ECOLOGY, BEHAVIOR AND BIONOMICS

Arthropod Recolonization in the Restoration of a Semideciduous Forest in Southeastern Brazil

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ABSTRACT - The use of arthropods for monitoring habitat changes has grown widely in the last decades. In Brazil, however, most of the studies in restored areas have involved only vegetation changes. The present study aimed at investigating recolonization patterns of epigeic arthropods in recently restored sites of semideciduous forests in southeastern Brazil. We compared the community structure of adjoining sites 5, 17, 29 and 36 months old with that at a nearby forest remnant (reference site). We also determined the most abundant species and looked for ecological indicator species of each site age. Arthropods were sampled using pitfall traps, and their assemblages were described and compared with multi- and univariate statistical methods. Species abundance and richness equivalent to the reference site were reached at five months after planting, however species composition was very distinctive not only in relation to the reference site, but also among restored sites. Some of the main species found in this restoration stage are common in agroecosystems or cerrado vegetation. Nevertheless, there was a clear trend of arthropod fauna in restored sites moving toward the fauna in the forest remnant over time. Our results also highlighted ants and termites because of their abundance and ants because of their high value as ecological indicators of restoration age.

KEY WORDS: Formicidae, seasonal forest, monitoring, ecological indicator

The landscape of southeastern Brazil has been entirely transformed over time by human activities (Dean 1997). Changes were especially dramatic in the inner lands originally covered by mesophytic seasonal forests (deciduous and semideciduous forests) since their soils are particularly suitable for agriculture (Oliveira-Filho & Ratter 2002). Such forests are now restricted to few small patches in the agricultural-urban matrix. Some attempts of restoration have been made in the last decades, but their effectiveness has not been properly evaluated. Long-term monitoring of sites where attempts have already been performed is necessary for evaluating restoration success and improving restoration protocols. If techniques involve tree planting, special attention should be dispensed to the first years of the restored site, when the greatest habitat changes occur due to the fast growing of pioneer trees.

Most of the studies in restored areas are concerned with recovery and development of vegetation, especially tree species (Amador & Viana 2000, Souza & Batista 2004), whereas fauna is usually ignored (but see Majer 1992).

Because of the high turnover and growth rates for most species, arthropods serve as probes that quickly respond to environmental changes. Another special attribute lies in their microgeographic distribution, which may reflect fine-scale heterogeneity in habitats to which most vertebrates are insensitive (Mattoni *et al* 2000). Arthropods often provide a more sensitive indication than plants of the overall state of the ecosystem in which they occur (Rosenberg *et al* 1986, Andersen & Sparling 1997). In addition, their assay is inexpensive and can be performed with a few simple trapping methods (Mattoni *et al* 2000). Pitfall trapping is a well-known method for sampling epigeic arthropods, which can be performed in almost any terrestrial habitat, making it very useful in comparing sites.

The aim of the present study was therefore to follow the recolonization of epigeic arthropods in restored sites representing the first three years after planting. Recolonization patterns were assessed by (1) comparisons of arthropod abundance, richness and diversity, (2) estimates of similarity, (3) detection of species that could be considered as ecological indicators for each site age. A forest remnant was included in the sampling design as a reference site.

Material and Methods

Study sites. The study was carried out in Ribeirão Preto (21°10'S; 47°50'W), northeast of São Paulo state, Brazil. The altitude ranges from 510 m to 800 m. The mean annual temperature is 22.6°C and average annual minimum and

maximum temperatures are respectively 19.2°C in June and July and 24.4°C in February. Mean annual rainfall is 1,468 mm concentrated in October-March (Kotchetkoff-Henriques *et al* 2005). The region is included in the Cerrado biome (IBGE & MMA 2004) or in the Cerrado – Tropical Atlantic transition (Ab´Sáber 1977). In fact, it is situated in an ecological tension zone (IBGE 1993), originally covered by a mosaic of cerrado (savannah) on sandy soils, and mesophytic seasonal forests on more fertile soils originating from basalt (Romariz 1964, Oliveira-Filho & Fontes 2000, Oliveira-Filho & Ratter 2002). The landscape currently comprises crop fields and urban areas (Kotchetkoff-Henriques 2003). The natural vegetation is reduced to only 3.89% of the municipality area and is dispersed over 102 patches ranging from 247 ha to less than 10 ha, most of them isolated and under different degrees of disturbance (Kotchetkoff-Henriques *et al* 2005).

Our focus was on the seasonal semideciduous forest. We selected two different systems: a 75 ha revegetated area (REV) at the University of São Paulo *campus* and a 78 ha forest remnant (FOR), located on Santa Adelaide Farm. FOR is an isolated forest remnant surrounded by sugar cane plantations and bordered by a highway on one side. The FOR site was characterized by three layers and a canopy about 10-15 m high with high vertical and horizontal heterogeneity. The number of tree species is around 68, with *Schyzolobium parahyba* (guapuruvu), *Cariniana estrellensis* (jequitibá), and *Galesia integrifolia* (pau-d'alho) as typical species in the area (Kotchetkoff-Henriques 2003). FOR was chosen as best fitting the reference site concept (Hobbs & Harris 2001, SER 2004), i.e., it occurs in the same life zone, semideciduous forest, reddish purple latosol soils (Oliveira & Prado 1983); it is close to the restoration project (about five kilometers); and it is exposed to similar natural disturbances. Although it may have been affected by selective logging and fire in the past, FOR has a high conservation value when compared to other forest patches in the region (Kotchetkoff-Henriques 2003).

The restoration project was established in an 11-year-old abandoned field dominated by the exotic grasses *Panicum maximum* and *Brachiaria decumbens* (Poaceae). The area was previously occupied by sugar cane plantations (17 years) and prior to that by coffee plantations (decades). The project was initiated by planting seedlings of about 60 different tree species that are typical of the semideciduous forest, such as *Guazuma ulmifolia, Trema micrantha, Cecropia pahystachya, Cederela fissilis, Chorisia speciosa, S. parahyba, C. estrellensis*, and *G. integrifolia*. Pre-planting management of land included clearing, ploughing and chemical fertilizer input, and after planting there was periodic slashing for weed control. The revegetated area is also surrounded by sugar cane plantations, abandoned fields, mixed vegetation of the *campus* (native and exotic trees and shrubs in a grassy matrix, gardens) and residential areas.

We adopted the "chronosequence approach" (Majer 1997) in which a range of sites which represent known ages after planting is sampled at the same time. The resulting differences are then taken to be representative of different stages in the restoration process. This strategy was well suited to the study of our sites, since they were originally part of a continuum and therefore had similar characteristics and also because the restoration procedures were standardized. In the revegetated area, we selected four adjoining sites: REV1, 36 months old, with 12 ha; REV2, 29 months old, with 16.6 ha; REV3, 17 months old, 1 ha; and REV4, 5 months old, with 5.6 ha. At sampling time, REV sites had a canopy 3-6 m high comprised with two layers, the first one composed by grasses and small saplings, and the second with the more developed saplings.

Sampling. Each of the five sites (FOR, REV1, REV2, REV3 and REV4) was sampled in five 10 x 10 m replicated quadrats, so that we had 25 sampling units. Quadrats were placed 50 m apart in a straight line and at least 10 m from the edge. At each quadrat, eight pitfall traps were set out on a grid design, which originally resulted in 40 traps/site. During sampling some traps were destroyed by animals so that the effective number of traps was 32, 38, 38, 40 and 39 respectively at FOR, REV1, REV2, REV3 and REV4. Pitfall traps consisted of double plastic cups (75 mm diameter, 250 ml), dug into the ground so that the cup border was flush with the soil surface. Each pitfall was filled with approximately 150 ml of saturated NaCl solution, which preserves the trapped specimens and does not attract the fauna (Brändle *et al* 2000). Some drops of detergent were added to the solution to break the surface tension, causing the specimens to sink. After traps were dug in, they were left in the field for one week prior to trapping, to avoid a digging-in effect (Greenslade 1973). Traps were then left sampling for seven days during May, in the early dry season.

All arthropods collected were classified according to the morphospecies concept recommended by Oliver and Beattie (1996). A code number was assigned to each morphospecies. When possible, their families were determined. Some of the most abundant and indicator morphospecies were identified by taxonomists.

Data analysis. A species accumulation curve was obtained for each site by taking the number of pitfall traps as sampling effort. Sample order was randomized 100 times in order to eliminate sampling error and heterogeneity among the units sampled, and the mean and standard deviation of S(n) (the number of species discovered) computed for each value of n between 1 and 40. Expected number of species E(S) and standard deviations SD were calculated using the Chao 2 classic formula (Colwell & Coddington 1994).

Individuals of each morphospecies trapped in the same sampling quadrat were grouped for calculations of species abundance, richness and Shannon diversity. In order to avoid bias due to the loss of some pitfalls, only six pitfalls (instead of eight) were considered per quadrat. Differences in the three variables among sites were evaluated using one-way ANOVAs and Student-Newman-Keuls test.

Cluster analysis, using the paired group method and Bray-Curtis similarity measures, was used to check the reliability of the pre defined groups and to depict relationships of arthropod assemblages from all sites. Prior to analysis, morphospecies abundance data were log (x+1) transformed for weighting contribution from the rarer species (Clarke 1993). An analysis of similarity (ANOSIM) using the Bray-Curtis coefficient was performed with 10,000 permutations for identifying significant differences between paired sites (Clarke & Warwick 1994).

The same transformed matrix was used for detrended correspondence analysis (DCA), producing a biplot in which sites and species were ordinated simultaneously (Gauch 1982). Characteristic species (indicator species) were identified for each site using the indicator value method (Dufrêne & Legendre 1997). The Monte Carlo test was used to determine the significance of the maximum IndVal recorded for each species. Those morphospecies with significant IndVals greater than 70% (subjective benchmark adopted by van Rensburg *et al* 1999, McGeogh *et al* 2002, Nakamura *et al* 2007) were then regarded as indicator species for the site in question.

The species accumulation curve and Chao 2 estimation were performed using the software EstimateS (Colwell 2006). SigmaStat (Jandel Scientific 1995) was used for ANOVA and post hoc tests. Cluster analysis and ANOSIM were performed with PAST software (Hammer *et al* 2001), while DCA, indicator species analysis and Monte Carlo test were performed with PC-ORD software (McCune & Mefford 1999).

Results

Community structure. Pitfall traps captured a total of 28,643 arthropods (no less than 4,000 per site) of 288 morphospecies. In spite of the high number of arthropods collected, the accumulation curves did not reach a plateau after around 40 samples/site and between 94 (REV1) and 142 (REV4) species captured (Fig 1). According to Chao 2 analysis, a plateau was expected to be achieved at estimated 278, 157, 155, 155 and 299 species at FOR, REV1, REV2, REV3 and REV4, respectively.

Abundance was not different among sites (Table 1). REV4 and FOR had the highest levels of species richness. Diversity did not differ much among sites. The only clear difference was between FOR (2.24) and REV1 (1.70) (Table 1).

Arthropod assemblage differed significantly among all sites (Table 2). In spite of being considered one of the most reliable coefficient performers, typically Bray-Curtis similarities tend to increase with increasing severity of matrix transformation (Clarke 1993). The absolute similarity levels (Fig 2) should thus be interpreted with some caution. In this case, it is the relative levels which have a natural interpretation.

Cluster analysis showed higher similarity among quadrats from the same site than among quadrats from different sites (Fig 2). β-diversity across sites was clearly represented in the dendrogram. Arthropods divided sites firstly into two clusters: FOR and REV (ANOSIM, $r = 0.9705$, $P < 0.0001$). From the REV cluster, in turn, REV4 and REV1 were progressively detached, and REV2 and REV3 were the most similar sites. The distance separating REV4 from the other REV sites was larger than the distance separating REV1, REV2 and REV3 from each other (Fig 2).

As seen in cluster analysis (Fig 2), DCA of the morphospecies abundance by sample matrix resulted in strong clustering of the samples along the first axis into two clusters, representing REV and FOR (Fig 3). Within the REV cluster, ordination discriminated the successional gradient on the first axis reaching from REV4 to REV1-REV2 samples. The second DCA axis discriminated the REV1 from REV2 samples. The eigenvalue for the first axis was 0.551, and for the second and third it was 0.180 and 0.123, respectively.

The most abundant species. Fig 3 also shows the DCA species scores for the 12 most abundant species (see Online Supplementary Material for the identification and abundance data for each species code). Nine out of the 12 most abundant species were ants (Formicidae), and they accounted for 73-88% of total abundance of epigeic arthropods per site, with the lowest and highest percentage at FOR and REV2, respectively. Termites (Termitidae) were also well represented, with three species whose abundances, summed up, represented an increasing percentage of total number of arthropods: 0.55% in REV4 to around 7% in REV1, and more than 8% in FOR. Phoridae sp1 accounted for no more than 3% in FOR and REV1, where it was more abundant.

Typically, many of the species found at the center of the DCA ordination are ubiquitous species, bimodally distributed species, or species whose distribution otherwise departs from a unimodal response curve (Ter Braak & Prentice 1988). *Atta* sp. (154) was a good example of this phenomenon (Fig 3). Despite its higher occurrence at REV2, this species was abundant at all sites sampled. The same occurred with *Megalomyrmex* sp. (150) and Phoridae sp. (82), even though they were a little more abundant at REV1. *Camponotus rufipes* Fabr. (151) was representative of the entire REV complex, with the exception of REV4, where its abundance was very low. In contrast, species found at the edges of the ordination diagram are generally abundant only at a given site. Typical species of the forest patch were *Camponotus* sp. (167), *Camponotus sericeiventris* (Guérin) (168), *Pheidole* sp. (172) and *Velocitermes* sp. (263). *Syntermes nanus* Constantino (262) was found predominantly in the REV1 cluster. Another species complex including *Crematogaster* sp. (149) and *Syntermes grandis* (Rambur) (261) had ordination optima within REV2-REV3 (Fig 3).

As Formicidae was the most abundant group among the epigeic arthropods, we decided to compare the structure of this subset of arthropod community among sites in the same way as done for the entire assemblage. As a result, the abundance of Formicidae did not differ among sites whereas species richness was higher at FOR in comparison with the REV sites (Table 3). The highest diversity levels were found at FOR, REV2 and REV3, and the lowest at REV4 (Table 3).

Indicator species. FOR and REV4, both extremes in the habitat gradient, had the higher absolute indicator species values among all the sites (see Online Supplementary Material for IndVal > 70%). Formicidae was the taxon with the most indicator species, seven out of 23, and all of them representative of the forest patch. Other indicator species of FOR belonged to the orders Araneae, Diptera, Dictyoptera and Hymenoptera. In REV4, the most representative species belonged to the orders Coleoptera, Hemiptera, Hymenoptera and Thysanoptera. Among the other sites, only REV1 had an indicator species, the termite *S. nanus* (Termitidae).

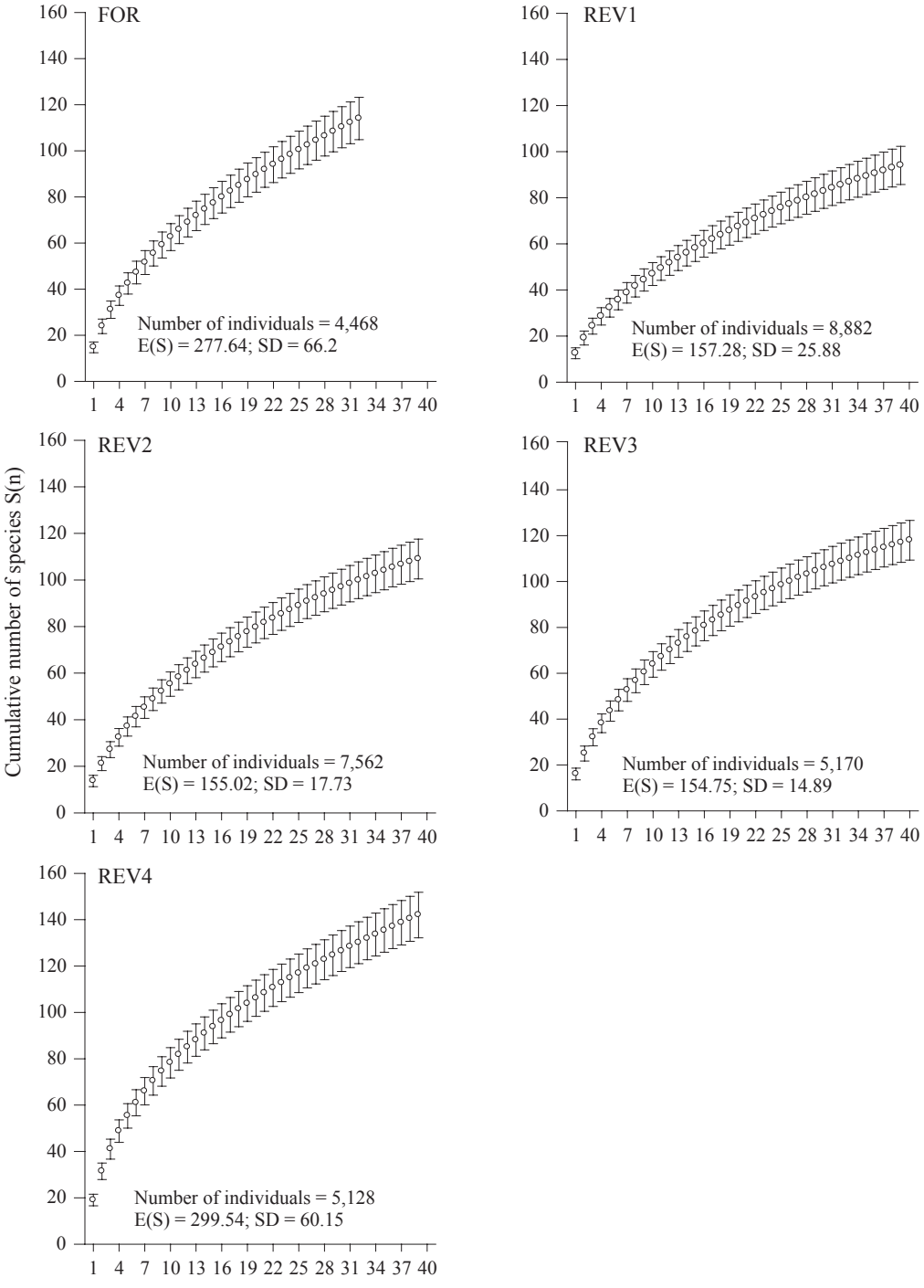

Fig 1 Species accumulation curves for arthropods from pitfall traps in the forest remnant (FOR) and at restored sites (REV1, REV2, REV3, REV4). Each point represents the mean of 100 randomizations of sample pooling order. Error bars are the corresponding standard deviations. Expected number of species E(S), and standard deviations (SD) were calculated using the Chao 2 formula.

Discussion

Despite the large number of individuals captured, the species accumulation curves suggested that we did not sample all the species available. Species accumulation curves of arthropods in the tropics and subtropics generally do not reach an asymptote due to the large set of rare species which accumulate with increasing sample size (Price *et al* 1995, Novotný & Basset 2000, Santos *et al* 2006, Grimbacher *et al* 2007). For such groups, more intensive sampling typically

Table 1 Comparison of species abundance, richness and diversity means (± SD) of epigeic arthropods in the forest remnant (FOR) and at restored sites (REV1-REV4).

	Abundance^{ns}	Richness	Diversity
FOR	792.6 ± 268.9	46.4 ± 5.8 ab	2.24 ± 0.3 a
REV1	1095.8 ± 319.2	31 ± 10.4 c	1.70 ± 0.2 b
REV2	1181.2 ± 556.5	36.8 ± 7.4 bc	1.77 ± 0.2 ab
REV3	932.2 ± 336.5	39.8 ± 3.4 bc	2.06 ± 0.1 ab
REV4	964.6 ± 291.3	54.6 ± 3.4 a	2.06 ± 0.4 ab

ANOVA, n = 5. Student-Newman-Keuls Test. Values followed by different letters in the same column are different ($P < 0.05$); ^{ns}non significant.

Table 2 ANOSIM pairwise comparisons (*R* statistic) of sites using the Bray-Curtis similarity matrix produced for the arthropod assemblage in the forest remnant (FOR) and at restored sites (REV1-REV4).

	FOR	REV1	REV2	REV3	REV4
FOR	-				
REV1	1.000[1]	-			
REV2	1.000[1]	0.792[1]	-		
REV3	1.000[1]	0.960[1]	0.692[1]	-	
REV4	1.000[1]	1.000[1]	1.000[1]	1.000[1]	-

[1]$P < 0.01$

never generates curves that completely flatten out and reach a plateau (Fisher 1999). Furthermore, several important epigeic taxa such as ants and termites have patchy distribution (Soares & Schoereder 2001, Nakamura *et al* 2003, 2007), which results in new species being found sporadically.

We did not actually intend to compile a species inventory but to achieve adequate spatial replication (Grimbacher *et al* 2007). Also, sampling was not seasonal, *i.e*. our data were obtained within a month. Therefore, our conclusions about arthropod communities and indicator species may not apply throughout the year as the measured parameters usually change with seasonality. Nevertheless we were successful in showing measurable assemblage-level responses to restoration age and reference habitat.

Among the attributes that demonstrate an appropriate trajectory of restored areas towards the intended goals or reference ecosystem, the first one is "similar assemblage of species and community structure" (SER 2004). In this study, we focused on this attribute, *i.e*., we analyzed community structure of composition of arthropods at the initial stage of the restoration process.

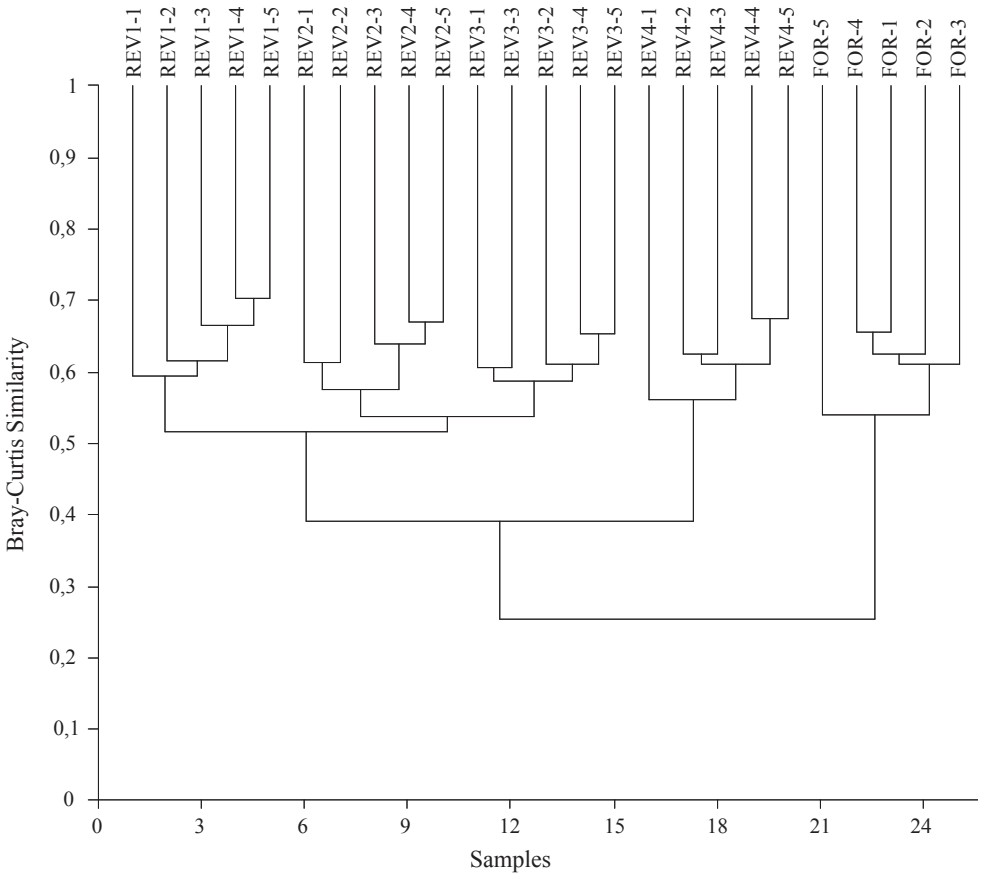

Fig 2 Dendrogram for hierarchical agglomerative clustering of arthropod samples in the forest remnant (FOR) and at restored sites (REV1-REV4), based on Bray-Curtis similarity matrices.

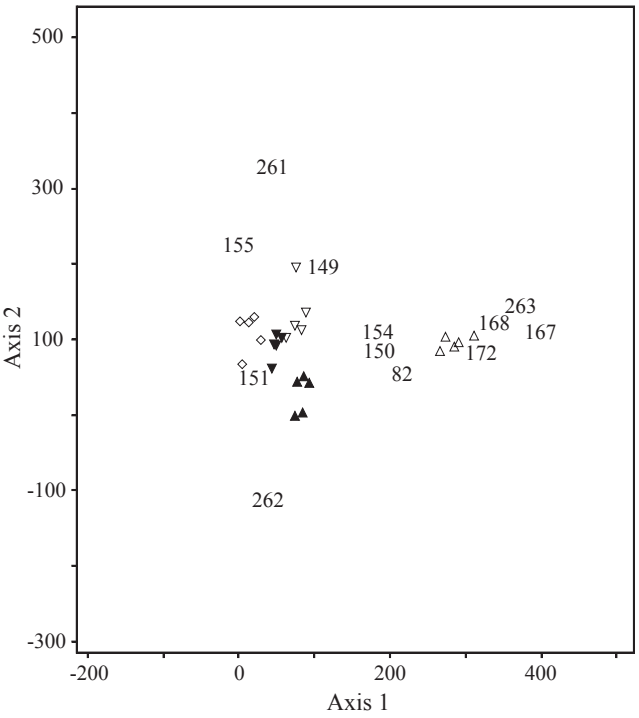

Fig 3 Ordination diagram of the first two axes of detrended correspondence analysis (DCA), showing sites and the 12 most abundant species. Species codes are related to the identification in Table 2. △= forest remnant, ▲ = REV1, ▽ = REV2, ▼ = REV3; ◇ = REV4 (all morphospecies included in the analysis).

Our results showed that even a 5-month-old restored site can reach arthropod abundance equivalent to that observed at the forest and that these levels do not necessarily change during the first three years after revegetation. Hamburg *et al* (2004) found a humped relationship between total ant abundance and rehabilitation age, with peak levels far higher than those at natural sites. However, the peak only occurred after 5-7 years, a period not sampled in our study.

Species richness, in turn, was also high in the first months after planting, with levels equivalent to that of the forest remnant. Even though species richness is considered to be the most easily restored component of biodiversity, recovery of species richness usually takes longer periods, *e.g.,* around 20-40 years for several animal taxa (Dunn 2004) or up to 5-15 years for ground-active beetles in rainforest restoration (Grimbacher *et al* 2007).

Table 3 Comparison of species abundance, richness and diversity means (± SD) of epigeic ants in the forest remnant (FOR) and at restored sites (REV1-REV4).

	Abundance^{ns}	Richness	Diversity
FOR	652.8 ± 250.2	17.4 ± 3.36 a	1.82 ± 0.27 a
REV1	947.8 ± 309.3	9.8 ± 2.17 b	1.46 ± 0.16 b
REV2	1060.6 ± 517.8	11.8 ± 3.03 b	1.61 ± 0.16 ab
REV3	830.8 ± 313.8	11.0 ± 2.34 b	1.76 ± 0.12 a
REV4	780.4 ± 330.7	8.4 ± 1.67 b	1.22 ± 0.16 c

ANOVA, n = 5. Student-Newman-Keuls Test. Values followed by different letters in the same column are different ($P < 0.05$); ^{ns}non significant.

After the five-month peak, richness decreased systematically with revegetation age. This finding was unexpected since, at least for ants, the opposite has been reported (Majer 1992, Bisevac & Majer 1999, Andersen *et al* 2003, Hamburg *et al* 2004). Sometimes, species richness at rehabilitation sites even exceeds reference sites in mid-succession (Jackson & Fox 1996). Even when a break in increasing richness occurs, it happens only after five years (Majer 1996). In our study, ant richness did not follow the decreasing pattern observed for the entire arthropod assemblage nor did it increase as reported in the above-mentioned studies, but showed a continuous level that was low in relation to the reference site.

Which process within the system could explain these patterns? Considering that the initial colonists of a site represent regional pool species and that a site is more likely to be colonized by abundant species than by rare species (Schowalter 2000), the explanation can be possibly found in the regional pool of arthropod species in the surrounding habitats such as cultivated lands and abandoned fields. Such areas serve as population sources of open-habitat or opportunistic arthropods, providing a fast input of species to the recently restored site, a habitat composed basically of tree samplings scattered in a sparse herb layer. One example is *Dorymyrmex* sp., which was abundant at the 5-month-old site and successively decreased in number with age of site. This species belongs to a genus that is typical of open areas (Shattuck & Barnett 2005). Some of the indicator species of the 5-month-old site, *e.g., Agalliana sticticollis* (Stål) (Cicadellidae) and *Astylus variegatus* (Germar) (Melyridae), are widespread insects with occurrence in crop systems indeed (Bennett 1967, Ferreira & Barrigossi 2006).

As habitat attributes change rapidly due mainly to the vegetation growing, these species are substituted by others more adapted to the new conditions. This conclusion is supported by the high turnover (β-diversity) of epigeic arthropod species found across all sites. Considering that there is no forest remnant in the close surroundings (the nearest one is our reference site, about 5 km away), the rate of colonization by forest species would be much slower, which explains the decline in species richness.

In fact, the vegetation structure of the 1- to 3-year-old sites resembled more that of a savannah than of a forest. Taking this into account and also the fact that the region of study is situated in a tension zone between cerrado and forest (IBGE 1993), it is not surprising that some of the main species found in this restoration stage are typical or common in cerrado vegetation. This is the case of the termites *Syntermes grandis* and *S. nanus* (Constantino 2005).

Despite the high dissimilarity between the forest patch and the revegetated area, epigeic arthropod assemblages of revegetated sites moved toward the forest patch score over time. It does not mean, however, that restored sites will ever achieve the same species composition of the forest remnant. Restored sites all over the world have not reached species composition of different living groups from reference sites, even several decades after restoration (Majer 1992, 1996,

Burger *et al* 2003, Grimbacher *et al* 2007). One of the few exceptions seems to be a rehabilitation site in Australia, which grouped with reference sites in multivariate analysis of ant assemblage (Andersen *et al* 2003).

The most abundant epigeic arthropods were ants and termites both in the restored sites and forest remnant, but with different species. The leaf-cutting ants (*Atta* sp.) were exceptions since they were equally abundant everywhere. The nine most abundant species of Formicidae accounted for more than 70% of total abundance of arthropods at all the sites studied. We did not determine, however, if ants in the restored area and mature forest were playing equivalent roles. On the other hand, termites found both in the restored sites (*S. grandis* and *S. nanus*) and reference site (*Velocitermes* sp.) interact with habitat in the same way, foraging for leaf litter (Constantino 2005). A proportional abundance of termites rose slower over time in comparison to ants, but in three years abundance of *S. nanus* approached abundance levels of *Velocitermes* sp. at the reference site.

Besides ants and termites, the only other very abundant species was a Phoridae, and it was probably linked to ant abundance, since the majority of parasitoid species of Phoridae attack adults of Formicidae (Feener Jr & Brown 1997).

Based on pitfall sampling, this study pointed to ants as the main local indicator taxa among epigeic arthropods, with seven out of 12 species being representative of the forest remnant, our restoration target. This finding corroborates the increasing recognition of ants as a useful group for land managers to monitor changes in terrestrial ecosystems (Majer & Kock 1992, Andersen & Sparling 1997, Hamburg *et al* 2004, Santos *et al* 2006). According to these researchers, ants are suitable for biomonitoring because of their a) high richness, diversity, abundance and biomass; b) ecological importance at all trophic levels; c) critical ecological role in soil turnover and structure, nutrient cycling, plant protection, seed dispersal and seed predation; d) easy sampling; e) wide geographic distribution; f) sensitivity to environmental changes; and f) relatively well-known taxonomy and dynamics within the community.

The main goal in the restoration of semideciduous forests in southeastern Brazil is for restored sites to resemble the small patches of mature forest that have resisted deforestation. These patches are disturbed in a variety of degrees (Nascimento *et al* 1999, Almeida 2000, Tabanez & Viana 2000) as a result of being submitted to a long period of isolation and to pressures from the anthropized matrix. Nevertheless, they are the only reference that persists of what were once magnificent seasonal forests. Our study contributes to the conservation efforts for this highly threatened ecosystem as it provides baseline information for understanding the dynamics of colonization of a subset of its biota at the first restoration stage.

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Online Supplementary Material 1

Pais M P, Varanda E M (2010) Arthropod Recolonization in the Restoration of a Semideciduous Forest in Southeastern Brazil. Neotrop Entomol 39(2): 198-206.

Number of individuals per site of the 12 most abundant species of epigeic arthropods in the forest remnant (FOR) and at restored sites (REV1-REV4).

Species code	Taxon	Abundance				
		FOR	REV1	REV2	REV3	REV4
	Diptera, Phoridae					
82	Phoridae sp.	124	199	59	59	73
	Hymenoptera, Formicidae					
149	*Crematogaster* sp.	62	313	802	567	51
150	*Megalomyrmex* sp.	1092	1766	1446	1289	1416
151	*Camponotus rufipes*	0	1287	911	617	16
154	*Atta* sp.	878	1959	2696	329	379
155	*Dorymyrmex* sp.	0	29	763	1127	1973
167	*Camponotus* sp.	428	0	0	0	0
168	*Camponotus sericeiventris*	251	0	0	0	0
172	*Pheidole* sp.	237	35	25	0	46
	Isoptera, Termitidae					
261	*Syntermes grandis*	0	0	274	26	0
262	*Syntermes nanus*	0	481	18	2	29
263	*Velocitermes* sp.	334	0	2	9	0
	All 288 morphospecies	4039	6706	7549	5120	5229

Online Supplementary Material 2

Pais M P, Varanda E M (2010) Arthropod Recolonization in the Restoration of a Semideciduous Forest in Southeastern Brazil. Neotrop Entomol 39(2): 198-206.

Percentage indicator values (IndVal > 70%) of epigeic arthropod species in the forest remnant (FOR) and at restored sites (REV1-REV4).

Species code	Taxon	Site	IndVal	P[1]
	Araneae, Theridiidae			
10	*Coleosoma floridanum*	FOR	80.0	0.0040
	Dictyoptera, Blattelidae			
23	*Xestoblatta* sp.	FOR	80.0	0.0010
	Coleoptera, Melyridae			
41	*Astylus variegatus*	REV4	78.1	0.0010
	Coleoptera, Tenebrionidae			
56	Tenebrionidae sp.	REV4	74.1	0.0040
	Diptera, Phoridae			
78	*Hypocera* sp.	FOR	80.0	0.0010
	Diptera, Drosophilidae			
93	Drosophilidae sp.	FOR	80.0	0.0040
	Hemiptera, Miridae			
116	Phylini sp.	REV4	86.5	0.0010
128	Miridae sp.	REV4	80.0	0.0030
	Hemiptera, Cicadellidae			
142	*Agalliana sticticollis*	REV4	77.6	0.0010
	Hemiptera, Aphididae			
143	*Aphis* sp.	REV4	90.4	0.0010
	Hymenoptera, Formicidae			
167	*Camponotus* sp.	FOR	100.0	0.0010
168	*Camponotus sericeiventris*	FOR	100.0	0.0010
170	*Linepithema* sp1	FOR	80.0	0.0020
176	*Linepithema* sp2	FOR	100.0	0.0010
171	*Cyphomyrmex* sp.	FOR	92.2	0.0010
173	*Odontomachus* sp.	FOR	100.0	0.0010
182	*Wasmannia* sp.	FOR	72.6	0.0040
	Hymenoptera, Chalcidoidea			
203	Chalcidoidea sp 1	FOR	100.0	0.0010
244	Chalcidoidea sp 2	REV4	100.0	0.0010
	Hymenoptera, Sphecidae			
220	*Prionyx chilensis*	REV4	77.2	0.0020
	Hymenoptera, Halictidae			
234	*Pereirapis* sp.	REV4	79.5	0.0010
	Isoptera, Termitidae			
262	*Syntermes nanus*	REV1	73.2	0.0010
	Thysanoptera			
286	Thysanoptera sp.	REV4	73.3	0.0010

[1]Monte Carlo test of significance of observed maximum indicator value for species.