FERNANDO AUGUSTO SCHMIDT

TROPICAL ANT DIVERSITY: DETERMINANT FACTORS, SPATIAL SCALES AND COMMUNITY CONGRUENCE

Tese apresentada à Universidade Federal de Viçosa, como parte das exigências do Programa de Pós-Graduação em Entomologia, para obtenção do título de *Doctor Scientiae*.

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(Coorientadora)

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Júlio Neil Cassa Louzada

Ricardo Ildefonso de Campos

José Henrique Schoereder
(Orientador)

All good work is done the way ants do things,

little by little.

Patrick Hearn

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SUMÁRIO

CHAPTER 1

PARTITION OF THE EFFECTS OF MULTI-SCALES FACTORS ON ANT DIVERSITY

CHAPTER 2

CONGRUENCE TRENDS AMONG TROPICAL ANT COMMUNITIES: A COMPARISON OF RAINFORESTS AND SAVANNAS IN BRAZIL AND INDONESIA

RESUMO

SCHMIDT, Fernando Augusto, D.Sc., Universidade Federal de Viçosa, fevereiro de 2012. **Diversidade de formigas tropicais: Fatores determinantes, escalas espaciais e congruência de comunidades**. Orientador: José Henrique Schoereder. Coorientadores: Carla Rodrigues Ribas e Tathiana Guerra Sobrinho.

Ecólogos têm descrito as comunidades de espécies em diferentes escalas espaciais, que podem variar de local a regional. Assim, diferentes mecanismos tem sido propostos para explicar os padrões de diversidade em cada escala espacial. Além disso, de acordo com o determinismo local, comunidades de diferentes regiões, porém em habitats similares devem apresentar padrões de diversidade congruentes. Nesta tese, nós desenvolvemos perguntas referentes à estrutura de comunidades de formigas em diferentes escalas espaciais. No primeiro capítulo nós verificamos: (i) quais são os principais fatores determinantes da estrutura de comunidades de formigas, e (ii) em que escala espacial esses fatores atuam. Nós desenvolvemos as análises com comunidades de formigas de floresta e savana associadas a diferentes microhabitats (arborícola, epigeíco e hipogéico). Nós realizamos seleção de modelos, para verificar a influência de recursos e condições agindo como fatores da escala em estudo ou da escala imediatamente superior na diversidade de formigas. Em geral, fatores locais e fatores de meso-escala desempenharam uma influência relativa similar na diversidade de espécies de formigas em escala local. Na meso-escala os parâmetros avaliados parecem ter pouca influência sobre a comunidade de espécies de formigas. Entretanto, verificamos que os fatores que influenciam as comunidades de formigas tanto na escala local quanto na meso-escla diferem entre os tipos de habitat e microhabitat. No segundo capítulo, nós testamos a hipótese que comunidades de formigas de habitats similares, independente de seus valores absolutos de diversidade idionsicráticos, compartilham padrões semelhantes da contribuição relativa da diversidade alfa em escala local e da diversidade beta ao longo de diferentes escalas para a diversidade gama. Além disso, nós verificamos se as comunidades de formigas apresentam padrões similares de saturação/insaturação de espécies em escala local. Nós amostramos formigas epigéicas em habitats de floresta tropical e savana no Brasil e Indonésia. Em cada país, para cada tipo de habitat, nós selecionamos três paisagens, onde as formigas foram coletadas em quatro áreas ao longo de dez armadilhas do tipo “pitfall” em cada área. Independente das diferenças nos valores absolutos de diversidade, em todos os biomas, a diversidade alfa em escala local e a diversidade beta entre as paisagens foram maiores que o esperado pelo acaso e a diversidade beta entre armadilhas (escala local) e entre as áreas foram menores que o esperado pelo acaso. Além disso, nós encontramos um padrão de insaturação de espécies em escala local. Nós associamos estes congruência de padrões à elevada capacidade de dispersão das formigas em escalas espaciais pequenas e intermediárias. Isto possibilita uma elevada diversidade de espécies nas comunidades locais e um constante fluxo de espécies entre elas. Entretanto, o padrão de diversidade beta semelhante na escala de paisagem sugere que em ambos os países, processos históricos podem ter restringido o fluxo de espécies entre paisagens de forma semelhante. Portanto, nós entendemos que perspectivas como as descritas nesta tese têm um grande potencial para oferecer explicações satisfatórias sobre a estrutura de comunidades de formigas. Nós sugerimos que assimilação de mecanismos alternativos ao determinismo local é essencial para a elaboração de futuras hipóteses em relação aos padrões de diversidade em comunidades de formigas tropicais.

ABSTRACT

SCHMIDT, Fernando Augusto, D.Sc., Universidade Federal de Viçosa, February, 2012. **Tropical ant diversity: Determinant factors, spatial scales and community convergruence**. Advisor: José Henrique Schoereder. Co-Advisors: Carla Rodrigues Ribas and Tathiana Guerra Sobrinho.

Community ecologists have described the species assemblages at different spatial scales, which range from local to regional. Different mechanisms have been proposed to explain the diversity patterns in each spatial scale. Moreover, according to local determinism predictions, communities from similar habitats in different regions should present congruent diversity patterns. In this thesis, we addressed questions regarding the structure of ant communities at multiple scales. In the first chapter, we verified: (i) what are the main driving factors to the structure of ant communities, and (ii) in which spatial scales these factors act. We carried out the analyses with ant communities from different habitat types (forest and savanna) and from different microhabitats (arboreal, epigaic and hypogaeic ants) within the same habitat type. We performed model selection to verify the influence of resources and concitions acting as factors at the studied scale or at the immediately larger scale to ant diversity. In general, local factors and meso-factors played a similar relative influence on the ant diversity at local scale. At mesoscale, the parameters evaluated seem to loss their influence on the ant communities. However, we verified that the determinant factors of ant communities at local scale and mesoscale are different according the habitat types and microhabitats. In the second chapter, we hypothesized that ant communities at similar habitats, independent on their idiosyncratic absolute diversity values present similar patterns of relative contribution of alpha diversity at local scale and beta diversity acrros multi-scale to gamma diversity. Moreover, we verify if the ant communities present similar patterns of species saturation/insaturation at local scale. We sampled epigaeic ants in rainforest and savanna habitats in Brazil and Indonesia. In each habitat type of each country, we selected three landscapes in which the ants were sampled in four sites along ten pitfall traps in each site. Regardless the differences on the absolute values of species diversity and variation, in all biomes, α-diversity at local scale and β-diversity among landscapes (β_3) were higher than expected by null models and β-diversity among pitfalls and among sites (β_1 and β_2 respectively) were lower. Moreover, we found a species insaturation pattern at local scale. We associated these convergent patterns among the

ant communities of all biomes to a high ant dispersal ability, which overcomes the local constraints, conferring a higher α-diversity at local scale and lower β-diversities among pitfall and among sites (β_1 and β_2 respectively). However, at large scales, historical restrictions could impose similar constraints on the ant dispersion among the ant communities at landscape scale resulting in the higher observed β-diversity. Therefore, we understand that perspectives, such as described in this thesis, have a great potential to offer satisfactory explanations about the ant community structure. We suggest that assimilation of alternative mechanisms, besides local determinism, are essential to the elaboration of future hypothesis regarding to the diversity patterns of tropical ant communities.

GENERAL INTRODUCTION

Community ecologists have described the species assemblages at different spatial scales, which range from local to regional (Ricklefs & Schluter 1993). In each spatial scale, different mechanisms have been proposed to explain the diversity patterns (Ricklefs 2004).

Species interactions (mainly competition) have been proposed as the major determinant factors to the structure of local communities. However, there is an exchange of species among local communities, which means an effect of external factors acting against the local restrictions (Ricklefs & Schluter 1993).

In this way, a set of local communities could be designated as a metacommunity, where the local assemblages are linked by the species dispersion (Holt 1993; Leibold et al. 2004). Usually, a metacommunity represents an area smaller than a whole biogeographically province or realm, and then they are spatially designated as mesoscale (Ricklefs & Schluter 1993).

At the mesoscale, the total species diversity (gamma diversity) could be partitioned in two components, the alpha diversity which is the species diversity within each local community and beta diversity, the species variation among the local communities (Whittaker et al. 2001). Thus competitive ability, colonization ability, patch use and habitat specialization are desirable traits to species coexistence at mesoscale, and ecologists have proposed mechanisms to explain the differences of species among local assemblages, such as patch dynamic, species-sorting, mass effects and the neutral perspective (Leibold et al. 2004).

At broad large scale, historical events have been reported as barriers on the species exchange among areas inside a common biogeographical realm (Ricklefs & Schluter 1993; Ricklefs 2004). However, according to local determinism predictions, communities from similar habitats in different regions should have congruent local diversity, which would be independent of regional diversity (Smith & Wilson 2002, Ricklefs 2004).

Ants, due to their conspicuous species diversity and key ecological functions (Hölldobler & Wilson 1999), have been used as models to test hypotheses regarding the structure and dynamics of ecological communities at several spatial scales (Lach 2010). Several studies have explained the ant species diversity patterns on different microhabitats (e.g. canopy, arboreal and ground) considering essentially the role of driving factors acting in the current focus scale (e.g. Ribas et al. 2003; Lassau & Hochuli 2004; Corrêa et al. 2006; Ribas and Schoereder 2007; Vargas et al. 2007; Yanoviak et al. 2007; Paolucci et al. 2010). Moreover, in a global scale, following biogeography approaches, studies have reported that ant diversity is limited by latitudinal gradients under the effects of climatic restrictions (Dunn et al. 2007; 2009).

However, there is a lack of studies including the effect of factors from large spatial scales (but see Spiesman & Cumming 2008; Vasconcelos et al. 2010; Mezger & Pfeiffer 2011), besides considering the role of factors acting at the focal scale. At broad scale also there are few studies that search for similarities on the structure of ant communities form similar habitats in different world regions (but see Campos et al. 2011)

We consider that studies about the relative effect of factors acting in different spatial scales on ant diversity and congruent trends among ant communities are very useful to understand the structure of tropical ant communities. Thus, in this thesis, we developed two studies, which in the first, we aimed to verify the determinant factors of ant diversity at local scale and mesoscale and in which scale they act. In the second study, we search for congruent trends among tropical ant communities from similar habitats types in Brazil and Indonesia.

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CHAPTER 1

Partition of the effects of multi-scales factors on ant diversity

Resumo

Comunidades ecológicas podem ser estudadas em diferentes escalas espaciais, desde assembléias locais até em um contexto global, através de uma abordagem biogeográfica. Em cada escala espacial a principal questão é verificar os efeitos de fatores que agem na escala foco, daqueles que agem em escalas superiores sobre a diversidade de espécies. Formigas têm sido utilizadas como modelos para estudos de ecologia de comunidades em diferentes escalas espaciais. Entretanto poucos trabalhos, consideram o papel de fatores que agem em distintos escalas espaciais na diversidade de formigas. Assim, usando uma abordagem de partição do efeito de fatores de distintas escalas espaciais na diversidade de espécies, nós verificamos: (i) quais são os principais fatores determinantes para a diversidade de formigas, e (ii) em que escala espacial eles agem. Nós também verificamos se há uma dependência da influência dos fatores em relação ao habitat (floresta e savana) e ao microhabitat (arborícola, epigeíco e hipogéico). Os habitats de floresta e savana foram representados pelos biomas, Floresta Atlântica e Cerrado. Em cada tipo de habitat, nós selecionamos três paisagens, onde as formigas foram coletadas em quatro áreas (meso-escala) em dez armadilhas do tipo “pitfall” (escala local) em cada área. Nós coletamos informações que foram utilizadas como estimativas da quantidade e heterogeneidade de recurso para as formigas de todos os microhabitats e como estimativa de condições para as formigas hipogéicas. Nós realizamos uma seleção de modelos, na qual o modelo global considerou a influência das estimativas de recursos e condições como fatores que agem na escala em foco e na escala imediatamente superior para a diversidade de formigas em escala local e meso-escala. Em geral, as estimativas de recurso e condições agiram como fatores locais e de meso-escala na diversidade de formigas em escala local. Na meso-escala os parâmetros avaliados parecem ter pouca influência sobre a diversidade e variação de espécies de formigas. Entretanto, verificamos que os fatores que influenciam as comunidades de formigas tanto na escala local quanto na meso-escla diferem entre os tipos de habitat e microhabitat. Assim, é importante se ter cuidado ao fazer generalizações a respeito da estrutura de comunidades de formigas que não consideram fatores idiossincráticos associados aos diferentes microhabitats e habitats das formigas.

Palavras-chaves: Cerrado, ecologia de comunidades, escala espacial, estratificação, Floresta Atlântica.

Abstract

Ecological communities can be studied at different spatial scales, from local assemblage to global-biogeography context. In each spatial scale, the major concern is the partitioning between the effects of factors acting at the focus scale and those operating at broad spatial scales on the species diversity. Ants have been used as models of ecological community studies at several spatial scales, however few studies have verified the effect of factors from large spatial scales besides the role of factors acting at the focal scale on ant diversity. Thus, following factor effects partitioning approaches on species diversity, we verified: (i) what are the main driving factors on species diversity, and (ii) in which spatial scales these factors act, at distinct spatial scales. We also investigate if there is a dependence of the factors effects regarding to the ant communities habitat type (forest and savanna) and to the microhabitat type (arboreal, epigaic and hypogaeic ants) within the same habitat type. The forest and savanna habitats landscapes were located in Atlantic rainforest and *Cerrado* (Brazilian savanna) biomes, respectively. In each habitat type, we selected three landscapes in which the ants were sampled in four sites (mesoscale) along ten pitfall traps (local scale) in each site. We collected data that were used as surrogates of resources amount and heterogeneity for the three ant microhabitats and conditions only for hypogaeic ants. We performed model selection, which in the global models were accounted the influence of resource and conditions surrogates acting as factors at the focus scale and at the immediately larger scale to ant diversity at local scale and mesoscale. In general, local factors and meso-factors play a similar relative influence on the ant species richness at local scale. At mesoscale, the parameters evaluated seem to loss their influence on the ant species diversity and variation. However, we verified that the determinant factors of ant communities at local scale and mesoscale are different according the habitat types and microhabitats. Hence, caution is important about broad generalization about the structure of ant communities which does not account for the idiosyncratic factors associated to the ant microhabitat and habitat types.

Key words: Atlantic rainforest, *Cerrado*, community ecology, spatial scale, stratification

Introduction

Ecological communities can be studied at different spatial scales, from local assemblage to global-biogeography context. In this way, it is expected that at each spatial scales different determinant factors should be responsible for the diversity patterns (Ricklefs & Schluter 1993).

Historically, interactions among species (mainly competition) have been reported as the major process responsible for the community structure at small (local) scale (Ricklefs 2004). The role of competition has been demonstrated by the influence of resource availability (quantity and variety), environmental heterogeneity on the species coexistence at local scale (Shorrocks & Sevenster 1998) and even at broad scales (Gilbert et al. 2008).

However, among local communities, there is an exchange of species by the species dispersal movement among them, which mean an effect of external factors that act against the local restriction (Ricklefs & Schluter 1993). In this way, set of local communities within a region could be also recognized as a metacommunity, where the local assemblages are linked by the species dispersion (Holt 1993; Leibold et al. 2004). Because they are areas smaller than whole biogeographical provinces or realms, they are spatially designated as mesoscale (Ricklefs & Schluter 1993).

At the mesoscale, besides the competitive ability, the colonization ability, patch use and habitat specialization are desirable species traits to the species coexistence in the metacommunity (Kneitel & Chase 2004). Building on these traits tradeoffs, Leibold et al. (2004) summarized four essential paradigms described in the community ecology literature as mechanisms responsible to species dispersion at mesoscale context, which are patch dynamic, species-sorting, mass effects and the neutral perspective (the absence of difference traits among the species).

The total species diversity (gamma diversity) within a large area (e.g. at mesoscale or metacommunity) could be partitioned in two components, the alpha diversity which is the species diversity within each local community (alpha diversity) and the beta diversity, the species variation among the local communities (Whittaker et al. 2001). In this way, according the effect of species dispersion movements on diversity components, alternative metacommunity paradigms could be reached (see details in Leibold et al. 2004).

At broad large scale, historical events related to tectonic dynamic effects (e.g. rising of mountain chain) and climate change (e.g. Pleistocene glacial cycles) have been reported as barriers on the species exchange among areas inside a common biogeographic realm (Ricklefs & Schluter 1993; Ricklefs 2004). In this way, the species diversity and species variation patterns at intermediate scales (i.e. mesoscale) also suffer an effect of external factors, but now related to the historical development of the whole region (Graham et al 2005; 2006).

Hence, in each spatial scale, the major concern is the partitioning between the effects of factors acting at the focus scale and the influence of those operating at broad spatial scales (Ricklefs 2004). This approach is desirable to a better understanding about the processes driving the community structure and their scale dependence.

Ants, due to their conspicuous species diversity and key ecological functions (Hölldobler & Wilson 1999), have been used as models to test hypotheses regarding the structure and dynamics of ecological communities at several spatial scales (Lach 2010). Several studies have explained the species ant diversity patterns on different microhabitats (e.g. canopy, arboreal and ground) considering essentially the role of driving factors acting in the current focus scale, such as resource availability (i.e. resource amount and variety), environmental heterogeneity and disturbance intensity (Ribas et al. 2003; Lassau & Hochuli 2004; Corrêa et al. 2006; Ribas and Schoereder 2007; Vargas et al. 2007; Yanoviak et al. 2007; Paolucci et al. 2010).

Recently, some studies have included the effect of factors from large spatial scales (Spiesman & Cumming 2008; Vasconcelos et al. 2010; Mezger & Pfeiffer 2011), besides considering the role of factors acting at the focal scale. Nevertheless, ant assemblages from specific habitats (e.g. forest and savanna) and microhabitats (e.g. canopy, arboreal and ground) have unique ecological structure and dynamics (Vasconcelos & Vilhena 2006; Blüthgen & Feldhaar 2010). This makes us to deduce that the relative effect of factors act at the focus and large scales on ant diversity could depend on the ant habitats and microhabitats.

Following factor effects partitioning approaches on species diversity, we verified: (i) what are the main driving factors on species diversity, and (ii) in which spatial scales these factors act, at focus sampling data scale or at immediately larger scale. We also investigate if there is a dependence of factors effects regarding to the ant communities habitat type (forest and savanna) and to the microhabitat type (arboreal, epigaic and hypogaeic ants) within the same habitat type.

Material and Methods

Habitat types

We sampled ant communities in savanna and rainforest habitats in Brazil (Table 1), which are known as *Cerrado* (Brazilian savanna) and Atlantic rainforest biomes (IBGE 2004), respectively. Both biomes contain several vegetation types. *Cerrado* encompass grasslands, shrublands, savannas and tropical deciduous forests (Coutinho 1978; Ribeiro & Walter 1998). In the Atlantic rainforest biome vegetation types such as lowland rainforest, coastal forest, freshwater swamp forest and semideciduous seasonal rainforest are described (IBGE 2004).

Table 1. Description of forest and savanna habitats sampled in Brazil. ARF = Atlantic rainforest biome. CER = *Cerrado* biome. * Although Atlantic rainforest is made up essential by forest formations, in VALE Natural Reserve we sampled ants in natural endemic grassland site (Jesus & Rolim 2005).

Habitat	**Biome**	**Conservation area**	**Vegetation**	**Area (ha)**	**Altitude (m)**	**Coordinates**
Rainforest	ARF	VALE Natural Reserve	Lowland rainforest at sandy soil and plain topography, grassland*	21,787	28 - 65	19°06'S 39°45'W
Rainforest	ARF	Rio Doce State Park	Semideciduous seasonal rainforest	35,976	230 - 515	19°29'S 42°28'W
Rainforest	ARF	Serra do Mar State Park	Lowland rainforest and coastal forest	315,390	0 - 1,320	23°27'S 45°15'W
Savanna	CER	Panga Ecological Station	Savanna and deciduos tropical forest	403.85	740 - 830	19°10'S 48°24'W
Savanna	CER	IBGE Ecological Reserve	Grassland and savanna	1,300	1,150	15°56'S 47°52'W
Savanna	CER	Grande Sertão Veredas National Park	Grassland, savanna and deciduous tropical forest	231,668	600 - 850	15°23’S 45°54’ W

Spatial scale definition

In each biome, we sampled the ants in three protected areas (Table 1), which we designated as landscape scale. The landscape scale was considered the largest spatial scales within each biome.

Within each landscape, we installed four transects that, depending on the vegetation variety in the protected areas, could encompass different vegetation types or not. We considered each transect as the mesoscale.

Along each transect we distributed 10 sampling units. The sampling units represented the smallest spatial scale, the local scale.

The distance among the protected areas (landscape scale) within the biomes was 277 to 684 Km in Atlantic rainforest and 267 to 519 Km in *Cerrado*. Within the protected area, we established 100 m straight transects (mesoscale) at least 500 m apart from each other. Finally, along each transect we set then sampling units (local scale) 10 m apart from each other.

Ant sampling and identification

In each sampling unit, we installed three pitfall traps, each one at arboreal, epigaeic and hypogaeic microhabitats. We considered arboreal, epigaeic and hypogaeic ants as all those ants foraging in trees, in the ground and/or litter and in the subterranean soil layers respectively.

Thus, in each transect we had a total of 30 traps (10 traps per microhabitat), but in sites without trees or shrubs, only epigaeic and hypogaeic traps were installed, dropping the total number of traps to 20.

The pitfall traps of all microhabitats consisted of plastic recipients (diameter = 8 cm; height = 12 cm) with an inner smaller recipient. Between these two recipients we put 200 ml of a solution of water, glycerol (5%) and salt (0.9%) that kept and killed the ants and avoided their contact with the baits. We set the baits, sardine (5 cm^3) and honey (10 cm^3), each one in small plastic pots (3.3 cm diameter; 5.0 cm height) that were put in the inner recipient.

We buried the epigaeic pitfall traps at the soil level (Bestelmeyer et al., 2000). We tied the arboreal pitfall traps at ca 1.3 m high to the trunks of trees (Ribas et al., 2003) allowing the sampling of ants running down and up on the trunk. We buried the hypogaeic pitfall traps under soil surface, 20 cm into the soil, and made some adaptations that allow the access of ants with subterranean habit to the trap (Schmidt and Solar, 2010). All the traps remained in the field by 48 hours.

We sorted and identified the collected ants to genera with the help of Bolton (1994) and Palacio and Fernández (2003) taxonomic keys. The subfamily classification followed the Bolton (2003) proposal.

We carried out ant species identification according with the Formicidae reference collection in the Community Ecology Laboratory – UFV, Brazil, where we deposited the voucher specimens. When the sampled ants did not correspond to the reference species, we sorted them in morpho-types according their external morphology.

Species diversity and explanatory variables

We analyzed ant species diversity at local and mesoscale. We considered the number of ant species (species richness) in each pitfall trap as local species diversity. To the mesoscale species diversity, we considered the decomposition of the total diversity (gamma diversity) in its components, alpha and beta diversity.

At mesoscale, we followed the additive diversity partitioning approach (Veech et al. 2002), where gamma diversity (γ) is the result of the sum between alpha diversity (α) and beta diversity (β). In our study, the total number of ant species sampled in each transect was considered as the γ-diversity at mesoscale. The α-diversity was considered the average amount of the γ-diversity (present in each transect) found in a single randomly-chosen sample (pitfall trap) and β-diversity was the average amount of the γ-diversity not found in a single randomly-chosen sample.

We collected data that were used as surrogates of resources amount and heterogeneity for the three ant microhabitats and conditions only for hypogaeic ants. The data were specific for each microhabitat (Table 2) and have been reported to have direct or indirectly influence on the ant diversity of each microhabitat (Ribas et al., 2003; Corrêa et al., 2006; Ribas and Schoereder, 2007; Vargas et al., 2007; Andersen and Brault, 2010; Paolucci et al. 2010).

Table 2. Description of resources and conditions surrogates for ants in three microhabitats in forest and savanna habitats in Brazil. RA = Resource amount. RH = Resource heterogeneity.

Surrogates	**Arboreal**	**Epigaeic**	**Hypogaeic**
RA	Number of trees* in an area of 10 m^2.	Litter depth measured with a digital caliper.	Soil respiration***: quantification of the carbon dioxide resulting from soil organism respiration.
RH	Number of tree species* in an area of 10 m^2.	Litter heterogeneity**: The Shannon evenness measure (J’) of the litter number of litter items and their frequency in an area of 200 cm^2.	Non-measured.
Conditions	Non-measured.	Non-measured.	Soil Moisture****: The amount of water among the soil particles. Soil texture****: The relative amount of soil fractions: clay, silt, fine sand and coarse sand.

*In Costal Atlantic rainforest biome we counted only trees with trunk circumference ≥ 15 cm at 1.3 m height. In *Cerrado,* we counted trees with trunk circumference ≥ 5 cm at 30 cm above soil level. **We counted the litter items and their frequency in the area of 200 cm^2 and used these data to calculated the Shannon evenness measure (J’) (Magurran 2003) which $J' = H'/H'_{max}$ where $H' = -\sum p_i/\log p_i$ and $H'_{max} = \log S$. The frequency of item “i” in a sample is p_i. ***We measured the soil respiration considering the CO_2 accumulation in inverted and closed chambers, where soil CO_2 was absorbed by an alkaline solution of NaOH during 24 hours and afterward titrated with HCl (Aquino & Assis 2005). ****We collected soil samplings which were processed at Soil Physics Laboratory – UFV.

We collected or measured the resource and condition data beside the place where the pitfall traps were set. However, for soil respiration (Table 2) we measured it at each two sampling units, due to the large structure and logistic to manage the equipments and chemical reagents in the field.

Model selection

We performed model selection analyses in the R statistical program (R Development Core Team 2009). We applied the IT – Information-Theoretic approach based on the second-order Akaike's Information corrected for small sample size (AICc)(Burnham & Andersen 2002).

We performed the essential steps for multimodel inference described by Grueber et al. (2011). We provided below a short description of each step.

We fitted global models by GLMM – Generalized Linear Mixed Models using the *glmer* function in the *lme4* package (Bates & Maechler 2009). The input variables were standardized by the *standardize* function in the *arm* package (Gelman et al. 2009), which fitted the models by Laplace approximation.

Afterward, we used the *MuMIn* package (Barton´ 2009). Thus, we got full submodel sets from global models by the use of the *dredge* function. The submodel sets were ranked considering the Akaike model weight (ω), resulting the top models got by the function *get.models*.

We considered a cut-off of 0.95 Akaike-weigth to model ranking. Regarding the model supporting the data, we considered only AICc difference (ΔAICc) up to 2 (two) among the models and the top model (model with the minimum AICc), because larger ΔAICc means that the model loss much information and fail to explain substantial data variation (Burnham & Andersen 2002).

Finally, we averaged the top models by *model.avg* function also in the *MuMIn* package undertaken by "zero" average shrinkage method. This average method is recommended when the aim of the study is to determine which factors have the strongest effect on the response variables (Nakagawa & Freckleton 2010).

Independent on the spatial scale, our aims were to find out (i) what are the main driving factors on species diversity at the studied scale and (ii) in which spatial scales the factors act. In this way, we construct global models that account for the influence of factors acting at the focus scale and at the immediately larger scale.

In the global model at local scale, the input variables were species richness as response variable, and the explanatory variables were resource amount and resource heterogeneity. We used the absolute value of resource amount and heterogeneity in each sampling unit as surrogate of the influence of local factors and their average was considered the effect of factors acting at the immediately larger scale, the mesoscale.

We considered local factors effects and meso-factors effects as fixed factors and transects and the protected areas (park) identity as random factors in the global models at local scale. We applied this model design with the data of arboreal and epigaeic ants.

In the global model of hypogaeic ant diversity at local scale, beside the resource data we also considered the condition data as an explanatory variable (Table 2.). The global model of hypogaeic ant diversity followed the same design of arboreal and epigaeic ants, but we also considered the coefficient of variation of the resource and condition data as the surrogate of the effect of factors acting at mesoscale. We ran separately the models with average and coefficient of variation of resource and conditions as meso-factors effects.

The global model at mesoscale had a similar structure as the models for local scale. However, the response variables were gamma, alpha and beta diversities.

The effect of factors acting at mesoscale was represented by the average of resource amount and heterogeneity, called as mesoscale factors. On the other hand, the effect of factors acting at the immediately larger scale, landscape scale, was represented by the protected area identities included in the model as park. The protected area identities also were included in the global models as random factor.

The global model of hypogaeic at mesoscale also considered resource and condition data. We ran separately global models with the average and coefficient of variation of resource and condition data.

In the hypogaeic model selection, for local scale and mesoscale, we previously verified the collinearity among the soil texture fraction (clay, silt, fine sand and coarse sand)(Table 2), because the sum of these fractions makes up the total soil texture of a single sample. We only considered clay as input variable in the model because it presented the largest collinearity with the other soil fractions.

We analyzed models with count data as response variable, such as species richness and gamma-diversity following Poisson distribution. We carried out models that had alpha and beta diversity, decimal data, under normal distribution.

Results

Ant fauna

We sampled 232 ant species from eight subfamilies, considering all the traps distributed in the two biomes and all microhabitats (arboreal, epigaeic and hypogaeic)(Appendix material-A1). We captured more ant species in *Cerrado* (162 species) than in Atlantic rainforest (133 species) considering all microhabitats together (Appendix material-A2 and A3) and separately (Table 3)

Table 3. Number of ant species sampled at three microhabitats in Atlantic rainforest and *Cerrado* biomes in Brazil. Total = the sum of number of single ant species considering the two biomes together. #spp.-Total = Total number of ant species.

Ant Subfamily	Atlantic rainforest	Cerrado	Total
Arboreal ants			
Dolichoderinae	7	6	12
Ecitoninae	1	0	1
Ectatomminae	2	1	3
Formicinae	14	22	29
Myrmicinae	26	29	43
Ponerinae	5	29	43
Pseudomyrmecinae	3	5	6
#spp.-Total	**58**	**65**	**99**
Epigaeic ants			
Dolichoderinae	6	14	19
Ecitoninae	4	3	5
Ectatomminae	4	9	9
Formicinae	18	27	33
Myrmicinae	55	71	104
Ponerinae	14	7	14
#spp.-Total	**103**	**133**	**187**
Hypogaeic ants			
Cerapachyinae	1	0	1
Dolichoderinae	1	2	2
Ecitoninae	2	4	5
Ectatomminae	2	5	6
Formicinae	5	8	11
Myrmicinae	31	30	47
Ponerinae	7	5	10
#spp.-Total	**49**	**54**	**82**

Myrmicinae was the most speciose subfamily in all microhabitats of both biomes followed by Formicinae (Table 3). Dolichoderinae and Ponerinae were the third most speciose subfamily in the arboreal and hypogaeic microhabitats respectively in both biomes. In the epigaeic microhabitat for Atlantic rainforest, Dolichoderinae was the third most speciose subfamily, but was replaced by Ponerinae in *Cerrado* (Table 3).

Cerapachyinae, Ecitoninae, Ectatomminae and Pseudomyrmecinae did not have a fixed position in the number of ant species ranking. However, some of these subfamilies were restricted to specific microhabitats and biomes (e.g. Cerapachyinae was only sampled with hypogaeic pitfall traps in Atlantic rainforest biome)(Table 3).

Model Selection

Model averaging at local scale

Independent on the biome, in general local factors and meso-factors play a similar relative influence on the ant species richness at local scale (see the RI values – relative importance in Table 4). However there were some particularities at the same microhabitat between the biomes (Table 4).

Average number of trees (NT_ave), a meso-factor, was an important predictor for arboreal ant species at local scale, though it had an expressive difference regarding its relative importance (RI) and effect direction (Atlantic rainforest - RI: 0.91 and negative effect; *Cerrado* – RI: 0.42 and positive effect (Table 4). However, the number of tree species, a local factor, presented a strong positive influence on arboreal ant species in Atlantic rainforest (RI: 0.92)(Table 4). An inspection on the Akaike-weights (ω) suggests that the explanatory variables considered in the models have a stronger influence on the arboreal ant species richness from Atlantic rainforest than in *Cerrado*, which the top model was fitted only with the intercept in absence of any explanatory variable (Table 4).

Litter depth and litter heterogeneity were the most important parameters to epigaeic species richness. However these factors play their influence at different spatial scales according the biome.

In Atlantic rainforest, litter heterogeneity (LH) was more influent than litter depth (LD) on the epigaeic species richness, both were local factors in the model selection and with positive effect on the epigaeic species richness (Table 4). In *Cerrado*, litter data were designated as meso-factors, which average litter depth (LD-ave) was more important predictor than average litter heterogeneity (LH_ave) and with a positive effect on epigaic ant species richness while average litter heterogeneity had a negative effect (Table 4).

We got better top models (bigger Akaike-weigths)(see ω-values in the Table 4) for hypogaeic species richness using the coefficient of variation of the explanatory variables than their averages (see Hypogaeic ants (A) and (B) in Table 4). Soil moisture was the most important predictor for local hypogaeic species richness however also playing their influence at different spatial scale according the biome.

In Atlantic rainforest, soil moisture was the most influent factor acting at local scale and with a positive effect on the hypogaeic ant species richness. However, others models (ΔAICc < 2) which considered soil respiration as local factor and meso-factor also gave support to local scale hypogaeic data (Table 4).

On the other hand, in *Cerrado* soil moisture showed similar relative importance values as local factor and as meso-factor (see RI-values in Table 4), both with negative effect on the hypogaeic ant species richness. Beside the model-1, models that considered average clay percentage and average soil respiration also were among the top models (ΔAICc < 2), although presenting the same low Akaike-weights (see ω-values in Table 4).

Table 4. AICc based model selection for ant species richness at local scale at three microhabitats in Atlantic rainforest (ARF) and *Cerrado* (CER) biomes, Brazil. Global models used surrogates of resource amount and heterogeneity and conditions (only for hypogaeic ants) as local factors effects and meso-factor effects (_ave). K = mumber of predictor variables. ΔAICc = AICc differences. ω = Akaiake weigths. SE = standard error. RI = relative importance. **Arboreal parameters:** *Local factors:* Number of trees (NT); number of species tree (ST); *Meso-factors:* average number of trees (NT_ave); average number of species tree (ST_ave). **Epigaeic parameters:** *Local factors:* Litter depth (LD); litter heterogeneity (LH); *Meso-factors:* average litter depth (LD_ave); average litter heterogeneity (LH_ave). **Hypogaeic parameters:** *Local factors:* Percentage of clay (C); soil moisture (M); soil respiration (SR); *Meso-factors:* average percentage of clay (C_ave); coefficient of variation of percentage of clay (C_cv); average of soil moisture (M_ave); coefficient of variation of soil moisture (M_cv); average of soil respiration (SR_ave); coefficient of variation of soil respiration (SR_cv). (A) model selection for hypogaeic ant species diversity considering the average of resource and condition as meso-factor effects. (B) model selection for hypogaeic ant species diversity considering the coefficient of variation of resource and condition as meso-factor effects.

Biome	**Microhabitat**	**Model ranks**	**Model**	**k**	**AICc**	**Δ**	**ω**	**ω - cumulative**	**Parameter**	**Estimate**	**SE**	**RI**
ARF	**Arboreal ants**	1	NT + NT_ave + ST	6	141.11	0.00	0.41	0.41	Intercept	0.32	0.26	
		2	NT_ave + ST	5	142.54	1.44	0.20	0.61	NT	-0.42	0.23	0.62
									NT_ave	-0.66	0.19	0.91
									ST	0.53	0.23	0.92
									ST_ave	-0.01	0.34	0.32
CER	**Arboreal ants**	1	Intercept only	3	88.40	0.00	0.21	0.21	Intercept	1.156	0.05	
		2	NT + NT_ave	5	89.64	1.24	0.11	0.32	NT	-0.201	0.16	0.41
		3	NT	4	89.75	1.35	0.11	0.43	NT_ave	0.27	0.25	0.42
		4	NT_ave	4	90.1	1.7	0.09	0.52	ST	0.061	0.15	0.23
									ST_ave	0.132	0.29	0.28
ARF	**Epigaeic ants**	1	LH	4	132.66	0.00	0.17	0.17	Intercept	1.54	0.08	
		2	LD + LH	5	132.95	0.29	0.15	0.32	LD	0.14	0.10	0.46

Table 4. Continue

Biome	Microhabitat	Model ranks	Model	k	AICc	Δ	ω	ω - cumulative	Parameter	Estimate	SE	RI
ARF	**Epigaeic ants**	3	LD	4	133.31	0.65	0.12	0.44	LD_ave	0.11	0.19	0.25
		4	Intercept only	3	133.43	0.77	0.11	0.55	LH	0.17	0.10	0.57
		5	LD_ave + LH	5	134.49	1.83	0.07	0.62	LH_ave	-0.01	0.2	0.23
		6	LD_ave	4	134.58	1.91	0.06	0.68				
CER	**Epigaeic ants**	1	LD_ave + LH_ave	5	129.71	0.00	0.34	0.34	Intercept	1.754	0.14	
		2	LD_ave + LH + LH_ave	6	131.56	1.85	0.14	0.48	LD	-0.031	0.08	0.23
									LD_ave	0.805	0.33	0.85
									LH	-0.074	0.11	0.27
									LH_ave	-0.694	0.32	0.68
ARF	**Hypogaeic ants (A)**	1	M	4	114.93	0.00	0.08	0.08	Intercept	0.59	0.07	
		2	SR_ave + M	5	115.23	0.30	0.07	0.15	C	0.52	0.52	0.38
		3	C + SR_ave	5	115.27	0.34	0.07	0.22	C_ave	0.24	0.67	0.31
		4	C_ave + SR_ave	5	116.00	1.08	0.05	0.27	SR	0.10	0.14	0.28
		5	SR + M	5	116.05	1.12	0.04	0.31	SR_ave	0.25	0.16	0.54
		6	C + SR_ave + M	6	116.33	1.41	0.04	0.35	M	0.56	0.30	0.55
		7	M_ave	4	116.47	1.55	0.04	0.39	M_ave	0.34	0.53	0.32
		8	SR_ave + M_ave	5	116.57	1.65	0.03	0.42				
		9	C_ave + SR_ave + M	6	116.71	1.78	0.03	0.45				
CER	**Hypogaeic ants (A)**	1	Intercept only	3	102.93	0.000	0.13	0.13	Intercept	0.675	0.07	
		2	SR_ave	4	103.34	0.41	0.11	0.24	C	-0.09	0.62	0.24
		3	M_ave	4	104.04	1.11	0.07	0.31	C_ave	-0.001	0.63	0.24
		4	C	4	104.29	1.36	0.07	0.38	SR_ave	-0.183	0.14	0.39

Table 4. Continue

Biome	**Microhabitat**	**Model ranks**	**Model**	**k**	**AICc**	**Δ**	**ω**	**ω - cumulative**	**Parameter**	**Estimate**	**SE**	**RI**
CER	**Hypogaeic ants**	5	M	4	104.31	1.37	0.07	0.45	M_ave	-0.861	1.31	0.33
	(A)	6	C_ave	4	104.32	1.39	0.06	0.51	M	0.67	1.36	0.30
		7	M_ave + M	5	104.73	1.8	0.05	0.56				
		8	SR_ave + M_ave	5	104.92	1.99	0.05	0.5				
ARF	**Hypogaeic ants**	1	M	4	114.93	0.00	0.19	0.19	Intercept	0.59	0.06	
	(B)	2	SR_cv + M	5	115.23	0.31	0.16	0.35	C_cv	0.33	0.49	0.29
		3	SR + M	5	116.05	1.12	0.11	0.46	SR	0.11	0.13	0.3
									SR_cv	0.19	0.15	0.41
									M	0.66	0.16	1.00
									M_cv	-0.30	0.44	0.32
CER	**Hypogaeic ants**	1	M_cv + M	5	100.65	0.00	0.22	0.22	Intercept	0.673	0.07	
	(B)	2	M_cv	4	102.37	1.71	0.09	0.31	C_cv	-0.01	0.43	0.32
		3	C_cv + M	5	102.54	1.88	0.09	0.4	SR_cv	-0.25	0.27	0.33
		4	SR_cv	4	102.54	1.89	0.09	0.49	M_cv	-0.378	0.23	0.58
		5	SR_cv + M_cv + M	6	102.85	2.19	0.07	0.56	M	-0.281	0.16	0.55

Model averaging at mesoscale

The model selection to the ant species diversity revealed that in general the most predictors act at mesoscale. However, several top models for the data of different microhabitats in both biomes were fitted considering only the intercept in absence of any explanatory variable (Table 5).

The average number of tree present in the Atlantic rainforest transects was the most import parameter to the arboreal mesoscale data accounting alone to the top models (with the minimal AICc) for all species diversity metrics (gamma, alpha and beta) and with a negative effect on all diversity metrics (Table 5). However, in the model selection to the arboreal species diversity of *Cerrado* the predictor variables did not give a strong support to the data and the top models were fitted only with the intercept (Table 5).

To the epigaeic ant species diversity metrics of Atlantic rainforest, litter parameters gave a weak support to the data, which models presented ΔAICc < 2 (smaller than two) in relation to the top models fitted only with the intercept (Table 5). However, litter depth and litter heterogeneity were important predictor to the epigaeic species diversity metrics in *Cerrado* which the first with a positive effect and the second with a negative effect. Park identity had a positive effect on γ-diversity and β-diversity, which means the influence of landscape factors (Table 5).

In general the best top models for hypogaeic ant species diversity were fitted in general only with the intercept in both biomes. In Atlantic rainforest only models that considered the average of the explanatory variables presented some support to the hypogaeic species diversity metrics, such as the positive effect of average soil moisture on α-diversity (see model-1values and soil moisture RI-value in Table 5 – ARF-Hypogaeic ants (A)) and the model-1 to β-diversity, which soil moisture had a negative effect and clay percentage, a positive effect.

In *Cerrado* the parameter that presented some effect on the hypogaeic ant species diversity was the soil moisture as average and coefficient of variation (see Table 5 – CER-Hypogaeic ants (A) (B)), in both with a negative effect on diversity metrics. However the top four models (ΔAICc < 2), which considered other soil variables (i.e. soil respiration and clay percentage) showed close Akaike-weights in models with β-diversity as response variable.

Table 5. AICc based model selection for ant species richness at meso-scale at three microhabitats in Atlantic rainforest (ARF) and *Cerrado* (CER) biomes, Brazil. Global models used surrogates of resource amount and heterogeneity and conditions (only for hypogaeic ants) as meso-factors effects and protected area identity (park) as landscape effect. K = mumber of predictor variables. ΔAICc = AICc differences. ω = Akaiake weigths. SE = standard error. RI = relative importance. **Arboreal parameters:** Average number of trees (NT_ave); average number of species tree (ST_ave). **Epigaeic parameters:** Average litter depth (LD_ave); average litter heterogeneity (LH_ave). **Hypogaeic parameters:** Average percentage of clay (C_ave); coefficient of variation of percentage of clay (C_cv); average of soil moisture (M_ave); coefficient of variation of soil moisture (M_cv); average of soil respiration (SR_ave); coefficient of variation of soil respiration (SR_cv). **Park identities in ARF:** Rio Doce State Park (PERD); Serra do Mar State Park (PESM); VALE Natural Reserve (VALE). **Park identities in CER:** Panga Ecological Station (PANGA); Grande Sertão Veredas National Park (PNGSV); IBGE Ecological Reserve (RECOR). (A) model selection for hypogaeic ant species diversity that considered the average of resource and condition. (B) model selection for hypogaeic ant species diversity that considered the coefficient of variation of resource and condition.

Biome	Microhabitat	Model ranks	Model	k	AICc	Δ	ω	ω - cumulative	Parameter	Estimate	SE	RI
ARF	**Arboreal ants**	Gamma diversity							Intercept	2.23	0.21	
		1	NT	3	20.21	0.00	0.49	0.49	PESM	-0.78	0.27	
		2	Intercept only	2	22.02	1.81	0.20	0.69	VALE	-0.06	0.22	
									NT	-0.46	0.19	0.58
									ST	-0.33	0.2	0.12
									Park			0.20
		Alpha diversity										
		1	NT	4	37.64	0.00	0.51	0.51	Intercept	1.54	0.37	
		2	Intercept only	3	38.09	0.45	0.41	0.92	NT	-0.96	0.35	0.51
		3	ST	4	41.19	3.55	0.09	1.01	ST	-0.55	0.46	0.09

Table 5. Continue

Biome	Microhabitat	Model ranks	Model	k	AICc	Δ	ω	ω - cumulative	Parameter	Estimate	SE	RI
		Beta diversity										
ARF	**Arboreal ants**	1	NT	4	62.81	0.00	0.64	0.64	Intercept	8.04	1.99	
									PESM	-6.12	2.53	
									VALE	-0.99	2.51	
									NT	-4.09	1.27	0.88
									ST	-0.32	2.32	0.20
									Park			0.10
CER	**Arboreal ants**	Gamma diversity										
		1	Intercept only	2	18.3	0.00	0.74	0.74	Intercept	2.9	0.07	
									ST	-0.24	0.16	0.26
		Alpha diversity										
		1	Intercept only	3	40.05	0.00	0.8	0.8	Intercept	3.49	0.39	
									ST	-1.25	0.69	0.20
		Beta diversity										
		1	Intercept only	3	62.95	0.00	0.45	0.45	Intercept	14.8	1.22	
		2	ST	4	63.52	0.57	0.34	0.79	NT	10.01	5.82	0.22
		3	NT + ST	5	64.4	1.46	0.22	1.01	ST	-6.98	6.11	0.55
ARF	**Epigaeic ants**	Gamma diversity										
		1	Intercept only	2	16.88	0.00	0.84	0.84	Intercept	2.96	0.06	
								0.84	LD	0.09	0.14	0.16

Table 5. Continue

Biome	Microhabitat	Model ranks	Model	k	AICc	Δ	ω	ω - cumulative	Parameter	Estimate	SE	RI
		Alpha diversity										
ARF	**Epigaeic ants**	1	Intercept only	3	51.65	0.00	0.63	0.63	Intercept	4.86	0.58	
									LD	0.66	0.91	0.18
									LH	0.55	1.22	0.19
		Beta diversity										
		1	Intercept only	3	67.23	0.00	0.46	0.46	Intercept	14.55	0.9	
		2	LD	4	68.59	1.36	0.24	0.7	LD	1.31	2.17	0.32
		3	LH	4	68.77	1.54	0.21	0.91	LH	-0.93	2.22	0.3
CER	**Epigaeic ants**	Gamma diversity										
		1	Park	4	25.45	0	0.34	0.34	Intercept	3.37	0.2	
		2	LD	3	26.37	0.92	0.22	0.56	PNGSV	-0.22	0.14	
		3	Intercept only	2	26.52	1.07	0.20	0.76	RECOR	-0.68	0.15	
		4	LD + LH	4	27.01	1.56	0.16	0.92	LD	0.39	0.24	0.46
									LH	-0.48	0.23	0.16
									Park	+		0.42
		Alpha diversity										
		1	LD + LH	5	61.60	0.00	0.40	0.40	Intercept	6.20	1.05	
		2	Intercept only	3	62.48	0.89	0.26	0.66	LD	4.25	2.42	0.65
		3	LD	4	62.57	0.97	0.25	0.91	LH	-3.76	2.82	0.50
		Beta diversity										
		1	LD + LH	5	68.37	0.00	0.80	0.80	Intercept	21.47	4.841	

Table 5. Continue

Biome	Microhabitat	Model ranks	Model	k	AICc	Δ	ω	ω - cumulative	Parameter	Estimate	SE	RI
CER	**Epigaeic ants**	Beta diversity										
		2	Park	5	72.45	4.08	0.10	0.90	PNGSV	-5.24	4.78	
		3	LD	4	73.61	5.24	0.06	0.96	RECOR	-13.93	4.67	
									LD	9.75	2.86	0.90
									LH	-8.21	2.25	0.80
									Park	+		0.14
ARF	**Hypogaeic ants**	Gamma diversity										
	(A)	1	Intercept only	2	14.71	0.00	0.49	0.49	Intercept	2.24	0.094	
		2	C	3	16.31	1.61	0.22	0.71	C	0.35	0.39	0.25
									SR	-0.12	0.19	0.10
									M	0.1	0.49	0.19
		Alpha diversity										
		1	M	4	32.05	0.00	0.42	0.42	Intercept	1.90	0.25	
		2	Intercept only	3	33.07	1.02	0.25	0.67	C	0.79	0.97	0.29
		3	C	4	33.24	1.19	0.23	0.9	SR	0.42	0.34	0.04
									M	1.24	0.61	0.48
		Beta diversity										
		1	C + M		61.58	0.00	0.29	0.29	Intercept	7.58	0.67	
		2	Intercept only		61.75	0.16	0.27	0.56	C	6.67	6.36	0.48
		3	C		62.8	1.21	0.16	0.72	SR	-1.12	1.5	0.16
			SR		63.17	1.59	0.13	0.85	M	-5.94	6.79	0.41
			M		63.38	1.8	0.12	0.97				

Table 5. Continue

Biome	**Microhabitat**	**Model ranks**	**Model**	**k**	**AICc**	**Δ**	**ω**	**ω - cumulative**	**Parameter**	**Estimate**	**SE**	**RI**
CER	**Hypogaeic ants**	Gamma diversity										
	(A)	1	Intercept only	2	13.57	0.00	0.64	0.64	Intercept	2.49	0.08	
									C	-0.07	0.17	0.11
									SR	0.06	0.17	0.11
									M	-0.12	0.17	0.13
		Alpha diversity										
		1	Intercept only	3	30.98	0.00	0.76	0.76	Intercept	1.99	0.16	
									SR	-0.43	0.34	0.14
									M	-0.32	0.35	0.1
		Beta diversity										
		1	Intercept only	3	64.43	0.00	0.27	0.27	Intercept	9.96	1.44	
		2	M	4	65.31	0.88	0.17	0.44	PNGSV	3.25	3.44	
		3	C	4	65.7	1.26	0.14	0.58	RECOR	0.7	3.44	
		4	SR	4	65.94	1.51	0.13	0.71	C	1.52	3.7	0.29
		5	C + M	5	66.2	1.76	0.11	0.82	SR	-0.09	2.31	0.21
									M	-2.44	3.75	0.33
									Park			0.1
ARF	**Hypogaeic ants**	Gamma diversity										
	(B)	1	Intercept only	2	14.71	0.00	0.52	0.52	Intercept	2.24	0.09	
		2	M	3	16.20	1.49	0.24	0.76	C	-0.23	0.21	0.16
									SR	0.02	0.19	0.08

Table 5. Continue

Biome	Microhabitat	Model ranks	Model	k	AICc	Δ	ω	ω - cumulative	Parameter	Estimate	SE	RI
ARF	**Hypogaeic ants (B)**	Gamma diversity							M	-0.31	0.22	0.24
		Alpha diversity										
		1	Intercept only	3	33.07	0.00	0.79	0.79	Intercept	1.9	0.39	
								0.79	C	-0.09	0.56	0.11
		Beta diversity										
			Intercept only	3	61.75	0.00	0.29	0.29	Intercept	7.58	0.67	
			M	4	62.15	0.40	0.23	0.52	C	2.77	4.73	0.38
			C + M	5	62.17	0.42	0.23	0.75	SR	0.51	1.49	0.11
			C	4	63.12	1.37	0.14	0.89	M	-4.38	4.05	0.46
			SR	4	63.74	1.99	0.11	1				
CER	**Hypogaeic ants (B)**	Gamma diversity										
		1	Intercept only	2	13.57	0.00	0.51	0.51	Intercept	2.48	0.08	
		2	SR	3	15.56	1.99	0.19	0.7	C	-0.17	0.19	0.13
									SR	-0.25	0.20	0.19
									M	-0.22	0.19	0.17
		Alpha diversity										
		1	Intercept only		30.98	0.00	0.66	0.66	Intercept	1.99	0.18	
		2	M		33.5	2.52	0.19	0.85	M	-0.64	0.32	0.19
		3	SR		33.92	2.94	0.15	1	SR	-0.56	0.33	0.15

Table 5. Continue

Biome	**Microhabitat**	**Model ranks**	**Model**	**k**	**AICc**	**Δ**	**ω**	**ω - cumulative**	**Parameter**	**Estimate**	**SE**	**RI**
CER	**Hypogaeic ants**	Beta diversity										
	(B)	1	M		63.96	0.00	0.28	0.28	Intercept	10.09	1.07	
		2	Intercept only		64.43	0.48	0.22	0.50	C	-0.46	2.95	0.27
		3	SR		64.99	1.03	0.17	0.67	SR	-1.09	2.39	0.24
		4	C		65.07	1.11	0.16	0.83	M	-2.99	2.19	0.46
		5	C + M		65.84	1.88	0.11	0.94				

Discussion

Ant fauna

Although Atlantic rainforest and *Cerrado* biomes are considered world's centers of biodiversity, they are also under highly fragmentation and land conversion pressure, which made them the two Brazilian biodiversity hotspots (Myers et al. 2000). Considered the conservation status of both biomes, we collected an expressive ant number of species which was quite similar to studies with more extensive sampling, such as Ribas et al. (2003), 133 ant species (*Cerrado* sites) and Silva & Brandão (2010), 171 ant species (Atlantic rain forest sites).

The difference on the number of species between the two biomes could be an effect of their area size. *Cerrado* is almost two times larger than Atlantic rainforest (IBGE 1994), though in our study the average area size of Atlantic rainforest landscapes were larger than those in *Cerrado* (Table 1).

In Australia, Andersen et al. (2007) comparing savanna and forest ant assemblages found a higher number of ant species in savanna sites, which make up a large landscape in the region when compared to rainforest, which is restricted to small patches. Although nowadays both Brazilian biomes are fragmented, Atlantic rainforest is historically the highest fragmented Brazilian biome, with high number of forest patches within different types of matrix and level of isolation (Ribeiro et al. 2009), which could enhance the difference on the number of species between the biomes.

Model Selection

Model averaging at local scale

The way that the number of trees and the number of tree species act as determinant factors for arboreal ants may be explained by three distinct mechanisms (Ribas et al. 2003). The number of trees could influence arboreal ant species by increasing the amount of resources; changing habitat conditions and increasing the area, causing a species–area pattern. Otherwise, the number of tree species could means an increasing in the variety of resources allowing the existence of a higher number of specialist species; increasing the amount of resources to generalist species or some other unmeasured factor may have influenced both ant and tree species richness.

The model selection allows us to observe that the local arboreal ant communities of each biome should be differently influenced by tree data (Table 4). In *Cerrado*, the high influence of average number of trees and its presence in the top models (ΔAIC < 2) make us deduce that variation on resource amount are more important to the arboreal ant species richness. On the other hand, in Atlantic rainforest, the number of tree species seems to assume the role of determinant factor.

Cerrado biome in Brazil encompasses a range of vegetation types, such as grasslands, savannas and tropical deciduous forests, which are markedly distinct by tree density (Coutinho 1978; Ribeiro & Walter 1998). Thus, the difference on the tree density among the *Cerrado* vegetation types could represent a gradient of resource amount and species-area (according the mechanisms proposed by Ribas et al. 2003) allowing a higher local number of arboreal ant species in sites with more trees. However, the number of tree in each sampling unit (local factor) had a negative effect which could act against the positive effect of average number of tree (meso-factor), contributing to the observed top model fitted only with the intercept.

Otherwise, Atlantic rainforest vegetation types are quite structurally similar, but distinct regarding the tree species composition (Veloso et al. 1991). Among the Atlantic rainforest sites, an increasing on the number of tree species could represent more resource heterogeneity for ants (Ribas et al. 2003). Thus the number of tree species should be a more prominent determinant factor to arboreal ant species richness within a landscape, where forest sites have a similar number of tree but different number of tree species.

However, in Atlantic rainforest biome, average number of tree (meso-factor) also presented in the top models (ΔAIC < 2) had an expressive negative effect on the local arboreal ant species in Atlantic rainforest biome. We deduce that average number of tree could be indirectly affecting arboreal ant species, by the enhancing of site viability to dominant ant species. High levels of ant species dominance have been reported as a major factor for low number of species in arboreal ant mosaics (Blüthgen & Stork 2007; Wielgoss et al. 2010).

Litter parameters affect local epigaeic ant community of the two biomes at different spatial scales (as local factors in Atlantic rainforest and as meso-factors in

Cerrado), and with distinct magnitudes and reverse directions. Litter parameters have been reported to be a driving factor to the species richness of epigaeic and litter ant assemblages (Theunis et al. 2005; Corrêa et al. 2006; Vargas et al. 2007; Mezger & Pfeiffer 2011) promoting the species coexistence by resource offering (amount and heterogeneity) and nest sites availability.

Resource and nest site availability seem to be mechanisms that explain the positive influence of litter depth and heterogeneity as local factor on local species richness in Atlantic rainforest sites. However, the magnitude (litter depth: 0.14; litter heterogeneity: 0.17; see Table 4) and the relative importance (litter depth: 0.46; litter heterogeneity: 0.57) of these parameters were weak such as described in others studies (e.g. Campos et al. 2003).

In *Cerrado*, litter parameters had high magnitudes and relative importance as meso-factors, although they had opposite directions (average litter depth – positive and litter heterogeneity – negative; see Table 5). This reverse direction effect of the litter parameters may reflect a differential response of ant species to litter rugosity according the body-size (Kaspari & Weiser 1999; Sarty et al. 2006).

Hence, in sites with more litter depth could mean more resource and nest sites availability for both small and large ant species. However, an enhancing only in the litter heterogeneity, considered an increasing on resource variability could mean also condition restrictions.

If we assume that sites with a uniform distribution of the litter items (with high litter heterogeneity) which could implicate in a narrow litter depth. Thus, it is expected an negative effect on the locomotion of large ant species (Sarty et al. 2007) due to the superficies rugosity and to small ant species by the less resource and nest sites availability (Theunis et al. 2005; Corrêa et al. 2006; Vargas et al. 2007; Mezger & Pfeiffer 2011).

The difference about the effect of soil moisture regarding with magnitude, relative importance and spatial scale on local hypogaeic ant species richness between the biomes could be attributed to the difference on their soil structure. In Atlantic rainforest, forest types are distributed at a great variability of soil types, such as coastal forests at sandy soils and lowland rainforests at deeper and richness soil types (Assis et al. 2011). *Cerrado*, although with a great range of soil types (Sano & Almeida 1998), does not present a strong variability on physical soil characteristics such as it observed in Atlantic rainforest soils.

These soil differences between the biomes probably support the opposite effect of soil moisture on the local hypogaeic ant species richness in Atlantic rainforest and *Cerrado*. Thus, soil moisture increasing in the Atlantic rainforest sites could help the ants to establish their nests, enhancing the number of ant species at local scale. On the other hand in *Cerrado*, high levels of soil moisture could require a stronger effort of ants to construct their nests and walk in the soil layers (Durso et al. *unpublished data*), which could decrease the local species richness.

Model averaging at mesoscale

The average number of trees was also the most important predictor with a negative direction for the three diversity components of the arboreal ants in Atlantic rainforest. Yanoviak et al. (2007) reported that the similarity among canopy ant assemblages was higher among trees sampled in the same forest patch than among trees sampled in different patches. Thus, regarding to the negative effect of the number of trees on β-diversity found in our study should happen because sites with more number of trees could facilitate the ant species dispersion (probably generalist ants) than in site with few trees and more isolate from each other.

To arboreal ant assemblages in *Cerrado* at mesoscale, the top models were again fitted only with the intercept for all diversity components. Although, the average number of tree had a positive effect to β-diversity, the average number of tree species was the most important predictor at mesoscale with a negative effect. Probably, like in the local scale, the top model was fitted only with the intercept due to the reverse effect of these predictors.

The litter parameters seem to loss their effects on epigaeic ant diversity at mesoscale in Atlantic rainforest, because the top models of all diversity components were fitted only with the intercept. Although with a positive direction, the effect of litter variables on epigaeic ant diversity components at mesoscale was weak such as reported for small spatial scales (Campos et al. 2003).

In *Cerrado*, beside the opposite effect of the litter parameters, was the only case in which we observed an effect of landscape factors (represented by the protected area identity; see CER-Epigaeic ants in the Table 5) on the epigaeic ant diversity. Hence we sampled more epigaeic ant species per transect (mesocale) in *Cerrado* protected areas with higher number of ant species in the following order: Panga Ecological Station (total epigaeic ant species: 78; ant species/transect: 35.5), Grande Sertão Veredas National Park (total epigaeic ant species: 69; ant species/transect: 27.5) and IBGE Ecological Reserve (total epigaeic ant species: 42; ant species/transect: 17.75).

Landscape factors also had a positive effect on β-diversity of epigaeic ant communities of *Cerrado*, although weak. Thus landscapes with larger species pool could offer a large amount of ant species to the local communities, enhancing γ-diversity at mesoscale.

This scenario for epigaeic ant species of *Cerrado* is in agreement with the proposal that factors acting at large scales (such as landscape scale) could have a relative importance on the epigaeic ant diversity at small scales (Spiesman & Cumming 2008; Vasconcelos et al. 2010; Mezger & Pfeiffer 2011). Thus, Panga Ecological Station beside has more varieties of savanna-like vegetation seems to be within a landscape less fragmented than the others (IBGE Ecological Reserve located in Brasília, Brazil capital; Grande Sertão Veredas National Park, surrounded by large extensions of soybean crops).

To the hypogaeic ant assemblages, like at local scale, soil moisture seems to be more influent to the ant diversity of Atlantic rainforest than in *Cerrado*. In Atlantic rainforest, soil moisture at the same time that enhances α-diversity within the local communities could decrease the β-diversity among them. Probably, soil moisture is acting like a filter on the hypogaeic ant species pool and selecting only a specific set of ant species to makes up the local communities.

In *Cerrado,* soil moisture just had a weak negative effect on the β-diversity in the hypogaeic ant assemblage. The effect of soil moisture on the hypogaeic ant species pool in *Cerrado* seem to be similar with this that happen in the Atlantic rainforest, selecting a specific set of ant species to live in the local communities.

Conclusion

We got different answer for our questions, depending on the spatial scale where the ant diversity was analyzed. In general, at local scale the model selection revealed that both local factors and meso-factors share the role as determinants of the ant species richness. At mesoscale, seems that the parameters evaluated were not so important to the ant diversity and when was detected some influence of them, this happen usually at the current mesoscale.

Building on ours result, we could conclude that at small scales (in this study at local scale) besides the structuring role of niche partitioning, factors originally from large scale also contribute to the number of species coexisting (Spiesman & Cumming 2008; Vasconcelos et al. 2010; Mezger & Pfeiffer 2011). At mesoscale ant communities seem to be more resistant to the influence of large factors effect and consequently to the entrance of ant species form a large species pool, exception for epigaeic ant assemblages in *Cerrado*.

Therefore, we attribute the differences on the model selection to the particularities of each ant microhabitat (arboreal, epigaeic and hypogaeic ants) and the habitat types (forest and savanna). Hence, caution is important about broad generalization about the structure of ant communities which does not account for the idiosyncratic factors associated to the ant microhabitat and habitat types.

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CHAPTER 2

Congruence trends among tropical ant communities: a comparison of rainforests and savannas in Brazil and Indonesia

Resumo

Ecólogos, de acordo com o determinismo local, tem investigado a congruência nos padrões de diversidade entre comunidades ecológicas em habitats similares. Embora as formigas tenham sido foco de estudos a respeito dos padrões de diversidade em diferentes escalas espaciais (de local à global), poucos trabalhos têm investigado o quão semelhante é a estrutura das comunidades de formigas pertencentes a habitats similares ao redor do mundo. Neste estudo nós verificamos a existência de tendências de congruência entre comunidades de formigas de florestas e savanas no Brasil e na Indonésia. Nós testamos a hipótese que comunidades de formigas de habitats similares, independente de seus valores absolutos de diversidade idionsicráticos, compartilham padrões semelhantes da contribuição relativa da diversidade alfa em escala local e da diversidade beta ao longo de diferentes escalas para a diversidade gama. Além disso, nós verificamos se as comunidades de formigas apresentam padrões similares de saturação/instaturação de espécies em escala local. Em cada país, para cada tipo de habitat, nós selecionamos três paisagens, onde as formigas foram coletadas em quatro áreas ao longo de dez armadilhas do tipo “pitfall” em cada área. No Brasil, os habitats de floresta e savana foram representados pelos biomas Floresta Atlântica e Cerrado. Na Indonésia foram amostrados habitats de floresta no oeste do país e habitats de savana no leste. Nós coletamos mais espécies de formigas no Brasil do que na Indonésia em todas as escalas espaciais nos dois tipos de habitats. A diversidade alfa em escala local e a diversidade beta entre as paisagens foram maiores que o esperado pelo acaso e a diversidade beta entre armadilhas (escala local) e entre as áreas foram menores que o esperado pelo acaso para todas as comunidades de formigas de todos os habitats. Além disso, nós encontramos um padrão de insaturação de espécies em escala local. Nós associamos esta congruência nos padrões de diversidade à elevada capacidade de dispersão das formigas em escalas espaciais pequenas e intermediárias. Isto possibilita uma elevada diversidade de espécies nas comunidades locais e um constante fluxo de espécies entre elas. Entretanto, o padrão de diversidade beta semelhante na escala de paisagem sugere que em ambos os países, processos históricos podem ter restringido o fluxo de espécies entre paisagens de forma semelhante. Assim, em nosso estudo parece que as tendências de congruência entre as comunidades de formigas estão associadas a uma similar capacidade de dispersão das espécies de formigas. Nós concluímos que processos baseados na dispersão de espécies possuem um papel expressivo para a coexistência de espécies de formigas e potencialmente oferecem uma explicação global para a estrutura de comunidades de formigas tropicais.

Palavras-chaves: Ecologia de comunidades, comparação transcontinetal, diversidade beta, padrões de diversidade.

Abstract

Ecologist, according with local determinism, have searched about congruence in diversity patterns among ecological communities at similar habitats. Although, ants have been the focus of several studies about diversity from local to global scale, few studies have investigated the similarities on the ant community structure among common habitats around the world. In this study we verified congruent trends among the ant communities of rainforests and savannas in Brazil and Indonesia. We hypothesized that ant communities at similar habitats, independent on their idiosyncratic absolute diversity values present similar patterns of relative contribution of alpha diversity at local scale and beta diversity acrros multi-scale to gamma diversity. Moreover, we verify if the ant communities present similar patterns of species saturation/insaturation at local scale. In each habitat type of each country, we selected three landscapes in which the ants were sampled in four sites along ten pitfall traps in each site. In Brazil rainforest and savanna landscapes were located in Atlantic rainforest and “Cerrado” (Brazilian savanna) biomes, respectively. In Indonesia, habitats in the western tropical rainforests and in the eastern savannas were sampled. We collected more ant species in Brazil than in Indonesia at all spatial scales for the two habitats types. The α-diversity at local scale and β-diversity among landscapes were higher than expected by null models and β-diversities among pitfalls traps (local scale) and among sites were lower than expected by null models for all ant communities of all biomes analyzed. Moreover, we found a species insaturation pattern at local scale. We associated these congruent patterns of diversity to the high dispersal of the ants at small-intermediated scales, which leads to high species diversity at local communities and a constant species flux among them. However, the similar pattern of β-diversity at large scales suggests that in both countries historical processes could restrict species flux between landscapes in a similar way. Hence, in our study seems that the congruent trends among the ant communities are related to similar dispersal ability of ant species in all biomes. We can conclude that alternative processes based on species dispersion have an expressive role on the ant species coexistence and potentially offer a broad global explanation to the structure of tropical ant communities.

Key words: Beta diversity, biodiversity patterns, community ecology, intercontinental comparison.

Introduction

Acording to local determinism, species coexistence in local communities is an outcome of species interaction, which would be influenced by the physical attributes of the environment (Schluter & Rickfles 1993; Rickfles 2004). In this way, Rickfles (2004) sumarised three predictions: “(1) diversity should be strongly correlated with physical aspects of the environment; (2) local diversity in comparable habitats should not vary between regions; (3) local diversity, at least above some ecological saturation level, should be independent of regional diversity.”

Thus, ecologists have searched for congruent or concordant patterns of divesrsity among similar or comparable ecological communities around the world (Schluter & Ricklefs 1993). Ricklefs & Latham (1993) highlighted that a tradeoff between local and regional diversity could be desirable for comparison about diversity patterns among regions.

Westoby (1993) considered regional diversity as a result of differences in the natural history of each region. Hence, the most study cases analyzed by the author, congruence among communities were considered as similar patterns of alpha and beta diversity between regions that have different regional diversity.

On hand, local diversities are congruents, which is attributed to the action of similar constraints in both regions, but regional diversity were different by the action of divergent differentiation diversities (beta diversity). On the other hand, local diversities are divergent reflecting the differences on the regional diversities, but with similar species variation reflecting congruent differentiation diversities.

Westoby (1993) reported that in the first case alpha diversity accounted for a few amount of the regional diversity and beta diversity had a larger contribution to gamma diversity. In the second, it was the opposite, alpha diversity represented a large amount of gamma diversity.

These different cases can be formulated using the diversity partitioning approach explicitly proposed by Lande (1996), that additively account the contribution of alpha (α) and beta (β) diversity components to the total-gamma diversity (γ). Independently of the absolute diversity values, in the additive partitioning, communities are comparable regarding the relative contribution of alpha and beta components to the gamma diversity, providing also the scale dependence of the diversity components across multiple spatial scales (Veech et al. 2002; Gering & Crist 2002).

Recently diversity partitioning approach has been applied to intercontinental comparison of ant communities at similar habitats (Campos et al. 2011). Hence, the relation of α, γ and β diversity components at multiple spatial scales could be useful to tool to evaluate ant community congruence trends in similar habitats across world regions.

In this study we verified cogruency trends among the ant communities of rainforests and savannas in Brazil and Indonesia. Regardless, the idiosincratic differences in the absolute species diversity and species variation among the regions, we hypothesized that ant communities at similar habitats present similar patterns of relative contribution of alpha diversity at local scale and beta diversity across multi-spatial scales to gamma diversity. Moreover, we verified if the ant communities present similar patterns of species saturation/insaturation at local scale.

Material and Methods

Habitat types

According to Olson (2001) at a global approach the rainforest and savanna habitats in both countries are considered Tropical and subtropical moist broadleaf forest and Tropical and subtropical grassland, savanna and shrublands biomes respectively. In Brazil, the rainforests and savannas were located in Atlantic rainforest and *Cerrado* (Brazilian savanna) biomes (IBGE 2004), respectively. In Indonesia, landscapes in the western tropical forests and in the eastern savannas were sampled (Partono et al. 2010).

The savanna landscapes in both countries encompassed a range of vegetation types that include grasslands, savannas, shrublands and tropical deciduous forests (Coutinho 1978; Ribeiro & Walter 1998; Partono et al. 2010)(Table 1). In both countries, we considered different varieties of tropical forests as rainforest habitats (IBGE 2004; Partono et al. 2010), such as lowland rainforest, coastal forest, freshwater swamp forest, semideciduous seasonal rainforest.

Although, Atlantic rainforest biome in Brazil is made up essential by forest habitats, some open vegetation composed generally by grass, herbaceous and shrubs are also considered as a vegetation type of Atlantic rainforest biome (Jesus & Rolim 2005).

Hence, in one of the protected areas of tropical rainforest in Brazil, we carried out ant samplings in a native endemic grassland to enhance the representativeness of vegetation types sampled in the Atlantic rainforest biome.

Table 1. Rainforest and savanna habitats sampled in Brazil and Indonesia. To each protected area is given a short description of vegetation, area, altitude and geographical coordinates.

Biome	Country	Protected area	Vegetation	Area (ha)	Altitude (m)	Coordinates
Savanna	Brazil	Ecological Station Panga	Savanna and deciduous tropical forest	403.85	740 - 830	19°10'S 48°24'W
		Ecological Reserve IBGE	Grassland and savanna	1,300	1,150	15°56'S 47°52'W
		Grande Sertão Veredas National Park	Grassland, savanna and deciduous tropical forest	231,668	600 - 850	15°23’S 45°54’W
Savanna	Indonesia	Komodo National Park	Grassland and savanna	173,300	0 - 735	8°23'S 119°22’E
		Bali Barat National Park	Grassland, savanna and deciduous tropical forest	19,002	0 - 1,986	8°05'S 114°25’E
		Baluran National Park	Savanna	25,000	0 - 1,247	7°29’S 114°17’E
Rainforest	Brazil	Natural Reserve VALE	Lowland rainforest at sandy soil and plain topography, grassland	21,787	28 - 65	19°06’S 39°45’W
		Rio Doce State Park	Semideciduous seasonal rain forest	35,976	230 - 515	19°29’S 42°28’W
		Serra do Mar State Park	Lowland rainforest and coastal forest	315,390	0 - 1,320	23°27’S 45°15’W
Rainforest	Indonesia	Gunung Halimun-Salak National Park	Lowland rain forest	113,357	500 - 1,929	6°37' S 106°21’E
		Ujung Kulong National Park	Lowland rain forest and coastal forest	122,956	0 - 620	6°30’S 102°02’E
		Way Kambas National Park	Lowland rain forest and freshwater swamp forest	125,621.30	0 - 50	4°37’ S 106°32’E

Spatial scale definition

In each country, the biomes (savanna or rainforest) were considered the largest spatial scale. Within each biome, in each country, we sampled the ants in three protected areas (Table 1) that we designated as the landscape scale.

Within each protected area (landscape scale), we installed four transects, which depending on the vegetation variety in the protected area, could encompass different vegetation types or not. We considered each transect as the site scale.

In each site, we distributed 10 pitfall traps. The pitfall traps represented the smallest spatial scale, the local scale.

The distance between landscapes within a biome ranged from 277 to 684 Km in the Atlantic rainforest (Brazil) and 150 to 207 Km in the tropical rainforest (Indonesia), 267 to 519 Km in *Cerrado* (Brazil) and 55 to 574 Km in the Indonesian savanna. Within each protected area (landscape sacle), we established the transects (site scale) at least 500 m apart from each other. Finally, along the transects, we set the pitfall traps (local scale) along a transect with 10 m between traps.

Ant sampling and identification

The pitfall traps consisted of plastic recipients (diameter = 8 cm; height = 12 cm) with an inner smaller recipient. Between these two recipients we put 200 ml of a solution of water, glycerol (5%) and salt (0.9%) that kept and killed the ants in the trap and avoided their contact with the baits. We set the baits, sardine (5 cm^3) and honey (10 cm^3), each one in small plastic pots (3.3 cm diameter; 5.0 cm height) that were put in the inner recipient.

In each site, we set the pitfall traps along a 100 m straight transect. The pitfall traps were buried so that the rim was level with the soil surface (Bestelmeyer et al. 2000) and remained in the field for 48 hours.

We sorted and identified the collected ants to genera with the help of the identification keys of Bolton (1994). Additionally, we used Palacio and Fernández (2003) taxonomic keys to identify the Neotropical ants and a compilation of taxonomic keys for Borneo ants (Fisher 2010). We adopted the subfamily classification proposed by Bolton (2003).

We carried out species identification (or morpho-species) of the ants collected in Brazil according to the Formicidae reference collection of the Community Ecology Laboratory – UFV, Brazil, where we deposited the voucher specimens. We sorted the ant species from Indonesia in morpho-species according morphological traits and compared with photos available at antbase.net (Pfeiffer & Katzmann 2011) and with the ant photo catalogs of Ant Course 2010 (Fisher 2010a). The voucher Indonesian ant specimens were sent to Entomology Laboratory at Center of Biology Research – LIPI, Indonesia.

Statistical analyses

To verify the similarity on the structure of ant communities, we carried out comparative analyses regarding the number of ant species and species variation at the three spatial scales sampled in the study. We used species richness as a measure of species diversity and beta diversity as a measure of species variation at specific spatial scales.

We obtained the species diversity and variation at the different spatial scales by the additive diversity partitioning analyses (Veech et al. 2002). In the additive diversity partitioning approach, the gamma diversity - (γ) is the result of the sum between alpha diversity (α) and beta diversity (β). Alpha is the average amount of the total diversity found in a single randomly-chosen sample and beta is the average amount of the total diversity not found in a single randomly-chosen sample. Thus alpha means the mean species diversity within the samples and beta is the mean species variation among the samples, also known as species turnover or species variation (see more details in Anderson et al. 2011).

The first analysis (i) was regarding the absolute species diversity at local, site and landscape scales and the species variation among pitfall traps (local scale) and among transects (site scale). We carried out analyses of variance, where the species diversity and beta diversity were the response variable and biome type was the categoric explanation variable. The number of samples in each scale was $n = 240$, local scale; $n = 24$, site scale and $n = 6$, landscape scale.

The second analysis (ii) was regarding the relative contribution of species diversity and variation to the gamma-biome diversity across a nested spatial scale

(Veech et al. 2002). Hence, in our case, the mean number of ant species per pitfall (the smallest spatial scale – local scale) was the α-diversity and $\beta_{1,}$ $\beta_{2,}$ $\beta_{3,}$ represented the species variation among pitfalls, among sites and among landscapes, respectively.

The α-diversities of site and landscapes scales were implicit and are obtained by the adding of β_1 and β_2 respectively. The sum of α-diversity and $\beta_{1,}$ $\beta_{2,}$ β_3 gives the γ-diversity for one biome, which equals the total number of ant species captured by the full sampling design within a biome (see *Spatial scale definition*).

We used individual-based randomizations (based on 1,000 randomizations), which reassign each individual to the dataset to any sample (Crist et al. 2003) producing an expected distribution of the diversity components under a null model. Each observed diversity component in a given spatial scale was compared with their expected distribution to determine if their value (lower or higher than expected values) was significantly different from the expected under the null model.

Finally, the third analysis (iii) was carried out to investigate species saturation/insaturation at local scale. We considered the mean number of ant species in the pitfall traps as the local species diversity and the number of ant species in the landscapes as regional species diversity.

To evaluate the effect of landscape species diversity on local species diversity we carried out analyses of covariance, in which local species diversity was the response variable and the landscape species diversity was the explanatory variable. The sampling number was the number of protected areas (n = 12).

Considering the recommendations of Srivastava (1999) about the drawbacks that data from different habitats (in our case rainforest and savanna) within the same region (in our case Brazil and Indonesia) could offer to local-regional species richness analyses, we include in the models the biome identity as an explanatory co-variable. Moreover, as the biomes are nested within the countries, we ran the analyses of covariance under linear mixed-effects models, where country identity was considered random factor and landscape species diversity and biome identity as fixed factors.

The comparative analyses (i) and (ii) were done with the ant communities from similar habitats between the countries (*Cerrado* – Brazil *versus* Savanna – Indonesia; Atlantic rainforest – Brazil *versus* Tropical rainforest - Indonesia) and within each country between the ant communities from different habitats (savanna *versus* rainforest). The analysis (iii) was done with the ant of all biomes sampled.

We carried out all the analyses were under R statistical software (R Development Core Team, 2009). The comparative analysis (ii) were developed using *Vegan* statistical package (Oksanen et al. 2011) and the models of analysis (iii) with *lme4* (Bates & Maechler 2012).

The models developed to the comparative analysis (i) were analyzed following Poisson distribution and with normal distribution for the models of comparative analysis (iii). We carried out residual analyses, to verify the suitability of the models and distributions of errors and the presence of outliers (Crawley, 2002) in the comparative analyses (i) and (iii)

Results

Ant fauna

Considering all habitats (rainforest and savanna) in Brazil, we captured 187 ant species and in Indonesia, 120 ant species. In the rainforest habitats, we sampled 103 ant species for Atlantic rainforest - Brazil (Appendix material A2 – Epigaeic ants) and 76 species for Tropical rainforest – Indonesia (Appendix material A4 – Tropical rainforest). In the savanna habitats, we collected 133 ant species in *Cerrado* – Brazil (Appendix material A3 – Epigaeic ants) and 58 species in Savanna – Indonesia (Appendix material A4 - Savanna).

Regarding the ant fauna, in Brazil the ant species belong to eight subfamilies (Appendix material A1 – Epigaeic ants) and in Indonesia to six subfamilies (Appendix material A4 – Total ants). Myrmicinae was the most speciose subfamily representing more than 50% of the ant species in all biomes, except in the Savanna - Indonesia (43%), followed by Formicinae which accounted for approximately 20% of the ant species (Figure 1).

The third most speciose ant subfamily was Ponerinae accounting for 10% of ant species (Figure 1). However, in *Cerrado*-Brazil, Dolichoderinae was the third most speciose ant subfamily. The remaining ant species (approximately 15 - 20%) belong to Cerapachyinae, and Dolichoderinae (exception in *Cerrado*-Brazil) in both countries and to Ecitoninae, Ectatomminae and Pseudomymicinae specific in Brazil and to Aenictinae only in Indonesia (Figure 1).

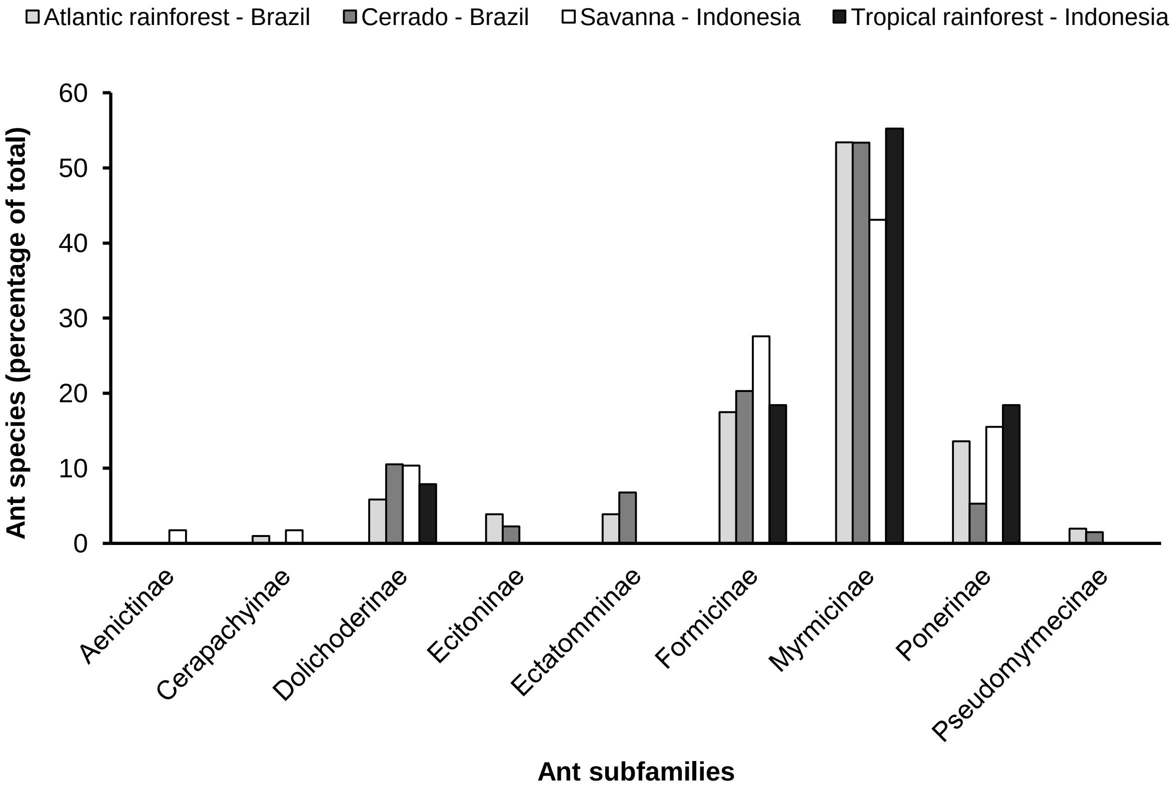

Figure 1. Percentage of the total number of ant species in each subfamily sampled in forest and savanna biomes in Brazil and Indonesia. Number of samples in each biome was 120 pitfall traps.

Absolute values of ant diversity

In general there are more ant species in Brazil than in Indonesia at all spatial scales (see the significance values in the Figure 2-legend) for forest biomes (Figure 2a) and savanna biomes (Figure 2b). Within each country, in Brazil there were more ant species at local and site scales in *Cerrado* than in Atlantic rainforest, but at landscape scale there was non- significant difference between the ant species diversity of the two biomes (Figure 3a - see the significance values in the Figure - legend). In Indonesia, the ant communities from rainforest were more speciose than ant savanna communities at local and site scales, but like in Brazil, at landscape scale there was no statistical difference between the ant communities of the two biomes (Figure 3b - see the significance values in the Figure – legend).

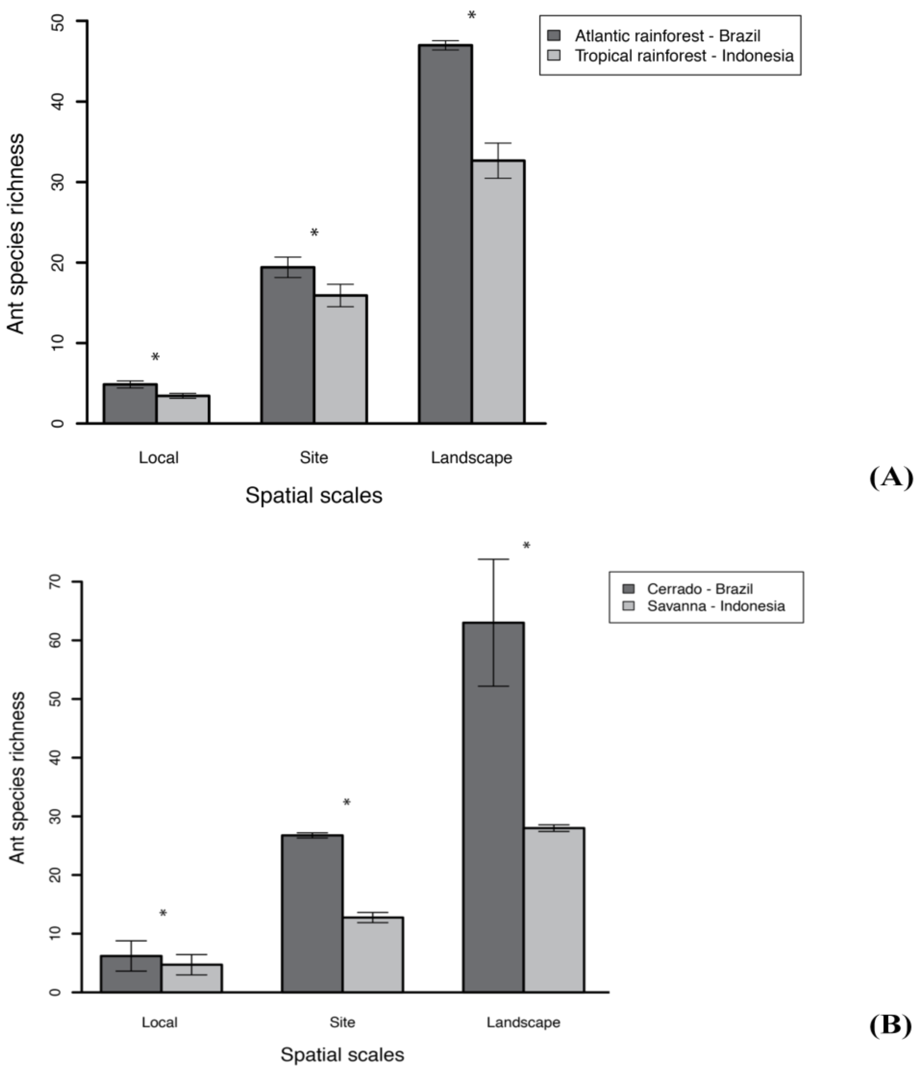

Figure 2. Ant species diversity (species richness) in rainforest and savannas biomes at three spatial scales: local scale (n=240), site scale (n=24), landscape scale (n=6). (A) Comparative analyses between Brazilian and Indonesian rainforest biomes. Local scale ($\chi^2 = 252.78$); Site scale ($\chi^2 = 27.21$); Landscape scale ($\chi^2 = 0.90$). (B) Comparative analyses between Brazilian and Indonesian savanna biomes. Local scale ($\chi^2 = 283.38$); Site scale ($\chi^2 = 44.28$); Landscape scale ($\chi^2 = 12.45$). Asterisks above the bars indicate statistical significance ($p < 0.05$).

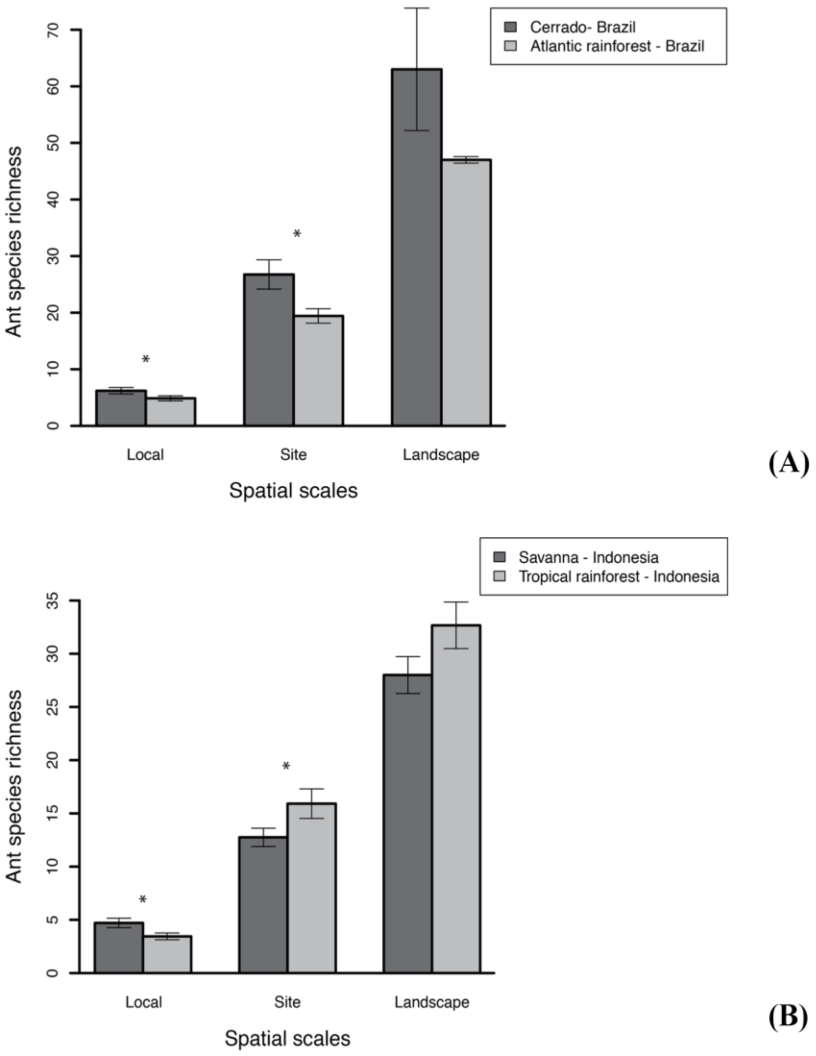

Figure 3. Comparative analyses of species richness between rainforest and savanna biomes within each country at three spatial scales: local scale (n=240), site scale (n=24), landscape scale (n=6). (A) Rainforest and savanna biomes in Brazil. Local scale (χ^2 = 349.92); Site scale (χ^2 = 47.77); Landscape scale (χ^2 = 11.85). (B) Rainforest and savanna biomes in Indonesia Local scale (χ^2 = 283.38); Site scale (χ^2 = 44.28); Landscape scale (χ^2 = 12.45). Asterisks above the bars indicate statistical significance ($p < 0.05$).

Regarding the species variation between the countries, Atlantic rainforest-Brazil presented more species variation among the sites than in Tropical rainforest-Indonesia (Figure 4a), and *Cerrado*-Brazil presented more species variation among the pitfalls than in Savanna-Indonesia (Figure 4b). Inside the countries, in Brazil *Cerrado* presented more species variation among pitfalls than in Atlantic rainforest (Figure 5a) and in Indonesia Tropical rainforest had more species variation among pitfalls than Savanna (Figure 5b).

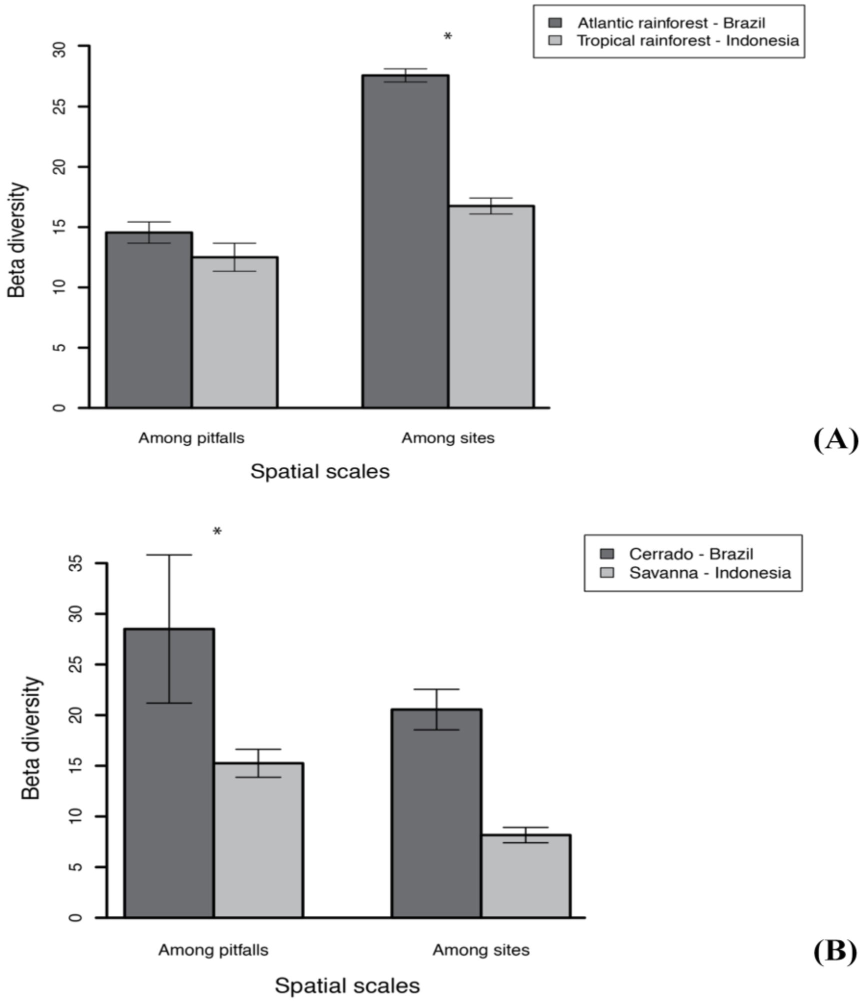

Figure 4. Comparative analyses of β-diversity at local scale (among pitfalls)(n = 24) and site scale (among sites)(n = 6) in rainforest and savannas biomes. (A) Comparative analyses between Brazilian and Indonesian rainforest biomes. Local scale ($F_{(1,22)} = 1.97$); Site scale ($F_{(1,4)} = 159.43$). (B) Comparative analyses between Brazilian and Indonesian savanna biomes. Local scale ($F_{(1,22)} = 33.57$); Site scale ($F_{(1,4)} = 3.16$). Asterisks above the bars indicate statistical significance ($p < 0.05$).

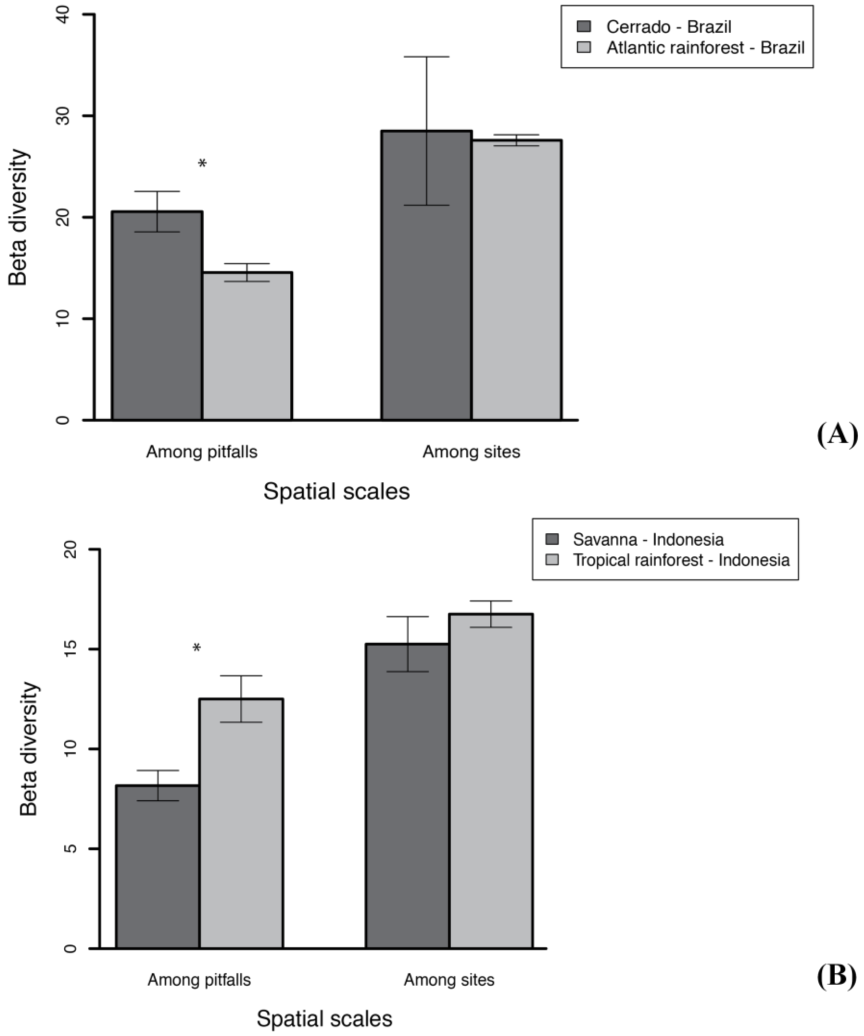

Figure 5. Comparative analyses of β-diversity at local scale (among pitfall)(n = 24) and at site scale (among sites)(n = 6) within each country. (A) Rainorest and savanna biomes in Brazil. Local scale ($F_{(1,22)} = 7.55$); Site scale ($F_{(1,4)} = 0.01$). (B) Rainforest and savanna biomes in Indonesia. Local scale ($F_{(1,22)} = 33.57$); Site scale ($F_{(1,4)} = 3.17$). Asterisks above the bars indicate statistical significance ($p < 0.05$).

Relative contribution of diversity components

The additive diversity partitioning showed that α-diversity at local scale and β-diversity among landscapes (β_3) were higher than expected by null models. β-diversity among pitfalls and among sites (β_1 and β_2 respectively) were lower than expected by null models for all ant communities of all biomes analyzed (Figure 6).

The contribution α-diversity at local scale to γ-diversity was approximately 4.5% in all biomes, exception in Savanna - Indonesia that was 8%. Regarding the contribution of β-diversity at specific scales to γ-diversity was 12 to 16% among pitfall (β_1); 25 to 28% among sites (β_2) and 50 – 53% among landscapes (β_3).

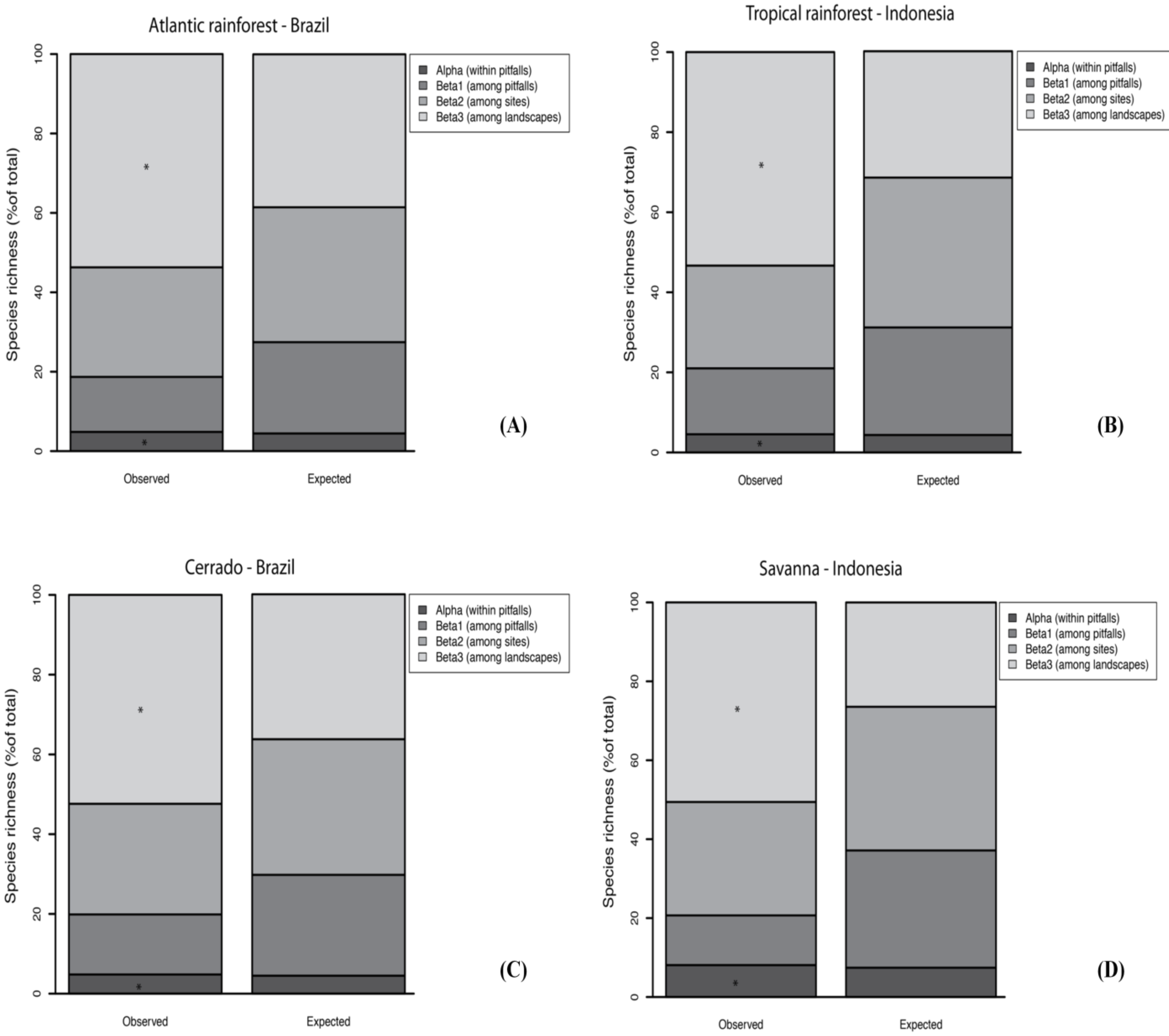

Figure 6. Additive partitioning of γ-diversity of ant communities from forest and savanna biomes in Brazil and Indonesia into local α-diversity component and β-diversity components at local (β_1), site (β_2) and landscape (β_3) scales. Asterisks represent observed diversity components significantly higher than expected by null models ($p < 0.05$).

Species saturation/insaturation at local scale

We detected a significant linear relationship between local species richness (mean number of ant species per pitfall traps) and regional species richness (number of ant species in the landscapes) ($F_{(1,10)} = 16.03$; $p > 0.05$). The biome identity was a non-significant term, thus by model simplification, the final model was fitted only with regional species richness as explanatory variable. Hence, we observed that protected areas (landscape scale) with higher ant species presented more ant species in the pitfall traps (local scale) (Figure 7).

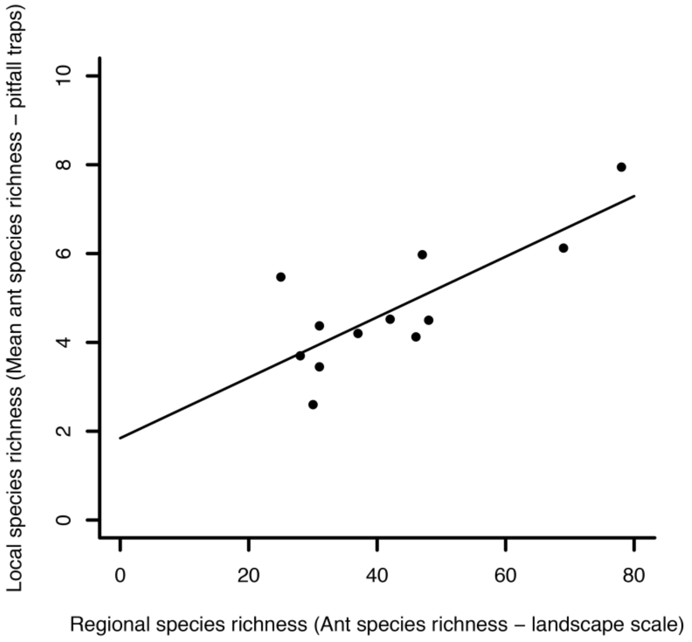

Figure 7. Relationship between local ant species diversity (mean number of species at pitfall traps) and regional ant species diversity (number of species at landscape scale) (n = 12)($F_{(1,10)} = 16.03$; $p < 0.05$).

Discussion

Although, the absolute diversity values and the idiosyncratic ant fauna in each countries point out to a dissimilar pattern, the relative contribution of diversity components to γ-diversity and species insaturation at local scale showed an interesting similarity between the ant communities. We consider these two similar patterns as evidences of congruence trends among the ant communities.

Ant fauna

Among the ant subfamilies, only Myrmicinae presented a quite similar pattern of proportionality in all the biomes (more than 50% of the ant species sampled in all biomes were mymicines). This result is in accordance with its world supremacy on epigaeic ant communities independently on the habitat type (Ward 2000).

However, the proportionality of some subfamilies seems to be affected by the biome type. The most evident case was Dolichoderinae, which enhanced two times its proportionality from rainforest to savanna in Brazil. Formicinae also increased its proportionality (approximately 1.5 times) from rainforest to savanna in Indonesia.

This reinforces the Dolichoderinae preference for hot-open habitats. The same could be said about the formicine ants, which have been reported as subordinate ants and co-occurring with the dominant dolichoderines in open xeric habitats (Andersen 1995; 1997).

The ant communities analyzed in our study in Brazil belong to the Neotropical region and in Indonesia essentially to the Indo-Malay region, but with a small part of savanna habitats (Komodo National Park) within the Australasia region (Olson 2001). These three regions have the highest number of ant genera, Neotropical and Indo-Malay each one host 128 native ant genera and Australasia region, 115 (Fisher 2010b).

The present-day exuberant biodiversity in these regions have been associated with the effects of glaciations/deglaciations cycles during the Pleistocene. During this time, in the tropical region, savanna and rainforest habitats experienced expansion and retraction movements of their range area, due to the interchanging periods of cold-dry and warm-wet climates that could lead to more intense vicariance events and speciation rates than in other stable environments (Voris 2000; Carnaval 2009; Werneck 2011).

Absolute values of ant diversity

Although the two countries could potentially host similar ant diversity, the higher number of ant species sampled at all spatial scales in Brazil could be an inherent result of the larger and more continuous areas of its rainforest and savanna than in Indonesia. Thus, differential effects of species-area relationship and island biogeography (Carvalho & Vasconcelos 1999; Sobrinho et al. 2003; Schoereder et al.

2004a-b; Ribas et al. 2005; Rizali et al. 2010) should happen in the two countries at the end of glaciations/deglaciation period.

This differential effect of species-area and island biogeography could be associated to the geographical differences between Indonesia and Brazil (insular *versus* continental). Thus, the small areas in Indonesia far from source areas of rainforest (Asia) and savanna (Australia)(Trainor & Andersen 2010), should not be as favorable for the ant establishment and persistence as the larger and more continuous areas of the equivalent habitats in Brazil.

The above explanation also fits well with the difference on the absolute values of species diversity and species variation between rainforest and savanna habitats within each country. In Indonesia, the area of forest habitats is far larger than the area of savannas, which could explain the pattern found. A similar pattern has been found by Vasconcelos & Vilhena (2006) in the Amazon region, where continuous forest habitats host two times more ant species than savanna patches (Vasconcelos & Vilhena 2006). Moreover, Taylor & Andersen (2010) reported that the ant fauna of Southeastern Asia savannas has essentially a forest origin, which allow us to deduce that it could be a poor species richness version of the forest ant fauna.

While the Amazon forest host higher number of ant species than *Cerrado* (Vascocelhos & Vilhena 2006), this is unlikely to apply to the smaller Atlantic rainforest in the Brazilian coast. *Cerrado* is almost two times larger than Atlantic rainforest (IBGE 1994) and is located in the middle of Brazilian territory surrounded by several other biomes, which could enhance the number of ant species.

Although nowadays both biomes are highly fragmented and endangered, the Atlantic rainforest is historically the biome that has suffered the highest levels of land conversion and human occupancy that resulted in several forest patches within an extremely fragmented landscape (Ribeiro 2009). This is a similar scenario reported by Andersen et al. (2007), who found far higher ant species richness in savanna habitats than in the small patches of rainforest in Australia.

Relative contribution of diversity components and species saturation/insaturation at local scale

Contrary to the absolute diversity results, additive diversity partitioning revealed congruent trends among the biomes. In all biomes the α-diversity at local scale and β-diversity among landscape (β_3) were higher than expected by null models and β-diversity among pitfall and among sites (β_1 and β_2 respectively) were lower. Moreover, in all biomes the observed relative contribution of the diversity components was very similar (Figure 6).

According to Crist et al. (2003), an observed α-diversity higher (or equal to) than expected by null model is interpreted as a non species aggregation, which means that a limitation to the occupancy of local communities by the ant species does not exist. The linear relationship between mean ant species per pitfall and ant species richness at landscape scale reinforces this pattern (Figure 7).

These results suggest that competition based on niche partitioning theory is not a constraint to the ant species coexistence at local communities, which have already been reported in other studies (Ribas & Schoereder 2002; Arnan et al. 2011). Thus, arguments based on neutral theory of community ecology have been proposed as an alternative explanation to the high ant species richness ant species at local scale (Andersen 2008).

Andersen (2008) proposes five theoretical propositions to the high local ant species richness. These propositions are elaborated assuming two assumptions, (i) large number of species must successfully establish, (ii) together with a high rate of species persistence of established colonies.

Among Andersen's theoretical propositions, we highlight the third: "Species richness in ant communities is to a large extent a function of propagule arrival, and is therefore strongly determined by regional species richness". He proposed that mass effect events could be responsible for the high local ant species richness and species insaturation by the constant influx of species arriving in the local communities.

Andersen's arguments are in agreement with Loreau (2001) who reports that species dispersal movements among spatial units tend to reduce the β-diversity and at the same time increase the α-diversity by species immigration, overcoming the constraints imposed by interspecific competition. In this context, if the species dispersal is allowed among the local communities, this could counteract local competitive exclusion maintaining more species from regional pool coexisting in the local communities. This coexistence, besides reducing β-diversity, means that α-diversity is a broad sample of γ-diversity in the region.

The statements and hypotheses described above are plausible explanations for the patterns that we found to the diversity components and species insaturation at local and site scales for the ant communities sampled in all biomes. Furthermore, some studies also have met low β-diversity and high α-diversity within sets of local ant communities (Ribas et al. 2005; Campos et al. 2011; Schmidt et al. *in preparation*; Marques & Schoereder *in preparation*). This could evidence the high dispersion capacity of ants among communities at small and intermediate scales (Mabelis & Chardon 2005), that according to Andersen (2008) and Loreau (2000) could overcome the interspecific competition constraints.

The β_3-diversity (species variation among landscapes) was the component with the higher contribution to the total gamma diversity of all biomes sampled. In all biomes, β_3-diversity accounted for around 50 % (min.: 50.57%; max.: 53.72%) of the total ant species richness (γ-diversity).

Moreover, absolute values of β-diversity in all biomes increased according to the spatial scale size enhancing, which in other words means ant communities at short and medium distance (in our case 10 m for local scale and at least 500 m for site scale) showed low β-diversities (β_1 and β_2). However, this dissimilarity increases approximately four times for ant communities sampled at different landscapes within the same biome, where the inter-distance considering all biomes range from 55 Km to 684 Km.

Campos et al. (2011) and Marques & Schoereder (*in preparation*), studying equivalent spatial scale designs, also found similar patterns (α-diversity at local scale and β-diversity among the largest scale higher than expected by null model). Both studies also pointed out the last β-diversity as the component with more contribution to γ-diversity. In these studies some β-diversity components at intermediate scale also had a significant contribution, which we credit to sampling particularities.

Soininen et al. (2007) summarized mechanisms described in ecological literature to explain the similarity decay (or β-diversity increasing) in ecological communities with the increase of distance. The mechanisms are not mutually exclusive and three distinct assumptions could be stated: (i) species differing in their ability to perform under different environment; (ii) spatial configuration and the nature of the landscape dictate the dispersal rate of organisms among sites, which means communities at heterogeneous landscapes will present lower similarity than this at homogeneous settings; and (iii) according to neutral theory (Hubbell 2001), community similarity decays with distance even if the homogeneous environment, due to organisms’ limited dispersal resulted of ecological drift, random dispersal and random speciation.

Comparing our β-diversity data with Soininen's assumptions review, seems that ecological drifts and neutral models context (Hubbell 2001) proposed by Andersen (2008) could be the mechanism to the ant species coexistence in our local and site scales. Hence, we can assume that, at small-intermediate scales, ant species should have a similar abilities to establish and survival at different environments.

The low β-diversities at local and site scale (β_1 and β_2) corroborate this assumption even though in heterogeneous landscapes such as our sampled savannas (e.g. grassland, savanna and tropical deciduous forest) and in the Natural Reserve VALE, a rainforest protected area, where ants were sampled in three forest sites and in one native endemic grassland. According the third theoretical proposal of Anderson (2008) a constant mass effect event could confer to ant species a reverse force against competition exclusion resulting in a similar ability to establish and survival at different environments.

Hence ant assemblages at small and intermediate scale host a great part of regional species pool. The Figure 7 stresses this relationship and could be intrepeted as one more evidence in favour of Anderson's theoretical proposals (Anderson 2008).

However, the spatial scale enhancing to landscape within the same biome shows a cut off on the ant species flux among the landscapes (high β-diversity). Following, the second assumption in Soininen (2007), the distance among our sampled landscapes could be enough to promote a spatial heterogeneity inside the common biome which could mean a dispersal barriers to the full ant species exchange among large areas.

Based on the historical development time of the sampled biomes, we could hypothesize that internal areas could be isolated from each other, probably by the action of some geographic or climatic constraints. These constraints could be played, for example, by the rising of mountain chains and by climatic fluctuation cycles during the early past time. Such cycles imposed lowering and rising of sea level (in Indonesia) and expansion and contraction of forest and savanna ranges in both regions, Neotropical and Indo-Malay (Voris 2000; Carnaval 2009; Werneck 2011).

Conclusion

If only the absolute diversity was considered in our study, we would draw a divergent scenario about the ant community structure, related to the geographic particularities of each continent. We associated this divergent pattern to dissimilar species-area relationship and island biogeography between the countries (continental *versus* insular).

On the other hand, regardless of the differences on the absolute diversity values, additive partitioning revealed a congruent pattern on the diversity components. We propose that processes playing out across both ecological and evolutionary times should be the responsible for the convergent trends on the contribution of α- and β-diversity to the γ-diversity in all biomes.

According to local determinism predictions (Rickfles 2004) the community congruence is a result of similar local biotic constraints. Hence, in our study seems that the congruent trends among the ant communities are related to similar dispersal ability among ant species in all biomes.

This similar dispersal ability could allow ant species overcomes the local constraints, conferring a higher α-diversity at local scale and lower β-diversities among pitfall and among sites (β_1 and β_2 respectively), which are corroborated by the species insaturtion at local scale in all biomes. On the other hand, at large scales, restrictions during the historical development of the biomes seem to limit in a similar way the ant dispersion among the ant communities at landscape scale resulting in the higher observed β-diversity in this scale.

Hence, our data support and confirm Andersen's theoretical propositions (Andersen 2008) that mass effect events are responsible for the high local ant species richness and species insaturation by the constant influx of species arriving in the local communities. We can conclude that alternative processes, based on species dispersion have an expressive role on ant species coexistence and potentially offer a broad global explanation to the structure of tropical ant communities.

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GENERAL CONCLUSION

We found interesting results about the species diversity and species variation on tropical ant communities in the two studies developed in this thesis. We consider that the major conclusion built in these chapters offer new perspectives to the study of ant community ecology.

Regarding the first chapter, the model selection approach allowed us to found out that ant species diversity at local scale is under the influence of both local factors and meso-factors. Increasing the spatial scale to mesoscale, the influence of the predictor variables considered in the models seem to lose their capacity of influencing species diversity and variation, because most models were fitted only with the intercept.

However, these results were dependent on the ant microhabitat (arboreal, epigaeic and hypogaeic) and we found differences in the same microhabitat according to the habitat type sampled (forest and savanna). Hence, we suggest that caution is important when broad generalization about the structure of ant communities are stated without accounting the idiosyncratic factors associated to the ant microhabitat and habitat types.

In the second chapter, we credit the congruence trends among the ant communities in all biomes to the similar dispersion ability of ant species. These findings support Andersen's theoretical propositions (Andersen 2008) that mass effect events are responsible for the high local ant species richness and species insaturation by the constant influx of species arriving in the local communities.

In this way, a high dispersal ability could allow ant species to overcome the local constraints, conferring a higher α-diversity at local scale and lower β-diversities among pitfall and among sites (β_1 and β_2 respectively), and species insaturation at local scale in all biomes. On the other hand, at large scales, restrictions during the historical development of the biomes seem to limit in a similar way the ant dispersion among the ant communities at landscape scale, resulting in the higher observed β-diversity in this scale.

Considering that competition has been considered the *hallmark* of ant ecology at local scale (Parr & Gibb 2010), our findings revealed that besides niche partitioning, others mechanisms also could enhance the ant species coexistence. This is showed in the Chapter 1 to epigaeic ants at local scale, in which meso-factors had a large relative importance and several top models were fitted with them.

The high ant dispersion invoked in the Chapter 2 to explain the high ant α-diversity and low β-diversity at local scale could be affected by the meso-factors described in Chapter 1. The model selection at mesoscale for ant assemblages of Atlantic rainforest and *Cerrado* biomes showed that at the same time some factors influences positively α-diversity and other affected negatively β-diversity. This make us deduce that these factors could be faciliting the ant dispersion among the local communities.

Therefore, we understand that perspectives such as described in this thesis, have a great potential to offer satisfactory explanations to the ant community structuring. We suggest that assimilation of alternative mechanisms, besides local determinism, are essential to the elaboration of future hypothesis regarding to the diversity patterns of tropical ant communities.

Appendix material

Appendix material A1. – Ant species sampled in Atlantic rainforest and *Cerrado* biomes in Brazil.

Appendix material A2. – Ant species sampled in Atlantic rainforest biome in Brazil.

Appendix material A3. – Ant species sampled in *Cerrado* biome in Brazil.

Appendix material A4. – Ant species sampled in tropical rainforest and savanna habitats in Indonesia.

Appendix material A1. – Ant species sampled in Atlantic rainforest and *Cerrado* biomes in Brazil. Species list for three ant microhabitats: arboreal, epigaeic and hypogaeic. #spp = Number of ant species. Total ants = The sum of single ant species considering the three microhabitats sampled in the two biomes.

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
Dolichoderinae	12	**Dolichoderinae**	19	**Cerapachyinae**	1	**Cerapachyinae**	1
Azteca cf. chartifex		Azteca sp. A		Acanthostichus laticornis		Acanthostichus laticornis	
Azteca instabilis		Dolichoderus sp. 1		**Dolichoderinae**	2	**Dolichoderinae**	23
Dorymyrmex sp. 1-coleção		Dorymyrmex sp. 1-coleção		Linepithema pr. cerradense		Azteca cf. chartifex	
Linepithema cf. aztecoides		Dorymyrmex sp. A		Linepithema sp. B		Azteca instabilis	
Linepithema pr. cerradense		Dorymyrmex sp. B		**Ecitoninae**	5	Azteca sp. A	
Linepithema sp. A		Dorymyrmex sp. C		Labidus coecus		Dolichoderus sp. 1	
Linepithema sp. B		Forelius sp. A		Labidus praedator		Dorymyrmex sp. 1-coleção	
Linepithema sp. C		Linepithema cf. aztecoides		Labidus sp. A		Dorymyrmex sp. A	
Linepithema sp. E		Linepithema pr. cerradense		Labidus sp. B		Dorymyrmex sp. B	
Linepithema sp. G		Linepithema sp. A		Nomamyrmex sp. A		Dorymyrmex sp. C	
Tapinoma sp. B		Linepithema sp. B		**Ectatomminae**	6	Forelius sp. A	
Tapinoma sp. C		Linepithema sp. E		Ectatomma brunneum		Linepithema cf. aztecoides	
Ecitoninae	1	Linepithema sp. F		Ectatomma edentatum		Linepithema pr. cerradense	
Labidus praedator		Linepithema sp. G		Ectatomma permagnum		Linepithema sp. A	
Ectatomminae	3	Linepithema sp. H		Ectatomma planidens		Linepithema sp. B	
Ectatomma muticum		Linepithema sp. I		Ectatomma sp. B		Linepithema sp. C	
Ectatomma sp. B		Linepithema sp. J		Gnamptogenys striatula		Linepithema sp. E	
Gnamptogenys striatula		Tapinoma sp. A		**Formicinae**	11	Linepithema sp. F	
Formicinae	29	Tapinoma sp. C		Acropyga sp. A		Linepithema sp. G	
Brachymyrmex pr. depilis		**Ecitoninae**	5	Brachymyrmex pr. depilis		Linepithema sp. H	
Brachymyrmex sp. 1-coleção		Labidus coecus		Brachymyrmex sp. 1-coleção		Linepithema sp. I	
Brachymyrmex sp. A		Labidus praedator		Brachymyrmex sp. B		Linepithema sp. J	
Camponotos trapezoideus		Neivamyrmex sp. A		Camponotos trapezoideus		Tapinoma sp. A	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
Formicinae		**Ecitoninae**		**Formicinae**		**Dolichoderinae**	
Camponotus atriceps		Neivamyrmex sp. B		Camponotus cingulatus		Tapinoma sp. B	
Camponotus blandus		Nomamyrmex sp. A		Camponotus genatus		Tapinoma sp. C	
Camponotus cingulatus		**Ectatomminae**	9	Camponotus sp. B		**Ecitoninae**	7
Camponotus crassus		Ectatomma brunneum		Camponotus sp. E		Labidus coecus	
Camponotus genatus		Ectatomma edentatum		Nylanderia pr. fulva		Labidus praedator	
Camponotus melanoticus		Ectatomma muticum		Nylanderia sp. A		Labidus sp. A	
Camponotus punctulatus		Ectatomma opaciventre		**Myrmicinae**	47	Labidus sp. B	
Camponotus rufipes		Ectatomma permagnum		Acromyrmex sp. C		Neivamyrmex sp. A	
Camponotus sericeiventris		Ectatomma planidens		Atta sexdens		Neivamyrmex sp. B	
Camponotus sp. 7-coleção		Ectatomma sp. A		Carebara sp. A		Nomamyrmex sp. A	
Camponotus sp. A		Ectatomma sp. B		Carebara sp. B		**Ectatomminae**	**9**
Camponotus sp. B		Gnamptogenys striatula		Carebara urichi		Ectatomma brunneum	
Camponotus sp. C		**Formicinae**	33	Centromyrmex cf. alfaroi		Ectatomma edentatum	
Camponotus sp. D		Acropyga sp. B		Cephalotes pusillus		Ectatomma muticum	
Camponotus sp. F		Acropyga sp. C		Crematogaster sp. D		Ectatomma opaciventre	
Camponotus sp. G		Brachymyrmex pr. depilis		Crematogaster sp. I		Ectatomma permagnum	
Camponotus sp. J		Brachymyrmex sp. 1-coleção		Cyphomyrmex sp. A		Ectatomma planidens	
Camponotus sp. L		Brachymyrmex sp. A		Megalomyrmex sp. C		Ectatomma sp. A	
Camponotus sp. M		Brachymyrmex sp. B		Monomorium sp. A		Ectatomma sp. B	
Camponotus sp. O		Camponotos trapezoideus		Mycocepurus goeldii		Gnamptogenys striatula	
Camponotus sp.1-coleção		Camponotus arboreus		Mycocepurus sp. A		**Formicinae**	42
Camponotus trapezoideus		Camponotus atriceps		Mycocepurus sp. B		Acropyga sp. A	
Camponotus vittatus		Camponotus blandus		Octostruma pr. stenognatha		Acropyga sp. B	
Myrmelachista sp. A		Camponotus cingulatus		Octostruma sp. A		Acropyga sp. C	
Nylanderia pr. fulva		Camponotus crassus		Pheidole sp. 6		Brachymyrmex pr. depilis	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
Myrmicinae	43	**Formicinae**		**Myrmicinae**		**Formicinae**	
Atta sexdens		Camponotus genatus		Pheidole sp. 30		Brachymyrmex sp. 1-coleção	
Cardiocondyla emery		Camponotus leydigi		Pheidole sp. 1		Brachymyrmex sp. A	
Carebara sp. D		Camponotus melanoticus		Pheidole sp. 11		Brachymyrmex sp. B	
Cephalotes atratus		Camponotus punctulatus		Pheidole sp. 14		Camponotos trapezoideus	
Cephalotes betoi		Camponotus rufipes		Pheidole sp. 15		Camponotus arboreus	
Cephalotes depressus		Camponotus sericeiventris		Pheidole sp. 17		Camponotus atriceps	
Cephalotes grandinosus		Camponotus sp. 1-coleção		Pheidole sp. 2		Camponotus blandus	
Cephalotes minutus		Camponotus sp. 7-coleção		Pheidole sp. 20		Camponotus cingulatus	
Cephalotes pusillus		Camponotus sp. 8-Coleção		Pheidole sp. 24		Camponotus crassus	
Cephalotes sp. 1		Camponotus sp. A		Pheidole sp. 25		Camponotus genatus	
Crematogaster sp. A		Camponotus sp. B		Pheidole sp. 26		Camponotus leydigi	
Crematogaster sp. C		Camponotus sp. D		Pheidole sp. 4		Camponotus melanoticus	
Crematogaster sp. D		Camponotus sp. E		Pheidole sp. 6		Camponotus punctulatus	
Crematogaster sp. E		Camponotus sp. F		Pheidole sp. 9		Camponotus rufipes	
Crematogaster sp. G		Camponotus sp. H		Pyramica cf. eggersi		Camponotus sericeiventris	
Crematogaster sp. H		Camponotus sp. K		Sericomyrmex sp. 1-coleção		Camponotus sp. 1-coleção	
Crematogaster sp. K		Camponotus sp. L		Solenopsis geminata-conf		Camponotus sp. 7-coleção	
Hylomyrma sp. A		Camponotus sp. N		Solenopsis sp. 1		Camponotus sp. 8-Coleção	
Monomorium sp. A		Camponotus vittatus		Solenopsis sp. 2		Camponotus sp. A	
Mycocepurus goeldii		Nylanderia pr. fulva		Solenopsis sp. 3		Camponotus sp. B	
Nesomyrmex sp. A		Nylanderia sp. A		Solenopsis sp. 4		Camponotus sp. C	
Pheidole sp. 1		**Myrmicinae**	104	Solenopsis sp. 5		Camponotus sp. D	
Pheidole sp. 10		Acromyrmex sp. A		Solenopsis sp. 6		Camponotus sp. E	
Pheidole sp. 12		Acromyrmex sp. B		Solenopsis sp. 7		Camponotus sp. F	
Pheidole sp. 14		Acromyrmex sp. C		Solenopsis sp. 9		Camponotus sp. G	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
Myrmicinae		**Myrmicinae**		**Myrmicinae**		**Formicinae**	
Pheidole sp. 2		Acromyrmex sp. D		Tranopelta sp. A		Camponotus sp. H	
Pheidole sp. 31		Acromyrmex sp. E		Wasmannia affinis		Camponotus sp. J	
Pheidole sp. 6		Acromyrmex sp. F		Wasmannia auropunctata		Camponotus sp. K	
Pheidole sp. 7		Apterostigma jubatum		Wasmannia sp. 3		Camponotus sp. L	
Pheidole sp. 9		Apterostigma sp. A		**Ponerinae**	10	Camponotus sp. M	
Solenopsis geminata-conf		Apterostigma sp. B		Dinoponera australis		Camponotus sp. N	
Solenopsis sp. 1		Atta sexdens		Hypoponera cf. opacipes		Camponotus sp. O	
Solenopsis sp. 2		Blepharidata conops		Hypoponera sp. 2-coleção		Camponotus sp.1-coleção	
Solenopsis sp. 3		Cardiocondyla emery		Hypoponera sp. A		Camponotus trapezoideus	
Solenopsis sp. 4		Carebara sp. C		Odontomachus chelifer		Camponotus vittatus	
Solenopsis sp. 5		Carebara sp. E		Odontomachus meinerti		Myrmelachista sp. A	
Solenopsis sp. 6		Carebara urichi		Pachycodyla venusta		Nylanderia pr. fulva	
Solenopsis sp. 7		Centromyrmex cf. alfaroi		Pachycondyla harpax		Nylanderia sp. A	
Solenosis sp. 1		Cephalotes pusillus		Pachycondyla venusta		**Myrmicinae**	125
Tetramorium sp. A		Crematogaster abstinens		Pachycondyla verenae		Acromyrmex sp. A	
Trachymyrmex sp. D		Crematogaster sp. B				Acromyrmex sp. B	
Tranopelta sp. A		Crematogaster sp. C				Acromyrmex sp. C	
Wasmannia auropunctata		Crematogaster sp. D				Acromyrmex sp. D	
Ponerinae	5	Crematogaster sp. E				Acromyrmex sp. E	
Pachycondyla sp. 4		Crematogaster sp. F				Acromyrmex sp. F	
Pachycondyla striata		Crematogaster sp. H				Apterostigma jubatum	
Pachycondyla venusta		Crematogaster sp. I				Apterostigma sp. A	
Pachycondyla verenae		Crematogaster sp. J				Apterostigma sp. B	
Pachycondyla villosa		Cyphomyrmex sp. 1-coleção				Atta sexdens	
		Cyphomyrmex sp. 2-coleção				Blepharidata conops	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
Pseudomyrmecinae	6	**Myrmicinae**				**Myrmicinae**	
Pseudomyrmex cubaensis		Cyphomyrmex sp. B				Cardiocondyla emery	
Pseudomyrmex elongatus		Cyphomyrmex sp. C				Carebara sp. A	
Pseudomyrmex gracilis		Cyphomyrmex sp. D				Carebara sp. B	
Pseudomyrmex pisinnus		Hylomyrma reitteri				Carebara sp. C	
Pseudomyrmex sp. A		Hylomyrma sp. B				Carebara sp. D	
Pseudomyrmex tenuis		Megalomyrmex sp. A				Carebara sp. E	
		Megalomyrmex sp. B				Carebara urichi	
		Megalomyrmex sp. C				Centromyrmex cf. alfaroi	
		Monomorium pharaonis				Cephalotes atratus	
		Monomrium sp. A				Cephalotes betoi	
		Mycetosoitis sp. A				Cephalotes depressus	
		Mycocepurus sp. B				Cephalotes grandinosus	
		Mycocepurus sp. C				Cephalotes minutus	
		Octostruma sp. A				Cephalotes pusillus	
		Pheidole sp. 30				Cephalotes sp. 1	
		Pheidole sp. 6				Crematogaster abstinens	
		Pheidole sp. 8				Crematogaster sp. A	
		Pheidole sp. 1				Crematogaster sp. B	
		Pheidole sp. 10				Crematogaster sp. C	
		Pheidole sp. 11				Crematogaster sp. D	
		Pheidole sp. 12				Crematogaster sp. E	
		Pheidole sp. 13				Crematogaster sp. F	
		Pheidole sp. 14				Crematogaster sp. G	
		Pheidole sp. 15				Crematogaster sp. H	
		Pheidole sp. 17				Crematogaster sp. I	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
		Myrmicinae				**Myrmicinae**	
		Pheidole sp. 18				Crematogaster sp. J	
		Pheidole sp. 19				Crematogaster sp. K	
		Pheidole sp. 2				Cyphomyrmex sp. 1-coleção	
		Pheidole sp. 20				Cyphomyrmex sp. 2-coleção	
		Pheidole sp. 21				Cyphomyrmex sp. A	
		Pheidole sp. 22				Cyphomyrmex sp. B	
		Pheidole sp. 23				Cyphomyrmex sp. C	
		Pheidole sp. 24				Cyphomyrmex sp. D	
		Pheidole sp. 25				Hylomyrma reitteri	
		Pheidole sp. 26				Hylomyrma sp. A	
		Pheidole sp. 28				Hylomyrma sp. B	
		Pheidole sp. 3				Megalomyrmex sp. A	
		Pheidole sp. 31				Megalomyrmex sp. B	
		Pheidole sp. 4				Megalomyrmex sp. C	
		Pheidole sp. 5				Monomorium pharaonis	
		Pheidole sp. 6				Monomorium sp. A	
		Pheidole sp. 7				Mycetosoitis sp. A	
		Pheidole sp. 9				Mycocepurus goeldii	
		Pyramica cf. eggersi				Mycocepurus sp. A	
		Rogeria sp. 2-coleção				Mycocepurus sp. B	
		Sericomyrmex sp. 1-coleção				Mycocepurus sp. C	
		Sericomyrmex sp. A				Nesomyrmex sp. A	
		Sericomyrmex sp. B				Octostruma pr. stenognatha	
		Solenopsis geminata-conf				Octostruma sp. A	
		Solenopsis sp. 1				Pheidole sp. 6	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
		Myrmicinae				**Myrmicinae**	
		Solenopsis sp. 2				Pheidole sp. 30	
		Solenopsis sp. 3				Pheidole sp. 6	
		Solenopsis sp. 4				Pheidole sp. 8	
		Solenopsis sp. 5				Pheidole sp. 1	
		Solenopsis sp. 6				Pheidole sp. 10	
		Solenopsis sp. 7				Pheidole sp. 11	
		Trachymyrmex sp. A				Pheidole sp. 12	
		Trachymyrmex sp. B				Pheidole sp. 13	
		Trachymyrmex sp. C				Pheidole sp. 14	
		Trachymyrmex sp. D				Pheidole sp. 15	
		Trachymyrmex sp. E				Pheidole sp. 17	
		Trachymyrmex sp. F				Pheidole sp. 18	
		Trachymyrmex sp. G				Pheidole sp. 19	
		Trachymyrmex sp. H				Pheidole sp. 2	
		Trachymyrmex sp. I				Pheidole sp. 20	
		Trachymyrmex sp. J				Pheidole sp. 21	
		Trachymyrmex sp. L				Pheidole sp. 22	
		Trachymyrmex sp. M				Pheidole sp. 23	
		Trachymyrmex sp. N				Pheidole sp. 24	
		Tranopelta sp. A				Pheidole sp. 25	
		Wasmania auropunctata				Pheidole sp. 26	
		Wasmannia affinis				Pheidole sp. 28	
		Wasmannia sp. 1				Pheidole sp. 3	
		Wasmannia sp. 2				Pheidole sp. 31	
		Wasmannia sp. 3				Pheidole sp. 4	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
		Myrmicinae				**Myrmicinae**	
		Wasmannia sp. 5				Pheidole sp. 5	
		Ponerinae	14			Pheidole sp. 6	
		Anochetus cf. oriens				Pheidole sp. 7	
		Hypoponera cf. foreli				Pheidole sp. 9	
		Hypoponera cf. opacipes				Pyramica cf. eggersi	
		Hypoponera sp. 2-coleção				Rogeria sp. 2-coleção	
		Hypoponera sp. C				Sericomyrmex sp. 1-coleção	
		Leptogenys sp. A				Sericomyrmex sp. A	
		Odontomachus bauri				Sericomyrmex sp. B	
		Odontomachus chelifer				Solenopsis geminata-conf	
		Odontomachus meinerti				Solenopsis sp. 1	
		Pachycondyla apicalis				Solenopsis sp. 2	
		Pachycondyla harpax				Solenopsis sp. 3	
		Pachycondyla venusta				Solenopsis sp. 4	
		Pachycondyla verenae				Solenopsis sp. 5	
		Pachycondyla villosa				Solenopsis sp. 6	
		Pseudomyrmecinae	3			Solenopsis sp. 7	
		Pseudomyrmex cubaensis				Solenopsis sp. 9	
		Pseudomyrmex pisinnus				Tetramorium sp. A	
		Pseudomyrmex tenuis				Trachymyrmex sp. A	
						Trachymyrmex sp. B	
						Trachymyrmex sp. C	
						Trachymyrmex sp. D	
						Trachymyrmex sp. E	
						Trachymyrmex sp. F	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
						Trachymyrmex sp. G	
						Trachymyrmex sp. H	
						Trachymyrmex sp. I	
						Trachymyrmex sp. J	
						Trachymyrmex sp. L	
						Trachymyrmex sp. M	
						Trachymyrmex sp. N	
						Tranopelta sp. A	
						Wasmannia affinis	
						Wasmannia auropunctata	
						Wasmannia sp. 1	
						Wasmannia sp. 2	
						Wasmannia sp. 3	
						Wasmannia sp. 5	
						Ponerinae	19
						Anochetus cf. oriens	
						Dinoponera australis	
						Hypoponera cf. foreli	
						Hypoponera cf. opacipes	
						Hypoponera sp. 2-coleção	
						Hypoponera sp. A	
						Hypoponera sp. C	
						Leptogenys sp. A	
						Odontomachus bauri	
						Odontomachus chelifer	
						Odontomachus meinerti	

A1 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Total ants	#spp.
						Ponerinae	
						Pachycodyla venusta	
						Pachycondyla apicalis	
						Pachycondyla harpax	
						Pachycondyla sp. 4	
						Pachycondyla striata	
						Pachycondyla venusta	
						Pachycondyla verenae	
						Pachycondyla villosa	
						Pseudomyrmecinae	6
						Pseudomyrmex cubaensis	
						Pseudomyrmex elongatus	
						Pseudomyrmex gracilis	
						Pseudomyrmex pisinnus	
						Pseudomyrmex sp. A	
						Pseudomyrmex tenuis	
Arboreal ants	99	**Epigaeic ants**	187	**Hypogaeic ants**	82	**Total ants**	232

Appendix material A2. – Ant species sampled in Atlantic rainforest biome in Brazil. Species list for three ant microhabitats: arboreal, epigaeic and hypogaeic. #spp = Number of ant species. Total ants = The sum of single ant species considering the three microhabitats.

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Biome	#spp.
Dolichoderinae	7	**Dolichoderinae**	6	**Cerapachyinae**	1	**Cerapachyinae**	1
Azteca cf. chartifex		Dolichoderus sp. 1		Acanthostichus laticornis		Acanthostichus laticornis	
Dorymyrmex sp. 1-coleção		Dorymyrmex sp. A		**Dolichoderinae**	1	**Dolichoderinae**	10
Linepithema sp. A		Linepithema sp. A		Linepithema sp. B		Azteca cf. chartifex	
Linepithema sp. B		Linepithema sp. B		**Ecitoninae**	2	Dolichoderus sp. 1	
Linepithema sp. C		Linepithema sp. E		Labidus coecus		Dorymyrmex sp. 1-coleção	
Linepithema sp. E		Tapinoma sp. A		Labidus praedator		Dorymyrmex sp. A	
Tapinoma sp. B		**Ecitoninae**	4	**Ectatomminae**	2	Linepithema sp. A	
Ecitoninae	1	Labidus coecus		Ectatomma brunneum		Linepithema sp. B	
Labidus praedator		Labidus praedator		Ectatomma sp. B		Linepithema sp. C	
Ectatomminae	2	Neivamyrmex sp. A		**Formicinae**	5	Linepithema sp. E	
Ectatomma muticum		Neivamyrmex sp. B		Acropyga sp. A		Tapinoma sp. A	
Gnamptogenys striatula		**Ectatomminae**	4	Brachymyrmex pr. depilis		Tapinoma sp. B	
Formicinae	14	Ectatomma brunneum		Brachymyrmex sp. B		**Ecitoninae**	4
Brachymyrmex pr. depilis		Ectatomma muticum		Camponotus sp. B		Labidus coecus	
Brachymyrmex sp. A		Ectatomma sp. B		Nylanderia pr. fulva		Labidus praedator	
Camponotos trapezoideus		Gnamptogenys striatula		**Myrmicinae**	31	Neivamyrmex sp. A	
Camponotus atriceps		**Formicinae**	18	Acromyrmex sp. C		Neivamyrmex sp. B	
Camponotus genatus		Acropyga sp. B		Atta sexdens		**Ectatomminae**	4
Camponotus punctulatus		Acropyga sp. C		Carebara sp. A		Ectatomma brunneum	
Camponotus sericeiventris		Brachymyrmex pr. depilis		Carebara urichi		Ectatomma muticum	
Camponotus sp. 7-coleção		Brachymyrmex sp. A		Centromyrmex cf. alfaroi		Ectatomma sp. B	
Camponotus sp. A		Brachymyrmex sp. B		Crematogaster sp. I		Gnamptogenys striatula	
Camponotus sp. B		Camponotos trapezoideus		Cyphomyrmex sp. A		**Formicinae**	24

A2 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Biome	#spp.
Formicinae		**Formicinae**		**Myrmicinae**		**Formicinae**	
Camponotus sp. C		Camponotus atriceps		Megalomyrmex sp. C		Acropyga sp. A	
Camponotus sp. D		Camponotus cingulatus		Octostruma pr. stenognatha		Acropyga sp. B	
Camponotus trapezoideus		Camponotus rufipes		Octostruma sp. A		Acropyga sp. C	
Myrmelachista sp. A		Camponotus sericeiventris		Pheidole sp. 6		Brachymyrmex pr. depilis	
Myrmicinae	26	Camponotus sp. 1-coleção		Pheidole sp. 1		Brachymyrmex sp. A	
Atta sexdens		Camponotus sp. 7-coleção		Pheidole sp. 14		Brachymyrmex sp. B	
Cardiocondyla emery		Camponotus sp. A		Pheidole sp. 15		Camponotos trapezoideus	
Cephalotes atratus		Camponotus sp. B		Pheidole sp. 17		Camponotus atriceps	
Cephalotes grandinosus		Camponotus sp. D		Pheidole sp. 2		Camponotus cingulatus	
Cephalotes minutus		Camponotus sp. H		Pheidole sp. 20		Camponotus genatus	
Cephalotes sp. 1		Nylanderia pr. fulva		Pheidole sp. 4		Camponotus punctulatus	
Crematogaster sp. A		Nylanderia sp. A		Pheidole sp. 6		Camponotus rufipes	
Crematogaster sp. C		**Myrmicinae**	55	Pheidole sp. 9		Camponotus sericeiventris	
Crematogaster sp. E		Acromyrmex sp. B		Pyramica cf. eggersi		Camponotus sp. 1-coleção	
Hylomyrma sp. A		Acromyrmex sp. C		Sericomyrmex sp. 1-coleção		Camponotus sp. 7-coleção	
Pheidole sp. 1		Acromyrmex sp. D		Solenopsis geminata-conf		Camponotus sp. A	
Pheidole sp. 10		Atta sexdens		Solenopsis sp. 1		Camponotus sp. B	
Pheidole sp. 14		Carebara urichi		Solenopsis sp. 4		Camponotus sp. C	
Pheidole sp. 2		Cephalotes pusillus		Solenopsis sp. 5		Camponotus sp. D	
Pheidole sp. 6		Crematogaster sp. B		Solenopsis sp. 6		Camponotus sp. H	
Pheidole sp.7		Crematogaster sp. C		Solenopsis sp. 7		Camponotus trapezoideus	
Solenopsis geminata-conf		Crematogaster sp. E		Solenopsis sp. 9		Myrmelachista sp. A	
Solenopsis sp. 1		Crematogaster sp. F		Wasmannia auropunctata		Nylanderia pr. fulva	
Solenopsis sp. 3		Crematogaster sp. I		Wasmannia sp. 3		Nylanderia sp. A	
Solenopsis sp. 4		Cyphomyrmex sp. 1-coleção		**Ponerinae**	7	**Myrmicinae**	70

A2 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Biome	#spp.
Myrmicinae		**Myrmicinae**		**Ponerinae**		**Myrmicinae**	
Solenopsis sp. 5		Cyphomyrmex sp. 2-coleção		Hypoponera cf. opacipes		Acromyrmex sp. B	
Solenopsis sp. 6		Cyphomyrmex sp. B		Hypoponera sp. 2-coleção		Acromyrmex sp. C	
Solenopsis sp. 7		Hylomyrma reitteri		Odontomachus chelifer		Acromyrmex sp. D	
Solenosis sp. 1		Megalomyrmex sp. A		Odontomachus meinerti		Atta sexdens	
Tetramorium sp. A		Megalomyrmex sp. B		Pachycodyla venusta		Cardiocondyla emery	
Wasmannia auropunctata		Megalomyrmex sp. C		Pachycondyla harpax		Carebara sp. A	
Ponerinae	5	Monomorium pharaonis		Pachycondyla verenae		Carebara urichi	
Pachycondyla sp. 4		Mycetosoritis sp. A				Centromyrmex cf. alfaroi	
Pachycondyla sp. 4		Mycocepurus sp. C				Cephalotes atratus	
Pachycondyla venusta		Octostruma sp. A				Cephalotes grandinosus	
Pachycondyla verenae		Pheidole sp. 8				Cephalotes minutus	
Pachycondyla villosa		Pheidole sp. 1				Cephalotes pusillus	
Pseudomyrmecinae	3	Pheidole sp. 10				Cephalotes sp. 1	
Pseudomyrmex elongatus		Pheidole sp. 13				Crematogaster sp. A	
Pseudomyrmex gracilis		Pheidole sp. 14				Crematogaster sp. B	
Pseudomyrmex pisinnus		Pheidole sp. 15				Crematogaster sp. C	
		Pheidole sp. 17				Crematogaster sp. E	
		Pheidole sp. 18				Crematogaster sp. F	
		Pheidole sp. 19				Crematogaster sp. I	
		Pheidole sp. 2				Cyphomyrmex sp. 1-coleção	
		Pheidole sp. 20				Cyphomyrmex sp. 2-coleção	
		Pheidole sp. 21				Cyphomyrmex sp. A	
		Pheidole sp. 22				Cyphomyrmex sp. B	
		Pheidole sp. 3				Hylomyrma reitteri	
		Pheidole sp. 4				Hylomyrma sp. A	

A2 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Biome	#spp.
		Myrmicinae				**Myrmicinae**	
		Pheidole sp. 5				Megalomyrmex sp. A	
		Pheidole sp. 6				Megalomyrmex sp. B	
		Pheidole sp. 7				Megalomyrmex sp. C	
		Pheidole sp. 9				Monomorium pharaonis	
		Pyramica cf. eggersi				Mycetosoritis sp. A	
		Rogeria sp. 2-coleção				Mycocepurus sp. C	
		Sericomyrmex sp. 1-coleção				Octostruma pr. stenognatha	
		Solenopsis geminata-conf				Octostruma sp. A	
		Solenopsis sp. 1				Pheidole sp. 6	
		Solenopsis sp. 3				Pheidole sp. 8	
		Solenopsis sp. 4				Pheidole sp. 1	
		Solenopsis sp. 5				Pheidole sp. 10	
		Solenopsis sp. 6				Pheidole sp. 13	
		Solenopsis sp. 7				Pheidole sp. 14	
		Wasmannia auropuncatata				Pheidole sp. 15	
		Wasmannia sp. 1				Pheidole sp. 17	
		Wasmannia sp. 2				Pheidole sp. 18	
		Wasmannia sp. 3				Pheidole sp. 19	
		Ponerinae	14			Pheidole sp. 2	
		Anochetus cf. oriens				Pheidole sp. 20	
		Centromyrmex cf. alfaroi				Pheidole sp. 21	
		Dinoponera lucida				Pheidole sp. 22	
		Hypoponera cf. foreli				Pheidole sp. 3	
		Hypoponera sp. 2-coleção				Pheidole sp. 4	
		Hypoponera sp. C				Pheidole sp. 5	

A2 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Biome	#spp.
		Ponerinae				**Myrmicinae**	
		Leptogenys sp. A				Pheidole sp. 6	
		Odontomachus chelifer				Pheidole sp. 7	
		Odontomachus meinerti				Pheidole sp. 9	
		Pachycondyla apicalis				Pyramica cf. eggersi	
		Pachycondyla harpax				Rogeria sp. 2-coleção	
		Pachycondyla venusta				Sericomyrmex sp. 1-coleção	
		Pachycondyla verenae				Solenopsis geminata-conf	
		Pachycondyla villosa				Solenopsis sp. 1	
		Pseudomyrmecinae	2			Solenopsis sp. 3	
		Pseudomyrmex pisinnus				Solenopsis sp. 4	
		Pseudomyrmex tenuis				Solenopsis sp. 5	
						Solenopsis sp. 6	
						Solenopsis sp. 7	
						Solenopsis sp. 9	
						Solenosis sp. 1	
						Tetramorium sp. A	
						Wasmannia auropuncatata	
						Wasmannia sp. 1	
						Wasmannia sp. 2	
						Wasmannia sp. 3	
						Ponerinae	16
						Anochetus cf. oriens	
						Dinoponera lucida	
						Hypoponera cf. foreli	
						Hypoponera cf. opacipes	

A2 - Continue

Arboreal ants	#spp.	Epigaeic ants	#spp.	Hypogaeic ants	#spp.	Biome	#spp.
						Ponerinae	
						Hypoponera sp. 2-coleção	
						Hypoponera sp. C	
						Leptogenys sp. A	
						Odontomachus chelifer	
						Odontomachus meinerti	
						Pachycodyla venusta	
						Pachycondyla apicalis	
						Pachycondyla harpax	
						Pachycondyla sp. 4	
						Pachycondyla venusta	
						Pachycondyla verenae	
						Pachycondyla villosa	
						Pseudomyrmecinae	4
						Pseudomyrmex elongatus	
						Pseudomyrmex gracilis	
						Pseudomyrmex pisinnus	
						Pseudomyrmex tenuis	
	58		**103**		**49**		**133**

Appendix material A3. – Ant species sampled in *Cerrado* biome in Brazil. Species list for three ant microhabitats: arboreal, epigaeic and hypogaeic. #spp = Number of ant species. Biome = The sum of single ant species sampled in all biome considering the three microhabitats.

Arboreal ant	#spp.	Epigaeic ant	#spp.	Hypogaeic ant	#spp.	Biome	#spp.
Dolichoderinae	6	**Dolichoderinae**	14	**Dolichoderinae**	2	**Dolichoderinae**	15
Azteca instabilis		Azteca sp. A		Linepithema pr. cerradense		Azteca instabilis	
Linepithema cf. aztecoides		Dorymyrmex sp. 1-coleção		Linepithema sp. B		Azteca sp. A	
Linepithema pr. cerradense		Dorymyrmex sp. B		**Ecitoninae**	4	Dorymyrmex sp. 1-coleção	
Linepithema sp. B		Dorymyrmex sp. C		Labidus coecus		Dorymyrmex sp. B	
Linepithema sp. G		Forelius sp. A		Labidus sp. A		Dorymyrmex sp. C	
Tapinoma sp. C		Linepithema cf. aztecoides		Labidus sp. B		Linepithema cf. aztecoides	
Ectatomminae	1	Linepithema pr. cerradense		Nomamyrmex sp. A		Linepithema pr. cerradense	
Ectatomma sp. B		Linepithema sp. B		**Ectatomminae**	5	Linepithema sp. B	
Formicinae	22	Linepithema sp. F		Ectatomma edentatum		Linepithema sp. F	
Brachymyrmex sp. 1-coleção		Linepithema sp. G		Ectatomma permagnum		Linepithema sp. G	
Camponotus atriceps		Linepithema sp. H		Ectatomma planidens		Linepithema sp. H	
Camponotus blandus		Linepithema sp. I		Ectatomma sp. B		Linepithema sp. I	
Camponotus cingulatus		Linepithema sp. J		Gnamptogenys striatula		Linepithema sp. J	
Camponotus crassus		Tapinoma sp. C		**Formicinae**	8	Tapinoma sp. C	
Camponotus genatus		**Ecitoninae**	3	Brachymyrmex pr. depilis		Forelius sp. A	
Camponotus melanoticus		Labidus coecus		Brachymyrmex sp. 1-coleção		**Ecitoninae**	5
Camponotus punctulatus		Labidus praedator		Bracymyrmex sp. B		Labidus coecus	
Camponotus rufipes		Nomamyrmex sp. A		Camponotos trapezoideus		Labidus praedator	
Camponotus sericeiventris		**Ectatomminae**	9	Camponotus cingulatus		Labidus sp. A	
Camponotus sp. A		Ectatomma brunneum		Camponotus genatus		Labidus sp. B	
Camponotus sp. B		Ectatomma edentatum		Camponotus sp. E		Nomamyrmex sp. A	
Camponotus sp. F		Ectatomma muticum		Nylanderia sp. A		**Ectatomminae**	9
Camponotus sp. G		Ectatomma opaciventre		**Myrmicinae**	30	Ectatomma brunneum	

A3 – Continue

Arboreal ant	#spp.	Epigaeic ant	#spp.	Hypogaeic ant	#spp.	Biome	#spp.
Formicinae		**Ectatomminae**		**Myrmicinae**		**Ectatomminae**	
Camponotus sp. J		Ectatomma permagnum		Atta sexdens		Ectatomma edentatum	
Camponotus sp. L		Ectatomma planidens		Carebara sp. B		Ectatomma muticum	
Camponotus sp. M		Ectatomma sp. A		Carebara urichi		Ectatomma opaciventre	
Camponotus sp. O		Ectatomma sp. B		Cephalotes pusillus		Ectatomma permagnum	
Camponotus sp.1-coleção		Gnamptogenys striatula		Crematogaster sp. D		Ectatomma planidens	
Camponotus trapezoideus		**Formicinae**	27	Monomorium sp. A		Ectatomma sp. A	
Camponotus vittatus		Brachymyrmex pr. depilis		Mycocepurus goeldii		Ectatomma sp. B	
Nylanderia pr. fulva		Brachymyrmex sp. 1-coleção		Mycocepurus sp. A		Gnamptogenys striatula	
Myrmicinae	29	Bracymyrmex sp. B		Mycocepurus sp. B		**Formicinae**	34
Carebara sp. D		Camponotos trapezoideus		Pheidole sp. 30		Brachymyrmex pr. depilis	
Cephalotes atratus		Camponotus arboreus		Pheidole sp. 1		Brachymyrmex sp. 1-coleção	
Cephalotes betoi		Camponotus atriceps		Pheidole sp. 11		Bracymyrmex sp. B	
Cephalotes depressus		Camponotus blandus		Pheidole sp. 14		Camponotos trapezoideus	
Cephalotes grandinosus		Camponotus cingulatus		Pheidole sp. 15		Camponotos trapezoideus	
Cephalotes pusillus		Camponotus crassus		Pheidole sp. 2		Camponotus arboreus	
Crematogaster sp. D		Camponotus genatus		Pheidole sp. 24		Camponotus atriceps	
Crematogaster sp. G		Camponotus leydigi		Pheidole sp. 25		Camponotus blandus	
Crematogaster sp. H		Camponotus melanoticus		Pheidole sp. 26		Camponotus cingulatus	
Crematogaster sp. K		Camponotus punctulatus		Pheidole sp. 6		Camponotus crassus	
Monomorium sp. A		Camponotus rufipes		Pheidole sp. 9		Camponotus genatus	
Mycocepurus goeldii		Camponotus sericeiventris		Solenopsis geminata-conf		Camponotus leydigi	
Nesomyrmex sp. A		Camponotus sp. 1-coleção		Solenopsis sp. 1		Camponotus melanoticus	
Pheidole sp. 1		Camponotus sp. 8-Coleção		Solenopsis sp. 2		Camponotus punctulatus	
Pheidole sp. 12		Camponotus sp. A		Solenopsis sp. 3		Camponotus rufipes	
Pheidole sp. 2		Camponotus sp. B		Solenopsis sp. 4		Camponotus sericeiventris	

A3 – Continue

Arboreal ant	#spp.	Epigaeic ant	#spp.	Hypogaeic ant	#spp.	Biome	#spp.
Myrmicinae		**Formicinae**		**Myrmicinae**		**Formicinae**	
Pheidole sp. 31		Camponotus sp. E		Solenopsis sp. 5		Camponotus sp. 1-coleção	
Pheidole sp. 6		Camponotus sp. F		Solenopsis sp. 6		Camponotus sp. 8-Coleção	
Pheidole sp. 7		Camponotus sp. K		Solenopsis sp. 7		Camponotus sp. A	
Pheidole sp. 9		Camponotus sp. L		Tranopelta sp. A		Camponotus sp. B	
Solenopsis geminata-conf		Camponotus sp. N		Wasmannia affinis		Camponotus sp. E	
Solenopsis sp. 1		Camponotus vittatus		**Ponerinae**	5	Camponotus sp. F	
Solenopsis sp. 2		Nylanderia pr. fulva		Dinoponera australis		Camponotus sp. G	
Solenopsis sp. 3		Nylanderia sp. A		Hypoponera sp. A		Camponotus sp. J	
Solenopsis sp. 4		**Myrmicinae**	71	Pachycondyla harpax		Camponotus sp. K	
Solenopsis sp. 6		Acromyrmex sp. A		Pachycondyla venusta		Camponotus sp. L	
Solenopsis sp. 7		Acromyrmex sp. D		Pachycondyla verenae		Camponotus sp. M	
Trachymyrmex sp. D		Acromyrmex sp. E				Camponotus sp. N	
Tranopelta sp. A		Acromyrmex sp. F				Camponotus sp. O	
Ponerinae	2	Apterostigma jubatum				Camponotus sp.1-coleção	
Pachycondyla striata		Apterostigma sp. A				Camponotus trapezoideus	
Pachycondyla villosa		Apterostigma sp. B				Camponotus vittatus	
Pseudomyrmecinae	5	Atta sexdens				Nylanderia pr. fulva	
Pseudomyrmex cubaensis		Blepharidata conops				Nylanderia sp. A	
Pseudomyrmex elongatus		Cardiocondyla emery				**Myrmicinae**	84
Pseudomyrmex gracilis		Carebara sp. C				Acromyrmex sp. A	
Pseudomyrmex sp. A		Carebara sp. E				Acromyrmex sp. D	
Pseudomyrmex tenuis		Carebara urichi				Acromyrmex sp. E	
		Cephalotes pusillus				Acromyrmex sp. F	
		Crematogaster abstinens				Apterostigma jubatum	
		Crematogaster sp. D				Apterostigma sp. A	

A3 – Continue

Arboreal ant	#spp.	Epigaeic ant	#spp.	Hypogaeic ant	#spp.	Biome	#spp.
		Myrmicinae				**Myrmicinae**	
		Crematogaster sp. H				Apterostigma sp. B	
		Crematogaster sp. J				Atta sexdens	
		Cyphomyrmex sp. C				Blepharidata conops	
		Cyphomyrmex sp. D				Cardiocondyla emery	
		Monomrium sp. A				Carebara sp. B	
		Mycocepurus sp. B				Carebara sp. C	
		Mycocepurus sp. C				Carebara sp. D	
		Hylomyrma reitteri				Carebara sp. E	
		Hylomyrma sp. B				Carebara urichi	
		Pheidole sp. 30				Cephalotes atratus	
		Pheidole sp. 6				Cephalotes betoi	
		Pheidole sp. 1				Cephalotes depressus	
		Pheidole sp. 11				Cephalotes grandinosus	
		Pheidole sp. 12				Cephalotes pusillus	
		Pheidole sp. 14				Crematogaster abstinens	
		Pheidole sp. 2				Crematogaster sp. D	
		Pheidole sp. 23				Crematogaster sp. G	
		Pheidole sp. 24				Crematogaster sp. H	
		Pheidole sp. 25				Crematogaster sp. J	
		Pheidole sp. 26				Crematogaster sp. K	
		Pheidole sp. 28				Cyphomyrmex sp. C	
		Pheidole sp. 3				Cyphomyrmex sp. D	
		Pheidole sp. 31				Hylomyrma reitteri	
		Pheidole sp. 4				Hylomyrma sp. B	
		Pheidole sp. 5				Monomorium sp. A	

A3 – Continue

Arboreal ant	#spp.	Epigaeic ant	#spp.	Hypogaeic ant	#spp.	Biome	#spp.
		Myrmicinae				**Myrmicinae**	
		Pheidole sp. 6				Mycocepurus goeldii	
		Pheidole sp. 7				Mycocepurus sp. A	
		Pheidole sp. 9				Mycocepurus sp. B	
		Solenopsis geminata-conf				Mycocepurus sp. C	
		Solenopsis sp. 1				Nesomyrmex sp. A	
		Solenopsis sp. 2				Pheidole sp. 30	
		Solenopsis sp. 4				Pheidole sp. 6	
		Solenopsis sp. 5				Pheidole sp. 1	
		Solenopsis sp. 6				Pheidole sp. 11	
		Solenopsis sp. 7				Pheidole sp. 12	
		Wasmannia auropunctata				Pheidole sp. 14	
		Wasmannia affinis				Pheidole sp. 15	
		Wasmannia sp. 5				Pheidole sp. 2	
		Trachymyrmex sp. A				Pheidole sp. 23	
		Trachymyrmex sp. B				Pheidole sp. 24	
		Trachymyrmex sp. C				Pheidole sp. 25	
		Trachymyrmex sp. D				Pheidole sp. 26	
		Trachymyrmex sp. E				Pheidole sp. 28	
		Trachymyrmex sp. F				Pheidole sp. 3	
		Trachymyrmex sp. G				Pheidole sp. 31	
		Trachymyrmex sp. H				Pheidole sp. 4	
		Trachymyrmex sp. I				Pheidole sp. 5	
		Trachymyrmex sp. J				Pheidole sp. 6	
		Trachymyrmex sp. L				Pheidole sp. 7	
		Trachymyrmex sp. M				Pheidole sp. 9	

A3 – Continue

Arboreal ant	#spp.	Epigaeic ant	#spp.	Hypogaeic ant	#spp.	Biome	#spp.
		Myrmicinae				**Myrmicinae**	
		Trachymyrmex sp. N				Sericomyrmex sp. A	
		Sericomyrmex sp. 1-coleção				Sericomyrmex sp. B	
		Sericomyrmex sp. A				Solenopsis geminata-conf	
		Sericomyrmex sp. B				Solenopsis sp. 1	
		Tranopelta sp. A				Solenopsis sp. 2	
		Ponerinae	7			Solenopsis sp. 3	
		Dinoponera australis				Solenopsis sp. 4	
		Hypoponera cf. opacipes				Solenopsis sp. 5	
		Odontomachus bauri				Solenopsis sp. 6	
		Odontomachus chelifer				Solenopsis sp. 7	
		Pachycondyla harpax				Trachymyrmex sp. A	
		Pachycondyla verenae				Trachymyrmex sp. B	
		Pachycondyla villosa				Trachymyrmex sp. C	
		Pseudomyrmecinae	2			Trachymyrmex sp. D	
		Pseudomyrmex cubaensis				Trachymyrmex sp. E	
		Pseudomyrmex tenuis				Trachymyrmex sp. F	
						Trachymyrmex sp. G	
						Trachymyrmex sp. H	
						Trachymyrmex sp. I	
						Trachymyrmex sp. J	
						Trachymyrmex sp. L	
						Trachymyrmex sp. M	
						Trachymyrmex sp. N	
						Tranopelta sp. A	
						Wasmannia affinis	

A3 – Continue

Arboreal ant	#spp.	Epigaeic ant	#spp.	Hypogaeic ant	#spp.	Biome	#spp.
						Myrmicinae	
						Wasmannia auropunctata	
						Wasmannia sp. 5	
						Ponerinae	10
						Dinoponera australis	
						Hypoponera cf. opacipes	
						Hypoponera sp. A	
						Odontomachus bauri	
						Odontomachus chelifer	
						Pachycondyla harpax	
						Pachycondyla striata	
						Pachycondyla venusta	
						Pachycondyla verenae	
						Pachycondyla villosa	
						Pseudomyrmecinae	5
						Pseudomyrmex cubaensis	
						Pseudomyrmex elongatus	
						Pseudomyrmex gracilis	
						Pseudomyrmex sp. A	
						Pseudomyrmex tenuis	
Total	**65**		**133**		**54**		**162**

Appendix material A4. – An14.02t species sampled in tropical rainforest and savanna habitats in Indonesia. #spp = Number of ant species. Total ants = The sum of single ant species considering the two habitat types.

Tropical rainforest	**#spp**	**Savanna**	**#spp**	**Total ants**	**#spp**
Dolichoderinae	6	**Aenictinae**	1	**Aenictinae**	1
Dolichoderus sp. 1		Aenictus sp. 1		Aenictus sp. 1	
Philidris sp. 1		**Cerapachyinae**	1	**Cerapachyinae**	1
Philidris sp. 2		Cerapachys sp. 1		Cerapachys sp. 1	
Tapinoma sp. 1		**Dolichoderinae**	6	**Dolichoderinae**	11
Technomyrmex sp. 1		Dolichoderus sp. 1		Dolichoderus sp. 1	
Technomyrmex sp. 2		Iridomyrmex sp. 1		Iridomyrmex sp. 1	
Formicinae	14	Iridomyrmex sp. 2		Iridomyrmex sp. 2	
Anoplolepis gracilipes		Iridomyrmex sp. 3		Iridomyrmex sp. 3	
Camponotus gigas		Tapinoma sp. 2		Philidris sp. 1	
Camponotus sp. 1		Tapinoma sp. 3		Philidris sp. 2	
Camponotus sp. 2		**Formicinae**	16	Tapinoma sp. 1	
Nylanderia sp. 1		Anoplolepis gracilipes		Tapinoma sp. 2	
Nylanderia sp. 2		Camponotus sp. 5		Tapinoma sp. 3	
Nylanderia sp. 3		Camponotus sp. 1		Technomyrmex sp. 1	
Nylanderia sp. 4		Camponotus sp. 2		Technomyrmex sp. 2	
Nylanderia sp. 5		Camponotus sp. 3		**Formicinae**	26
Nylanderia sp. 6		Camponotus sp. 4		Anoplolepis gracilipes	
Oecophylla smaragdina		Camponotus sp. 5		Camponotus sp. 5	
Polyrachis abdominalis		Nylanderia sp. 1		Camponotus gigas	
Polyrachis sp. 2		Nylanderia sp. 7		Camponotus sp. 1	
Plagiolepis sp. 1		Paratrechina sp. 1		Camponotus sp. 2	
Mymicinae	42	Polyrhachis sp. 3		Camponotus sp. 3	
Acanthomyrmex sp. 1		Polyrhachis sp. 4		Camponotus sp. 4	
Aphaenogaster sp. 1		Polyrhachis sp. 5		Camponotus sp. 5	
Aphaenogaster sp. 2		Polyrhachis sp. 7		Nylanderia sp. 1	
Aphaenogaster sp. 3		Polyrhachis sp. 8		Nylanderia sp. 2	
Aphaenogaster sp. 4		Polyrhachis sp. 6		Nylanderia sp. 3	
Aphaenogaster sp. 6		**Mymicinae**	25	Nylanderia sp. 4	
Cataulacus sp. 1		Cardiocondyla sp. 1		Nylanderia sp. 5	
Crematogaster sp. 1		Cardiocondyla sp. 2		Nylanderia sp. 6	
Lophomyrmex sp. 1		Crematogaster sp. 2		Nylanderia sp. 7	
Monomorium floricola		Crematogaster sp. 3		Oecophylla smaragdina	
Monomorium sp. 1		Meranoplus bicolor		Paratrechina sp. 1	
Monomorium sp. 2		Monomorium sp. 5		Plagiolepis sp. 1	
Monomorium sp. 3		Monomorium sp. 6		Polyrachis abdominalis	
Monomorium sp. 4		Monomorium sp. 7		Polyrachis sp. 2	
Myrmicaria brunnea		Monomorium sp. 8		Polyrhachis sp. 3	
Oligomyrmex sp. 1		Pheidole sp. 10		Polyrhachis sp. 4	
Oligomyrmex sp. 2		Pheidole sp. 11		Polyrhachis sp. 5	
Oligomyrmex sp. 3		Pheidole sp. 12		Polyrhachis sp. 6	

A4 - Continue

Tropical rainforest	#spp	Savanna	#spp	Total ants	#spp
Mymicinae		**Mymicinae**		**Formicinae**	
Pheidoe sp. 4		Pheidole sp. 5		Polyrhachis sp. 7	
Pheidole sp. 8		Pheidole sp. 9		Polyrhachis sp. 8	
Pheidole sp. 1		Pheidologeton sp. 2		**Mymicinae**	62
Pheidole sp. 10		Pheidologeton sp. 6		Acanthomyrmex sp. 1	
Pheidole sp. 2		Solenopsis sp. 1		Aphaenogaster sp. 1	
Pheidole sp. 3		Solenopsis sp. 2		Aphaenogaster sp. 2	
Pheidole sp. 4		Tetramorium sp. 8		Aphaenogaster sp. 3	
Pheidole sp. 5		Tetramorium sp. 10		Aphaenogaster sp. 4	
Pheidole sp. 6		Tetramorium sp. 5		Aphaenogaster sp. 6	
Pheidole sp. 7		Tetramorium sp. 6		Cardiocondyla sp. 1	
Pheidole sp. 8		Tetramorium sp. 7		Cardiocondyla sp. 2	
Pheidole sp. 9		Tetramorium sp. 11		Cataulacus sp. 1	
Pheidologeton sp. 1		Tetramorium sp. 9		Crematogaster sp. 1	
Pheidologeton sp. 2		**Ponerinae**	9	Crematogaster sp. 2	
Pheidologeton sp. 3		Anochetus sp. 1		Crematogaster sp. 3	
Pheidologeton sp. 4		Diacamma sp. 2		Lophomyrmex sp. 1	
Pheidologeton sp. 5		Diacamma sp. 3		Meranoplus bicolor	
Proatta butteli		Leptogenys sp. 3		Monomorium floricola	
Solenopsis sp. 1		Odontomachus sp. 3		Monomorium sp. 1	
Strumigenys sp.1		Odontoponera denticulata		Monomorium sp. 2	
Tetramorium sp. 1		Odontoponera sp. 4		Monomorium sp. 3	
Tetramorium sp. 2		Odontoponera transversa		Monomorium sp. 4	
Tetramorium sp. 3		Pachycondyla sp. 3		Monomorium sp. 5	
Tetramorium sp. 4				Monomorium sp. 6	
Ponerinae	14			Monomorium sp. 7	
Diacamma sp. 1				Monomorium sp. 8	
Diacamma sp. 2				Myrmicaria brunnea	
Odontomachus sp. 1				Oligomyrmex sp. 1	
Odontomachus sp. 2				Oligomyrmex sp. 2	
Odontoponera denticulata				Oligomyrmex sp. 3	
Odontoponera sp. 3				Pheidoe sp. 4	
Odontoponera transversa				Pheidole sp. 8	
Hypoponera sp. 1				Pheidole sp. 1	
Leptogenys sp. 2				Pheidole sp. 10	
Leptogenys sp.1				Pheidole sp. 11	
Pachycondyla sp. 1				Pheidole sp. 12	
Pachycondyla sp. 2				Pheidole sp. 2	
Pachycondyla sp. 3				Pheidole sp. 3	
Pachycondyla sp. 4				Pheidole sp. 4	
				Pheidole sp. 5	
				Pheidole sp. 6	
				Pheidole sp. 7	
				Pheidole sp. 8	

A4 - Continue

Tropical rainforest	#spp	Savanna	#spp	Total ants	#spp
				Mymicinae	
				Pheidole sp. 9	
				Pheidologeton sp. 1	
				Pheidologeton sp. 2	
				Pheidologeton sp. 3	
				Pheidologeton sp. 4	
				Pheidologeton sp. 5	
				Pheidologeton sp. 6	
				Proatta butteli	
				Solenopsis sp. 1	
				Solenopsis sp. 2	
				Strumigenys sp.1	
				Tetramorium sp. 8	
				Tetramorium sp. 1	
				Tetramorium sp. 10	
				Tetramorium sp. 11	
				Tetramorium sp. 2	
				Tetramorium sp. 3	
				Tetramorium sp. 4	
				Tetramorium sp. 5	
				Tetramorium sp. 6	
				Tetramorium sp. 7	
				Tetramorium sp. 9	
				Ponerinae	19
				Anochetus sp. 1	
				Diacamma sp. 1	
				Diacamma sp. 2	
				Diacamma sp. 3	
				Hypoponera sp. 1	
				Leptogenys sp. 2	
				Leptogenys sp. 3	
				Leptogenys sp.1	
				Odontomachus sp. 1	
				Odontomachus sp. 2	
				Odontomachus sp. 3	
				Odontoponera denticulata	
				Odontoponera sp. 3	
				Odontoponera sp. 4	
				Odontoponera transversa	
				Pachycondyla sp. 1	
				Pachycondyla sp. 2	
				Pachycondyla sp. 3	
				Pachycondyla sp. 4	
Tropical rainforest	76	**Savanna**	58	**Total ants**	120