the oldest secondary stage. We therefore assume that mature secondary forests can host a highly diverse spider community, but do not serve as surrogate habitats for all old/primary forest dwelling genera or species. A classification of forests by the diversity and structure of spider assemblages would separate young (< 15 years) from median to old forests (> 30 years), in good accordance with results on beetles (Hopp et al. 2010), but not on ants (Bihn et al. 2008a).

Our study did not show a succession of spider diversity from species-poor young secondary vegetation toward a species-rich old-growth fauna, but rather a turnover of spider genera along the successional gradient, strongest between the two young and the two older stages; i.e., between ages of 20 to 30 years. We interpret the high alpha diversity and turnover between sites of the same stage as an expression of a rich regional spider fauna, maintained by the mosaic landscape of forests of different ages and mainly stochastic processes in the establishment of spider assemblages in early successional stages. Our study region presents a highly diverse mosaic texture, with large patches of old-growth forest acting as refuges for spiders (Rodrigues et al. 2009), never far away even from the youngest secondary stages. This variation in vegetation complexity, and the large set of microhabitats provided, is able to host highly diverse spider assemblages (Ricetti & Bonaldo 2008). We assume that ideal preconditions for colonization and repopulation of secondary habitats have been met in the region. Spiders survived the deforestation and fragmentation of the coastal forests in Paraná due to the constant availability of retreat habitats for later resettlement.

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Appendix 1.—List of morphospecies of adult spiders recorded in the forest stages (H – herbaceous, A – arboreal, M – medium, F – old-growth forest) of the two nature reserves Cachoeira (Ca) and Itaqui (It) (specimens from all methods and replicate sites pooled).

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Amaurobiidae								
Amaurobiidae sp. 1	0	0	0	1	0	0	0	6
Amaurobiidae sp. 2	0	0	0	0	0	1	0	0
Amaurobiidae sp. 3	0	0	0	1	0	0	0	0
Amaurobiidae sp. 4	0	0	3	2	0	0	3	1
Anapidae								
Anapidae sp.	0	0	0	0	0	0	1	0
Anyphaenidae								
Amaurobioidinae sp. 1	1	0	0	0	0	0	0	0
Aysha sp. 1	11	2	0	1	7	1	1	1
Aysha sp. 2	1	0	0	0	0	0	0	0
Aysha sp. 4	0	0	0	1	0	0	0	0
Buckupiella imperatriz Brescovit 1997	4	1	0	0	4	0	0	0
gen. 1 sp. 1	16	0	0	0	0	0	0	0
Patrera cita (Keyserling 1891)	0	10	19	18	0	2	15	9
Temnida sp. 1	0	0	0	0	1	0	0	0
Wulfila sp. 1	0	0	0	0	0	1	0	0
Wulfilopsis sp. 1	2	1	1	3	8	2	10	4
Araneidae								
Araneidae sp. 8	0	1	0	0	0	0	0	0
Acacesia tenella (L. Koch 1871)	1	0	0	0	7	0	0	0
Acacesia yacuiensis Glueck 1994	0	0	0	0	0	2	1	0
Alpaida biasii Levi 1988	0	0	0	0	3	0	0	0
Alpaida canoa Levi 1988	0	0	2	0	0	0	1	0
Alpaida rubellula (Keyserling 1892)	0	0	0	1	0	0	0	0
Alpaida septemmammata (O.P.-Cambridge 1889)	0	0	0	0	0	0	0	1
Alpaida sp. 3	0	0	0	1	0	0	0	0
Alpaida sp. 5	2	0	0	0	0	0	0	0
Alpaida tijuca Levi 1988	1	0	1	0	0	1	3	0
Alpaida truncata (Keyserling 1865)	0	0	1	0	0	0	0	0
Araneus iguacu Levi 1991	0	1	0	2	0	2	3	3
Araneus tijuca Levi 1991	0	0	2	1	2	1	1	0
Araneus unanimus (Keyserling 1879)	0	0	0	1	0	0	0	0
Araneus uniformis (Keyserling 1879)	0	0	0	0	1	0	0	0
Bertrana rufostriata Simon 1893	1	0	0	0	7	0	0	0
Bertrana sp. 1	0	0	0	0	2	0	0	0
Cyclosa fililineata Hingston 1932	1	0	4	8	1	2	1	2
Cyclosa morretes Levi 1999	0	0	0	3	0	0	0	2
Enacrosoma anomalum (Taczanowski 1873)	0	0	0	0	0	1	0	0
Eustala sp. 1	1	0	0	1	0	0	0	0
Eustala sp. 2	1	0	0	0	1	0	0	0
Eustala sp. 3	0	0	0	0	3	0	0	0
Eustala sp. 4	0	0	0	0	2	0	0	0
Eustala sp. 6	1	0	0	0	1	0	0	0
Eustala sp. 8	0	0	0	0	3	0	0	0
Hypognatha sp. 1	0	0	1	0	0	0	0	0
Kaira echinus (Simon 1897)	0	1	0	0	0	0	0	0
Kapogea sellata (Simon 1895)	0	0	1	0	1	0	0	0
Mangora blumenau Levi 2007	4	0	2	14	0	4	6	2
Mangora bocaina Levi 2007	0	1	0	0	1	4	1	0
Mangora botelho Levi 2007	0	0	1	0	0	0	0	0
Mangora caparu Levi 2007	1	0	1	3	0	0	3	1
Mangora chacobo Levi 2007	0	0	0	0	0	1	0	0
Mangora manicore Levi 2007	4	3	3	3	1	0	1	5
Mangora melanocephala (Taczanowski 1874)	1	0	0	0	2	0	0	0
Mangora missa Levi 2007	0	1	0	0	0	0	1	1
Mangora sp. 1	0	1	7	10	0	2	2	0
Mangora sp. 2	0	0	0	0	0	0	1	2

Appendix 1.—Continued.

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Metazygia manu Levi 1995	0	0	0	0	1	0	1	0
Micrathena crassispina (C.L. Koch 1836)	0	0	0	0	0	0	0	1
Micrathena excavata (C.L. Koch 1836)	0	0	1	1	0	1	0	1
Micrathena sanctispiritus Brignoli 1983	0	0	0	1	0	0	0	0
Micrathena triangularis (C.L. Koch 1836)	1	2	0	0	0	0	1	0
Micrepeira albomaculata Schenkel 1953	0	0	0	1	0	0	0	0
Parawixia audax (Blackwall 1863)	3	0	0	0	2	0	1	2
Parawixia kochi (Taczanowski 1873)	0	0	0	0	1	0	0	0
Parawixia monticola (Keyserling 1892)	0	0	0	0	0	0	3	1
Scoloderus cordatus (Taczanowski 1879)	0	0	1	0	2	0	0	4
Scoloderus gibber (O.P.-Cambridge 1898)	1	1	0	0	0	0	0	0
Testudinaria gravatai Levi 2005	0	0	0	1	0	2	0	0
Verrucosa sp. 1	0	1	1	2	0	1	1	3
Wagneriana eupalaestra (Mello-Leitão 1943)	0	0	2	1	0	0	0	0
Wagneriana heteracantha (Mello-Leitão 1943)	0	0	2	0	0	0	0	0
Wagneriana iguape Levi 1991	0	1	1	1	0	1	2	1
Wagneriana janeiro Levi 1991	0	1	1	6	0	1	3	1
Wagneriana taim Levi 1991	3	0	0	0	2	0	0	1
Wixia sp. 1	0	1	0	0	0	0	0	0
Caponiidae								
Caponiidae sp.	0	0	0	0	0	0	1	0
Corinnidae								
Castianeira sp. 1	0	0	0	0	1	0	0	0
Castianeira sp. 2	0	1	0	0	0	0	0	0
Corinna sp. 1	0	1	0	1	0	0	1	0
Corinna sp. 2	1	1	0	0	0	0	0	0
Corinna sp. 3	0	1	0	0	0	0	0	0
Corinna sp. 4	0	0	0	0	0	0	1	0
Corinna sp. 5	1	0	0	0	2	0	1	0
Corinna sp. 6	0	0	0	0	0	1	0	0
Corinna sp. 7	0	0	0	0	0	0	1	0
Ianduba varia (Keyserling 1891)	3	2	0	1	1	0	0	0
Myrmecium sp. 1	0	0	1	0	0	0	0	1
Trachelas sp. 1	0	1	0	1	0	0	1	0
Trachelas sp. 2	0	0	0	0	0	0	1	0
Ctenidae								
Ctenus medius Keyserling 1891	1	3	4	4	0	1	3	2
Ctenus ornatus (Keyserling 1877)	1	0	0	0	0	0	0	0
Ctenus sp. 1	0	0	0	1	0	0	0	0
Isoctenus janeirus (Walckenaer 1837)	0	0	0	1	0	0	4	0
Isoctenus ordinario Polotow & Brescovit 2009	0	0	0	1	0	2	4	1
Isoctenus strandi Mello-Leitão 1936	7	11	4	16	4	11	15	21
Deinopidae								
Deinopis sp. 1	0	0	1	2	0	0	0	0
Dictynidae								
Thallumetus sp. 1	0	0	20	25	0	0	6	7
Dipluridae								
Trechona rufa Vellard 1924	0	0	0	0	0	0	1	0
Gnaphosidae								
Gnaphosidae sp.	0	0	0	0	2	0	0	0
Hahniidae								
Hahniidae sp. 1	0	0	5	10	0	0	0	0
Hahniidae sp. 2	0	0	0	0	0	0	1	0
Hahniidae sp. 3	0	0	1	0	0	0	0	0
Hahniidae sp. 4	0	0	2	0	0	0	0	0
Hahniidae sp. 5	1	0	1	0	0	0	0	0

Appendix 1.—Continued.

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Hahniidae sp. 6	0	0	0	0	0	0	1	0
Hahniidae sp. 7	0	0	0	0	4	0	8	0
Hersiliidae								
Ypypuera crucifera (Vellard 1924)	0	2	0	0	0	0	0	0
Linyphiidae								
Linyphiidae indet. 1	0	0	0	0	1	0	0	0
Linyphiidae indet. 2	0	0	0	0	3	0	0	0
Linyphiidae sp. 1	0	3	0	0	0	21	1	0
Linyphiidae sp. 2	2	0	0	0	0	1	0	0
Linyphiidae sp. 3	0	0	2	0	0	5	7	2
Anodoration claviferum Millidge 1991	22	5	0	0	0	0	0	0
Anodoration sp. 1	2	0	0	0	81	15	0	0
Asemostera tacuapi Rodrigues 2007	0	0	1	0	3	0	0	1
Dubiaranea sp.	0	0	1	0	0	0	0	0
Dubiaranea sp. 1	2	0	0	0	0	0	0	0
Dubiaranea sp. 2	0	0	0	0	0	1	0	0
Exechopsis conspicua Millidge 1991	0	0	0	0	0	0	0	2
Exechopsis sp.	1	6	2	0	0	16	5	0
Exechopsis sp. 1	0	1	0	0	0	0	1	2
Exechopsis sp. 2	1	0	0	0	0	0	0	0
Exocora sp.	0	0	0	2	0	3	0	0
Exocora sp. 1	0	0	2	0	0	0	0	1
Labicymbium sp.	3	0	0	0	0	0	0	0
Labicymbium sp. 1	0	3	0	0	0	1	0	0
Lepthyphantes sp.	0	0	1	0	0	0	0	0
Lepthyphantes sp. 2	1	0	0	0	0	0	0	0
Linyphiinae indet. 1	0	0	0	1	0	0	0	0
Linyphiinae indet. 2	2	0	0	0	0	0	0	0
Meioneta sp.	0	0	0	0	0	0	0	1
Meioneta sp. 1	0	2	0	0	1	1	8	8
Meioneta sp. 2	0	0	0	0	0	0	8	0
Meioneta sp. 3	0	0	0	0	3	0	0	0
Meioneta sp. B	0	3	0	0	0	0	0	0
Moyosi prativaga (Keyserling 1886)	0	1	0	0	0	0	0	0
Moyosi sp.	0	1	0	0	0	0	0	0
Moyosi sp. 1	1	0	0	0	0	1	0	0
Psilocymbium sp.	5	0	0	0	0	0	0	0
Psilocymbium sp. 1	6	0	1	0	0	0	0	0
Psilocymbium sp. 2	1	0	0	0	0	0	0	0
Scolecura sp.	1	0	0	0	0	0	0	0
Sphecozone diversicolor (Keyserling 1886)	17	0	0	0	19	0	0	0
Sphecozone labiata (Keyserling 1886)	0	3	0	0	0	0	0	5
Sphecozone personata (Simon 1894)	10	13	2	1	0	5	7	7
Sphecozone sp.	1	0	0	0	0	0	0	0
Sphecozone sp. 1	3	5	0	0	6	0	0	0
Sphecozone tumidosa (Keyserling 1886)	0	1	0	0	0	2	0	0
Sphecozone venialis (Keyserling 1886)	0	0	0	34	0	8	39	19
Vesicapalpus simplex Millidge 1991	0	0	0	0	0	0	1	0
Liocranidae								
Gen. 1 sp. 1	1	0	0	0	0	0	0	0
Lycosidae								
Agalenocosa sp. 1	7	0	0	0	0	0	0	0
Hogna sp. 1	0	2	0	0	2	0	0	0
Hogna sp. 2	4	2	0	0	0	0	0	0
Hogna sternalis (Bertkau 1880)	0	5	0	0	3	0	0	0
Lobizon sp. 1	0	0	0	9	0	0	0	3
Lobizon sp. 2	0	4	0	3	11	0	0	0
Lycosa erythrognatha Lucas 1836	0	0	0	0	1	0	0	0

Appendix 1.—Continued.

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Lycosa inornata Blackwall 1862	3	0	0	0	1	0	0	0
Lycosinae sp. 1	0	0	0	5	0	0	0	0
Mimetidae								
Ero sp. 1	2	2	8	7	2	2	3	5
Ero sp. 2	2	0	0	0	0	1	0	0
Gelanor sp. 1	0	0	0	1	0	0	0	1
Mimetinae sp. 1	0	0	1	0	0	0	0	0
Miturgidae								
Radulphius sp. 1	1	1	0	0	0	0	0	1
Strotarchus sp. 1	0	1	0	0	0	0	0	0
Teminius insularis (Lucas 1857)	0	0	0	0	1	0	0	0
Mysmenidae								
Mysmenidae sp. 1	0	0	0	1	0	0	0	0
Itapua sp.	1	2	1	0	0	0	0	0
Itapua sp. 1	0	0	1	0	0	0	0	0
Microdipoena sp. 1	0	0	0	0	2	6	2	24
Nemesiidae								
Acanthogonatus sp. 1	0	0	1	1	0	1	2	0
Pycnothele sp. 1	0	0	2	1	0	0	0	0
Nesticidae								
Eidmanella sp.	0	0	0	1	0	0	0	0
Ochyroceratidae								
Ochyrocera sp. 1	0	0	0	0	1	1	3	1
Ochyrocera sp. 2	0	0	0	3	0	0	1	3
Ochyrocera sp. 3	0	0	0	0	0	1	0	0
Oonopidae								
Gamasomorpha sp.	0	0	1	0	0	0	0	0
gen. 2 sp. 1	0	0	0	0	0	1	0	0
Neoxyphinus sp. 1	0	0	0	3	0	1	0	0
Oonops sp. 1	2	2	1	1	3	3	3	1
Oonops sp. 2	0	0	0	0	0	4	2	0
Orchestina sp. 1	0	0	0	0	0	0	4	0
Predatoroonops sp. 1	0	1	0	3	0	0	2	1
Triaeris stenaspis Simon 1891	0	0	0	0	1	0	0	0
Oxyopidae								
Hamataliwa sp. 1	0	2	1	0	0	0	0	0
Hamataliwa sp. 2	0	1	0	0	2	0	1	0
Oxyopes salticus Hentz 1845	1	0	0	0	0	0	0	0
Peucetia flava Keyserling 1877	0	0	0	0	1	0	0	0
Palpimanidae								
Palpimanidae sp.	0	0	1	0	0	0	0	0
Notiothops birabeni (Zapfe 1961)	0	0	0	0	0	0	0	1
Philodromidae								
Cleocnemis sp. 1	0	0	0	0	0	1	0	0
Pholcidae								
Pholcidae sp. 1	11	5	3	3	0	0	0	0
Mesabolivar aff. *brasiliensis* (Moenkhaus 1898)	0	0	0	1	0	0	0	0
Mesabolivar aff. *cyaneotaeniatus* (Keyserling 1891)	0	0	0	3	0	0	0	0
Mesabolivar aff. *guapiara* Huber 2000	0	0	0	1	0	4	1	6
Mesabolivar brasiliensis (Moenkhaus 1898)	0	1	3	11	0	0	0	0
Mesabolivar cyaneotaeniatus (Keyserling 1891)	0	0	0	2	0	0	0	0
Mesabolivar luteus (Keyserling 1891)	0	9	1	24	0	4	7	4
Mesabolivar rudilapsi Machado, Brescovit & Francisco 2007	1	0	2	0	0	6	1	2
Mesabolivar sp. 1	0	0	0	0	1	0	3	0

Appendix 1.—Continued.

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Mesabolivar sp. 2	0	2	0	0	0	3	0	2
Metagonia aff. *bonaldoi* Huber 2000	0	1	0	1	0	0	0	0
Metagonia furcata Huber 2000	0	0	1	1	0	1	0	0
Metagonia sp. 1	0	3	2	5	0	5	4	0
Metagonia sp. 2	0	0	0	0	0	1	0	0
Ninetines sp. 1	0	0	0	0	0	0	0	2
Ninetines sp. 2	0	1	1	0	0	0	1	1
Tupigea nadleri Huber 2000	0	2	0	1	0	0	6	0
Tupigea sp. 1	0	1	3	0	0	0	0	0
Pisauridae								
Architis brasiliensis (Mello-Leitão 1940)	2	2	18	20	0	3	1	7
Architis capricorna Carico 1981	1	0	0	0	0	0	0	0
Prodidomidae								
gen. sp.	0	0	0	0	0	0	2	0
Salticidae								
Salticidae sp. 26	1	0	0	0	0	0	0	0
Salticidae sp. 38	0	0	0	0	1	0	0	0
Salticidae sp. 45	0	0	0	0	0	1	0	0
Salticidae sp. 46	0	0	0	0	0	1	0	0
Salticidae sp. 54	0	0	0	0	0	0	3	0
Salticidae sp.	0	0	0	0	0	0	2	0
Amphidraus sp. 1	0	1	1	0	0	0	0	0
Amycinae sp.1	0	0	2	0	0	0	1	1
Amycinae sp.2	0	1	0	0	0	1	0	0
Arnoliseus graciosa Braul & Lise 2002	0	4	1	4	0	0	2	3
Asaphobelis physonychus Simon 1902	3	2	2	1	1	1	0	1
Atelurius sp. 1	1	0	0	0	0	0	1	0
Chira spinosa Mello-Leitão 1945	1	0	0	0	1	0	0	0
Chira thysbe Simon 1902	2	0	0	0	0	0	0	0
Coryphasia sp. 1	0	0	0	1	0	0	0	0
Coryphasia sp. 2	0	2	3	0	0	1	1	0
Cotinusa sp. 1	2	1	2	0	0	0	0	1
Cotinusa sp. 2	0	0	0	0	0	1	1	0
Cylistella sp. 1	0	0	1	1	0	3	2	0
Cyllodania sp. 1	0	0	0	0	1	0	0	0
Dendryphantinae sp.1	1	0	0	0	0	0	0	0
Dendryphantinae sp.2	0	0	0	0	1	0	0	0
Euophryinae sp. 2	0	0	0	2	0	0	1	0
Euophryinae sp. 3	2	0	0	0	0	0	0	0
Euophryinae sp. 4	0	0	0	2	0	0	0	0
Euophryinae sp. 5	1	0	0	0	0	0	0	0
Euophryinae sp. 6	0	3	0	0	1	1	0	0
Euophryinae sp. 7	0	0	1	0	0	1	1	2
Euophryinae sp. 8	1	0	0	0	1	0	0	0
Euophryinae sp. 9	1	0	0	1	0	0	0	0
Euophryinae sp. 10	0	0	1	0	0	0	1	2
Euophryinae sp. 11	0	0	0	0	0	0	0	1
Euophryinae sp. 12	0	0	0	0	0	0	1	0
Euophryinae sp. 13	0	0	0	0	0	1	0	0
Euophryinae sp. 14	0	0	0	0	0	1	0	0
gen. n. sp. 1	0	0	1	0	0	0	0	0
Hyetussinae sp. 1	0	0	1	3	0	0	0	2
Ilargus sp. 1	0	0	0	0	1	0	0	0
Itata sp. 1	0	0	0	1	0	0	0	0
Lyssomanes sp. 1	0	0	0	0	0	0	0	1
Lyssomanes sp. 2	0	0	0	0	0	0	1	0
Maeota dichrura Simon 1901	0	1	0	0	5	1	0	1
Noegus sp. 1	8	9	11	7	5	4	7	10
Ramboia sp. 1	3	0	0	0	2	0	4	0

Appendix 1.—Continued.

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Romitia sp. 1	2	0	0	0	1	1	0	0
Semnolius sp. 1	0	1	0	0	1	0	0	1
Semora napaea Peckham & Peckham 1892	0	0	0	0	4	0	0	0
Synemosyna lauretta Peckham & Peckham 1892	1	0	0	0	3	0	0	0
Synemosyninae sp. 1	0	0	0	1	0	2	3	0
Tanybelus aeneiceps Simon 1902	0	0	0	0	0	0	0	1
Tariona sp. 1	18	38	19	19	1	7	33	28
Tariona sp. 3	0	3	0	0	0	0	0	0
Tariona sp. 4	5	4	0	0	0	0	0	0
Tariona sp. 5	2	0	0	0	0	0	0	0
Tariona sp. 6	0	0	0	0	1	1	0	0
Vinnius uncatus Simon 1902	3	0	0	0	0	0	0	0
Scytodidae								
Scytodes antonina Rheims & Brescovit 2009	6	2	9	0	7	6	3	3
Scytodes globula Nicolet 1849	0	0	0	1	0	0	0	0
Scytodes sp. 1	0	0	2	1	0	1	1	0
Sparassidae								
Olios sp. 1	1	0	0	1	0	0	0	0
Symphytognathidae								
Anapistula sp. 1	0	0	1	0	0	0	0	0
Synotaxidae								
Synotaxus sp. 1	0	0	0	0	0	1	0	1
Tetragnathidae								
Azilia histrio Simon 1895	1	0	0	0	0	0	0	1
Chrysometa boraceia Levi 1986	0	0	0	0	2	0	2	0
Chrysometa ludibunda (Keyserling 1893)	0	2	1	2	1	1	13	2
Chrysometa sp.	0	0	0	1	0	0	3	0
Cyrtognatha sp. 1	9	3	1	0	4	0	2	0
Glenognatha sp. 1	1	0	0	0	0	0	0	0
Leucauge sp.	0	0	0	0	0	1	0	1
Leucauge sp. 1	0	1	1	0	0	2	0	5
Leucauge sp. 2	0	0	1	0	0	0	5	0
Tetragnatha sp.	0	2	0	0	0	0	0	0
Theridiidae								
Theridiidae sp. 1	0	0	0	0	0	0	0	1
Achaearanea sp. 1	0	0	0	0	0	1	0	0
Achaearanea sp. 18	0	0	0	1	0	0	0	0
Achaearanea tingo Levi 1963	0	1	1	0	0	1	0	0
Ameridion unanimum (Keyserling 1891)	0	0	0	0	4	0	0	0
Anelosimus ethicus (Keyserling 1884)	0	0	0	0	1	0	0	0
Anelosimus nigrescens (Keyserling 1884)	1	0	0	0	0	0	0	0
Argyrodes elevatus Taczanowski 1873	0	0	0	1	0	0	0	0
Argyrodes sp. 1	0	0	0	0	0	1	0	1
Ariamnes attenuatus (O.P.-Cambridge 1881)	0	0	2	1	0	0	1	2
Ariamnes longissimus Keyserling 1891	1	1	0	0	1	1	0	0
Ariamnes sp. 2	0	0	0	0	0	0	1	0
Chrosiothes niteroi Levi 1964	0	0	0	3	13	4	7	9
Chrosiothes perfidus Marques & Buckup 1997	0	1	1	3	2	3	0	5
Chrosiothes sp. 1	0	0	0	2	0	0	0	0
Chrysso gounellei Levi 1962	1	13	0	0	0	1	0	0
Chrysso nigrosterna Keyserling 1891	0	0	0	0	0	3	3	0
Chrysso rubrovittata (Keyserling 1884)	0	0	0	0	1	0	0	0
Chrysso sp. 3	1	2	0	1	0	0	0	6
Chrysso sp. 32	0	0	0	0	0	0	0	1
Coleosoma sp. 1	0	0	0	0	2	0	0	0
Cryptachaea altiventer (Keyserling 1884)	2	1	0	0	1	0	0	0
Cryptachaea digitus (Buckup & Marques 2006)	0	0	0	0	0	0	0	3

Appendix 1.—Continued.

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Cryptachaea cinnabarina (Levi 1963)	0	0	0	0	0	0	1	2
Cryptachaea hirta (Taczanowski 1873)	0	0	0	0	8	0	0	0
Cryptachaea isana (Levi 1963)	3	0	0	0	0	0	0	0
Cryptachaea jequirituba (Levi 1963)	0	0	0	0	0	2	0	0
Cryptachaea migrans (Keyserling 1884)	0	0	0	3	0	0	0	0
Cryptachaea passiva (Keyserling 1891)	2	2	3	6	2	5	2	7
Cryptachaea rioensis (Levi 1963)	0	0	0	0	0	0	1	0
Cryptachaea sicki (Levi 1963)	0	0	0	0	0	0	0	1
Cryptachaea sp. 1	0	0	0	0	0	0	1	0
Cryptachaea taim (Buckup & Marques 2006)	1	0	1	1	0	2	4	3
Cryptachaea triguttata (Keyserling 1891)	0	4	3	2	1	3	3	0
Dipoena atlantica Chickering 1943	0	0	0	0	1	1	0	1
Dipoena bryantae Chickering 1943	0	0	0	0	0	1	0	0
Dipoena cordiformis Keyserling 1886	0	0	1	0	0	0	0	0
Dipoena duodecimpunctata Chickering 1943	0	0	0	1	0	0	0	0
Dipoena ira Levi 1963	4	0	0	1	1	0	1	1
Dipoena keyserlingi Levi 1963	1	0	0	0	0	0	2	0
Dipoena pumicata (Keyserling 1886)	1	4	3	2	3	0	1	1
Dipoena pusilla (Keyserling 1886)	0	0	4	5	0	2	0	1
Dipoena santacatarinae Levi 1963	5	1	4	0	0	0	0	0
Dipoena sp.	1	0	0	0	0	0	1	2
Dipoena sp. 2	8	10	11	3	1	20	42	4
Dipoena sp. 3	0	0	0	0	0	0	1	0
Dipoena sp. 6	0	0	0	0	0	3	0	0
Dipoena sp. 8	1	0	0	0	3	0	0	0
Dipoena sp. 12	5	9	5	12	3	4	11	9
Dipoena sp. 21	0	1	0	0	0	0	0	0
Dipoena sp. 22	0	0	0	0	0	0	1	1
Dipoena sp. 58	0	0	0	0	0	2	0	0
Dipoena variabilis (Keyserling 1886)	0	1	0	1	0	0	0	1
Emertonella taczanowskii (Keyserling 1886)	0	0	0	1	1	1	0	0
Episinus sp.	0	0	0	0	0	1	0	0
Episinus sp. 1	3	2	6	4	9	6	17	5
Episinus sp. 2	0	0	0	0	21	0	0	0
Episinus teresopolis Levi 1964	1	0	0	0	2	0	0	0
Euryopis sp.	1	0	0	0	0	0	0	0
Euryopis sp. 1	2	0	0	0	2	1	0	0
Exalbidion sp. 1	6	1	0	3	1	1	0	0
Exalbidion sp. 2	0	1	0	0	0	0	0	0
Faiditus acuminatus (Keyserling 1891)	0	0	0	0	0	2	0	0
Faiditus sp. 1	0	0	1	1	0	0	0	0
Faiditus sp. 2	0	1	0	1	0	0	1	1
Faiditus sp. 3	0	0	0	3	0	0	1	0
gen. 2 sp. 2	0	0	0	0	0	0	1	0
Guaraniella mahnerti Baert 1984	0	0	0	0	4	15	31	5
Guaraniella sp.	0	0	0	0	0	0	1	0
Guaraniella sp. 1	3	0	0	5	0	0	0	0
Hadrotarsinae sp. 1	0	0	0	0	0	0	1	0
Hadrotarsinae sp. 2	0	0	0	0	3	0	0	0
Hadrotarsinae sp. 3	0	0	0	3	0	0	0	0
Helvibis sp. 1	2	3	0	0	0	0	1	0
Hetschkia gracilis Keyserling 1886	14	5	2	0	4	0	1	0
Janula bicorniger (Simon 1894)	0	1	13	6	0	2	21	32
Neopisinus cognatus (O.P.-Cambridge 1893)	0	1	0	0	0	0	0	0
Phycosoma altum (Keyserling 1886)	4	6	2	0	13	2	0	0
Rhomphaea sp. 1	1	0	1	1	0	0	0	0
Rhomphaea sp. 2	0	0	1	0	0	0	0	1
Spintharus gracilis Keyserling 1886	2	10	8	25	1	10	74	30
Stemmops sp. 2	1	0	0	0	0	0	0	0
Styposis selis Levi 1964	0	0	0	0	1	1	0	1
Tekellina crica Marques & Buckup 1993	1	0	0	0	0	0	2	0

Appendix 1.—Continued.

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Tekellina sp. 3	0	0	0	1	0	0	0	0
Tekellina sp. 4	0	0	0	0	0	0	0	1
Theridion biezankoi Levi 1963	1	0	0	0	0	0	1	0
Theridion minutissimum Keyserling 1884	0	1	0	0	0	0	0	0
Theridion opolon Levi 1963	0	0	1	0	0	0	0	0
Theridion plaumanni Levi 1963	11	2	0	0	43	0	0	1
Theridion quadripartitum Keyserling 1891	0	0	1	3	0	0	0	0
Theridion sp. 1	1	0	0	0	1	0	0	0
Theridion sp. 2	0	0	0	1	0	0	0	0
Theridion sp. 11	0	0	0	0	0	1	0	0
Theridion sp. 28	0	0	0	0	0	0	0	1
Theridion sp. 32	1	12	1	23	0	0	0	8
Theridion sp. 36	0	0	0	1	0	0	0	0
Theridion sp. 40	0	1	0	0	0	0	0	0
Theridion sp. 47	0	0	1	1	0	0	0	0
Theridion sp. 63	0	0	0	1	0	0	0	0
Theridion sp. 68	0	0	0	1	1	0	0	0
Theridion teresae Levi 1963	1	0	0	0	1	0	0	1
Theridula gonygaster (Simon 1873)	0	0	0	0	1	0	0	0
Thwaitesia affinis O.P.-Cambridge 1882	7	9	7	1	2	7	12	41
Thwaitesia sp. 1	0	0	1	1	0	0	0	0
Thymoites anicus Levi 1964	8	2	0	0	4	0	0	0
Thymoites melloleitaoni (Bristowe 1938)	0	0	0	1	0	15	1	1
Thymoites sp.	1	0	0	0	0	1	0	0
Thymoites sp. ?	0	0	0	0	0	2	0	0
Thymoites sp. 1	4	1	2	4	1	0	1	0
Thymoites sp. 2	5	0	1	3	0	0	0	0
Thymoites sp. 4	1	0	0	0	0	0	1	2
Thymoites sp. 5	0	0	1	0	0	0	0	0
Thymoites sp. 7	0	0	2	3	0	7	1	0
Thymoites sp. 12	1	0	0	0	0	0	0	0
Wamba crispulus (Simon 1895)	4	1	0	0	0	0	0	0
Wirada sp. 1	0	0	0	0	0	0	1	0
Theridiosomatidae								
gen. indet. 1	0	1	0	0	1	0	0	0
gen. indet. 3	1	0	1	5	0	0	0	0
gen. indet. 4	0	0	0	1	0	0	0	1
gen. sp. 1	0	0	1	0	0	0	0	1
Chthonos sp.	1	0	0	0	0	0	0	0
Chthonos sp.1	0	0	0	0	0	1	3	0
Chthonos sp.2	0	0	0	0	0	0	1	0
Naatlo sp.	0	0	2	0	0	2	0	1
Naatlo sp. 1	0	0	0	0	0	0	1	0
Plato sp. 1	0	0	0	0	0	0	0	1
Theridiosoma sp. 1	5	0	0	1	0	0	0	0
Theridiosoma sp. 3	0	0	0	2	0	0	0	0
Theridiosoma sp. 4	0	0	0	1	0	0	0	1
Thomisidae								
Acentroscelus sp. 1	0	2	1	0	0	0	1	1
Aphantochilus taurifrons (O.P.-Cambridge 1881)	0	0	1	1	0	1	0	0
Deltoclita sp. 1	1	0	1	1	2	1	2	0
Epicadinus sp. 1	0	1	0	2	0	0	2	1
Misumenops sp. 1	1	0	0	0	0	0	0	0
Onocolus sp. 1	0	0	7	1	0	0	0	1
Titidius sp. 1	8	10	1	0	2	5	0	0
Tmarus sp. 1	3	12	4	3	9	3	9	5
Tmarus sp. 2	4	7	2	0	2	2	2	1
Tmarus sp. 3	0	0	1	1	0	0	0	0
Tmarus sp. 4	0	0	0	1	0	0	0	0
Tmarus sp. 5	0	1	0	0	0	0	0	0

Appendix 1.—Continued.

Taxon	Locality and Stage							
	Ca-H	Ca-A	Ca-M	Ca-F	It-H	It-A	It-M	It-F
Titanoecidae								
Goeldia sp. 1	0	0	0	0	7	0	0	0
Trechaleidae								
Neoctenus comosus Simon 1897	0	0	0	0	1	0	0	0
Uloboridae								
Conifaber sp. 1	0	1	0	0	0	0	0	0
Miagrammopes sp. 1	0	1	8	6	0	2	2	3
Miagrammopes sp. 2	4	0	8	8	0	3	9	9
Uloborus sp.	0	0	0	0	0	0	0	1
Uloborus sp. 1	0	0	0	1	0	0	1	3
Zodariidae								
Zodariidae sp.	0	0	0	0	0	0	1	0
Zoridae								
gen. 1 sp. 14	8	0	0	0	0	0	0	0
gen. 1 sp. A	30	74	88	103	21	110	107	64
gen. 1 sp. B	0	2	1	0	0	5	1	1
gen. 1 sp. C	20	28	2	21	16	50	31	20
gen. 1 sp. D	14	0	20	12	0	0	0	0
gen. 1 sp. E	1	0	0	0	0	0	0	0
gen. 1 sp. F	0	1	0	0	0	0	0	0
gen. 1 sp. G	0	3	0	1	0	2	1	2

* Nomenclature (order) of the morphospecies originates from the system of the experts/hosting institutions: IBSP - Instituto Butantan, São Paulo; MCN: Museu de Ciências Naturais da Fundação Zoobotânica, Porto Alegre.