UNIVERSIDADE FEDERAL DE MINAS GERAIS

Instituto de Ciências Biológicas

Programa de Pós-Graduação em Ecologia, Conservação e Manejo da Vida Silvestre

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TESE DE DOUTORADO

PADRÕES E MECANISMOS ESTRUTURADORES DA DIVERSIDADE TAXONÔMICA E FUNCIONAL DE COMUNIDADES DE FORMIGAS NA CADEIA DO ESPINHAÇO

FLÁVIO SIQUEIRA DE CASTRO

BELO HORIZONTE

2019

Flávio Siqueira de Castro

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Orientador: Dr. Frederico de Siqueira Neves

Co-orientadores: Dr. Ricardo Ribeiro de Castro Solar e Dr. Pedro Giovâni da Silva

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043 Castro, Flávio Siqueira de.
Padrões e mecanismos estruturadores da diversidade taxonômica e funcional de comunidades de formigas na Cadeia do Espinhaço [manuscrito] / Flávio Siqueira de Castro. – 2019.
159 f. : il. ; 29,5 cm.

Orientador: Dr. Frederico de Siqueira Neves. Co-orientadores: Dr. Ricardo Ribeiro de Castro Solar e Dr. Pedro Giovâni da Silva.
Tese (doutorado) – Universidade Federal de Minas Gerais, Instituto de Ciências Biológicas. Programa de Pós-Graduação em Ecologia, Conservação e Manejo da Vida Silvestre.

1. Ecologia. 2. Formigas. 3. Biodiversidade. 4. Campo rupestre. 5. Serra do Cipó. I. Neves, Frederico de Siqueira. II. Solar, Ricardo Ribeiro de Castro. III. Silva, Pedro Giovâni da. IV. Universidade Federal de Minas Gerais. Instituto de Ciências Biológicas. V. Título.

Ficha e laborada pela Biblioteca do Instituto de Ciências Biológias da UFMG CDU: 502.7
Ficha elaborada pela Biblioteca do Instituto de Ciências Biológias da UFMG

Ficha catalográfica elaborada por Fabiane Cristielle M. Reis – CRB: 6/2680

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Ata da Defesa de Tese

N° 193
Entrada: 2015/2

Flávio Siqueira de Castro

No dia 20 de dezembro de 2019, às 14:00 horas, na sala 236, bloco I3 do Instituto de Ciências Biológicas da Universidade Federal de Minas Gerais, teve lugar a defesa de tese de doutorado no Programa de Pós-Graduação em Ecologia, Conservação e Manejo da Vida Silvestre, de autoria do(a) doutorando(a) Flávio Siqueira de Castro, intitulada: "**PADRÕES E MECANISMOS ESTRUTURADORES DA DIVERSIDADE TAXONÔMICA E FUNCIONAL DE COMUNIDADES DE FORMIGAS NA CADEIA DO ESPINHAÇO**". Abrindo a sessão, o(a) orientador(a) e Presidente da Comissão, Doutor(a) Frederico de Siqueira Neves, após dar a conhecer aos presentes o teor das normas regulamentares do trabalho final, passou a palavra para o(a) candidato(a) para apresentação de seu trabalho. Estiveram presentes a Banca Examinadora composta pelos Doutores: Fernando Augusto de Oliveira e Silveira (UFMG), Danilo Rafael Mesquita Neves (UFMG), Ricardo Ildefonso de Campos (UFV), Lucas Navarro Paolucci (UFLA) e demais convidados. Seguiu-se a arguição pelos examinadores, com a respectiva defesa do(a) candidato(a). Após a arguição, apenas os senhores examinadores permaneceram no recinto para avaliação e deliberação acerca do resultado final, sendo a decisão da banca pela:

☑Aprovação da tese, com eventuais correções mínimas e entrega de versão final pelo orientador diretamente à Secretaria do Programa, no prazo máximo de 30 dias;
☐Reavaliação da tese com avaliação pelos membros da banca do documento revisado, sem nova defesa, no prazo máximo de 30 dias, sob possibilidade de reprovação;
☐Reformulação da tese com indicação de nova defesa em data estabelecida a critério do Colegiado em observância às Normas Gerais da Pós-graduação na UFMG a ao Regimento do PPG-ECMVS;
☐Reprovação

A banca indica esta tese aos Prêmios CAPES e UFMG de teses? ☐SIM ☒NÃO

Nada mais havendo a tratar, o Presidente da Comissão encerrou a reunião e lavrou a presente ata, que será assinada por todos os membros participantes da Comissão Examinadora.

Belo Horizonte, 20 de dezembro de 2019.

Comissão Examinadora	Assinatura
Doutor(a) Frederico de Siqueira Neves	
Doutor(a) Fernando Augusto de Oliveira e Silveira	
Doutor(a) Danilo Rafael Mesquita Neves	
Doutor(a) Ricardo Ildefonso de Campos	
Doutor(a) Lucas Navarro Paolucci	

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Tese defendida em 20 de dezembro de 2019 e aprovada pela banca examinadora constituída pelos membros:

Doutor(a) Fernando Augusto de Oliveira e Silveira

Doutor(a) Danilo Rafael Mesquita Neves

Doutor(a) Ricardo Ildefonso de Campos

Doutor(a) Lucas Navarro Paolucci

Doutor(a) Frederico de Siqueira Neves
(Presidente da Banca)

Sumário

Agradecimentos

Dedico o trabalho ao meu filho Lucas e minha família Siqueira de Castro. Ao meus pais José Carlos e Stellita, irmãos Rodrigo, Marcelo e Renata agradeço o amor e a parceria eterna. Às minhas cunhadas Lara e Taís, agradeço as horas de descontração em família e por me proporcionarem, junto com meus irmãos, o convívio com meus sobrinhos Lívia, Cauê e Lorena. Agradeço aos avós (*in memoriam*) e a todos Laender de Castro e Antunes de Siqueira por todos os momentos vividos! Agradeço especialmente tia Beth, que considero uma “mãedrinha”, e tio Claúdio, grande físico e pesquisador, o cara que sempre me incentivou a não desistir da ciência e, principalmente, do doutoramento.

Agradeço também aos meus amigos irmãos do Véritas, Gim, Cari, Leandro e Nepá! A todos do Churras Do Véritas e aos filhos da PUC Minas, Queroz, Geraldo, Dorinha, Dudu, Gabriel, Regis, e a todos integrantes do Pé de Cedro! Agradeço ao GSG (Grupo de discussão de Ecologia) e seus integrantes, por todas as discussões e artigos compartilhados durante o doutorado!

Agradeço ao meu orientador e amigo Dr. Frederico de Siqueira Neves. Obrigado pela amizade e por me ensinar, aprendi muito nesses quatro anos! E obrigado por sempre insistir para eu voltar para as formigas! Agradeço especialmente o Dr. Lucas Neves Perillo (repetindo suas palavras), “o sócio de tese”. Cheguei com o projeto em andamento e assumi a responsabilidade pelas comunidades de formigas. Foram mais de 50 dias de campo, 5 picos, cachaça, caminhadas, chuva e Aculeata pelas montanhas do Espinhaço, sempre subindo pra direção norte seguindo o Uno verde ou dentro dele. Valeu demais!

Aos coorientadores: ao Dr. Ricardo Solar, Bob, pela amizade, discussões e contribuições para a tese; ao Dr. Pedro Giovâni da Silva pela paciência, conversas, análises estatísticas, sugestões de literatura, escrita (no andamento e fechamento da tese) e pelo constante apoio e amizade.

Agradeço ao povo das cidades por onde passamos e aconteceram os projetos PELD e Espinhaço: as mineiras Belo Horizonte, Ouro Branco, Ouro Preto, Lavras Novas, Barão de Cocais, Catas Altas, Mariana, Santa Bárbara, Brumal, Cardeal Mota, Jaboticatubas, Itambé do Mato Dentro, Santana do Riacho, Lapinha, Serro, Santo Antônio do Itambé, Capivari, Diamantina, São Gonçalo do Rio Preto, Botumirim, Grão Mogol, Monte Azul, Formosa, Montezuma, Mamonas, Gameleiras, Espinosa, e as baianas Caetité, Abaíra, Catolés, Catolés de Cima, Rio de Contas, Brumadinho, Palmeiras, Capão, Mucugê, Pati, Ruínha, Brejo de Cima, Paiol, Jussiape e Guiné. Em todos esses lugares vivem pessoas do Espinhaço, o povo das montanhas. São eles que tornam cada uma dessas localidades únicas, além das paisagens e rica biodiversidade.

No projeto PELD (Capítulo 1), agradeço a Cedro Têxtil, ICMBio-PARNA Serra do Cipó, Pousada Serra Morena e Pouso do Elefante pelo suporte e logística. Agradeço ao pessoal da Reserva Vellozia, especialmente ao professor Dr. GW Fernandes, coordenador do projeto PELD e coautor no primeiro capítulo. Obrigado pela hospitalidade, conversas e contribuições para o trabalho. Agradeço aos amigos que sempre ajudaram em campo ou laboratório, especialmente Rayana Mello, Matheus Couto, Humberto Brant e Marina Catão. Agradeço ao Flávio Camarota e Scott Powel (*Cephalotes*), Alexandre Ferreira (*Pheidole*), Rodolfo Probst (*Camponotus*, *Myrmelachista* e *Octostruma*) e ao Mayron Escárraga (Dolichoderinae) pelas identificações das formigas. Agradeço ao Flávio Camarota, Lucas Perillo e Rafael Leitão por todos os valiosos comentários no manuscrito.

No projeto Espinhaço (Capítulo 2) agradeço algumas das pessoas que de alguma forma contribuíram no trabalho e para que ele acontecesse: Rodrigo Nescau e Laurinha (Montes Claros). Plínio, Vinicius, Lucas e Luiz (Porteirinha, P.E. Serra Nova). Ao Seo Zé Camilo (Alitôta), João (Dão), Marcos (Prego) e José Custódio Jorge, Alessandre Custódio Jorge, Gandú de Capivara, Chico de Mamonas no Pico da Formosa. À do Zé do Pilão e Dona Maria, Sinvaldo e Marli em Brumadinho (Pico das Almas). À Catarina e Ângela em Rio de Contas. Edmundo, Janho Barbosa de Azevedo, Sr. Antônio e Sr. Melquíades em Catolés (Pico do Barbado) e ao Dê em Guiné (Chapada Diamantina).

Agradeço aos amigos: Matteus Carvalho, que, depois de mim (além do Dr. Perillo e Dr. Fred Neves), foi o maior coletor do projeto (Bolo Doido foi em 4 picos!), Heron Hilário, Ivan Monteiro, Caio Marques, Arleu Viana, João Pedro (Jota), Daniela Melo, Luisa Azevedo, André Araújo, Núbia Campos, Frederico Neves, Humberto Brant, Rayana Melo e Jéssica Martins. Muito obrigado pela parceria!

Agradeço aos estagiários e integrantes do Laboratório de Ecologia de Insetos LEI (de 2013 aos dias atuais). Sem eles seria impossível processar tanto material: Caio Silveira, Thaís Tavares, Lucas Freitas, Lorenzzo Monteran, Bruna Vaz, Franklin Logan, Júlia Toffalini, Matheus Galvão, Isabella Villani, Laura Braga, Isa Mariah, Bruna Boa Sorte, Mellina Galantini, Maria Eliza Nogueira, Mariana Côrtes, Matheus Belchior, Poliana Gomes, Paola Mitraud, Daniel Vieira, Natalia Santoro, Ana Profeta, Ícaro, Catarina Dias e Bernardo (Museo). Aos amigos e parceiros de laboratório e projetos do lab e da UFMG Luiz Eduardo, Ludmila Hufnagel, Marina Beirão, Paloma Marques, Rodrigo Massara, Tadeu Guerra, Newton Barbosa, Ju Kuchenbecker, Matheus Couto (Jão), Amanda Dias, Fernando Pinho, Paulin, Leo Dias, Arleu Viana, Marcela, Ana Luiza, Vanessa Monteiro e Rayana Mello e à todos os outros integrantes da Villa Parentoni, da Varandinha e Grelo no Asfalto. Agradeço a todos os professores e colegas da ECMVS. Muitos aprendizados e excelente convívio. Obrigado Cris e Fred, secretaria do PPG-ECMVS, por tudo!

Agradeço ao Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) por financiar o projeto PELD-Campo Rupetre, Serra do Cipó, e a Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG) por financiar o projeto Espinhaço. Agradeço também a CAPES pela bolsa de doutorado.

Agradeço também minha banca de qualificação (Capítulo 1), composta pelos Dr. Milton Barbosa, Dr. Rafael Leitão e Dr. Flávio Camarota, além de Dr. Lucas Perillo como suplente.

E, finalizando, agradeço aos membros da banca examinadora, composta pelos professores: Dr. Fernando Silveira, Dr. Danilo Neves, Dr. Ricardo Campo e Dr. Lucas Paolucci, além dos suplentes Dr. Flávio Camarota e Dr. Milton Barbosa.

Resumo

Montanhas são modelos ideais para o estudo dos padrões e entendimento dos processos que determinam a distribuição das espécies no espaço-tempo. Apresentam condições ambientais extremas para a distribuição da biodiversidade, com comunidades restritas e alta diversidade taxonômica e funcional de espécies. Nesse sentido, utilizo as formigas encontradas nas montanhas da Cadeia do Espinhaço como objetos de estudo. A tese está dividida em dois capítulos. Tem como objetivo determinar os padrões taxonômicos e funcionais e os mecanismos estruturadores das comunidades de Formicidae em gradientes espaço-temporais ao longo da Cadeia do Espinhaço, em diferentes escalas espaciais. Além disso, investigar os aspectos biogeográficos dessas comunidades em campo rupestre e avaliar como comunidades de formigas respondem às diferentes variáveis ambientais. No primeiro capítulo, investigamos padrões de diversidade taxonômica e funcional (diversidades α e β) de formigas em uma paisagem montanhosa da Cadeia do Espinhaço (Serra do Cipó) e os mecanismos associados a esses padrões em diferentes dimensões espaço-temporais. No segundo capítulo, avaliamos os padrões de diversidade funcional das comunidades de formigas e atributos individuais das espécies (cor e tamanho do corpo) em uma extensiva amostragem no campo rupestre ao longo de 12 montanhas em diferentes elevações na Cadeia do Espinhaço. Verificamos quais são os efeitos das variáveis ambientais na estrutura funcional da diversidade das comunidades de formigas e em atributos individuais das espécies em montanhas antigas. Foram testadas três hipóteses macroecológicas associadas à variação clinal de cores do tegumento para verificar o papel da variação da cor do tegumento e do tamanho do corpo em um gradiente geoclimático tropical de elevação e latitude. Descobrimos que a variação da elevação e os efeitos das variáveis geoclimáticos do gradiente de elevação são mais importantes na estruturação das diversidades taxonômica e funcional de formigas do que a variação latitudinal e os efeitos de suas variáveis geoclimáticas.

Palavras chaves: Diversidade; Atributos Funcionais; Campo Rupestre; Formigas; Cadeia do espinhaço

Abstract

Mountains are considered ideal models for the study of patterns and understanding of the processes that determine species distribution in space-time., Exhibit extreme environmental conditions for biodiversity distribution, presenting restricted communities and high taxonomic and functional diversity of species. In this sense, I use the ants found in the mountains of the Espinhaço Range as objects of study. The thesis is divided into two chapters. The goal is to determine the taxonomic and functional patterns and structuring mechanisms of the Formicidae communities in spatiotemporal gradients along the Espinhaço Range, at different spatial scales. In addition, to elucidate biogeographic aspects of these communities in rupestrian field and evaluate how ant communities respond to different environmental variables. In the first chapter, we investigated patterns of taxonomic and functional diversity (α and β diversity) of ants in a mountainous landscape of the Espinhaço Range (Serra do Cipó) and the mechanisms associated with these patterns in different spatio-temporal dimensions. In the second chapter, we evaluated patterns of functional diversity of ant communities and individual species attributes (colour and body size) in an extensive rupestrian field sampling over 12 mountains at different elevations in the Espinhaço Range. We verified the effects of environmental variables on the functional structure of ant community diversity and individual species attributes in ancient mountains. Three macroecological hypotheses associated with clinal tegument colour variation were tested to verify the role of tegument colour and body size variation in a tropical geoclimatic gradient of elevation and latitude. We found that elevation variation and the effects of elevation gradient geoclimatic variables are more important in structuring the taxonomic and functional diversity of ants than latitudinal variation and the effects of their geoclimatic variables.

Keywords: Diversity;Traits; Campo Rupestre; Formigas; Cadeia do espinhaço

Introdução Geral

O entendimento e determinação dos padrões de diversidade, além dos processos envolvidos na estruturação das comunidades, estão entre as principais questões a serem respondidas na ecologia. A utilização de múltiplas escalas e métricas de biodiversidade em resposta aos processos ecológicos é fundamental para auxiliar na resolução dessas questões (Anderson *et al.*, 2011; Barton *et al.*, 2013; Tuomisto, 2010). A utilização das múltiplas escalas de diversidade proposta por Whittaker (1960) se mostra uma abordagem bem adequada para nos ajudar a elucidá-las, focando em padrões de diversidade β (uma medida da variabilidade da composição de espécies entre as amostras), evidenciando a dissimilaridade entre comunidades, ao relacionar tanto a diversidade de espécies na escala local (α) como a diversidade em larga escala (γ). Baselga (2010) trouxe uma abordagem mais focada em componentes da diversidade β (substituição e aninhamento), que pode ser aplicada tanto para a diversidade taxonômica (TD), representada pela riqueza e abundância das espécies, ou funcional (FD), relacionada às funções ecológicas de cada espécie (Baselga, 2013; Jost, 2007; Petchey & Gaston, 2006; Violle *et al.*, 2007).

Quando definimos os padrões de diversidade taxonômica consideramos que todas as espécies são diferentes umas das outras, mas desconsideramos que cada uma tem sua função ecológica (Villéger, Grenouillet, & Brosse, 2013). Para a diversidade funcional, os padrões refletem a variação dos atributos funcionais ou atributos funcionais (“traits”) entre as espécies da comunidade (Petchey & Gaston, 2006; Violle *et al.*, 2007). Atributos funcionais são características biológicas mensuráveis dos organismos em nível individual e que tem influência ou relação direta em suas performances (“fitness”) e funções ecológicas (Violle *et al.*, 2007). Analisando os padrões de diversidade com diferentes abordagens (e.g., TD e FD) podemos identificar os processos associados às origens e manutenção da biodiversidade e dos serviços prestados pelas diferentes comunidades ecológicas (Anderson *et al.*, 2011; Barton *et al.*, 2013). Dado o cenário atual de mudanças globais, elucidar os mecanismos que direcionam os padrões de distribuição da biodiversidade é essencial para orientar, por exemplo, futuras ações efetivas de conservação dos ambientes naturais (Cooke *et al.*, 2013; Lassau & Hochuli, 2004).

Gradientes ambientais, como gradientes latitudinais e de elevação, são excelentes modelos para entendermos os mecanismos envolvidos na estruturação da biodiversidade (Colwell *et al.*, 2008; Gaston, 2000; Janzen, 1967). No gradiente latitudinal, por exemplo, a riqueza de espécies em geral aumenta em baixas latitudes (Gaston, 2000), além de apresentarem variações nos padrões de diversidade funcional (Stevens *et al.*, 2003; Villéger *et al.*, 2013; Lamanna *et al.*, 2014). No entanto, cada latitude pode apresentar uma composição taxonômica diferente devido à variação nas condições ambientais, com padrões de redundância funcional ao longo do gradiente (Silva & Brandão, 2014) ou diminuição da riqueza funcional em direção às latitudes mais elevadas (Lamanna *et al.*, 2014). Além disso, exibem uma grande variação na riqueza de espécies e nas condições ambientais de uma localidade para outra (por exemplo, longitude e altitude), com uma variedade de topografias e condições climáticas do Sul para o Norte (Gaston, 2000).

Da mesma maneira, gradientes de elevação apresentam variação semelhante nos padrões de riqueza de espécies, com diminuição geral da riqueza de espécies devido ao aumento da elevação (Gaston, 2000; Peters *et al.*, 2016; Longino & Branstetter, 2019). Dessa forma, também é esperada uma menor riqueza funcional ou maior redundância funcional com o aumento da elevação (ver Bishop *et al.*, 2014; Tiede *et al.*, 2017). O filtro ambiental no topo das montanhas, devido à variação nas condições geoclimáticas (menores temperaturas, aumente da umidade, radiação solar, além da diminuição de área de ocupação pelas espécies), é uma força severa e seletiva para a ocorrência das espécies de insetos (Bishop *et al.*, 2014; Nunes *et al.*, 2016, 2017; Tiede *et al.*, 2017). Gradientes de elevação são espacialmente heterogêneos e por isso podem abrigar diferentes espécies, uma consequência direta do maior número de micro-habitat, abrigos e locais de forrageamento (Dunn *et al.*, 2010; Körner, 2007; Lessard *et al.*, 2007; Munyai & Foord, 2012). A compreensão de quais mecanismos e processos determinam a estruturação e distribuição das comunidades biológicas em montanhas é de extrema importância, sendo utilizado, por exemplo, como parâmetro para a identificação de mudanças nos padrões de diversidade em função de alterações no clima (Parmesan, 2006; Pecl *et al.*, 2017). Segundo Minx *et al.* (2017), os topos de montanhas são uma das principais áreas afetadas com o aumento de temperatura global. Com o aquecimento global são esperadas alterações na distribuição das espécies e na estrutura taxonômica e funcional das comunidades nesses gradientes ambientais, em escala local (montanha) ou regional (a cordilheira) (Brousseau, Gravel, & Handa, 2018; Longino & Branstetter, 2018; Parmesan, 2006; Rahbek *et al.*, 2019).

As montanhas tropicais, em geral, não possuem uma forte variação anual de temperatura se comparadas às montanhas de regiões temperadas, removendo-se o efeito de baixas temperaturas a ponto de congelamento, importante variável com grande influência na biota de regiões temperadas (Colwell *et al.*, 2008; Janzen, 1967). As montanhas tropicais são consideradas ótimos ambientes para investigarmos quais são os mecanismos estruturadores dos padrões de diversidade das comunidades, no espaço e no tempo, em diferentes escalas espaciais (gradientes de elevação e latitudinal, por exemplo). Além disso, montanhas podem ser consideradas um espaço pequeno o suficiente para permitir que todas as espécies regionais tenham acesso a todas as partes do gradiente (se comparados aos gradientes latitudinais), minimizando os efeitos de limitação de dispersão (Longino & Colwell, 2011).

Dentre as cadeias montanhosas tropicais, destaca-se a Cadeia do Espinhaço no Brasil. É uma região tropical megadiversa e extremamente ameaçada por distintas ações antrópicas como mineração, agropecuária e incêndios criminosos (Fernandes *et al.*, 2016; 2018; Domingues & Andrade, 2011). A Cadeia do Espinhaço é a maior cordilheira do Brasil e possui um dos ecossistemas campestres mais antigos e com maior biodiversidade da América do Sul, o campo rupestre, considerado uma paisagem climaticamente tamponada, antiga e infértil (OCBIL, *old climate buffered infertile landscape*) (Hopper, 2009; Silveira *et al.*, 2016). A ocorrência de espécies restritas a elevações especificas é relativamente comum no campo rupestre (e.g. anfíbios - Leite *et al.* 2008;

aves - Chaves *et al.* 2015; formigas - Costa *et al.* 2015; plantas - Mota *et al.* 2018), tornando-o fonte valiosa de estudos sobre os padrões de distribuição geográfica de espécies ao longo de gradientes de elevação, bem como sobre seus padrões de diversidade funcional e quais os efeitos das variáveis do habitat sobre as comunidades.

Formigas exibem uma grande diversidade de estratégias de história de vida (Hölldobler & Wilson, 1990). Vivem em todo o planeta, exceto nos polos e em ambientes acima de 3000 m de elevação ao nível do mar (Bharti *et al.*, 2013; Dunn *et al.*, 2009). Exercem múltiplas funções ecológicas, atuando com predadoras, dispersoras de sementes, herbívoras (cortadeiras) (Baccaro *et al.*, 2015; Hölldobler & Wilson, 1990) e na bioturbação de solos (movimentação de solos por agentes biológicos, com transferência de material biológico e geológico entre solo e superfície), com grande importância na estruturação de solos tropicais (Lavelle, 2002). Também respondem rapidamente às alterações da estrutura da vegetação (Kaspari *et al.*, 2003; Ribas *et al.*, 2003; Solar *et al.*, 2016). Dessa forma, a estrutura da comunidade de formigas pode diferir entre ambientes (por exemplo, campo e floresta) em função das diferenças estruturais dos habitats, como diferenças na complexidade estrutural e heterogeneidade da vegetação; presença ou ausência de serapilheira, e pelas diferentes condições microclimáticas, com variações em sombreamento ou insolação; variação na amplitude de temperatura e umidade (Brühl *et al.*, 1999; Fernandes *et al.*, 2016; Munyai & Foord, 2012). Em regiões tropicais também observamos uma variação sazonal nos padrões de diversidade de espécies de formigas, ocorrendo maior abundância e riqueza de espécies nos períodos mais úmidos e quentes (estação chuvosa) do que nos períodos mais secos e frios (estação seca) (Castro *et al.*, 2012; Esquivel-Muelbert *et al.*, 2017; Leal & Oliveira, 2000; Montine *et al.*, 2014).

Em geral, a riqueza de formigas em gradientes montanhosos apresenta o padrão de distribuição linear ou com efeito de pico intermediário ("*mid-elevation peak*") com o aumento da elevação (Costa *et al.*, 2015; Longino & Branstetter, 2018; Longino & Colwell, 2011), ocorrendo elevadas taxas de substituição de espécies (*turnover*) ao longo do gradiente de elevação (Bishop *et* *al.*, 2015; Brühl *et al.*, 1999; Nowrouzi *et al.*, 2018). Já em gradientes latitudinais, como por exemplo do Cerrado, as comunidades de formigas apresentam um padrão latitudinal inverso, com a diminuição da riqueza de espécies em direção ao nordeste mais seco e quente do Brasil (Vasconcelos *et al.*, 2018). Da mesma forma, comunidades de formigas na Mata Atlântica apresentam um elevado *turnover* de espécies do sul para o norte, e o padrão de riqueza de espécies invertido , aumentando em direção ao sul, mas com redundância funcional ao longo de todo gradiente, sob forte efeito da diminuição da temperatura em latitudes mais altas (Silva & Brandão, 2014). As formigas constituem um grupo termofílico (“amante do calor”; Hölldobler & Wilson, 1990; Kaspari *et al.*, 2000) e seus amplos padrões na tolerância térmica começaram a ser revelados apenas recentemente (Bishop *et al.* 2017; Costa *et al.*, 2018; Kaspari *et al.*, 2015; Nowrouzi *et al.*, 2018).

Nas regiões tropicais ocorre uma variação sazonal em padrões de diversidade de formigas, geralmente com uma maior abundância e riqueza de espécies no períodos mais quentes e úmido (estação chuvosa) do que no período seco e frio (estação seca) (Castro *et al.*, 2012; Montine *et al.*, 2014; Esquivel-Muelbert *et al.*, 2017; Marques *et al.*, 2017). As comunidades de formigas também respondem à estrutura da vegetação, respondendo positivamente em função do aumento na complexidade e heterogeneidade estrutural do habitat (Kaspari *et al.*, 2003; Solar *et al.*, 2016). Por isso, a composição da comunidade de formigas pode diferir entre os ambientes (por exemplo, campos e florestas) devido a diferenças estruturais em habitat (ou seja, diferenças na complexidade estrutural e heterogeneidade da vegetação e presença ou ausência de serapilheira), além das diferentes condições microclimáticas resultantes, ou seja, maior sombreamento ou insolação, variação nas faixas de temperatura e umidade (Andersen, 2019; Brühl *et al.*, 1999; Fernandes *et al.*, 2016; Lasmar *et al.*, 2020; Munyai & Foord, 2012). Da mesma forma, os padrões de estratégias ou características funcionais podem variar entre diferentes habitats e condições climáticas, como consequência de filtros ambientais (por exemplo, variabilidade climática, heterogeneidade de habitat) (Dunn *et al.*, 2009; Arnan *et al.*, 2018), e pode representar um subconjunto aninhado das estratégias funcionais disponíveis ao longo de um gradiente de elevação (Bishop *et al.*, 2015) ou latitudinal (Silva & Brandão, 2014). Nesses cenários, as variáveis de macrohabitat podem atuar como filtros ambientais, limitando o estabelecimento de espécies incapazes de tolerar condições abióticas de um determinado habitat (Keddy, 1992), o que pode influenciar os padrões de distribuição das espécies e de suas características. Estudos realizados em grandes escalas espaciais para compreender os efeitos dos gradientes ecológicos na distribuição de espécies, como gradientes de elevação e latitude na estrutura taxonômica e funcional de comunidades de formigas, ainda são negligenciados, especialmente em regiões tropicais (Tiede *et al.*, 2017)

Visando elucidar lacunas no conhecimento de padrões espaço temporais em montanhas tropicais, temos como objetivo descrever os padrões taxonômicos e funcionais e mecanismos estruturadores das comunidades de Formicidae em gradientes espaço-temporais ao longo da Cadeia do Espinhaço, em diferentes escalas espaciais; em um gradiente de elevação em uma montanha e em um gradiente latitudinal em uma Cadeia de montanhas. Temos o objetivo de elucidar aspectos biogeográficos dessas comunidades no campo rupestre e avaliar como comunidades de formigas respondem às diferentes variáveis ambientais. A tese está organizada em dois capítulos, cada um visando investigar objetivos propostos, na escala local (montanha) e na escala regional (cordilheira) e darão origem a dois manuscritos.

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Capítulo 1: Environmental drivers of taxonomic and functional diversity of ant communities in a tropical mountain

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Artigo submetido para o periódico *Insect Conservation and Diversity* (Qualis Capes A2, Impact Factor 2.313)

Status: Major Revision

Insect Conservation and Diversity

Section: Original Research

Environmental drivers of taxonomic and functional diversity of ant communities in a tropical mountain

Running title: Ant taxonomic and functional diversity

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Abstract

1. We investigated the patterns of taxonomic (TD) and functional (FD) α and β diversities of ants in a mountainous landscape along three dimensions, namely one temporal (seasonal) and two spatial dimensions: between habitats – grassland and forest habitats (horizontal), and among elevation bands (vertical). In addition, we tested the effects of environmental variables (mean elevation and temperature, and normalized difference vegetation index – NDVI) on taxonomic and functional α and β-diversities.

2. The β-diversities of the two spatial dimensions are the main components of TD. The α-diversities of the two spatial dimensions exhibit contrasting patterns to drive taxonomic α-diversity, indicating differences in the community at local scale on grassland and forest habitats. The FD is almost entirely represented by the α-diversity component, with very low contribution of β-diversity.

3. Regarding environmental drivers, the decrease in temperature caused by increased elevations and seasonal variations had a negative effect on taxonomic α-diversity. There were no effects of environmental variables on functional α-diversity.

4. Despite the high turnover of ant species occurring along spatial dimensions, the communities were functionally redundant. The changes in species richness and composition patterns in this mountain were strongly influenced by variables correlated with elevation and habitat structure.

5. Species composition changed across all dimensions, but the core traits and functions remained unchanged. Differences observed in the composition of ant communities over relatively short geographic distances highlight the importance to conserve the entire mountain, ensuring the maintenance of the ant diversity and associated ecosystem functions.

Keywords: turnover; nestedness; ground-dwelling ants; Espinhaço Mountain Range; *campo rupestre*; rupestrian grassland

Introduction

Understanding how communities are structured in space and time, and the underlying mechanisms driving diversity patterns are among the central goals of ecology and conservation biology (Gaston, 2000; Vellend, 2016). To achieve this goal, it is important to evaluate multiple scales and metrics of biodiversity in response to ecological processes (Tuomisto, 2010; Anderson *et al.*, 2011; Barton *et al.*, 2013). The use of multiple scales of diversity proposed by Whittaker (1960) is an adequate approach to elucidate these questions, focusing on β-diversity (a measure of species composition variability among samples), which links local diversity (α) to broad-scale diversity (γ). Baselga (2010) brought a complimentary process-focused approach to describe β-diversity into turnover (species substitution) and nestedness (species loss). Understanding how the total diversity is partitioned into α and β-diversity, as well as how β-diversity is decomposed into its components (turnover and nestedness; Baselga 2010), is extremely important to identify which mechanisms support the observed biodiversity patterns.

Taxonomic diversity, mainly based on species richness, considers that all species are different from each other but overlooks that species can play distinct ecological roles (Villéger *et al.*, 2013). Functional diversity, on the other hand, reflects the variety of functional traits among all species in the community (Petchey & Gaston, 2006). Functional traits are measurable biological characteristics of organisms that influence their performance or fitness and ecosystem functioning (Violle *et al.*, 2007). The approaches proposed by Whittaker (1960) and Baselga (2010) have increasingly been applied to both taxonomic (TD) and functional (FD) diversity (Petchey & Gaston, 2006; Jost, 2007; Villéger *et al.*, 2013). Analysing diversity patterns with different approaches (e.g., TD and FD) allows to identify the processes associated with the origin and maintenance of biodiversity and the associated services provided by the different species (Anderson *et al.*, 2011; Barton *et al.*, 2013). Thus, elucidating the mechanisms underpinning the patterns of biodiversity distribution is key to guide future effective conservation actions (Lassau & Hochuli, 2004; Cooke *et al.*, 2013) given the current scenario of global changes.

Mountainous environments are spatially heterogeneous and can harbour many species, as a direct consequence of the greater number of microhabitats, shelters, and foraging sites (Körner, 2007; Munyai & Foord, 2012). Elevation gradients can also be considered spatially small (if compared to latitudinal gradients) to allow all species pool to have access to the whole gradient, minimizing the effects of dispersal limitation (Longino & Colwell, 2011). These environments have extreme environmental characteristics (e.g., increasing elevation leading to lower temperature, primary productivity, and species-area ratio) and are considered ideal models for investigating the spatial patterns and processes that determine the distribution of biodiversity (Gaston, 2000; Longino & Colwell, 2011; Smith, 2015; Longino & Branstetter, 2019). Similarly, mountains are also suitable systems for identifying changes in diversity patterns due to changes in climate (Parmesan, 2006; Pecl *et al.*, 2017). Tropical mountains have higher temperatures at low elevations and overall wetter conditions than temperate mountains (McCain & Grytnes, 2010). In addition to the vertical dimension, the occurrence of different habitats (e.g., field and forest, Lasmar *et al.*, 2020) along the mountain that possess a seasonal climate includes two important factors to be addressed (habitat type and seasonality), since forests can buffer daily variations in temperature and maintain the humidity, ultimately changing the patterns of species distribution. The effects of these different factors and their interactions on both taxonomic and functional diversity of communities still need to be comprehensively addressed.

Among the tropical mountains, the ancient Espinhaço Range (1100 km length, emerged nearly 640 Ma; Alkmin, 2012) is a tropical region extremely endangered (e.g., mining, agriculture, deforestation) and biodiverse (Silveira *et al.*, 2016; Fernandes *et al.*, 2018). Located in an ecotone region amid three biomes, the Cerrado to the west, the Atlantic Forest to the east (two biodiversity hotspots; Mittermeier *et al.*, 2004), and the Caatinga to the north (Giulietti *et al.*, 1997; Fernandes, 2016; Silveira *et al.*, 2016), Espinhaço has great strategic importance for the conservation of unique natural environments in Brazil (Domingues *et al.*, 2011; Fernandes *et al.*, 2018). The environments found in the Espinhaço Range are formed mainly by rocky grassland ecosystem, the *campo rupestre* (Silveira *et al.*, 2016), permeated by forests such as riparian forests and forest islands (*capões de mata*) (Coelho *et al.*, 2018b), forming vegetation mosaics along the elevational and latitudinal gradients (Giulietti *et al.*, 1997; Silveira *et al.*, 2016). The occurrence of species restricted to specific elevations is relatively common in the *campo rupestre* (Leite *et al.*, 2008; Chaves *et al.*, 2015; Costa *et al.*, 2015; Mota *et al.*, 2018), making it a valuable system to investigate the patterns of species distribution along elevation gradients.

In general, patterns of ant species richness present a linear decrease or a mid-elevation peak with increasing elevation (Longino & Colwell, 2011; Longino & Branstetter, 2019; Lasmar *et al.*, 2020), with high species replacement rates (turnover) along the elevation gradient (Brühl *et al.*, 1999; Bishop *et al.*, 2015; Nowrouzi *et al.*, 2016). Moreover, in tropical regions a seasonal variation in ant diversity patterns occurs, with usually greater abundance and richness of species in the wetter and hotter periods (rainy season) than in the drier and colder periods (dry season) (Castro *et al.*, 2012; Montine *et al.*, 2014; Esquivel-Muelbert *et al.*, 2017; Marques *et al.*, 2017). Ant communities also respond to vegetation structure (Kaspari *et al.*, 2003; Solar *et al.*, 2016) and like so, ant community composition may differ between environments (e.g., grassland and forest) due to structural differences in habitats (i.e., differences in structural complexity and heterogeneity of vegetation, presence or absence of leaf litter) and the resulting different microclimatic conditions (i.e., greater shading or insolation, variation in temperature and humidity ranges) (Andersen, 2019; Brühl *et al.*, 1999; Fernandes *et al.*, 2016; Lasmar *et al.*, 2020; Munyai & Foord, 2012). Similarly, patterns of functional strategies or traits could vary among different habitats and climatic conditions, as a consequence of environmental drivers (e.g., climatic variability, heterogeneity of habitat)

(Dunn *et al.*, 2009; Arnan *et al.*, 2018) and could represent a nested subset of the available functional strategies along an elevational gradient (Bishop *et al.*, 2015).

Here, we aimed to determine the patterns of taxonomic and functional diversity of ants in different spatio-temporal dimensions (horizontal, vertical, or seasonal) along a tropical mountainous landscape, as well as to explore the environmental variables driving such patterns. In this study, three spatio-temporal dimensions were considered (adapted from Basset *et al.*, 2015): one temporal dimension (dry and rainy season) and two spatial dimensions: between habitats within the same elevational range (horizontal dimension), and across different elevations (vertical dimension). Our main prediction was that environmental filters related to elevation (vertical dimension) and habitat (horizontal dimension) would be the main drivers of both taxonomic and functional α and β-diversities. In addition, since temperature and humidity rise during the rainy season (Ferrari *et al.*, 2016) and ant communities present a seasonal richness pattern, we hypothesized that α and β-diversities (TD and FD) would vary along the spatio-temporal gradient studied and we expect they would be higher in the hotter and wetter period, mainly in lower elevations, due to the combined effects of habitat and climate factors occurring along the elevation gradient. Specifically, we expect the following:

(i) We expected to find a lower taxonomic diversity (TD) of ants in higher elevations. Diversity is not uniformly distributed throughout space (Whittaker, 1960) and ant richness decreases with increasing elevation (i.e., patterns usually present a linear decrease or a mid-elevation peak with increasing elevation) (Smith, 2015; Longino & Branstetter, 2019). In our case, we expected a linear taxonomic decrease as found for other insect groups (i.e., wasps, termites, galling insects, and dung beetles) in the same system (Coelho *et al*., 2018a; Nunes *et al.*, 2016; 2017; Perillo *et al.*, 2017). Ants are responsive to the habitat openness and to vegetation structure type (Kaspari *et al.*, 2003; Solar *et al.*, 2016; Andersen, 2019), which could result in different communities among grassland and forest. In addition, although the vegetation heterogeneity or complexity on *campo rupestre* could decrease with elevation increases (Mota *et al.*, 2018), the habitat type is kept considering the same vegetation type (forest or grassland). Nonetheless, we expect higher turnover between elevations followed by among habitats. Once ants could be considered an ecological indicator of climatic variation *campo rupestre* ecosystem (Costa *et al.*, 2018), with greater richness in hot and warm season rather than cold and dry season, we expect to found patterns related to a real effect of seasonal climatic conditions on ant communities. Thus, seasonally, we expect to find greater nestedness since the dry season communities were subsets of the communities found in the rainy season.

(ii) Despite the low richness in higher elevations, we also expected that the taxonomic β-diversity would be explained mainly by the turnover pattern, with different ant communities found across the elevational gradient (i.e., high elevations communities will not be subsets of lowland ant communities). Along elevational gradients, there are high species replacement rates (turnover) (Bishop *et al.*, 2015; Nowrouzi *et al.*, 2018). In the *campo rupestre*, ants and other insects (i.e., wasps, termites, galling insects, and dung beetles) typically exhibit elevational turnover patterns (Coelho *et al.*, 2018a; Nunes *et al.*, 2016, 2017; Perillo *et al.*, 2017). Generally, the turnover of ant species in tropical mountains is related to a simplification of the vegetation structure with elevation, and also to a decrease in temperature and increase in rainfall along the elevation (Brühl *et al.*, 1999; Dunn *et al.*, 2009), which is the case of the Espinhaço Range (Fernandes *et al.*, 2016).

(iii) We expect that functional β-diversity would be mostly driven by nestedness across the elevational gradient, as found for other insects such as ants, dung beetles, galling insects, and termites (Bishop *et al.*, 2015; Coelho *et al.*, 2018a; Nunes *et al.*, 2016, 2017). At higher elevations or under harsher climatic conditions, many organisms (including ants) display a shrank or clustered pattern of phylogenetic diversity due to the species richness decrease with an increase in elevation (Smith, 2015; Smith *et al.*, 2014; Machac *et al.*, 2011). Thus, we predict that ant communities there will be poor at higher elevations and the functional diversity could diminish as well and become restricted to particular ant phenotypes in response to harsh environmental conditions in mountain ecosystems (Smith, 2015).

Material and Methods

Study area

The study was conducted in Serra do Cipó, located in the southern portion of the Espinhaço Range (Fig. 1), dominated by Cerrado vegetation and *campo rupestre*, with the occurrence of riparian forests, *capões de mata* (forest islands), and semi-deciduous and deciduous seasonal forest (Giulietti *et al.*, 1997; Silveira *et al.*, 2016). The climate is mesothermic (Cwb in the Köppen classification), with dry winters and rainy summers, mean annual rainfall of 1500 mm and average annual temperature ranging from 17.4 to 19.8ºC (Ferrari *et al.*, 2016; Silveira *et al.*, 2016). Environmental variables, such as temperature and humidity, tend to decrease and rainfall tends to increase as a function of increasing elevation, following the expected patterns for mountainous environments (Ferrari *et al.*, 2016; Silveira *et al.*, 2016; Fernandes *et al.*, 2016). Located in a region of high biodiversity, the Serra do Cipó comprises a private area of environmental protection (APA Morro da Pedreira) and a National Park of integral protection (PARNA Serra do Cipó), besides being part of the Espinhaço Range Biosphere Reserve (Domingues *et al.*, 2011; Fernandes *et al.*, 2018).

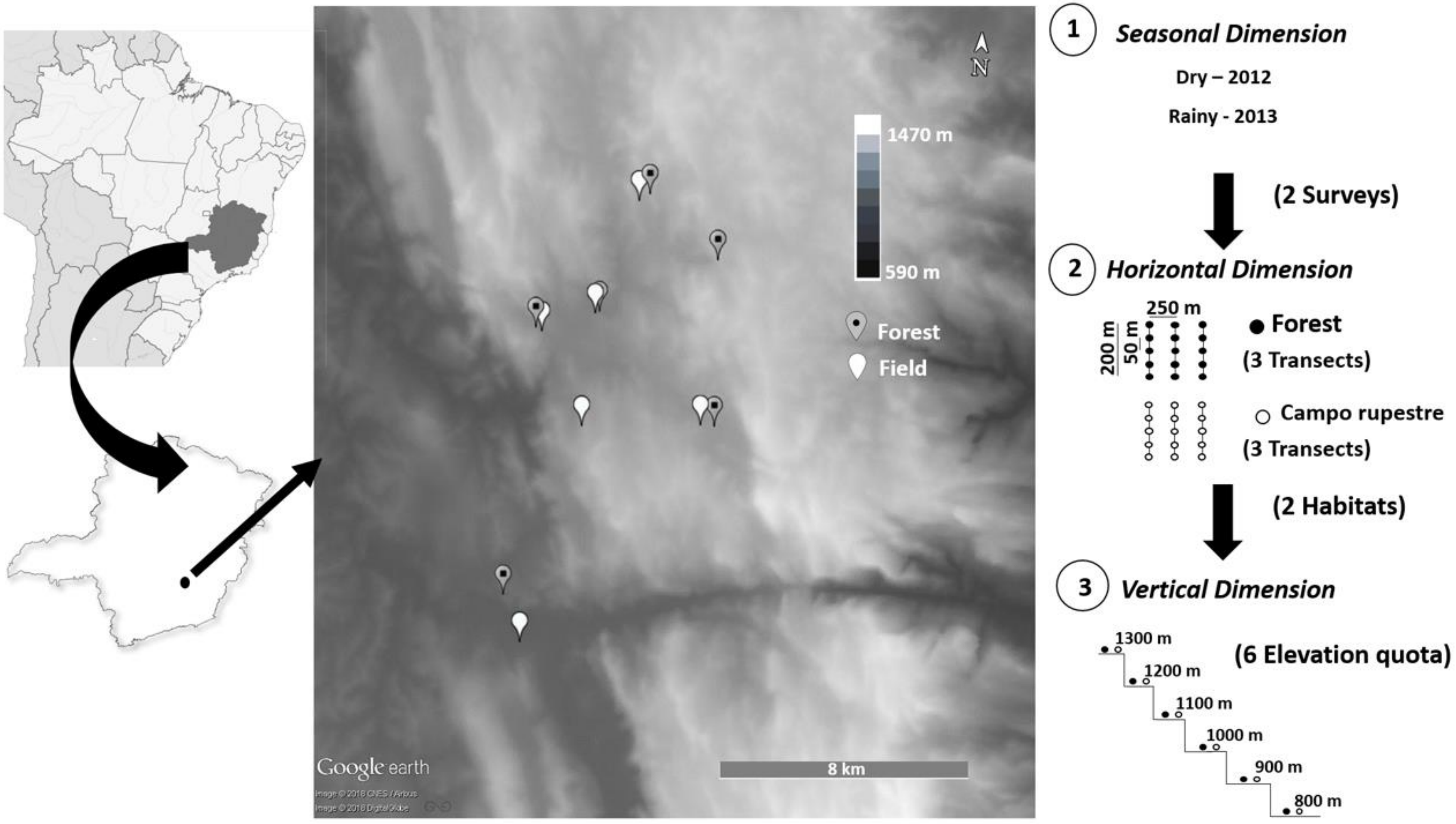

Fig 1. Map of the study area with the location of each transect at the six sampling sites of PELD/CRSC—Long-Term Ecological Research. Serra do Cipó, Minas Gerais State, Brazil. The three sampling spatio-temporal dimensions considered: (1) temporal dimension (between seasons); (2) horizontal dimension (between habitats – grassland and forest); and (3) vertical dimension (among elevations).

The sampled areas are established in the permanent plots of the Long Term Ecological Research Project Campos Rupestres (PELD CRSC/CNPq Project) along a gradient of elevation in the Serra do Cipó National Park, Minas Gerais State, Brazil (19º22'01"S, 43º32'17"W) (Fernandes *et al.*, 2016; Silveira *et al.*, 2019). The elevation gradient has a range of 500 m, ranging from 800 to 1300 m (meters above the sea level). The Cerrado vegetation (Neotropical savanna) occurs at 800 m and the transition from Cerrado to *campo rupestre* occurs at 900 m (Silveira *et al.*, 2019). However, between 1000 and 1300 m is where the *campo rupestre sensu lato* occurs (for more details see Silveira *et al.*, 2019), which are areas with mountainous vegetation, typically rocky grassland and shrubby vegetation, with quartzitic outcrops and sandy, rocky or flooded grasslands, permeated by forest areas with transitional vegetation such as riparian forests (among 800 and 1200 m) and natural forest fragments of Atlantic Forest, *capões de mata* or Forest Islands (among 1200 and 1300 m, see Coelho *et al.*, 2018b). The floristic similarity between riparian forests and *capões de mata* is also quite high (Coelho *et al.* 2018b; Meguro *et al.*, 1996). The *campo rupestre sensu stricto* (where woodlands do not occur) is a very old ecosystem, climatically buffered and infertile landscape (OCBILs), with high concentrations of Al^{+3} in the soil; possibly the oldest grassland ecosystem to the east of South America (Silveira *et al.*, 2016).

Sampling of ants

Sampling was carried out in the *campo rupestre* and forest environments (riparian forests and *capões de mata*), during the dry (July to August, 2012) and rainy (January to February, 2013) seasons, at six sampling sites pre-established by the PELD CRSC/CNPq Project (Silveira *et al.*, 2019). Sample sites were distributed along an elevational gradient in six distinct elevation plots among 800 and 1300 m, spaced every 100 m of elevation and geographically distant by at least three kilometres. In each elevation, three linear transects were arranged in the *campo rupestre* and other three transects were arranged in the forest environment closest to each *campo rupestre* (riparian forests among 800-1200 m and *capões de mata* at 1300 m), totalling 18 forest transects (Fig. 1). Each transect was 200 m of extension in the north-south direction, distant from each other by 250 m, totalling 18 transects along the gradient. In each transect, five pitfall traps were arranged 50 m apart (a plastic pot with 14 cm diameter × 9 cm height with 500 ml of a saline-detergent solution). The spacing of 50 meters between traps is considered enough to avoid interference related to the foraging range of ants belonging to the same colony (Leponce *et al.*, 2004). All pitfall traps remained in the field for 48 hours per survey (Bestelmeyer *et al.*, 2000). Each transect was considered an independent sample replicate (data from traps were pooled) in further analyses (6 elevations × 6 transects × 2 seasons, N = 72).

Identification of ant species and description of functional traits

The ants were identified to species and morphospecies by comparison with the Collection of Formicidae from *campo rupestre* of the Laboratory of Insect Ecology at the Universidade Federal de Minas Gerais, Brazil, and with the help of experts of different ant taxonomic groups. We followed Baccaro *et al.*, (2015) and Ants of Bolton World Catalog (Bolton *et al.*, 2005) classifications.

Ant species were described in terms of functional traits that provide information about the ecological functions, linked to diet, nesting, foraging capacity, thermoregulation, and habitat association (Fichaux *et al.*, 2019; Paolucci *et al.*, 2016; Leal *et al.*, 2012; Bishop *et al.*, 2016; Barden, 2017; Tiede *et al.*, 2017). Seven traits were described to each species: Weber's length, femur length, mandible length, colour (mesossoma), polymorphism, integument sculpture, and functional groups (six morphological traits and one ecological trait; Table 1).

Table 1. List of morphological and ecological traits measured and their hypothesized ecological functions

Traits	Measure	Abbrev. /Unit	Ecological functions
Morphological Traits			
Weber's length	Continuous	WL (μm)	Proxy for total size, related to habitat complexity (Weber, 1938; Kaspari & Weiser, 1999).
Femur length	Continuous	HFL(μm)	Indicator of foraging speed, associated to habitat complexity (Feener *et al.*, 1988; Yates *et al.*, 2014).
Mandible length	Continuous	ML(μm)	Indicative of diet (Brandão *et al.*, 2009).
Colour (Mesossoma)	Continuous	V (%) *	Thermal melanism: dark individuals has an benefit in cool climates compared to a lighter one (Clusella *et al.*, 2007); Indicative of thermotolerance and, directly related to temperature variation and solar radiation (e.g. ants in cold environments may be darker integument rather than in warm environments with greater UV-B rates) (Bishop *et al.*, 2016).
Polymorphism	Categorical	1 = monomorphic; 2 = dimorphic; 3 = polymorphic	Polymorphism of the workers, attribute related to the ability to develop different tasks in the

Traits	Measure	Abbrev. /Unit	Ecological functions
			colony (e.g., foraging, protection, internal activities of the nest; Wills *et al.*, 2017).
Integument Sculpture	Ordinal	1 = cuticle smooth/shiny; 2 = superficial wrinkles/pits; 3 = surface heavily textured	Protection from desiccation. Thickened cuticles enhanced the dehydration tolerance (Nation, 2008; Terblanche, 2012)
Ecological Trait			
Functional Groups	Categorical	AA = Army Ants; AD = Arboreal Dominant; AP = Arboreal Predator; AS = Arboreal Subordinate; CO = Cryptic Omnivores; CP = Cryptic Predators; DD = Dominant Dolichoderinae; EO = Epigeic Omnivores; EP = Epigeic Predators; Hatt = High Attini; Latt = Low Attini; Opp = Opportunist;	Functional groups based on global-scale responses of ants to environmental stress and disturbance. Also, indicative of ecological tasks, such as nesting, foraging, and diet habits (Andersen, 1995; Leal *et al.*, 2012; Paolucci *et al.*, 2016). All groups were based on the classification used by Paolucci *et al.*, (2016), except for Seed Harvester group (Johnson, 2015) here represented by *Pogonomyrmex naegelli*, which was not present in this list.

Traits	Measure	Abbrev. /Unit	Ecological functions
		SC = Subordinate Camponotini SH = Seed Harvester;	

* The HSV cylindrical-coordinate colour model (Smith, 1978), whereas: H = Hue shows the dominant wavelength; S = Saturation, indicates the amount of dominant wavelength (H) present in the colour; and V = Value, defines the amount of bright in the colour. We analysed only the variable V, which measured in % of colour brightness (e.g., white colour presents 100% of bright while black colour has 0% of bright) (as proposed by Bishop *et al.*, 2016).

We followed the guide for identification of functional attributes for ants (*The Global Ants trait Database* – GLAD; Parr *et al.*, 2017) to perform the morphological measurements, except for the variable “Colour”. Ant colour was obtained from the HSV colour model (Smith, 1978) using only the variable V (colour brightness), as proposed by (Bishop *et al.*, 2016). Differently from Bishop *et al.*, (2016), who considered a predominant colour between head, mesosoma, and gaster, we performed the capture of HSV values of the predominant colour on the mesosoma of each specimen. We measured only the mesosoma because it is an important body part for acquiring heat for body activities (not only for flight) in Hymenoptera, whose warmth transfer occurs via hemolymph from mesossoma to head, gaster, and legs when the thoracic muscles are activated (Terblanche, 2012). All continuous data, except Weber’s length and colour brightness, were divided by Weber’s length to correct for individual body size, because traits were not normally distributed (Arnan *et al.*, 2018; Fichaux *et al.*, 2019).

We performed image acquisition using Microscope Digital Camera LC30 OLYMPUS$^{®}$ mounted on a stereomicroscope SZ61 OLYMPUS$^{®}$. Measurements were made with a digital capture micrometre (accurate to 0.01 mm) provide in the LC Micro 2.2 OLYMPUS$^{®}$ software. We take measures of the randomly selected individuals of every species recorded in the dataset. At least six individuals were measured when possible, and whenever it was not possible, we take measures of available individuals (only minor workers were used; N = 2760 images from 920 individuals measured; average = 4.72 individuals per species). Categorical and ordinal morphological traits used (polymorphism and integument sculpture) were attributed using genera/species information available at AntWeb (www.antweb.org) and AntWiki website (www.antwiki.org) (Guénard *et al.*, 2017) and by own observations .

Taxonomic and functional diversity

Taxonomic diversity (TD) and functional diversity (FD) were calculated for each of the 72 transects. The TD was calculated by species richness in each transect and the functional diversity (FD) was calculated using the mean value functional attribute data for the species in each transect (Table 1; Supplementary Material I Table S1). To obtain functional diversity we calculated a species dissimilarity matrix based on all ant traits using the Gower distance (Villéger *et al.*,2008) with the “trova” function (i.e., TRait OVerlAp) of the R software (de Bello *et al.*, 2011). Gower distance measures the dissimilarity of traits between species using different types of data: categorical, ordinal or continuous (see de Bello *et al.*, 2011; Nunes *et al.*, 2016 for more details). We then used the dissimilarity matrix to calculate the Rao index, which estimates FD based on species incidence and Gower dissimilarities at each sampling point. We used the “Rao” R function to calculate Rao index considering Jost’s correction (de Bello *et al.*, 2010).

Environmental variables

Climatic variables were obtained along the elevation gradient using a meteorological monitoring tower (equipped with an Onset HOBO$^{®}$ U30 data logger) located at every 100 m of elevation on grassland, adjacent to the sampling sites of the PELD CRSC/CNPq Project, between April 2012 and February 2013. The climatic variables measured were the mean air temperature, mean air humidity, and accumulated rainfall for each survey period (dry, July to August/2012, and rainy, January to February/2013, seasons) and for each elevation (Supplementary Material I Table S2).

As explanatory variables, the environmental variables used were: (1) average air temperature (ºC), mean air humidity (%), accumulated rainfall (mm) at each elevation (predictive variables of ant activities, which varies in space and time; Kaspari *et al.*, 2015), (2) mean elevation per transect along the elevational gradient; and (3) Normalized Difference Vegetation Index (NDVI): Mean NDVI and Standard Deviation of NDVI, as indirect measures of heterogeneity and structural complexity of vegetation, respectively (Costanza *et al.*, 2011; Flores *et al.*, 2018), for each transect among seasons, across elevations, and habitats.

In order to obtain the vegetation cover indices, we calculated the Mean NDVI (with mean values of vegetation cover per environment/sampled elevation) and the Standard Deviation of NDVI for each transect (Costanza *et al.*, 2011; Flores *et al.*, 2018) (Supplementary Material I Table S2). NDVI indexes were calculated from LANDSAT 7 images (with 30 m buffer resolution) (NASA, 2009) from the dry season (April and June 2012) and from the rainy season (December 2012 and February 2013). The images are available at the National Institute for Space Research (INPE) database (http://www.dgi.inpe.br/CDSR/). The QGIS 2.18.0 software was used for the geo-referencing and atmospheric correction of the images (according to NASA, 2009) and later for obtaining the Mean NDVI and Standard Deviation of NDVI for each sampling unit (Costanza *et al.*, 2011; Flores *et al.*, 2018).

For all variables, the multicollinearity was tested via Pearson correlation to define the variables to be used in the models as explanatory predictors (i.e., all of which with correlation values lower than ± 0.7; Supplementary Material I Table S3). Among these variables we selected mean elevation, mean air temperature, and the indirect measure of vegetation (Mean NDVI). These variables play crucial roles in species diversity patterns and ant community structure (Longino & Branstetter 2019; Fernandes *et al.*, 2016; Kaspari *et al.*, 2015).

Data analysis

We estimated the sufficiency of our samples based on a sample coverage value. The sample coverage measures the inventory completeness and using richness values for a specified sample size or a specified level of sample coverage allows to make statistical comparisons based on these estimates (Chao & Jost, 2012; Chao *et al.*, 2013). The sample-size- and coverage-based rarefaction and extrapolation curves were calculated only for Hill numbers of $q = 0$ (species richness) by doubling the reference sample sizes and finding a common value of sample coverage between sites to estimate species richness (Chao & Jost, 2012; Chao *et al.*, 2013). We used 50 bootstraps to determine confidence intervals. Analyses were done using iNEXT (Hsieh *et al.*, 2016), available at https://chao.shinyapps.io/iNEXTOnline/.

We evaluated patterns along three spatio-temporal dimensions: (1) one temporal dimension (between dry and rainy seasons); and two spatial dimensions: (2) between habitats, *campo rupestre* and forest environments (horizontal dimension), and (3) between elevation bands (vertical dimension). To test our hypotheses, we estimated the taxonomic and functional diversity of the ant communities for each dimension. The γ-diversity was partitioned into α-diversity (local scale or transects) and β-diversity (which was partitioned into βS – between rainy and dry seasons; βH – between habitats; and βV – between elevations), for both TD and FD.

We performed these analyses with the "adipart" (additive diversity partitioning, for taxonomic approach) and "hiersimu" (hierarchical null model testing, for functional approach) which works with a statistic returned by a function assessed according to a nested hierarchical sampling design, both of the "vegan" package (Oksanen *et al.*, 2018) in the R software (R Core Team, 2017). The function "adipart" calculates α, β and γ-diversity values for species richness, Shannon and Simpson diversity in a sampling hierarchy (our three dimensions). We used the function "adipart" only to describe the species richness per dimension. The function "hiersimu" works almost in the same way as "adipart", but it has an additional argument that can be used to partition functional metrics such as Rao's quadratic entropy (a measure of functional diversity). As proposed by de Bello *et al.*, (2010), we used the "Rao" function of the R software to estimate the FD and perform the partitioning (using the function "hiersimu") into α, β (for each dimension), and γ considering the Gower distance in the distribution of the species in each transect. To compare the TD and FD partition results, we transformed the values of each diversity component into a percentage of γ-diversity. After that, we also performed the partition of each taxonomic β-diversity (β-TD) and functional β-diversity (β-FD) into turnover and nestedness components to verify if the taxonomic and functional dissimilarities between ant communities in the three spatio-temporal dimensions are explained by replacement or gain/loss of species/functional groups. We used the Jaccard dissimilarity index and the "beta.multi" function of the "betapart" R package (Baselga *et al.*, 2013; Baselga & Orme, 2012).

We calculated the variation of the taxonomic (TD) and functional (FD) composition of the ant community (β_{SOR}) for each transect in all spatio-temporal dimensions. Then, we partitioned the TD and FD into the components derived from (β_{SOR}) into species turnover (β_{SIM}) and species gain/loss or nestedness (β_{NES}) using the β-diversity partitioning method components. We used the “beta.multi” and “functional.beta.multi” function of the R package “betapart” to partition TD an FD β-diversity (Baselga & Orme, 2012). In this analysis, we used the same functional approach described above.

Finally, we constructed two generalized linear mixed models (GLMMs) using the function *glmer* from “lme4” R package (Bates *et al.*, 2015) to evaluate the effects of all spatio-temporal dimensions (seasonal, horizontal, and vertical) and associated environmental variables on taxonomic (α-TD) and functional (α-FD) richness. We considered ant taxonomic richness (α-TD) and functional richness (α-FD, i.e., Rao index) per transect as response variables, and the three spatio-temporal dimensions (seasonal, horizontal, and vertical) (model 1), mean elevation, mean temperature and mean NDVI (model 2) were used as fixed variables. We used “transect identity” as a random variable to remove the effect of temporal pseudoreplication. The Poisson and Gaussian distributions were used for taxonomic and functional variable responses. In addition, we performed two generalized linear models (GLM) to test if β-TD (species turnover) and β-FD (functional turnover) as response variables are related with spatio-temporal dimensions (model 1) and the same fixed variables presented above (model 2). For each model, we verified whether the error distribution was adequate (Crawley 2013) using the “rdiagnostic” tool of the “RT4Bio” package and consequent approval of the appropriate minimum model through the gradual omission of nonsignificant terms. The binomial distribution corrected for overdispersion was used for taxonomic and functional variable responses. Model adequacy and distribution adjustment were checked using residual analysis (Crawley, 2013). All analyzes were performed using the R software (R Core Team, 2017).

Results

We recorded 2,548 ant individuals belonging to eight subfamilies, 50 genera, and 195 species/morphospecies. Most of the genera sampled belongs to the subfamily Myrmicinae (27 genera or 55% of the total), followed by Ponerinae (seven), Formicinae, Dolichoderinae, and Dorylinae (four in each). The subfamilies with the highest species richness were Myrmicinae (101 species), Formicinae (33 species), Ponerinae (18 species), and Dolichoderinae (16 species). Together, these four subfamilies accounted for 86.2% of the species sampled throughout the system. The genera with most species were *Pheidole* (36 species), *Camponotus* (27 species), and *Solenopsis* and *Linepithema* (seven species each). Considering all samples, 18 doubletons and 44 singletons (31.8%) were recorded (Supplementary Material I Table S4).

Rarefaction-extrapolation accumulation curves suggested high sample coverage for all sites (Fig. 2a, b). The high sample completeness was found for site at 900 m (sample coverage = 0.921, S_{obs} = 90), followed by site at 800 m (sample coverage = 0.901, S_{obs} = 128), 1100 m (sample coverage = 0.880, S_{obs} = 76), 1300 m (sample coverage = 0.871, S_{obs} = 83), 1200 m (sample coverage = 0.817, S_{obs} = 85), and 1000 m (sample coverage = 0.800, S_{obs} = 73).

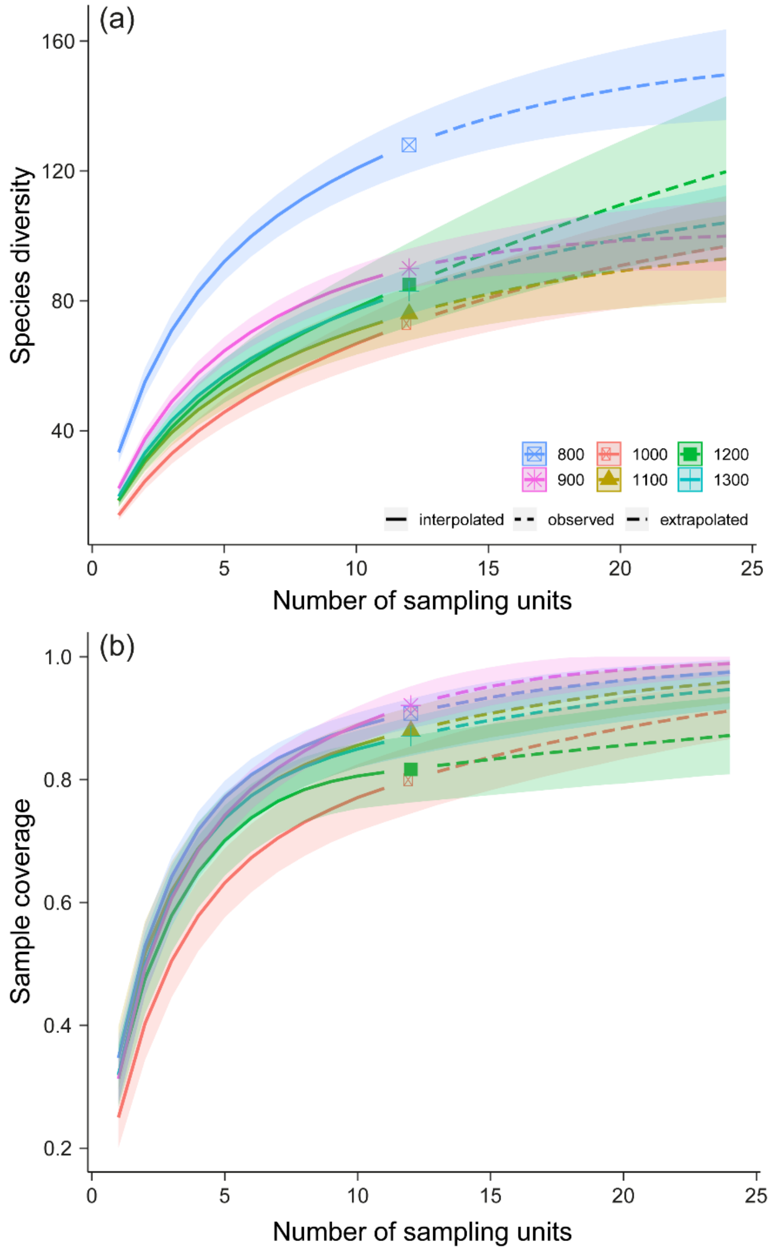

Fig 2. Rarefaction-extrapolation species accumulation curves of ant richness along the elevational gradient: (a) total sampling; (b) Sampling areas. Colour code: green = 800 m; light blue = 900 m; dark orange = 1000 m; dark blue = 1100 m; lilac = 1200 m; purple = 1300 m.

Partition of taxonomic and functional diversity

The partitioning of taxonomic diversity revealed that the relative contribution of the β-TD component was 89.2% to γ-TD, with 54.3% relative to β-TDV (vertical dimension), 19.2% relative to β-TDH (horizontal dimension), and 15.7% relative to β-TDS (temporal dimension). The contribution of α-TD was only 10.8%. In relation to the relative contributions to γ-FD, the total β-FD component was 3.2%, being 0.7% relative to β-FDV (vertical dimension), 0.8% relative to β-FDH (horizontal dimension) and 1.7% relative to β-FDS (temporal dimension). The main contribution to γ-FD was of the α-FD component, with 96.8% of contribution (Fig. 3).

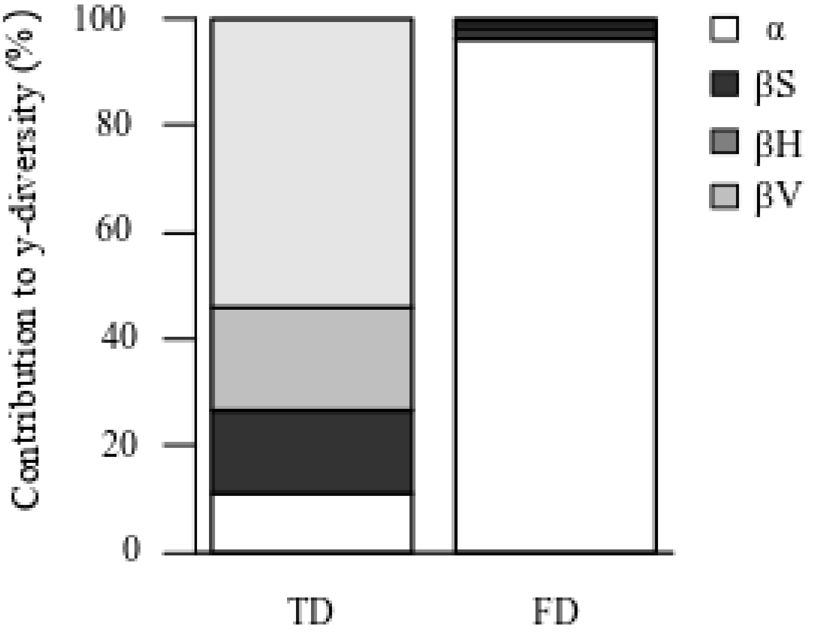

Fig 3. The contribution of α, β1 (βS), β2 (βH) and β3 (βV) to both taxonomic diversity (γ-TD) and functional diversity (γ-FD). α is the average diversity, βS is the between-season diversity (temporal dimension), βH is the between-habitat diversity (horizontal dimension), and βV is the between-elevation diversity (vertical dimension).

When we partitioned each β-TD (i.e., β-TDH, β-TDV and β-TDS) into the turnover and nestedness components, we verified that regardless of the spatio-temporal dimension evaluated, β-TD was mainly caused by the turnover component (Fig. 4). Despite the β-FD being very small for all dimensions, nestedness was the main cause of the pattern found for temporal dimension (β-FDS), while turnover was the main mechanism for horizontal and vertical dimensions (β-FDH e β-FDV) (Fig. 4).

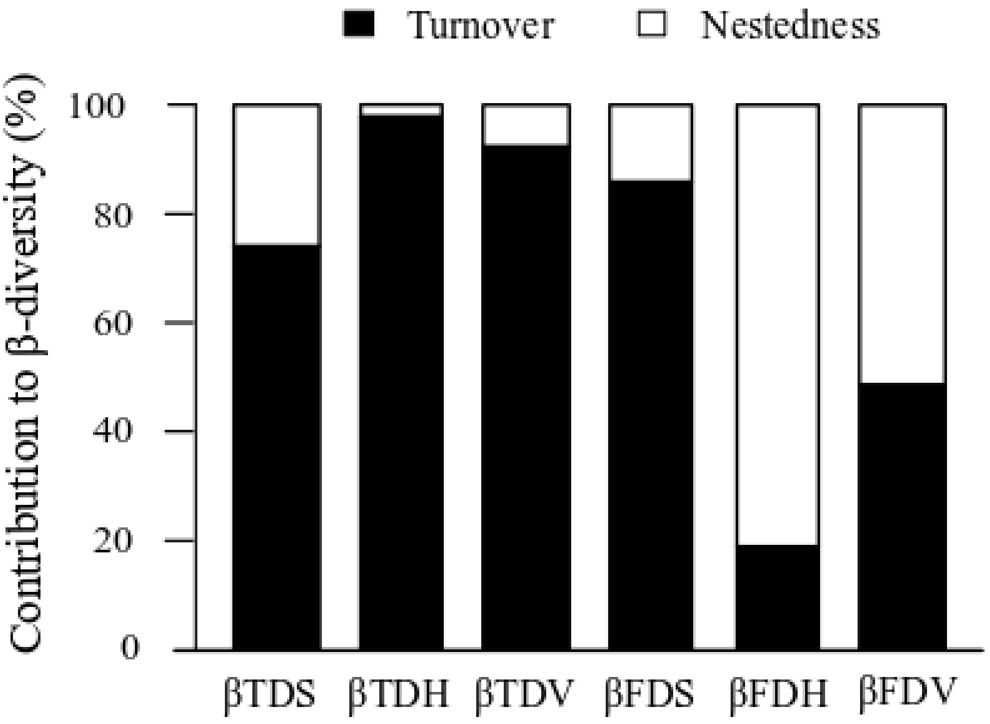

Fig 4. The relative contribution of turnover and nestedness to taxonomic and functional β-diversity for each spatio-temporal dimension evaluated. For taxonomic diversity (TD): β-TDS = temporal dimension; β-TDH = horizontal dimension; β-TDV = vertical dimension. For functional diversity (FD): β-FDS = temporal dimension; β-FDH = horizontal dimension; β-FDV = vertical dimension.

Effect of elevation and environmental variables on taxonomic and functional diversity

Ant species richness decreased in *campo rupestre* and increased in forest communities as a function of the increase in elevation (Table 2). The richness was also different between habitats (Table 2), being greater in the *campo rupestre* (128 spp.) rather than in forest (113 spp.). Evident effects were observed in the interaction of these two explanatory variables on species richness (Table 2). Although we observed evident effects in relation to the vertical dimension, the effects were negative for *campo rupestre* communities and positive for forest communities (Fig. 5a). There were evident positive effects of the seasonal dimension on species richness, whereas the rainy season presented greater species richness than dry season in both habitats (Fig. 5a; Table 2). We observed negative effects of the interaction of seasonal and vertical dimension with decreased on functional richness (α-FD), especially in dry season (Fig. 5b; Table 2).

Table 2. GLMM model's results with α-TD (species richness) and α-FD (Rao index) as responses variables. The response variables denote a model with Poisson error distribution for complete models and for minimal adequate models. In all models, sample unit (transect) was the random variable. d.f. = Degrees of freedom; Chisq = Type II Wald chi-square tests; Pr(>Chisq) = P-values (significance codes: *** ≤ 0.001; **≤ 0.01; * ≤ 0.05).

Response variables	**Explanatory variables**	**Chisq.**	**Pr(>Chisq)**
Model 1			
Dimensions			
α-TD – Richness[a]	**Season**	**16.8828**	**0.03976*****
d.f.residuals = 64	**Mean Elevation**	**5.4562**	**0.0195***
	Habitat	**34.4278**	**0.000004424*****
	Season : Mean Elevation	0.0000	0.9973
	Season : Habitat	0.2426	0.6224
	Mean Elevation : Habitat	**40.1003**	**0.0000002413*****
α-TD – Richness[b]	**Season**	**16.8956**	**0.03949*****
d.f.residuals = 66	**Mean Elevation**	**5.4576**	**0.01948****
	Habitat	**34.4313**	**0.000004416*****
	Mean Elevation : Habitat	**40.1035**	**0.0000002409*****
α-FD – Rao[a]	Season	0.5445	0.460589

d.f.residual = 64	Mean Elevation	2.0474	0.152469
	Habitat	2.6022	0.106717
	Season : Mean Elevation	**10.7650**	**0.001034****
	Season : Habitat	0.1252	0.723442
	Mean Elevation : Habitat	0.8080	0.368698
α-FD – Rao[b]	Season	0.5588	0.4547273
d.f.residual = 67	Mean Elevation	1.6931	0.1931936
	Season : Mean Elevation	**10.9405**	**0.0009408*****
Model 2			
Environmental variables			
α-TD – Richness[a]	Mean Elevation	0.0000	0.99973
d.f.residuals = 64	Mean NDVI	0.8621	0.32525
	Mean Temperature	**17.2647**	**0.03252**
	Mean Elevation : Mean NDVI	3.6933	0.05463
	Mean Elevation : Mean Temp	0.2590	0.61082
	Mean NDVI : Mean Temp	0.1230	0.72583
α-TD – Richness[b]	Mean Elevation	0.0138	0.90641
d.f.residuals = 66	Mean NDVI	0.8841	0.34709
	Mean Temperature	**17.4700**	**0.02919**
	Mean Elevation : Mean NDVI	**3.9692**	**0.04634**
α-FD – Rao[a]	Mean Elevation	0.0004	0.9834

d.f.residual = 64	Mean NDVI	0.0006	0.9811
	Mean Temperature	0.0004	0.9844
	Mean Elevation : Mean NDVI	0.0004	0.9832
	Mean Elevation : Mean Temp	0.0026	0.9592
	Mean NDVI : Mean Temp	0.0000	0.9983

[a] Complete model

[b] Minimal adequate model

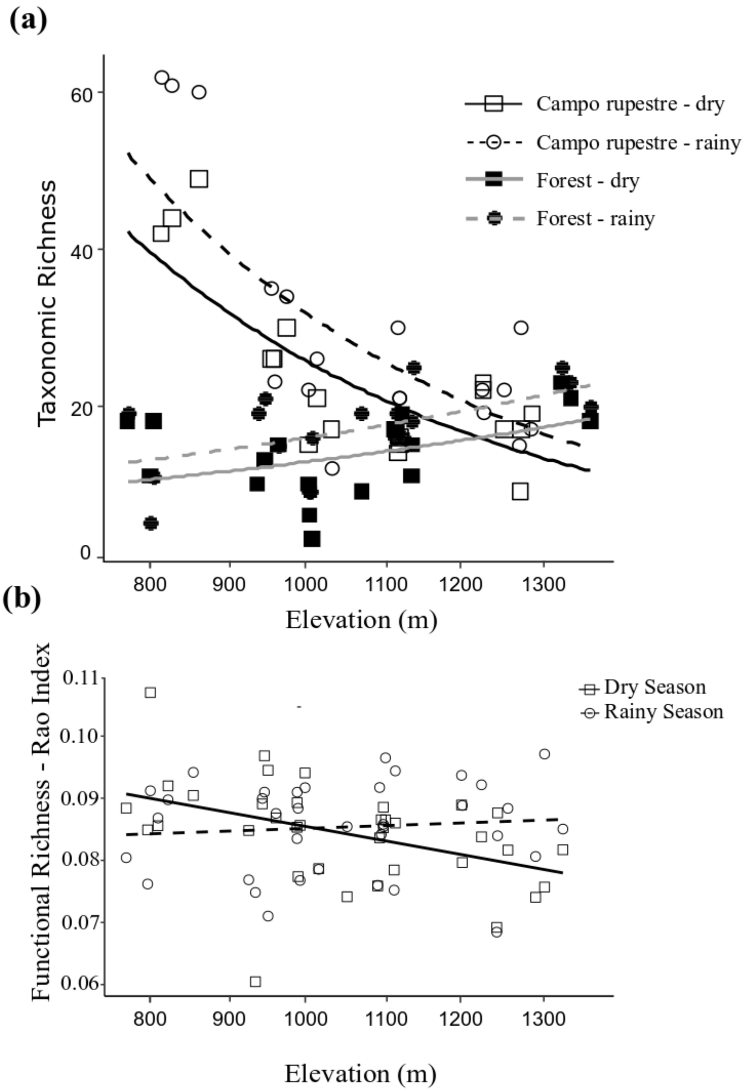

Fig 5. Taxonomic (a) and functional (b) ants' richness (α-TD and α-FD along an elevational gradient in Serra do Cipó, Minas Gerais State, Brazil. Each point denotes the diversity of an elevation per season (sampling unit).

We observed negative effects on species richness due to the decreasing temperature as a function of the increase in elevation and between seasons as well (Table 2; Supplementary Material I Table S3). When we considered only mean elevation or mean NDVI, no evident effects were observed on species richness, although we observed clear effects in the interaction of these explanatory variables (Table 2). No evident effects were observed of all environmental variables tested for functional richness (α-FD).

In relation to β-TD (taxonomic turnover) and β-FD (functional turnover) patterns, we observed positive effects of the interaction between habitat and elevation for β-TD (Table 3; Fig. 6a) and a positive effect of habitat on β-FD patterns(Table 3; Fig. 6a). As found for functional richness (α-FD), no evident effects were observed of environmental variables tested for functional turnover (Table 3) and for taxonomic turnover as well.

Table 3. GLM model's results with β-TD (species turnover) and β-FD (functional turnover) as responses variables. The response variables denote a model with binomial error distribution corrected for overdispersion for complete models and for minimal adequate models. d.f. = Degrees of freedom; Chisq = Type II Wald chi-square tests; Pr(>Chisq) = P-values (significance codes: *** ≤ 0.001; **≤ 0.01; * ≤ 0.05).

Response variables	**Explanatory variables**	**Chisq.**	**Pr(>Chisq)**
Model 1			
Dimensions			
β-TD – Turnover[a]	Season	1.0444	0.3068
d.f.residuals = 17	Mean Elevation	1.1433	0.28496
	Habitat	2.5572	0.10979
	Season : Mean Elevation	0.025	0.87441

	Season : Habitat	2.3008	0.12931
	Mean Elevation : Habitat	**5.0324**	**0.02488***
β-TD – Turnover[b]	Mean Elevation	1.1216	0.28957
d.f.residuals = 20	Habitat	2.5150	0.11277
	Mean Elevation : Habitat	**4.9515**	**0.02607***
β-FD – Turnover[a]	Season	0.7948	0.372638
d.f.residuals = 17	**Mean Elevation**	**11.2007**	**0.000818*****
	Habitat	0.0406	0.840243
	Season : Mean Elevation	0.0181	0.892905
	Season : Habitat	2.5217	0.112292
	Mean Elevation : Habitat	1.4858	0.222869
β-FD – Turnover[b]	**Habitat**	**11.3830**	**0.0007411*****
d.f.residuals = 22			
Model 2			
Environmental variables			
β-TD – Turnover[a]	Mean Elevation	3.0212	0.08218
d.f.residuals = 17	Mean NDVI	1.7413	0.18698
	Mean Temperature	1.4301	0.23174
	Mean Elevation : Mean NDVI	1.3237	0.24993
	Mean Elevation : Mean Temp	0.0005	0.98233
	Mean NDVI : Mean Temp	3.5423	0.05982

β-FD – Turnover[b]	Mean Elevation	0.3338	0.5635
d.f.residuals = 17	Mean NDVI	0.0128	0.9099
	Mean Temperature	1.0331	0.3094
	Mean Elevation : Mean NDVI	2.5799	0.1082
	Mean Elevation : Mean Temp	0.7195	0.3963
	Mean NDVI : Mean Temp	0.0510	0.8214

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[a] Complete model

[b] Minimal adequate model

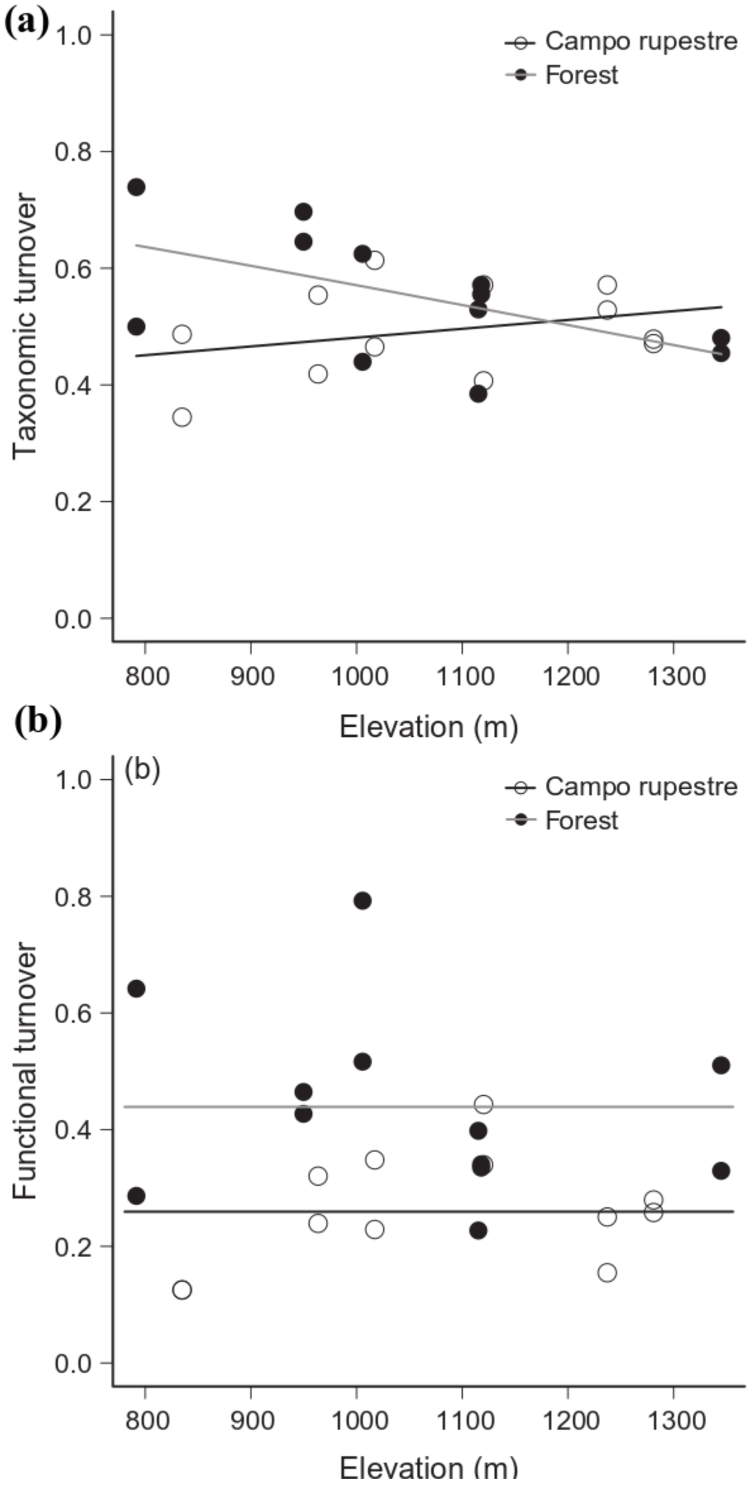

Fig 6. Taxonomic (a) and functional (b) turnover (β-TD and β-FD) of ants along an elevational gradient in Serra do Cipó, Minas Gerais State, Brazil. Each point denotes the β-diversity of an elevation per season (sampling unit).

Discussion

The main contribution to the changes in taxonomic diversity occurred along the vertical dimension (i.e., elevation), followed by the horizontal dimension (i.e., habitats). Total functional β-diversity was lower than taxonomic β-diversity and an evident effect of the environmental variables on the species richness due to the decrease in mean temperature with increasing elevation, and lower Mean NDVI values in *campo rupestre* environments at higher elevations (lower habitat structural heterogeneity). Despite the high turnover of ant species occurring across all spatio-temporal dimensions, the communities are functionally or ecologically redundant, i.e., species change between habitats and elevations, but the main functional characteristics and ecological functions remain basically unchanged.

The differences in TD patterns between the horizontal and vertical dimensions can also be explained by the variation in vegetation structure in both dimensions. In the same system, Fernandes *et al.*, (2016) found high β-TD of ants among elevations, and the main explanations were a decrease in the structural heterogeneity and changes in climate (decrease in average temperature) along the habitats and the elevational gradient. In Serra do Cipó, there is a decrease in the structural heterogeneity of the grassland areas with elevation (Santos *et al.*, 2011; Conceição *et al.*, 2016). We observed an evident shift in the climate and vegetation with increasing elevation on *campo rupestre*, determining changes in composition (high β-TD) and decreases of ant species richness. Moreover, the species richness of forest communities increased as a function of elevation rise. As seen by Lasmar *et al.* (2020) when evaluating elevational patterns in ants diversity, it is important to highlight the potential bias of different kinds of vegetation types across elevational gradients, showing the importance to preserve them. Probably, this pattern reflects seasonal riverbank conditions, which are subject to fluctuation in water level due to its geomorphological structure and slope. In forest environments between 800 and 1200 m, considered as riparian forests, seasonal flood-prone streams occur (Rosgen, 1994; Galdean *et al.*, 2000). Flooding can act as a physical filter for ant communities and literally drown entire colonies, diminishing species richness, and abundance, interfering with the establishment of ground dwelling ants (Ballinger *et al.*, 2007).

The weather conditions in the studied area are considered climatically seasonal (Ferrari *et al.*, 2016), but we observed small contribution of the seasonal dimension to changes in species composition and community traits (β-TDS and β-FDS). Since we use a passive sampling method and ants usually have increased activity in higher temperatures (Kaspari *et al.*, 2015), the chance of capturing ants increases in the hotter seasons of the year. Similarly, we observed fewer species in the dry season than in the rainy season (decrease of α-TD) with a consequent decrease in functional richness (α-FD) along the elevational gradient in the dry season. In addition, in the rainy season, we verified a greater richness of specialist predators (cryptic predators), evidencing the influence of the climatic variations on β-FD.

A possible explanation for the FD pattern found here is that species are functionally redundant, i.e., although there is a great replacement of species and a decrease in species richness in the vertical dimension, the main ecological functions remained along the gradient. We identified ant communities with similar characteristics and non-random attribute patterns along the elevation and, consequently, we can consider communities ecologically similar along these gradients as demonstrated by Smith (2015), which revision paper included data from a survey in Serra do Cipó (Araújo & Fernandes, 2003). Walker (1992) argues that functional redundancy (or ecological redundancy) occurs when there is no effect of the variation in species composition and richness on FD. Similar patterns of β-TD and β-FD of terrestrial social and non-social insects were observed in the same system of the PELD/CRSC Project (e.g., termites; dung beetles, Nunes *et al.*, 2016, 2017). The explanation for the α-TD patterns found was related to environmental filters, mainly in relation to vertical (negative effect of temperature and humidity variation) and horizontal dimensions (variation of the vegetation heterogeneity).

When we consider the β-TD decomposition into turnover and nestedness, the vertical and horizontal dimensions (β-TDV and β-TDH) contributed with more than half of the explanation in the variation of species composition along the elevation gradient, being explained by the turnover of species along the vertical and horizontal dimensions. These results confirm the patterns previously found for terrestrial insects in the *campo rupestre* (Coelho *et al.*, 2018a; da Silva *et al.*, 2018; Nunes *et al.*, 2016; 2017; Perillo *et al.*, 2017). Although β-FDV and β-FDH were also explained mainly by trait turnover, it is not possible to state that this pattern actually exists, since β-FD was very low and contributed with 3.2% of γ-FD, which was 96.8% explained by the α-component, showing a functional redundancy in all spatio-temporal dimensions addressed (Villéger *et al.*, 2013). It may be important to include more functional characteristics related to habitat and thermal tolerance, especially traits with continuous measurements (as proposed by Petchey & Gaston, 2006) to increase the accuracy of FD estimates.

In general, the high taxonomic diversity of the communities that we found resemble those found for ants and other taxa in the *campo rupestre* (Leite *et al.*, 2008; Fernandes *et al.*, 2016; Nunes *et al.*, 2016, 2017; Silveira *et al.*, 2016; Pereira *et al.*, 2017; Perillo *et al.*, 2017). Also, these high taxonomic diversity pattern and the generic composition found for ants in the *campo rupestre* was very similar with Cerrado (Vasconcelos *et al.*, 2018) and Atlantic Forest biomes. The *campo rupestre sensu stricto* fits into the OCBIL definition, as being an old, climatically buffered infertile landscape (Hopper *et al.*, 2016; Silveira *et al.*, 2016). It is probably one of the oldest ecosystems of the South American continent and most of the geological formations where they occur are approximately 640 m.y.a. (millions years ago) (Alkmin, 2012). Possibly, ants already existed in the *campo rupestre,* since the origin of the current ants happened between 115 to 135 m.y.a. (Brady *et al.*, 2006; Branstetter *et al.*, 2017).

In this paper, we found that ant communities are very similar functionally despite the changes in local environmental conditions among elevations, but also with compositional restrictions regarding the characteristics of spatial dimensions (i.e., habitats and elevation bands). Taxonomic differences in community composition as a consequence of the high β-TD along the gradient over relatively short geographic distances emphasize the importance of conserving the entire mountain, since with the loss of any part of the community, either at higher elevations or not, there will be a loss of diversity, although there is no loss of the main ecological functions (or traits) evaluated in this study. Comparisons of TD and FD patterns demonstrated the high importance of using different diversity facets at distinct scales (Anderson *et al.*, 2011; Barton *et al.*, 2013; Bishop *et al.*, 2015). With information about the patterns of the multiple facets of diversity (TD, FD and including phylogenetic diversity – PD; Cianciaruso *et al.*, 2009; Anderson *et al.*, 2011), we can directly relate our observations and discoveries about biodiversity to applied ecology. For example, in designing public policies or identifying priority areas for biodiversity conservation and cultural diversity, one of the main objectives of the biosphere reserves in the world (Unesco, 1996).

Acknowledgments

We thank all friends involved in data collection during fieldwork, especially Rayana Melo, Humberto Brant, Matheus Couto, and Marina Catão. We also thank Flávio Camarota and Scott Powel (*Cephalotes*), Alexandre Ferreira (*Pheidole*), Rodolfo Probst (*Camponotus*, *Myrmelachista*, and *Octostruma*), and Mayron Escárraga (Dolichoderinae) for ant identification. We also thank Milton Barbosa, Flávio Camarota, Lucas Perillo, and Rafael Leitão for all useful comments on our manuscript. We thank the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for funding this Long-Term Ecological Research (PELD-CRSC-17 - 441515/ 2016-9), and Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG - CRA - APQ-00311-15) for financial support. GWF and FSN received a Research Productivity Fellowship from CNPq. RRCS is supported by Pesquisa & Desenvolvimento of Agência Nacional de Energia Elétrica and

Companhia Energética de Minas Gerais (P&D ANEEL/CEMIG, PROECOS project GT-599), FAPEMIG (APQ-00288-17) and CNPq (428298/2018-4) research project grants. This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001. FSN, PGdS, and FSC thank the CAPES for grants. We are also grateful to Cedro Têxtil, Reserva Vellozia, ICMBio-PARNA Serra do Cipó, Pousada Serra Morena and Pouso do Elefante and GSG for logistical support. The author(s) declare(s) that there is no conflict of interest regarding the publication of this article.

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Supporting information

Table S1. Species captured and traits used to calculate functional diversity (FD): (1) morphological traits (a) WL: Weber's length (µm); (b) HFL: Hind femur length (µm); (c) ML: Mandible length (µm); (d) V: measure of color brightness (%); (e) Workers polymorphism: categorical (monomorphic, dimorphic and polymorphic); (f) integument sculpture (ordinal data (smooth/often shine, intermediate and texturized); and (2) ecological traits or life history traits (a): functional groups based on global-scale responses of ants to environmental stress and disturbance (Andersen, 1995; Leal *et al*,. 2012; Paolucci *et al.*, 2016). AA = Army Ants; AD = Arboreal Dominant; AP = Arboreal Predator; AS = Arboreal Subordinate; CO = Cryptic Omnivores; CP = Cryptic Predators; DD = Dominant Dolichoderinae; EO = Epigeic Omnivores; EP = Epigeic Predators; Hatt = High Attini; Latt = Low Attini; OPP = Opportunist; SC = Subordinate Camponotini SH = Seed Harvester.

Species	**WL**	**HFL**	**ML**	**V**	**Workers' polymorphism**	**Integument sculpture**	**Functional groups**
Acromyrmex balzani	2558.66	1.04	0.40	0.54	polymorphic	intermediate	Hatt
Acromyrmex coronatus	1759.29	1.11	0.49	0.38	polymorphic	intermediate	Hatt
Acromyrmex sp2	2235.66	1.13	0.51	0.62	polymorphic	intermediate	Hatt
Acromyrmex sp5	2411.54	1.17	0.50	0.34	polymorphic	intermediate	Hatt
Acromyrmex subterraneus	3107.80	1.12	0.46	0.62	polymorphic	intermediate	Hatt
Anochetus inermis	1378.50	0.69	0.45	0.48	monomorphic	intermediate	EP
Apterostigma gr. *pilosum* sp1	1281.67	1.08	0.47	0.36	monomorphic	intermediate	Latt
Apterostigma gr. *pilosum* sp2	1602.61	0.95	0.30	0.28	monomorphic	intermediate	Latt
Apterostigma gr. pilosum sp3	1272.44	0.97	0.30	0.34	monomorphic	intermediate	Latt
Atta sexdens rubropilosa	3788.38	1.41	0.45	0.34	polymorphic	intermediate	Hatt
Brachymyrmex pictus	371.70	0.89	0.33	0.41	monomorphic	smooth	OPP
Brachymyrmex prox. *Cordemoyi*	475.97	0.89	0.36	0.26	monomorphic	smooth	OPP
Brachymyrmex sp4	451.42	0.75	0.47	0.27	monomorphic	smooth	OPP
Brachymyrmex sp5	704.81	0.87	0.44	0.63	monomorphic	smooth	OPP
Camponotus (Hypercolobopsis) sp3	1775.89	0.74	0.25	0.62	dimorphic	intermediate	SC
Camponotus (Hypercolobopsis) sp6	1732.71	0.82	0.29	0.52	dimorphic	intermediate	SC
Camponotus (Hypercolobopsis) sp7	1742.19	0.82	0.27	0.63	dimorphic	intermediate	SC
Camponotus (Myrmaphaenus) sp1	2452.25	0.83	0.36	0.14	dimorphic	intermediate	SC
Camponotus (Myrmaphaenus) sp5	1434.07	0.88	0.30	0.12	dimorphic	intermediate	SC
Camponotus (Tanaemyrmex) sp2	1931.61	0.87	0.26	0.11	dimorphic	intermediate	SC
Camponotus arboreus	2152.96	0.79	0.27	0.14	dimorphic	intermediate	SC
Camponotus atriceps	2590.19	0.90	0.28	0.46	dimorphic	intermediate	SC

Species	**WL**	**HFL**	**ML**	**V**	**Workers' polymorphism**	**Integument sculpture**	**Functional groups**
Camponotus blandus	2031.42	0.84	0.29	0.12	dimorphic	intermediate	SC
Camponotus cingulatus	2699.53	1.00	0.28	0.38	dimorphic	intermediate	SC
Camponotus crassus	1602.19	0.87	0.32	0.13	dimorphic	intermediate	SC
Camponotus latangulus	1446.18	0.90	0.36	0.38	dimorphic	intermediate	SC
Camponotus lespesii	4288.06	0.97	0.25	0.20	dimorphic	intermediate	SC
Camponotus leydigi	2817.51	0.80	0.28	0.45	dimorphic	intermediate	SC
Camponotus melanoticus	2856.95	0.90	0.26	0.24	dimorphic	intermediate	SC
Camponotus novogranadensis	1608.14	0.73	0.32	0.15	dimorphic	intermediate	SC
Camponotus renggeri	3157.38	0.89	0.28	0.14	dimorphic	intermediate	SC
Camponotus rufipes	3196.31	0.92	0.27	0.14	dimorphic	intermediate	SC
Camponotus senex	1628.06	0.95	0.33	0.15	dimorphic	intermediate	SC
Camponotus sericeiventris	3694.48	0.97	0.26	0.14	dimorphic	intermediate	SC
Camponotus sexguttatus	1889.19	0.84	0.27	0.13	dimorphic	intermediate	SC
Camponotus sp14	1956.54	0.78	0.27	0.18	dimorphic	intermediate	SC
Camponotus sp19	3493.04	0.80	0.30	0.20	dimorphic	intermediate	SC
Camponotus sp20	3174.94	0.85	0.26	0.46	dimorphic	intermediate	SC
Camponotus sp4	3679.38	0.92	0.23	0.35	dimorphic	intermediate	SC
Camponotus sp5	3179.61	0.92	0.27	0.54	dimorphic	intermediate	SC
Camponotus vittatus	2690.20	0.93	0.26	0.61	dimorphic	intermediate	SC
Cardiocondyla cf. *obscurior*	501.44	0.59	0.37	0.68	monomorphic	intermediate	AD
Carebara urichi	509.08	0.63	0.47	0.60	dimorphic	intermediate	CO
Cephalotes atratus	4140.30	0.86	0.27	0.13	dimorphic	intermediate	AS
Cephalotes pusillus	1338.89	0.70	0.31	0.16	dimorphic	intermediate	AS
Crematogaster acuta	985.77	0.89	0.56	0.30	polymorphic	intermediate	AD
Crematogaster brasiliensis	786.65	1.06	0.50	0.23	polymorphic	intermediate	AD
Crematogaster prox. *erecta* sp1	758.01	0.83	0.45	0.34	polymorphic	intermediate	AD
Crematogaster prox. *obscurata* sp1	637.96	0.80	0.40	0.63	polymorphic	intermediate	AD
Crematogaster sp6	799.19	0.98	0.47	0.32	polymorphic	intermediate	AD
Cyphomyrmex gr. *rimosus* sp1	830.77	0.78	0.43	0.51	monomorphic	intermediate	Latt
Cyphomyrmex gr. *rimosus* sp2	1002.22	0.88	0.39	0.41	monomorphic	intermediate	Latt
Cyphomyrmex gr. *rimosus* sp3	858.61	0.83	0.40	0.39	monomorphic	intermediate	Latt
Dolichoderus bispinosus	1911.95	0.94	0.35	0.10	monomorphic	intermediate	AD
Dolichoderus diversus	1886.54	0.90	0.28	0.22	monomorphic	smooth	AD
Dolichoderus lutosus	1391.76	0.77	0.33	0.66	monomorphic	smooth	AD
Dorymyrmex brunneus	1224.75	1.00	0.37	0.39	monomorphic	smooth	OPP
Dorymyrmex goeldii	1198.94	1.02	0.33	0.29	monomorphic	smooth	OPP
Dorymyrmex pyramicus	1015.13	1.03	0.39	0.81	monomorphic	smooth	OPP

Species	**WL**	**HFL**	**ML**	**V**	**Workers' polymorphism**	**Integument sculpture**	**Functional groups**
Dorymyrmex sp5	785.73	1.05	0.36	0.62	monomorphic	smooth	OPP
Eciton cf. *vagans*	2813.05	0.99	0.35	0.36	polymorphic	intermediate	AA
Eciton mexicanum	2972.83	1.16	1.05	0.51	polymorphic	intermediate	AA
Ectatomma brunneum	3602.40	0.77	0.39	0.17	monomorphic	textured	EP
Ectatomma edentatum	2760.84	0.76	0.41	0.22	monomorphic	textured	EP
Ectatomma opaciventre	4758.47	0.93	0.40	0.53	monomorphic	textured	EP
Ectatomma permagnum	3607.01	0.77	0.41	0.16	monomorphic	textured	EP
Ectatomma planidens	2368.66	0.72	0.41	0.40	monomorphic	textured	EP
Ectatomma tuberculatum	3546.31	0.81	0.45	0.39	monomorphic	textured	AP
Forelius brasiliensis	839.50	1.18	0.43	0.61	monomorphic	smooth	DD
Forelius maranhaoensis	685.37	1.21	0.52	0.35	monomorphic	smooth	DD
Forelius sp2	536.26	0.91	0.42	0.54	monomorphic	smooth	DD
Gnamptogenys gp *striatula* sp.n. A	1085.81	0.57	0.43	0.46	monomorphic	textured	EP
Gnamptogenys sp3	1889.60	0.66	0.40	0.14	monomorphic	textured	EP
Gnamptogenys striatula	1467.21	0.84	0.38	0.21	monomorphic	textured	EP
Gnamptogenys sulcata	1297.90	0.64	0.41	0.25	monomorphic	textured	EP
Heteroponera sp1	1192.50	0.63	0.28	0.27	monomorphic	textured	EP
Hylomyrma balzani	1076.35	0.76	0.52	0.25	monomorphic	textured	EO
Hylomyrma prox. *Reitteri*	1164.23	0.80	0.53	0.24	monomorphic	textured	EO
Hylomyrma sp4	1049.22	0.72	0.50	0.28	monomorphic	textured	EO
Hypoponera distinguenda	935.95	0.54	0.36	0.33	monomorphic	smooth	CP
Hypoponera sp1	1144.60	0.58	0.39	0.25	monomorphic	smooth	CP
Hypoponera sp3	1629.02	0.55	0.44	0.23	monomorphic	smooth	CP
Hypoponera sp4	790.79	0.55	0.37	0.39	monomorphic	smooth	CP
Hypoponera sp5	1563.29	0.65	0.34	0.23	monomorphic	smooth	CP
Kalathomyrmex emeryi	860.48	0.68	0.50	0.67	monomorphic	intermediate	Latt
Labidus coecus	1433.98	0.98	0.37	0.30	polymorphic	intermediate	AA
Labidus praedator	1602.77	1.00	0.47	0.23	polymorphic	intermediate	AA
Leptogenys aff. *Górgona*	1550.62	0.69	0.29	0.15	monomorphic	smooth	EP
Leptogenys crudelis	2933.08	0.68	0.27	0.11	monomorphic	smooth	EP
Linepithema aztecoides	730.18	0.83	0.35	0.36	monomorphic	smooth	EO
Linepithema cerradense	732.48	0.84	0.34	0.65	monomorphic	smooth	EO
Linepithema cf. *pulex*	864.22	0.67	0.33	0.59	monomorphic	smooth	EO
Linepithema gallardoi	757.60	0.77	0.33	0.39	monomorphic	smooth	EO
Linepithema iniquum	858.67	0.75	0.34	0.38	monomorphic	smooth	EO
Linepithema micans	813.12	0.80	0.36	0.54	monomorphic	smooth	EO
Megalomyrmex sp1	1157.27	0.90	0.34	0.46	monomorphic	smooth	EO

Species	**WL**	**HFL**	**ML**	**V**	**Workers’ polymorphism**	**Integument sculpture**	**Functional groups**
Mycetarotes sp1	1063.75	0.89	0.47	0.72	monomorphic	intermediate	Latt
Mycetophylax gr. *strigatus* sp4	829.21	0.57	0.44	0.47	monomorphic	intermediate	Latt
Mycetophylax gr. *strigatus* sp5	795.90	1.04	0.74	0.70	monomorphic	intermediate	Latt
Mycetophylax gr. *strigatus* sp6	730.09	0.81	0.51	0.60	monomorphic	intermediate	Latt
Mycetophylax lectus	712.06	0.81	0.45	0.57	monomorphic	intermediate	Latt
Mycocepurus goeldii	920.92	0.85	0.49	0.39	monomorphic	intermediate	Latt
Myrmelachista catharinae	688.57	0.79	0.32	0.13	monomorphic	smooth	AS
Myrmicocrypta sp1	922.00	0.84	0.45	0.66	monomorphic	intermediate	Latt
Neivamyrmex cf. *swainsonii*	596.01	0.53	0.30	0.54	polymorphic	intermediate	AA
Neivamyrmex pseudops	1356.80	1.12	0.42	0.46	polymorphic	intermediate	AA
Neivamyrmex sp2	1099.18	0.71	0.35	0.46	polymorphic	intermediate	AA
Neoponera crenata	2138.10	0.74	0.45	0.15	monomorphic	intermediate	EP
Neoponera latinoda	2814.77	0.76	0.48	0.15	monomorphic	smooth	EP
Neoponera villosa	4643.72	0.79	0.48	0.14	monomorphic	smooth	AP
Nomamyrmex esenbeckii	2531.03	0.85	0.38	0.54	polymorphic	intermediate	AA
Nylanderia sp1	783.41	0.95	0.40	0.57	monomorphic	smooth	OPP
Ochetomyrmex semipolitus	495.81	0.69	0.48	0.69	monomorphic	intermediate	EO
Octostruma balzani	576.86	0.70	0.32	0.50	monomorphic	textured	CP
Octostruma iheringi	759.18	0.72	0.31	0.45	monomorphic	textured	CP
Octostruma stenognatha	675.45	0.70	0.30	0.42	monomorphic	textured	CP
Odontomachus bauri	4343.87	0.93	0.47	0.27	monomorphic	intermediate	EP
Odontomachus brunneus	2551.31	0.85	0.45	0.29	monomorphic	intermediate	EP
Odontomachus chelifer	4888.06	0.89	0.46	0.31	monomorphic	intermediate	EP
Odontomachus meinerti	2426.02	0.81	0.46	0.39	monomorphic	intermediate	EP
Oxyepoecus prox. *bruschi* sp1	566.91	0.64	0.46	0.30	monomorphic	intermediate	EP
Oxyepoecus prox. *bruschi* sp2	628.51	0.63	0.42	0.37	monomorphic	intermediate	EP
Oxyepoecus sp5	496.43	0.62	0.42	0.39	monomorphic	intermediate	EP
Pachycondyla harpax	2632.19	0.64	0.43	0.15	monomorphic	intermediate	EP
Pachycondyla striata	4269.56	0.73	0.44	0.15	monomorphic	intermediate	EP
Pheidole ambígua	839.68	0.94	0.46	0.50	dimorphic	intermediate	EO
Pheidole capilata	839.16	0.92	0.50	0.27	dimorphic	intermediate	EO
Pheidole dorsata	467.19	0.82	0.50	0.39	dimorphic	intermediate	EO
Pheidole gertrudae	867.83	1.08	0.52	0.41	dimorphic	smooth	EO
Pheidole jelskii	1142.97	1.12	0.39	0.32	dimorphic	intermediate	EO
Pheidole oxyops	1246.70	1.22	0.41	0.32	dimorphic	intermediate	EO
Pheidole prox. *Reclusi*	811.69	0.93	0.50	0.18	dimorphic	intermediate	EO
Pheidole radoszkowskii	742.21	0.94	0.41	0.55	dimorphic	intermediate	EO

Species	**WL**	**HFL**	**ML**	**V**	**Workers' polymorphism**	**Integument sculpture**	**Functional groups**
*Pheidole scolioceps**	NA	NA	NA	NA	dimorphic	intermediate	EO
Pheidole sensitiva	733.25	1.05	0.48	0.19	dimorphic	intermediate	EO
Pheidole sp1	1167.29	1.05	0.39	0.24	dimorphic	intermediate	EO
Pheidole sp13	457.99	0.77	0.48	0.57	dimorphic	intermediate	EO
Pheidole sp14	728.83	0.82	0.52	0.59	dimorphic	intermediate	EO
Pheidole sp15	991.17	0.88	0.45	0.24	dimorphic	smooth	EO
Pheidole sp17	775.01	0.91	0.51	0.28	dimorphic	intermediate	EO
Pheidole sp18	852.64	1.12	0.33	0.60	dimorphic	intermediate	EO
Pheidole sp2	747.97	0.94	0.43	0.65	dimorphic	intermediate	EO
Pheidole sp20	839.89	0.94	0.42	0.58	dimorphic	intermediate	EO
Pheidole sp24	836.95	1.11	0.43	0.35	dimorphic	intermediate	EO
Pheidole sp25	851.55	0.83	0.51	0.23	dimorphic	intermediate	EO
Pheidole sp29	776.94	1.05	0.42	0.64	dimorphic	intermediate	EO
Pheidole sp32	518.70	0.78	0.50	0.73	dimorphic	intermediate	EO
Pheidole sp39	851.45	0.97	0.41	0.55	dimorphic	intermediate	EO
Pheidole sp40	839.40	1.05	0.49	0.55	dimorphic	intermediate	EO
Pheidole sp45	479.71	0.77	0.50	0.57	dimorphic	intermediate	EO
Pheidole sp5	703.17	0.87	0.53	0.20	dimorphic	intermediate	EO
Pheidole sp51	572.01	0.73	0.52	0.61	dimorphic	intermediate	EO
Pheidole sp52	925.53	0.97	0.43	0.44	dimorphic	intermediate	EO
Pheidole sp53	822.60	1.01	0.42	0.51	dimorphic	intermediate	EO
Pheidole sp6	719.71	0.93	0.41	0.75	dimorphic	intermediate	EO
Pheidole sp7	886.39	1.06	0.42	0.61	dimorphic	intermediate	EO
Pheidole sp8	443.76	0.78	0.51	0.58	dimorphic	intermediate	EO
Pheidole subarmata	529.95	0.85	0.54	0.51	dimorphic	intermediate	EO
Pheidole susannae	1006.22	1.02	0.40	0.49	dimorphic	intermediate	EO
Pheidole termitobla	646.55	0.82	0.51	0.40	dimorphic	intermediate	EO
Pheidole vafra	777.43	1.00	0.42	0.47	dimorphic	intermediate	EO
Pogonomyrmex naegelii	1495.75	0.85	0.50	0.35	monomorphic	textured	SH
Procryptocerus schmitti	1194.11	0.55	0.26	0.13	monomorphic	textured	AS
Pseudomyrmex gr. *pallidus* sp1	1105.60	0.47	0.29	0.67	monomorphic	intermediate	AS
Pseudomyrmex gracilis	2282.01	0.63	0.34	0.22	monomorphic	intermediate	AS
Pseudomyrmex sp1	2263.75	0.45	0.25	0.63	monomorphic	intermediate	AS
Pseudomyrmex sp2	1532.20	0.51	0.26	0.55	monomorphic	intermediate	AS
Pseudomyrmex sp3	1893.88	0.54	0.30	0.61	monomorphic	intermediate	AS
Pseudomyrmex sp4	1479.88	0.55	0.28	0.26	monomorphic	intermediate	AS
Pseudomyrmex sp7	1232.77	0.48	0.26	0.49	monomorphic	intermediate	AS

Species	**WL**	**HFL**	**ML**	**V**	**Workers' polymorphism**	**Integument sculpture**	**Functional groups**
Pseudomyrmex termitarius	1799.27	0.66	0.39	0.49	monomorphic	intermediate	AS
Rasopone sp2	1688.18	0.54	0.40	0.15	monomorphic	intermediate	EP
Sericomyrmex sp1	1410.22	0.82	0.46	0.42	monomorphic	intermediate	Hatt
Sericomyrmex sp2	1648.22	0.80	0.46	0.86	monomorphic	intermediate	Hatt
Sericomyrmex sp4	1462.01	0.84	0.50	0.51	monomorphic	intermediate	Hatt
Sericomyrmex sp5	1114.70	0.91	0.60	0.49	monomorphic	intermediate	Hatt
Solenopsis (Diplorhoptrum) sp1	409.27	0.68	0.54	0.59	monomorphic	smooth	CO
Solenopsis globularia sp1	648.48	0.63	0.40	0.35	polymorphic	smooth	EO
Solenopsis globularia sp2	641.62	0.63	0.39	0.44	polymorphic	smooth	EO
Solenopsis saevissima	1042.91	0.77	0.40	0.52	polymorphic	smooth	EO
Solenopsis sp2	679.61	0.42	0.48	0.72	polymorphic	smooth	CO
Solenopsis sp7	583.28	0.59	0.44	0.22	polymorphic	smooth	EO
Solenopsis substituta	939.42	0.83	0.40	0.24	polymorphic	smooth	EO
Strumigenys gr. *louisianae* sp3*	NA	NA	NA	NA	monomorphic	textured	CP
Strumigenys schulzi	428.46	0.60	0.27	0.64	monomorphic	textured	CP
Trachymyrmex sp1	1538.49	0.81	0.45	0.43	monomorphic	intermediate	Latt
Trachymyrmex sp2	1768.12	0.89	0.43	0.29	monomorphic	intermediate	Latt
Trachymyrmex sp3	1456.10	0.88	0.46	0.55	monomorphic	intermediate	Latt
Trachymyrmex sp4	1092.95	0.79	0.42	0.43	monomorphic	intermediate	Latt
Trachymyrmex sp5	1720.18	0.85	0.46	0.43	monomorphic	intermediate	Latt
Trachymyrmex sp6	1490.50	0.86	0.48	0.44	monomorphic	intermediate	Latt
Tranopelta gilva	560.92	0.61	0.47	0.68	monomorphic	intermediate	CO
Wasmannia affinis	589.15	0.78	0.42	0.59	monomorphic	textured	EO
Wasmannia auropunctata	469.98	0.85	0.42	0.48	monomorphic	textured	EO
Wasmannia lutzi	676.39	0.80	0.38	0.71	monomorphic	textured	EO

***Morphological traits not measured.**

Table S2. Environmental variables used in GLMM's models and PERMANOVA. Units: Mean Elevation: m a.s.l (above sea level); Mean Air Humidity: relative %; Mean Air Temperature: °C; NDVI Mean: mean; NDVI Std. Dev.: std. dev; Accumulated Rainfall: mm.

Season	**Habitat**	**Elevation band**	**Mean Elevation**	**Mean Air Humidity**	**Mean Air Temperature**	**Mean NDVI**	**Std. Dev NDVI.**	**Accumulated Rainfall**
Dry	Campo rupestre	800	834.74	68.7	19.21	0.35	0.27	0
Dry	Forest	800	791.55	68.7	19.21	0.57	0.06	0
Dry	Campo rupestre	900	963.51	70.51	18.59	0.16	0.16	0.1
Dry	Forest	900	949.62	70.51	18.59	0.29	0.13	0.1
Dry	Campo rupestre	1000	1017.11	73.04	17.87	0.44	0.12	0
Dry	Forest	1000	1005.52	73.04	17.87	0.30	0.21	0
Dry	Campo rupestre	1100	1120.29	75.98	17.01	0.30	0.17	0.3
Dry	Forest	1100	1117.94	75.98	17.01	0.29	0.24	0.3
Dry	Campo rupestre	1200	1237.21	75.5	17.08	0.23	0.18	0.4
Dry	Forest	1200	1115.11	75.5	17.08	0.25	0.23	0.4
Dry	Campo rupestre	1300	1281.19	77.19	16.23	0.33	0.10	0.1
Dry	Forest	1300	1345.17	77.19	16.23	0.29	0.17	0.1
Rainy	Campo rupestre	800	834.74	73.49	23.13	0.41	0.07	126.75
Rainy	Forest	800	791.55	73.49	23.13	0.30	0.27	126.75
Rainy	Campo rupestre	900	963.51	77.52	22.63	0.28	0.11	250.92
Rainy	Forest	900	949.62	77.52	22.63	0.25	0.15	250.92
Rainy	Campo rupestre	1000	1017.11	78.1	22.25	0.30	0.16	211.96
Rainy	Forest	1000	1005.52	78.1	22.25	0.44	0.06	211.96
Rainy	Campo rupestre	1100	1120.29	80.18	21.38	0.31	0.07	267.28
Rainy	Forest	1100	1117.94	80.18	21.38	0.41	0.05	267.28
Rainy	Campo rupestre	1200	1237.21	82.89	20.83	0.22	0.14	229.29
Rainy	Forest	1200	1137.56	82.89	20.83	0.21	0.16	229.29
Rainy	Campo rupestre	1300	1281.19	85.14	19.97	0.20	0.13	238.49
Rainy	Forest	1300	1345.17	85.14	19.97	0.38	0.12	238.49

Table S3. Pearson's correlation coefficient (r) between samples and environmental variables collected on the elevation gradient. An r-value greater than 0.7 was the parameter to consider correlated variables (bold). Mean_Eleva – Mean values of elevation (m a.s.l.); NDVI_Mean - NDVI Mean values; Mean_Hum - Mean values of air humidity or Humidity (%); Mean_Temp - Mean values of air temperature (°C); Pluv - Accumulated rainfall or precipitation (mm); NDVI_Std dev - NDVI Standard deviation values.

	Mean_Eleva	NDVI_Mean	Mean_Hum	Mean_Temp	Pluv	NDVI_Std dev
Mean_Eleva	-					
NDVI_Mean	-0.35	-				
Mean_Hum	**0.72**	-0.29	-			
Mean_Temp	-0.45	0.11	0.25	-		
Pluv	0.13	-0.08	**0.74**	**0.80**	-	
NDVI_Std dev	-0.11	-0.47	-0.28	-0.30	-0.43	-

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Table S4. Records of Formicidae species sampling in six elevation cotes, in Rainy and Dry Season and two habitats with different vegetal structures, campo rupestre, and forest at Serra do Espinhaço, Minas Gerais, Brazil.

	Dry Season												Rainy Season											
	Campo Rupestre						Forest						Campo Rupestre						Forest					
Subfamily/Species	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300
Dolichoderinae																								
Dolichoderus bispinosus																			X					
Dolichoderus diversus													X											
Dolichoderus lutosus																			X					
Dorymyrmex brunneus	X	X	X	X			X	X		X				X		X			X			X		
Dorymyrmex goeldii	X	X	X	X	X	X							X	X	X	X	X	X						
Dorymyrmex pyramicus	X	X	X	X	X								X	X	X	X	X	X						
Dorymyrmex sp5	X		X													X								
Forelius brasiliensis	X	X											X		X									
Forelius maranhaoensis	X		X										X		X	X								
Forelius sp2		X	X		X	X							X	X	X	X	X							
Linepithema aztecoides	X	X						X		X			X	X		X				X		X		
Linepithema cerradense	X																							
Linepithema cf. *pulex*									X	X	X	X									X	X	X	X
Linepithema gallardoi										X														
Linepithema iniquum										X												X	X	
Linepithema micans	X	X	X	X	X	X					X		X	X	X	X	X	X					X	
Dorylinae																								
Eciton cf. *vagans*														X										
Eciton mexicanum		X																						
Labidus coecus					X							X				X			X					X
Labidus praedator			X		X								X				X						X	
Neivamyrmex cf. *swainsonii*													X											
Neivamyrmex pseudops													X		X	X	X							
Neivamyrmex sp2						X																		
Nomamyrmex esenbeckii															X	X								
Ectatomminae																								
Ectatomma brunneum	X	X		X				X					X	X								X		
Ectatomma edentatum	X	X		X	X	X			X	X			X	X	X	X	X	X		X				
Ectatomma opaciventre	X												X	X	X									
Ectatomma permagnum	X	X											X					X						
Ectatomma planidens	X		X										X		X									
Ectatomma tuberculatum	X												X	X										
Gnamptogenys gr *striatula* sp nov A**												X												X

	Dry Season												Rainy Season											
	Campo Rupestre						Forest						Campo Rupestre						Forest					
Subfamily/Species	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300
Gnamptogenys sp3				X												X	X							
Gnamptogenys striatula												X				X						X		X
Gnamptogenys sulcata													X	X	X	X	X	X						
Formicinae																								
Brachymyrmex pictus	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X		X	X	X
Brachymyrmex prox. *cordemoyi*	X	X			X	X								X	X	X	X	X					X	
Brachymyrmex sp4								X		X										X			X	
Brachymyrmex sp5									X														X	
Camponotus (*Hypercolobopsis*) sp3						X											X							
Camponotus (*Hypercolobopsis*) sp6	X																							
Camponotus (*Hypercolobopsis*) sp7	X	X																						
Camponotus (*Myrmaphaenus*) sp1	X				X								X				X							
Camponotus (*Myrmaphaenus*) sp5	X													X	X	X	X							
Camponotus (*Tanaemyrmex*) sp2	X																							
Camponotus arboreus																			X	X			X	
Camponotus atriceps							X	X	X	X	X								X	X	X			
Camponotus blandus	X	X	X										X	X	X	X	X							
Camponotus cingulatus	X												X											
Camponotus crassus			X		X		X						X				X							
Camponotus latangulus																					X			
Camponotus lespesii							X	X		X	X	X								X		X	X	X
Camponotus leydigi	X	X											X	X										
Camponotus melanoticus	X	X	X	X	X	X	X	X		X		X	X	X	X	X	X	X	X			X	X	X
Camponotus novogranadensis	X				X								X				X			X				
Camponotus renggeri	X	X					X	X					X	X					X	X			X	
Camponotus rufipes	X	X	X	X	X	X				X		X	X	X	X	X	X	X				X	X	X
Camponotus senex	X	X	X			X							X	X	X	X	X	X						
Camponotus sericeiventris							X	X											X	X				
Camponotus sexguttatus								X											X	X				
Camponotus sp14										X		X												
Camponotus sp19												X												
Camponotus sp20																				X			X	
Camponotus sp4																								X
Camponotus sp5											X								X		X	X	X	
Camponotus vittatus	X	X											X	X										
Myrmelachista catharinae									X			X									X			
Nylanderia sp1								X			X	X										X	X	X
Heteroponerinae																								
Heteroponera sp1																								X
Myrmicinae																								

	Dry Season												Rainy Season											
	Campo Rupestre						Forest						Campo Rupestre						Forest					
Subfamily/Species	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300
Acromyrmex balzani	X	X											X											
Acromyrmex coronatus							X												X				X	
Acromyrmex sp2	X												X											
Acromyrmex sp5											X													X
Acromyrmex subterraneus	X	X	X		X	X	X		X		X		X	X			X	X					X	X
Apterostigma gr. *pilosum* sp1	X	X										X	X	X		X								
Apterostigma gr. *pilosum* sp2				X												X					X		X	
Apterostigma gr. *pilosum* sp3												X												X
Atta sexdens rubropilosa	X	X	X				X	X		X			X	X						X		X		
Cardiocondyla cf. *obscurior*							X																	
Carebara urichi																					X			
Cephalotes atratus	X												X											
Cephalotes pusillus	X	X		X	X			X					X	X			X			X		X		
Crematogaster acuta	X	X	X		X	X							X	X	X		X							
Crematogaster brasiliensis																					X			
Crematogaster prox. *erecta* sp1							X	X	X						X					X	X			
Crematogaster prox. *obscurata* sp1													X											
Crematogaster sp6											X													
Cyphomyrmex gr. *rimosus* sp3							X			X		X								X		X	X	X
Cyphomyrmex gr. *rimosus* sp1													X											
Cyphomyrmex gr. *rimosus* sp2	X		X		X							X	X		X	X		X						X
Hylomyrma balzani												X										X	X	X
Hylomyrma prox. *reitteri*																		X						
Hylomyrma sp4**												X											X	X
Kalathomyrmex emeryi	X			X	X									X										
Megalomyrmex sp1																	X							
Mycetarotes sp1					X																			
Mycetophylax gr. *strigatus* sp6					X	X							X				X							
Mycetophylax gr. *strigatus* sp4						X											X							
Mycetophylax gr. *strigatus* sp5		X		X									X		X			X						
Mycetophylax lectus		X		X									X			X	X	X						
Mycocepurus goeldii	X	X	X	X	X		X			X			X	X	X	X	X		X				X	
Myrmicocrypta sp1		X											X											
Ochetomyrmex semipolitus	X		X										X		X			X						
Octostruma balzani							X												X					
Octostruma iheringi													X											
Octostruma stenognatha																								X
Oxyepoecus prox. *bruschi* sp1						X				X								X		X				
Oxyepoecus prox. *bruschi* sp2			X			X												X						
Oxyepoecus sp5												X												

	Dry Season												Rainy Season											
	Campo Rupestre						Forest						Campo Rupestre						Forest					
Subfamily/Species	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300
Pheidole ambigua												X												X
Pheidole capilata	X		X										X			X								
Pheidole dorsata								X												X		X		
Pheidole gertrudae		X		X			X	X		X				X	X	X			X	X		X	X	
Pheidole jelskii	X	X		X			X		X		X	X	X	X					X	X	X	X	X	X
Pheidole oxyops	X	X	X	X	X			X		X			X	X	X	X	X	X	X	X		X		
Pheidole prox. *reclusi*																				X				
Pheidole radoszkowskii	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
Pheidole scolioceps							X																	
Pheidole sensitiva															X					X			X	
Pheidole sp1	X	X				X							X	X			X	X						
Pheidole sp13	X	X			X								X	X			X							
Pheidole sp14	X												X		X									
Pheidole sp15				X		X												X						
Pheidole sp17		X											X	X										
Pheidole sp18	X												X						X					
Pheidole sp2	X	X											X	X										
Pheidole sp20								X		X		X								X				X
Pheidole sp24																				X				
Pheidole sp25										X												X		
Pheidole sp29	X	X				X		X		X	X	X	X	X				X		X		X	X	X
Pheidole sp32		X		X									X	X		X	X							
Pheidole sp39	X	X	X		X		X	X					X	X	X				X					
Pheidole sp40													X											
Pheidole sp45					X		X	X	X	X	X	X									X	X	X	X
Pheidole sp5	X							X					X					X		X				
Pheidole sp51												X												
Pheidole sp52							X	X		X	X								X	X	X	X	X	
Pheidole sp53								X		X	X									X		X	X	
Pheidole sp6	X												X											
Pheidole sp7	X							X		X		X												X
Pheidole sp8	X				X								X											
Pheidole subarmata	X	X	X		X								X	X	X		X			X				X
Pheidole susannae										X										X		X		
Pheidole termitobla							X					X												X
Pheidole vafra							X					X							X	X				X
Pogonomyrmex naegelii	X	X	X	X	X								X	X	X	X	X	X						
Procryptocerus schmitti																				X				
Sericomyrmex sp1	X			X									X			X		X						
Sericomyrmex sp2	X												X											

	Dry Season												Rainy Season											
	Campo Rupestre						Forest						Campo Rupestre						Forest					
Subfamily/Species	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300
Sericomyrmex sp4													X											
Sericomyrmex sp5								X																
Solenopsis (*Diplorhoptrum*) sp1	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X
Solenopsis globularia sp1		X	X		X									X		X	X	X						
Solenopsis globularia sp2			X			X									X			X						
Solenopsis saevissima	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	
Solenopsis sp2	X		X													X								
Solenopsis sp7	X		X			X												X						
Solenopsis substituta	X	X	X		X								X				X							
Strumigenys gr. *louisianae* sp3																								X
Strumigenys schulzi													X					X						
Trachymyrmex sp1	X				X	X							X	X		X		X						
Trachymyrmex sp2	X												X					X						
Trachymyrmex sp3	X									X		X	X					X						
Trachymyrmex sp4	X													X										
Trachymyrmex sp5		X			X	X						X	X	X		X		X						X
Trachymyrmex sp6		X											X											
Tranopelta gilva				X																				
Wasmannia affinis							X					X												X
Wasmannia auropunctata	X	X		X	X								X	X			X	X		X		X		
Wasmannia lutzi										X		X									X	X	X	X
Ponerinae																								
Anochetus inermis													X		X								X	
Hypoponera distinguenda									X														X	
Hypoponera sp1	X		X		X	X							X					X		X				X
Hypoponera sp3													X											
Hypoponera sp4									X															
Hypoponera sp5												X												X
Leptogenys aff. *gorgona*												X												
Leptogenys crudelis																								X
Neoponera crenata																					X			
Neoponera latinoda																					X			
Neoponera villosa													X											
Odontomachus bauri									X		X								X		X	X	X	
Odontomachus brunneus	X												X		X									
Odontomachus chelifer	X						X												X					
Odontomachus meinerti											X									X	X			
Pachycondyla harpax												X							X		X		X	X
Pachycondyla striata			X				X		X	X	X	X				X			X		X	X	X	X
Rasopone sp2	X																X							

	Dry Season												Rainy Season											
	Campo Rupestre						Forest						Campo Rupestre						Forest					
Subfamily/Species	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300	800	900	1000	1100	1200	1300
Pseudomyrmicinae																								
Pseudomyrmex gr. *pallidus* sp1	**X**												**X**	**X**					**X**					
Pseudomyrmex gracilis													**X**											
Pseudomyrmex sp1																							**X**	**X**
Pseudomyrmex sp2																				**X**				
Pseudomyrmex sp3																							**X**	
Pseudomyrmex sp4																			**X**					
Pseudomyrmex sp7										**X**														
Pseudomyrmex termitarius	**X**	**X**	**X**	**X**	**X**	**X**							**X**	**X**	**X**	**X**	**X**	**X**						
Species richness	79	51	38	29	39	29	30	30	16	34	21	37	89	51	39	42	41	40	31	40	22	33	40	40

**** Species under description**

S1. Methods – Composition analysis: PERMANOVA and NMDS

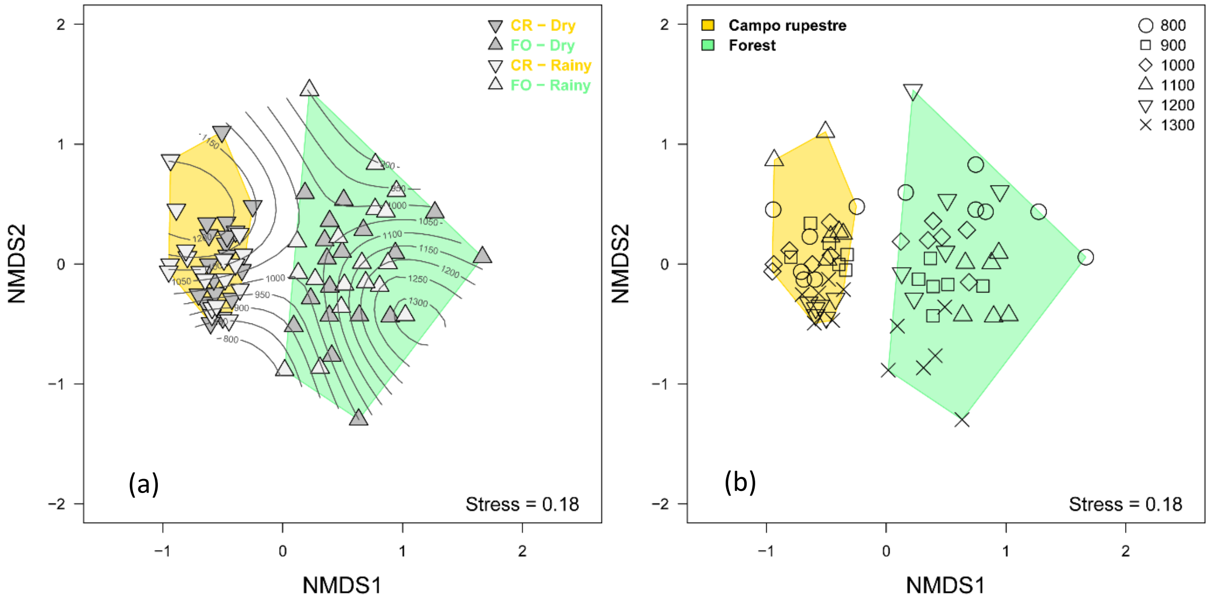
We used the Permutational multivariate analysis of variance (PERMANOVA) (Anderson, 2017) to test the significance of the effects of each spatio-temporal dimension on ant species composition. The effects of each spatio-temporal dimension on the species composition were plotted using the Non-metric multidimensional scaling (NMDS) based on a Jaccard dissimilarity matrix. We performed the same analyzes (PERMANOVA and NMDS) to verify the effects of environmental variables on species composition. We used the "adonis" function for the PERMANOVA and Permdisp analyzes (both with Sorensen index) and the "metaMDS" function for NMDS, "ordihull" for group definition (e.g. fields and forests) and "ordisurf" for adjusting continuous variables (e.g. NDVI, mean temperature) in the NMDS. All functions belong to the "vegan" package (Oksanen *et al.*, 2018) of the R software (R Core Team, 2017).

Permanova (Sorensen):

Response Variable	Df	SumsOfSqs	MeanSqs	F.Model	R^2	Pr(>F)	
Season	1	0.201	0.201	0.914	0.009	0.484	
Habitat	**1**	**4.803**	**4.803**	**21.894**	**0.227**	**0.001**	***
Elevation	**1**	**1.256**	**1.256**	**5.724**	**0.059**	**0.001**	***
Residuals	68	14.919	0.219	0.704			
Total	71	21.179	1				

Permdisp (Sorensen): Habitat and Elevation

	Df	SumSq	MeanSq	F.value	Pr(>F)	
HABITAT						
Groups	**1**	**0.095**	**0.095**	**14.704**	**0.000**	***
Residuals	70	0.451	0.006			
ELEVATION						
Groups	5	0.03822	0.007645	1.4848	0.2067	
Residuals	66	0.33982	0.005149			



S1. Figure 1. NMDS plot showing the similarity of ants' species composition. Representation of the species composition of two habitats per season (a) and for each elevation quota(b). The polygon denotes habitats (Field and Forest), which differed in diversity from each other in the PERMANOVA analysis.

There are differences in composition between habitats and elevations, but not between seasons. Among habitats, a forest composition is also more heterogeneous than the campo rupestre.

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Capítulo 2: Snow-free mountaintops are dominated by tiny and dark ants

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Artigo a ser submetido para o periódico *Biological Journal of the Linnean Society, Special Issue on OCBIL Theory.*

Biological Journal of the Linnean Society

Section: Special Issue on OCBIL Theory.

Snow-free mountaintops are dominated by tiny and dark ants

Running title: Snow-free mountaintops' tiny dark ants

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Abstract

In this study, we performed surveys in the rainy season in *campo rupestre* ecosystem in 12 mountains at different elevation across the Espinhaço mountain range, from Minas Gerais to Bahia, Brazil. First, we aimed to evaluate the effects of environmental variables on the functional structure of functional diversity of ant communities in snow-free mountaintops. Then, we tested three macroecological hypotheses associated to ants' integument colour cline variation (thermal melanism hypothesis; melanism desiccation hypothesis; and photo-protection hypothesis) relating them to mean temperature, vapor pressure deficit and solar radiation to determine the role of colour and body size variation in a tropical elevational and latitudinal geo-climatic gradient. We found ants' communities functionally redundant due to an increase of geographical distance. Despite the redundant functional pattern across the latitudinal gradient, ant species tend to be tinier and darker on mountaintops than ants of lower sites in the *campo rupestre*. Besides the elevational effects, the main drivers of functional ant diversity acting as environmental filters on ants' communities were the decrease in mean temperature and vapor pressure deficit. This result is associated to the thermal melanism hypothesis, which occurs in old mountains of Espinhaço mountain range, an old climatic buffered infertile landscape (OCBIL), but not in new mountains in landscapes characterised by fertile soils (young, often disturbed, fertile landscapes - YODFEL). These findings highlight the importance of the climatic variables on ants' community functional structuring and enhance our understanding of its drivers in the current scenario of the global warming crisis.

Keywords: traits; functional diversity; ground-dwelling ants; Espinhaço Mountain Range; geographical gradients; *campo rupestre*; OCBIL.

Introduction

Understanding how communities are structured in space and time, unveiling the mechanisms underpinning such diversity patterns and determining the role of the species to ecosystem functioning are among the central themes of ecology and conservation biology (Gras *et al.*, 2016; Vellend, 2016; Schluter & Pennell, 2017). Patterns of diversity distribution respond to both deterministic (niche-related; e.g., environmental filtering) and non-deterministic (neutral; e.g., dispersal limitation) ecological mechanisms. Deterministic mechanisms take into account the biotic and abiotic interactions between species and between species and their habitat of occurrence (Keddy, 1992). Non-deterministic mechanisms are related to stochastic processes (Gleason, 1926; Eliot, 2007) and we can consider among them the dispersal limitation or dispersion distance, which in many cases is guided by natural physical barriers like rivers, lakes, and mountains (especially considering their mountains range). These barriers can limit species' distribution via landscape attributes and, in the same way, prevent other species from relocating (Måren *et al.*, 2018).

The habitat concept is defined by the interactions between its abiotic and biotic components, which determines the patterns of diversity, co-occurrence, and distribution of biological communities (Southwood, 1977). We can only determine where these species are distributed knowing the associations between species and their habitats. However, using only this taxonomic approach, the ecological role of each species and their ecological function on a given ecosystem is broadly neglected (Petchey & Gaston, 2006), especially when the focus is arthropod diversity. Arthropods comprise one of the most abundant animal group in terms of biomass and species richness (Basset *et al.*, 1998), and hence, they play crucial and diverse functional roles in different ecosystems (Losey & Vaughan, 2006). Therefore, the functional diversity approach

(FD) can be very useful and relevant for little known taxa or communities with many undescribed species, such as ants (Gibb & Parr, 2013; Yates *et al.*, 2014). Functional diversity can be defined as the value and variation of species and their morphological, ecological or behavioural characteristics (e.g., traits), which influence the functioning of communities (Petchey & Gaston, 2006).

The use of species traits (e.g., morphological, ecological or behaviour attributes) to describe the functional structure and estimate the ecological functions of communities (Dolédec *et al.*, 1996; Vandewalle *et al.*, 2010; Leitão *et al.*, 2018), enable a directly to species responses to changing environmental conditions in local or regional scales. Functional structure (FS) is an important approach to elucidate these differences in species traits across environmental gradients (Mason *et al.*, 2005; Villégere *et al.*, 2008; Mouillot *et al.*, 2013) when considering the multifaceted aspect of the functional diversity: (1) functional richness (FRic) is related to the range of trait combination in the community; (2) functional evenness (FEve) shows how similar one community is to another in terms of ecological functions; (3) functional divergence (FDiv) demonstrates how much a set of attributes can differ from one community to another; and (4) functional originality (FOri), which indicates how original a given attribute or set of them can be in a community structure. Besides, when we argue how environmental filters could acting on biodiversity, β-diversity is among the better approaches to investigate diversity patterns, either using taxonomically or functionally attributes, as well as what factor explain the changes in those patterns (Tuomisto, 2010). The β-diversity approach describes the length of compositional dissimilarities between sites and could reveal the mechanisms that drive these differences (Baselga, 2010; Tuomisto, 2010; Ricotta, 2017). β-diversity can also be used in the functional diversity perspective, describing the length of functional dissimilarities on functional composition, and, in the same way, reveals the mechanisms underlying these differences

(Swenson *et al.*, 2011). Using these multi-functional indices listed above, plus functional β-diversity approach, we could explain the extent of the functional dissimilarity between communities (Mason *et al.*, 2005; Villéger *et al.*, 2011), their responses to environmental changes, and hence, determine which mechanisms act as environmental filters on communities and species traits (Mouillot *et al.*, 2013; Leitão *et al.*, 2018).

Large-scale assessments of ecological gradients' effects such as elevational and latitudinal gradients on the functional structure (FS) of ant communities are yet neglected, especially in tropical regions (Tiede *et al.*, 2017). In these scenarios, macrohabitat variables could act as environmental filters limiting the establishment of species unable to tolerate abiotic conditions of a given habitat (Keddy, 1992), which may drive the species traits' patterns. Many studies testing macroecological hypotheses could be found for many organisms and they show the potential distribution of organisms due to changes in geo-climatic gradients. For ectothermic organisms, these patterns usually are related to the variation in the tegument colour of species (e.g., cline variation on integument) (Clusella *et al.*, 2007; Clusella-Trullas *et al.*, 2008; Moura *et al.*, 2017), which include studies on ant communities in temperate snow-covered mountains (Bishop *et al.*, 2016) and lowland tropical forest (Law *et al.*, 2019). As pointed by Law *et al.* (2019), three of these macroecological hypotheses (related to integument colour cline variation) are very useful to determine the role of the colour variation on ectothermic, organism (Figure 1a): (1) thermal melanism hypothesis (TMH), which predicts that colder environments (e.g., at higher elevations and latitudes) have individuals with more melanin (i.e., pattern of darker integument) (Clusella Trullas *et al.*, 2007). Darker ants, for example, can assimilate more heat from solar radiation than lighter individuals in a temperate mountain range in higher latitudes (Bishop *et al.*, 2016); (2) melanism desiccation hypothesis (MDH), which points that drier environments with greater vapor pressure deficit (VPD) have darker individuals (Kalmus, 1941;

Clusella-Trullas *et al.*, 2008). Kalmus (1941) found in *Drosophila melanogaster*. a positive relationship between the increase of melanisation and body desiccation resistance, by decreasing the cuticular permeability. In a vertical gradient in tropical forest, Law *et al.* (2019) showed that canopy ants, inhabiting a drier and hotter environment, are darker than understory or ground/subterranean dwelling ants; and (3) photo-protection hypothesis (PPH), which predicts that the melanin provides protection against UV-B radiation being, a driving mechanism behind the integument brightness colour variation. In environments with greater UV-B radiation, a rise in melanisation rates could be found in many ectothermic such as insects (ants, Bishop *et al.*, 2016; Law *et al.*, 2019; *Drosophila melanogaster*, Bastide *et al.*, 2014; carabid beetles, Schweiger & Beierkuhnlein, 2016) and lizards (Clusella-Trullas *et al.*, 2008). Since ultraviolet radiation has deleterious effects on the fitness of ectothermic organisms (such as ants), the increase in melanisation rates could promote protection to the dangerous effects of UV-B radiation. Besides, in many cases body size is also an important attribute for a better fitness of an ectothermic organism (Clusella Trullas *et al.*, 2007; Clusella-Trullas *et al.*, 2008; Bishop *et al.*, 2016) and also could be considered a trade-off in the variation of colour patterns (specifically on cline variation of colour from dark to bright) and size variation as well (Clusella Trullas *et al.*, 2007; Clusella-Trullas *et al.*, 2008; Schweiger & Beierkuhnlein, 2016).

Mountain ecosystems are an important scenario to describe functional diversity and species trait patterns because they present high variation among small (e.g., different isocline band on elevation gradient) and large spatial scales (e.g., different latitudes across the latitudinal mountain range gradient). In the latitudinal gradient, species richness increases at low latitudes, however, each latitude may present a different taxonomic composition due to the variation on environmental conditions (Gaston, 2009; Stein *et al.*, 2014). For instance, ant communities of Cerrado present a reverse pattern with decrease species richness in direction to drier and hotter northeast of Brazil (Vasconcelos *et al.*, 2018); ant communities in the Atlantic Forest have high species turnover from south to north of Brazilian coast with an inverted species richness pattern as well (Silva & Brandão, 2014), and ants of *campo rupestre*, whereas taxonomic diversity decreases due to increased elevation and the turnover rates increases due to increased distance among mountains Latitudinal gradients also present a variation in functional diversity patterns (Stevens *et al.*, 2003; Villéger *et al.*, 2013; Lamanna *et al.*, 2014). They may present a very similar functional pattern between latitude, despite the changes in species composition, with a great functional redundancy across the gradient, as occurs with ants from the Atlantic Forest (Silva & Brandão, 2014). Notably, this gradient exhibits a great variation in species richness and environmental conditions from a locality to another (e.g., longitude and elevation), with a variety of topographies and climatic weathers conditions through the south to north (Gaston, 2009; Dunn *et al.*, 2009; Stein *et al.*, 2014) (Figure 1b). Elevational gradients present similar variation in species richness with decreasing species richness due to increased elevation (Gaston, 2000; Peters *et al.*, 2016; Longino & Branstetter, 2019; Perillo *et al.* in prep.), and due to low species richness, a lower functional richness and higher functional redundancy is expected (Bishop *et al.*, 2014; Tiede *et al.*, 2017; Castro *et al.* in prep.). As the latitudinal gradient, the elevation gradient causes a decreased species richness at mountaintops due to the variation in geo-climatic conditions, which sometimes become very harsh and selective on species occurrence (Bishop *et al.*, 2014; Nunes *et al.*, 2016, 2017; Tiede *et al.*, 2017; Castro *et al.* in prep.) (Figure 1c). Therefore, examining how environmental factors at local (between elevations at the same mountain) and regional scales (between mountains across a latitudinal gradient) drive functional diversity patterns is an important contribution to our understanding of how ecological communities change in response to climatic variations locally and regionally. Also, it could enhance our knowledge about how species traits changes in response to predicted global climatic variations.

Here, we aimed to determine the patterns of functional diversity of ants across elevational and latitudinal gradients and to describe what are the effects of environmental variables on functional structure of ant communities (functional richness, functional evenness, functional divergence, and functional originality) and ant species traits (colour brightness). Thus, we considered as explanatory variables the variations on climatic conditions (i.e., variations of temperature and UV-B radiation, and vapor pressure deficit) across elevational and latitudinal gradients, as well as the geographic distance (i.e., elevation range and latitude). Then, we expect these variables will be important drivers to determine both functional α and β diversity patterns, as seen for taxonomic α and β diversity patterns of Aculeata, ants, wasps, and bees (Bishop *et al.*, 2014; Tiede *et al.*, 2017; Perillo *et al* in prep). Specifically, we expect that the functional β diversity will be higher as the environments become warmer and drier, that is, approaching the equator or in lower sites. As the taxonomic diversity decreases due to increased elevation and the turnover rates increases due to increased distance among mountains (geographic distance) (Perillo *et al*. in prep.), we expect a decrease in functional α or functional richness (FRic), functional divergence (FDiv) and functional originality (FOri), and an increase of functional evenness (FEve) due to the decrease on mean temperature (Silva & Brandão, 2014). Because sites with more similar environmental and climatic conditions may have more similar functional diversity than less similar ones (da Silva *et al.*, 2018; Heino *et al.*, 2019), we also expect a positive relationship between functional β diversity and environmental distance due to different climatic conditions between elevation or latitude ranges.

Additionally, we tested whether these three macroecological hypotheses explain ant's cuticle brightness at elevational and latitudinal gradients in snow-free mountaintops in the Espinhaço Mountain Range, a megadiverse and endangered old climatically buffered infertile landscape (OCBIL) (Hopper, 2009; Silveira *et al.*, 2016). The Espinhaço Mountain Range is the longest mountain range in Brazil and has one of South America's oldest and most biodiverse open ecosystems, the *campo rupestre* (Hopper, 2009; Silveira *et al.*, 2016). Considering both geo-climatic gradients, following the thermal melanism hypothesis (TMH) we expect cuticle colour to get lighter as temperature increases. However, if melanin cline is a driver directly related to dissection protection (MDH) or solar protection (PPH), we expect to find darker ants where the vapor pressure deficit (VPD) rates and UV-B radiation increase (Figure 1). Since we are dealing with a colour-body size trade-off relationship (Clusella-Trullas *et al.*, 2008; Schweiger & Beierkuhnlein, 2016), we hypothesize that ants' body size decreases due to the warmer weather conditions as found for mountaintop ants in snow-free mountains (Bishop *et al.*, 2016).

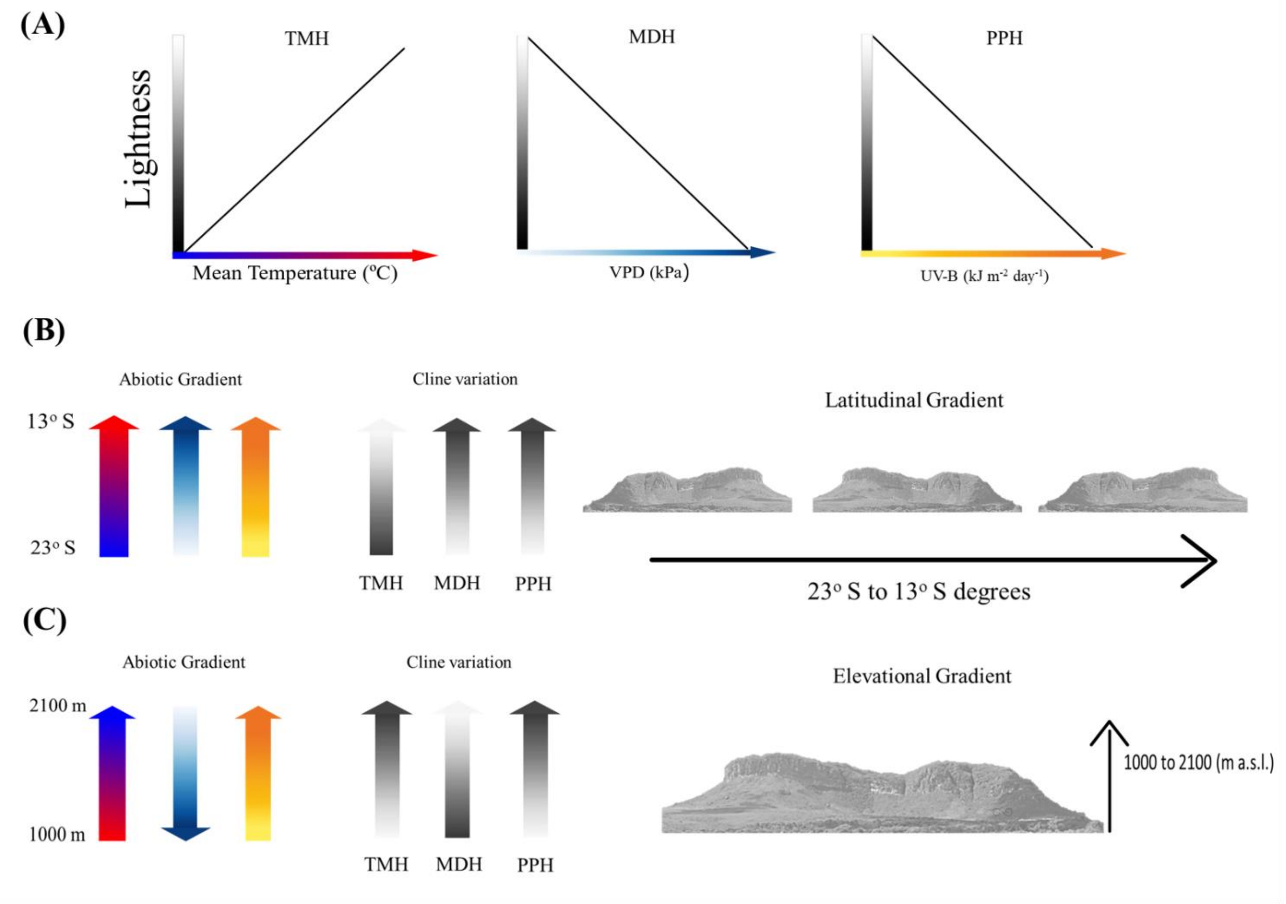

Fig. 1. Predictions for elevational and latitudinal gradients in abiotic factors (temperature, vapor pressure deficit, VPD, and UV-B radiation) and in melanism according to the three hypotheses (TMH, thermal melanism; MDH, melanism-desiccation; PPH, photo-protection).

Material and Methods

Study sites

The study was carried out across the entire extension of Espinhaço mountain range (Figure 2; Appendix 1 – A.1), the biggest mountainous formation that extends for more than 1,200 km north-south in the southeast and northeast of Brazil (Giulietti *et al.*, 1997; Fernandes, 2016; Silveira *et al.*, 2016). The Espinhaço mountain range is at the ecotone of three Brazilian vegetation domains: Cerrado (Brazilian savanna) to the west, Atlantic rainforest to the east, and Caatinga (with scrubby xeromorphic vegetation, such as Dry Forests) in its north eastern (Silveira *et al.*, 2016). Our study was conducted across an extensive latitudinal gradient (ranging from 12ºS to 20ºS) with samples distributed in elevation ranges from 1,100 to 2,072 m a.s.l. (meters above sea level) where *campo rupestre* occurs. All sampling were performed in a single ecosystem: *campo rupestre*, which is among the oldest neotropical grassland formations (Silveira *et al.*, 2016).

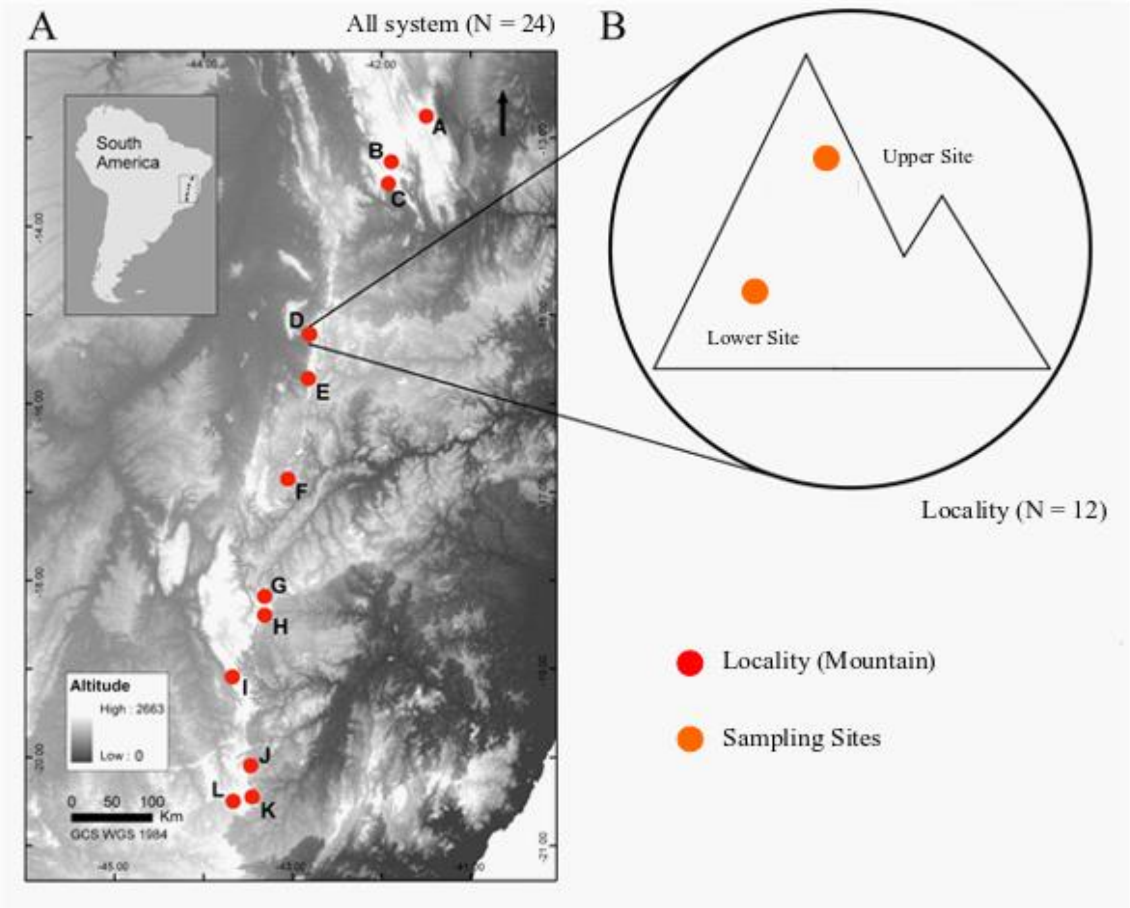

Fig. 2. (A) Map of 12 sample mountains thought *Espinhaço* Mountain Range. A: Parque Nacional Chapada Diamantina; B: Pico do Barbado; C: Pico das Almas; D: Pico da Formosa; E: Parque Estadual Serra Nova; F: Botumirim; G: Parque Estadual do Rio Preto; H: Parque Estadual Pico do Itambé; I: Pico do Breu; J: RPPN Santuário do Caraça;

K: Pico do Itacolomi, Ouro Preto; L: Ouro Branco. (B) Schematic sampling design: yellow circle corresponds to a sample unit composed by two sample sites, lower and upper in each mountian (N=24 sites with 40 pitfall trap sets).

The *campo rupestre* is a neotropical grassland mosaic in association with vegetation complexes on rocky outcrops (Giulietti *et al.*, 1997; Fernandes, 2016; Silveira *et al.*, 2016), formally classified as an old, climate-buffered, and infertile landscape (OCBIL) (Hopper, 2009; Silveira *et al.*, 2016). This ecosystem mainly occurs in the Espinhaço mountaintop surfaces (mostly above 900 m) within all vegetation domains represented, with high species richness and a considerable number of endemic and threatened plants (e.g., the endemic *Trembleya laniflora* [Melastomataceae] - Soares and Morellato, 2018; *Coccoloba cereifera* and *C. acrostichoides* [Polygonaceae] - (Melo, 2000); and the threatened *Philcoxia minensis* [Plantaginaceae] and *Mitracarpus pusillus* [Rubiaceae]), and animal species (e.g., the endemic butterfly *Yphthimoides cipoensis* [Nymphalidae] and the threatened *Strymon ohausi* [Lycaenidae] - Rosa et al., 2019).

Sampling design

We defined 12 sample mountains along the Espinhaço Mountain range considering the latitudinal and elevational gradients (mean distance: approx. 67 km; minimum distance: approx. 20 km; maximum distance: approx. 216 km apart), selecting only sites within *campo rupestre* ecosystem (Figure 2; Appendix 1 – A.1). In each mountain, we selected two sample sites at different elevations in *campo rupestre*: one at the mountain base (lower site: approximately at 1000 m), and another near the mountain summit (upper site: ranging from approximately 1300 to 2100 m). Thus, the minimum and maximum distance between the up-down was 300 to 1100 m respectively.

In each mountain site (N=12), we installed five sets of pitfall traps separated from each other by 200 m at each elevation site (i.e., five sets on lower site and five at the upper site; Figure 2). Each set of traps (50 m length and 20 m width) was composed of four pitfall traps arranged in parcel corners. Each trap remained in the field for 48 hours, totalling 23,040 hours of sampling effort. Each locality was sampled once, during the rainy season (November to February).

Identification of species

Ants were identified to species and morphospecies by comparison with the Collection of Formicidae from *campo rupestre* of the Laboratory of Insect Ecology at the Universidade Federal de Minas Gerais, Brazil. We followed Baccaro *et al*., (2015) and Bolton *et al.*(2005) for ants classifications, and we had help of experts of different ant taxonomic groups (see Acknowledgements)..

Definition of functional traits

We described each ant species in terms of functional traits, which provides information about ants' ecological functions, such as body size, diet habit, foraging capacity, nesting, thermoregulation, and habitat association (following consolidated Fichaux *et al.*, 2019; Paolucci *et al.*, 2016; Leal *et al.*, 2012; Bishop *et al.*, 2016; Barden, 2017; Tiede *et al.*, 2017). Six traits were described to each species: Weber's length (WL), hind femur length (HFL), mesossoma colour (% of colour brightness), polymorphism, integument sculpture, and functional groups (five morphological traits and one ecological trait) (Table 1).

267 **Table 1.** List of morphological and ecological traits measured and their related ecological functions.

Traits	**Measure**	**Abbreviation/Unit**	**Ecological functions**
Morphological traits			
Weber's length	Continuous	WL (μm)	Proxy for total size, related to habitat complexity (Weber, 1938; Kaspari & Weiser, 1999).
Femur length	Continuous	HFL (μm)	Indicator of foraging speed, associated with habitat complexity (Feener *et al.*, 1988; Yates *et al.*, 2014).
Colour (Mesossoma)	Continuous	V (%) *	Thermal melanism: dark individuals has a benefit in cool climates compared to a lighter one (Clusella Trullas *et al.*, 2007); Indicative of thermotolerance and, directly related to temperature variation and solar radiation (e.g. ants in cold environments may be darker integument rather than in warm environments with greater UV-B rates) (Bishop *et al.*, 2016).

Traits	Measure	Abbreviation/Unit	Ecological functions
Polymorphism	Categorical	1 = monomorphic; 2 = dimorphic; 3 = polymorphic	Polymorphism of the workers, attribute related to the ability to develop different tasks in the colony (e.g., foraging, protection, internal activities of the nest; Wills *et al.*, 2017).
Integument Sculpture	Ordinal	1 = cuticle smooth/shiny; 2 = superficial wrinkles/pits; 3 = surface heavily textured	Protection from desiccation. Thickened cuticles enhanced dehydration tolerance (Nation, 2008; Terblanche, 2012)
Ecological Trait			
Functional Groups	Categorical	AA = Army Ants; AD = Arboreal Dominant; AP = Arboreal Predator; AS = Arboreal Subordinate; CO = Cryptic Omnivores; CP = Cryptic Predators; DD = Dominant Dolichoderinae; EO = Epigeic Omnivores; EP = Epigeic Predators; Hatt = High Attini; Latt = Low Attini;	Functional groups based on global-scale responses of ants to environmental stress and disturbance. Also, indicative of ecological tasks, such as nesting, foraging, and diet habits (Andersen, 1995; Leal *et al.*, 2012; Paolucci *et al.*, 2016). All groups were based on the classification used by Paolucci *et al.*, (2016), except for the Seed Harvester group

Traits	Measure	Abbreviation/Unit	Ecological functions
		Opp = Opportunist; SC = Subordinate Camponotini SH = Seed Harvester; UT = Underground tender	(Johnson, 2015) here represented by *Pogonomyrmex naegelli*, which was not present in this list.

* The HSV cylindrical-coordinate colour model (Smith, 1978), whereas: H = Hue shows the dominant wavelength; S = Saturation, indicates the amount of dominant wavelength (H) present in the colour; and V = Value, defines the amount of bright in the colour. We analysed only the variable V, which measured in % of colour brightness (e.g. white colour presents 100% bright while black colour has 0% of bright) (as proposed by Bishop *et al.*, 2016).

To perform the morphological measurements, except for the trait "Colour", we followed the guide for identification of functional attributes for ants (The Global Ants Trait Database – GLAD; Parr *et al.* 2017). We used the HSV colour model (Smith, 1978) to obtain the ant's colour, using only the variable V (colour brightness or lightness), as proposed by Bishop et al. (2016). Differently, from Bishop *et al.* (2016), who considered a predominant colour between head, mesosoma, and gaster, we performed the capture of HSV values of the predominant colour only in mesosoma of each specimen. All continuous data were divided by Weber's length (except for Weber's length and colour brightness) to generate correction for individual body size, because these data (continuous traits measured) were not normally distributed (Arnan *et al.*, 2018; Fichaux *et al.*, 2019).

Body measurements were made using a digital capture micrometre (accurate to 0.01 mm) provide in the LC Micro 2.2 OLYMPUS® software. We carried out image acquisition using Microscope Digital Camera LC30 OLYMPUS® mounted on a stereomicroscope SZ61 OLYMPUS®. We randomly selected individuals of every species recorded in the dataset to take the measures. At least six individuals were measured per species or all individuals for species with fewer individuals (e.g. only one measure per trait for singletons). We took measures of available individuals (only minor workers were used; N = 1386 images from 693 individuals measured; average = 4.1 individuals per species). We used genera/species information available at AntWeb (https://www.antweb.org) and AntWiki website (https://www.antwiki.org) (Guénard *et al.*, 2017) (and by our own observations) to attribute categorical and ordinal morphological traits to each species (polymorphism and integument sculpture).

Macrohabitats variables

We used WorldClim data (version 2, 1970-2000) (https:// www.worldclim.org) extracted for each collection site geographical coordinates (N=24: 12 upper and 12 lower sites) as climatic explanatory variables (mean and variance) that may shape environmental site patterns, such as temperature, wind speed, precipitation, vapor pressure deficit, and solar radiation. Additionally, we used as geographical variables the elevation data for each sampling site (m a.s.l.), and its respective latitudinal and longitudinal position (decimal degrees) (Appendix 1 – A.2).

Functional diversity metrics

Functional structure (FS) of Functional Diversity (FD) was measured using a multidimensional framework proposed by Mouillot *et al.* (2013). With this approach, we can access a particularly useful way to characterize functional spatial-temporal changes in communities. We first computed the functional distance between each pair of species using the Gower distance since functional traits were not all continuous, which allows considering different types of traits (see de Bello *et al.*, 2011; Leitão *et al.*, 2016; Nunes *et al.*, 2016 for more details) (Appendix 1 – A.3). A principal coordinate analysis (PCoA) on each functional distance matrix was built to a multidimensional functional space and then the different functional indexes of assemblage structure was estimated (Mouillot *et al.* 2013). The number of PCoA axes (i.e. dimensions) was chosen based on the quality of the functional space, with "quality functional space" function (Maire *et al.*, 2015) of the R software (R Core Team, 2019). This function shows the extent to which it accurately represents the initial functional distances between species pairs. Thus, we kept the first six PCoA axes with the minimum number of axes that yield a high-quality functional space (Maire *et al.*, 2015).

Then, we calculated the functional indices using the "multidimFD" function in the "FD" R package (Laliberté & Legendre, 2010). After that, we selected four functional indices: FRic (Functional Richness) – volume of the functional space filled by all species within the community, which shows the range of trait combination; FEve (Functional Evenness) – the regularity of the distribution and relative abundance of species in functional space for a given community, which applies only to the distribution of abundance in given niche space; FDiv (Functional divergence) – the proportion of total abundance supported by species with the most extreme trait values within a community and indicates the degree of niche differentiation; and FOri (Functional originality) – the isolation of a species in the functional space occupied by a given community and reflects the degree of uniqueness of species traits. The raw values of each index were standardized between 0 and 1 by dividing them, respectively, by the maximum distance to the barycentre and by the maximum nearest-neighbour distance observed overall species present in dataset (Mouillot *et al.*, 2013; Leitão *et al.*, 2016).

Data analysis

Species richness at each mountain (lower and upper sites) were estimated using the sample completeness of our samples based on a sample coverage value (Chao & Jost, 2012; Chao *et al.*, 2013). Analyses were done using iNEXT (Hsieh *et al.*, 2016), available at https://chao.shinyapps.io/iNEXTOnline/.

To verify the relationship between functional dissimilarity and environmental distance we calculated functional β-diversity dissimilarity among sites (N=24) based on the Jaccard dissimilarity coefficient. Thus, using the "functional.beta.pair" function of betapart (Baselga & Orme, 2012) to produce a dissimilarity matrix based on each site with Jaccard dissimilarity coefficient. Then we modelled the variation in biological dissimilarities using Generalized Dissimilarity Modelling (GDM: Ferrier et al., 2007). With GDM we could modelling spatial variation in functional community composition between pairs of geographical locations, and it can be based on any dissimilarity matrix as response. In our case, the response matrix was the pairwise Jaccard dissimilarity matrix (functional β-diversity) for each site. GDM is based on matrix regression and is specified based on a link function defining the relationship between the response (i.e., dissimilarity matrix) and predictor environments variables (Ferrier *et al.*, 2007), to uncover the effects of ecological distance on functional diversity. For all variables, the multicollinearity was tested via Pearson correlation to define the variables to be used in the models as explanatory predictors (i.e., all of which with correlation values lower than ± 0.6; Appendix 1 – A.2). Among these variables we kept eleven variables used in the analysis (Appendix 1 – A.2). Finally, we assessed the impacts of the predictor variables on this matrix using the functions "gdm" and "gdm.varImp" available in the "gdm" R package (Manion *et al.*, 2018). The GDM with Jaccard dissimilarity matrix is an important functional diversity approach, which allows us to elucidate the differences in functional β-diversity and, then, the extent of the functional dissimilarity between communities, their responses to environmental changes, and so, determine which mechanisms will act as environmental filters on communities.

Differences in functional diversity indices (FRic, FEve, FDiv, and FOri) among mountains (latitudinal gradient) and between upper and lower sites (elevational gradient) were evaluated using generalized linear models (GLM – binomial error family, corrected for overdispersion) (Crawley, 2013). We performed four models (Model 1 to Model 4), considering each functional index as response variables using the related variables to the three melanism hypothesis (i.e., mean temperature, vapor deficit pressure [VPD] and mean solar radiation [UVB-B]; Appendix 1 – A.2) and the interaction between elevation and latitude as explanatory variables.

We also used assembly weighted averages (AWM) of lightness (the V variable of HSV, Table 1), as proposed in Bishop *et al.* (2016) and Law *et al.* (2019) and body size (Weber's Length – WL, Table 1), calculated for each community (N=24):

$$\mathrm{AWM} = \sum_{i}^{S} p_i x_i$$

where *S* is the number of species in each community site, *pi* is the proportional abundance of each species and *xi* is the trait value (lightness – AWM V - or body size – AWM WL) of each species (Appendix 1 – A.4). For ant's proportional abundance, we used the proportion of incidence of each species per site (Castro *et al.*, 2012; Banschbach & Ogilvy, 2014), e.g., there were 20 pitfall traps per site then if a species has fallen on all pitfall traps, the frequency equals 1; if a species has fallen in six traps, the frequency equals 0.3.

Generalized linear models (GLM) were also used to assess how much variation in assemblage-weighted lightness (AWM V) and assemblage-weighted body size (AWM WL) could be explained by the elevational and latitudinal gradients. We tested six models, contemplating in the first three models the AWM V as response variable (Model 5 to Model 7, with binomial corrected for overdispersion). In every model, we test the effect of each melanism hypothesis, mean temperature (related to TMH), mean VPD (related to MDH) and mean UVB-B (related to PPH), respectively, plus elevation (m a.s.l.) and latitude (DD) values for each site as explanatory variables, considering the interaction between these two geographical variables. For the other models (Model 8 to Model 10, with Gaussian distribution), we used the AWM WL as response variable and the same explanatory variables described above for AWM V.

All models were corrected for overdispersion for complete models to the minimal adequate models. The significance of the tests in models was determined by computing an analysis of deviance using the F test (Crawley, 2013). All analyses were performed in R software (R Core Team, 2019).

Results

Taxonomic structure

We collected 2,357 specimens distributed among 169 morphospecies and seven ants' subfamilies (Appendix 1 – A.5). The most representative subfamilies in numbers of records were Myrmicinae (47.0%), Formicinae (26.6%), Dolichoderinae (12.2%), and Ectatominae (6.8%). The richer subfamilies were Myrmicinae (61.5%), Formicinae (14.2%), Dolichoderinae (6.5%), Ponerinae (6.5%), and Ectatominae (5.9%). Most subfamilies occurred on all mountains and elevations, except for Dorylinae, which did not occur on any upper sites. We found a high number of singletons (49 spp. - 28.9%) and doubletons (15 spp. - 8.8%). Only two morphospecies were sampled on all mountains, *Ectatomma edentatum* (Ectatomminae) and *Pheidole oxyops* (Myrmicinae). Additionally, we found 29 (17.2%)

morphospecies sampled exclusively on upper sites, 73 spp. (43.2%) exclusively on lower sites, and 68 spp. (40.2%) on both sets of sites.

Rarefaction-extrapolation accumulation curves suggested high sample coverage for all sites (Appendix 1 – A.6.a; A.6.b; A.7), where the lower sites presented the higher values of species richness. The sample completeness found for the upper sites was high (sample coverage ranging from 0.741 to 0.969). Also, we found high sample completeness for the lower sites (sample coverage ranging from 0.832 to 0.938).

Functional structure (FS)

Functional β-diversity of ant communities did not change along the latitudinal gradient, nor on the elevation gradient as a function of geo-climatic gradient changes. There were no differences in the explained deviance among the pairwise functional dissimilarity of ants according to GDM analysis. The environmental distance explained only 3.64% of the pairwise functional diversity dissimilarity model (Table 2).

Table 2. Summary of the Generalized Dissimilarity Modelling (GDM) of Jaccard dissimilarity (β-diversity) and the predictor variable impacts.

	Dissimilarity
GDM deviance	17.71
Explained (%)	3.64
p-value	0.69
Variables impacts	
Latitude	0.97
Elevation	0.36
UVB-B (mean)	0.42
Temperature Max (mean)	0.98
Temperature (mean)	0.97
UVB-B (variance)	0.42
Precipitation (variance)	0.92

Nonetheless, we found a significant decrease in functional richness (FRic) due to an increase in elevation (Model 1, Table 3; Figure 3), independently of the latitudinal variation (Model 1, Table 3; Figure 3b). We do not find any effects of spatial variables (elevation and latitude) on other functional metrics FEve, FDiv and FOri (Table 3; Figure 3).

Table 3. Results of generalized linear models with functional metrics (FRic = Functional Richness; FEve = Functional Evenness; FDiv = Functional Divergence; FOri = Functional Originality) as responses variables across the elevational and latitudinal gradients. The response variables denote a model with binomial error distribution corrected for overdispersion (quasibinomial). d.f = Degrees of Freedom; F = Fisher value's; Pr(>F) = P-values (significance codes: *** ≤ 0.001; **≤ 0.01; * ≤ 0.05); VPD = Vapor Pressure Deficit; UV-B = Ultra-violet radiation band B.

Response variables	**Explanatory variables**	**F**	**Pr(>F)**
Model 1			
FRic [a]	**Mean Temperature**	**4.8458**	**0.04182 ***
d.f. = 23/ d.f. residuals = 17	Mean VPD	0.1011	0.75439
	Mean UV-B	0.3264	0.57527
	Elevation	**9.3781**	**0.00705 ****
	Latitude	**4.4694**	**0.04959 ***
	Elevation: Latitude	0.6687	0.42482
FRic[b]	**Elevation**	**8.7094**	**0.007383 ****
d.f. = 23/ d.f. residuals = 22			

Response variables	Explanatory variables	F	Pr(>F)
Model 2			
FEve[a]	**Mean Temperature**	**15.9627**	**0.0009366 *****
d.f. = 23/ d.f. residuals = 17	Mean VPD	0.2728	0.6082310
	Mean UV-B	0.9555	0.3420281
	Elevation	1.8275	0.1941359
	Latitude	0.4635	0.5051834
	Elevation: Latitude	3.4674	0.0799683
FEve[a]	**Mean Temperature**	**14.699**	**0.0009036 *****
d.f. = 23/ d.f. residuals = 22			
Model 3			
FDiv[a]	Mean Temperature	0.0093	0.92437
d.f. = 23/ d.f. residuals = 22	Mean VPD	0.6529	0.43024
	Mean UV-B	2.4890	0.13307
	Elevation	2.3770	0.14154
	Latitude	0.0646	0.80235
	Elevation: Latitude	3.3630	0.08424
FDiv[b]	Mean Temperature	0.0089	0.9259
d.f. = 23/ d.f. residuals = 18	Mean VPD	0.6249	0.4395
	Mean UV-B	2.3822	0.1401

Response variables	**Explanatory variables**	**F**	**Pr(>F)**
	Elevation	2.2750	0.1488
	Latitude	0.0619	0.8064
Model 4			
FOri[a]	Mean Temperature	0.0119	0.91454
d.f. = 23/ d.f. residuals = 22	Mean VPD	0.0251	0.87591
	Mean UV-B	0.6414	0.43427
	Elevation	0.0111	0.91751
	Latitude	0.4924	0.49236
	Elevation: Latitude	4.1998	0.05619
FOri[b]	Mean Temperature	0.0103	0.9202
d.f. = 23/ d.f. residuals = 18	Mean VPD	0.0219	0.8840
	Mean UV-B	0.5587	0.4644
	Elevation	0.0096	0.9229
	Latitude	0.4289	0.5208

[a] Complete model
[b] Minimal adequate model

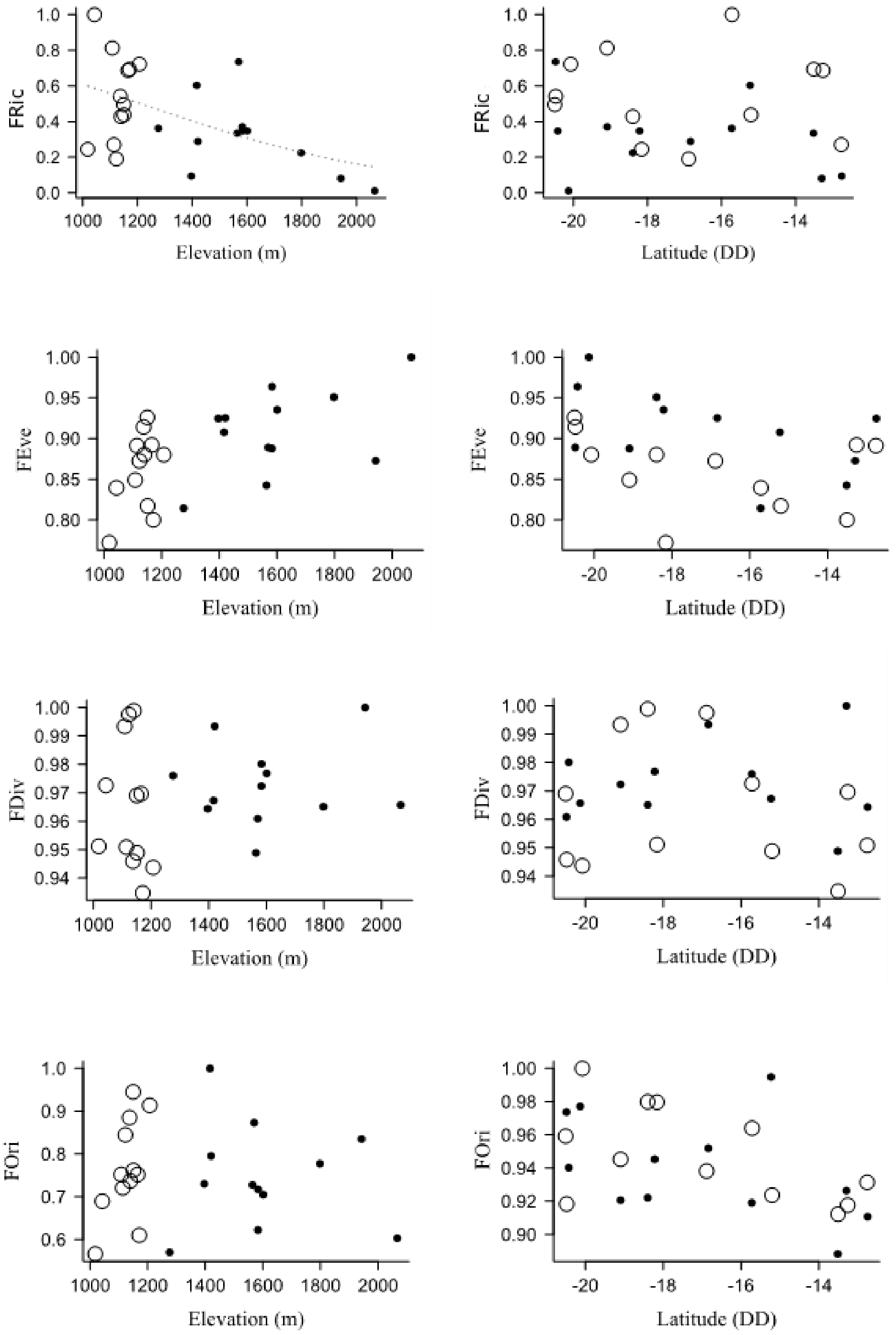

Fig. 3. Results of generalized linear models between functional diversity metrics and geographical variables of elevation and latitude.Legend: FRic – Functional richness; FEve – Functional evenness; FDiv – Functional divergence; FOri – Functional originality. Elevation: meters above sea level (m

a.s.l.); Latitude: decimal degrees. Colour and size dots: black tiny dots – upper sites; white big dots – lower sites.

Also, no effects of environmental variables on functional metrics were observed (Table 3), with exception of functional evenness (FEve). We found a negative effect on FEve due to increased mean temperature (Model 2, Table 3; Figure 4).

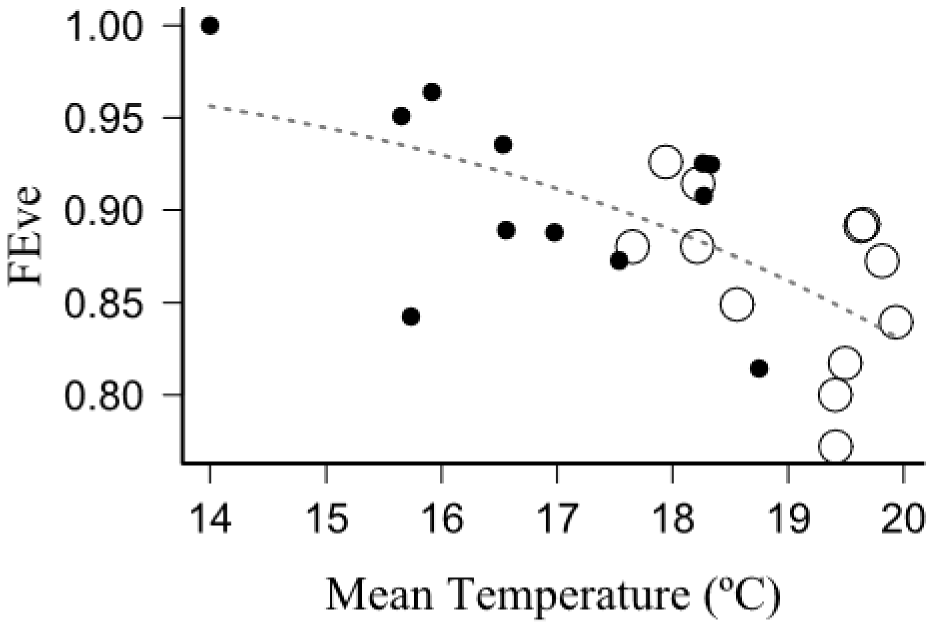

Fig. 4. Results of generalized linear models between functional evenness and mean temperature. Colour and size dots: black tiny dots – upper sites; white big dots – lower sites.

Effects of environmental filters on ant's traits - Testing three hypotheses of cuticle colour and body size on elevational and latitudinal gradients

We found a positive effect of assemblage-weighted lightness (AWM V) and assemblage-weighted body size (AWM WL), being body size a predictor of lightness on ants (Anova: F $_{(1,22)}$ = 52.573, p= 2.902e-07, R^2= 0.69; Figure 5).

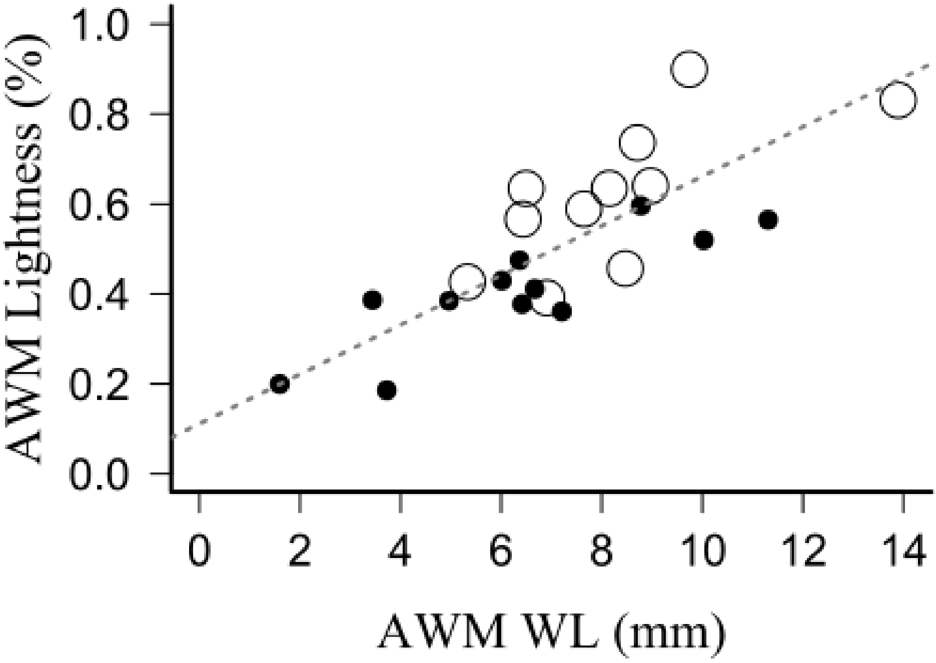

Fig. 5. Results of correlation between assemblage-weighted lightness (AWM V) and assemblage-weighted body size (AWM WL). Colour and size dots: black tiny dots – upper sites; white big dots – lower sites.

Increasing the elevation, regardless of the latitude, has a negative effect on the assemblage lightness (Table 4; Figure 6) and body size (Table 4; Figure 7a).

Table 4. Results of generalized linear models with AWM index of lightness (with Mean of colour brightness - AWMV) and AWM index of body size proxy (with Mean Weber's Length – AWMWL) variables as responses variables across the elevational and latitudinal gradients. Each model was performed to test the three melanism hypothesis: TMH (Thermal Melanism Hypothesis), MDH (Melanism Dissection Hypothesis) and PPH (Photo-Protection Hypothesis). The response variables denote a model with quasibinomial error distribution for the AWM V index and Gaussian error distribution for the AWM WL index. All models corrected for overdispersion for complete models and for minimal adequate models. d.f = Degrees of Freedom; F = Fisher value's; Pr(>F) = P-values (significance codes: *** ≤ 0.001; **≤ 0.01; * ≤ 0.05); VPD = Vapor Pressure Deficit; UV-B = Ultra-violet radiation band B.

Response variables	**Explanatory variables**	**F**	**Pr(>F)**
***Model 5* – TMH**			
AWM V [a]	**Mean Temperature**	**9.9125**	**0.005291 ****
d.f. = 23/ d.f. residuals = 19	**Elevation**	**6.2709**	**0.021549 ***
	Latitude	1.3825	0.254197
	Elevation: Latitude	0.7877	0.385902
AWM V [b]	**Mean Temperature**	**9.7985**	**0.005058 ****
d.f. = 23/ d.f. residuals = 21	**Elevation**	**6.1988**	**0.021244 ***
***Model 6* – MDH**			
AWM V [a]	**Mean VPD**	**9.9304**	**0.005258 ****

Response variables	Explanatory variables	F	Pr(>F)
d.f. = 23/ d.f. residuals = 19	**Elevation**	**8.3119**	**0.009527 ****
	Latitude	0.8504	0.367989
	Elevation: Latitude	0.5088	0.484344
AWM V [b]	**Mean VPD**	**10.3195**	**0.004181 ****
d.f. = 23/ d.f. residuals = 21	**Elevation**	**8.6376**	**0.007840 ****
Model 7 **– PPH**			
AWM V [a]	Mean UV-B	3.3542	0.082758
d.f. = 23/ d.f. residuals = 19	**Elevation**	**14.4169**	**0.001218 ****
	Latitude	1.8328	0.191680
	Elevation: Latitude	1.3626	0.257531
AWM V [b]	**Elevation**	**16.296**	**0.0005513 *****
d.f. = 23/ d.f. residuals = 22			
Model 8 **– TMH**			
AWM WL[a]	Mean Temperature	4.3732	0.05018
d.f. = 23/ d.f. residuals = 19	Elevation	1.1678	0.29339
	Latitude	1.3243	0.26410
	Elevation: Latitude	0.4198	0.52478

Response variables	**Explanatory variables**	**F**	**Pr(>F)**
AWM WL^b	Mean Temperature	4.2080	0.05292
d.f. = 23/ d.f. residuals = 21	Latitude	0.0839	0.77487
Model 9 **– MDH**			
AWM WL ^{a}	Mean VPD	3.8867	0.06341
d.f. = 23/ d.f. residuals = 19	Elevation	1.7827	0.19760
	Latitude	1.2692	0.27394
	Elevation: Latitude	0.3292	0.57287
AWM WL^b	Mean VPD	4.0216	0.05864
d.f. = 23/ d.f. residuals = 21	Elevation	1.8445	0.18954
	Latitude	1.3133	0.26533
Model 10 **-PPH**	Mean UV-B	2.1102	0.16264
AWM WL ^{a}	**Elevation**	**4.4788**	**0.04774 ***
d.f. = 23/ d.f. residuals = 19	Latitude	0.0005	0.98313
	Elevation: Latitude	0.6211	0.44036
AWM WL^b	**Elevation**	**5.8302**	**0.02451 ***
d.f. = 23/ d.f. residuals = 22			

Response variables	Explanatory variables	F	Pr(>F)

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[a] Complete model

[b] Minimal adequate model

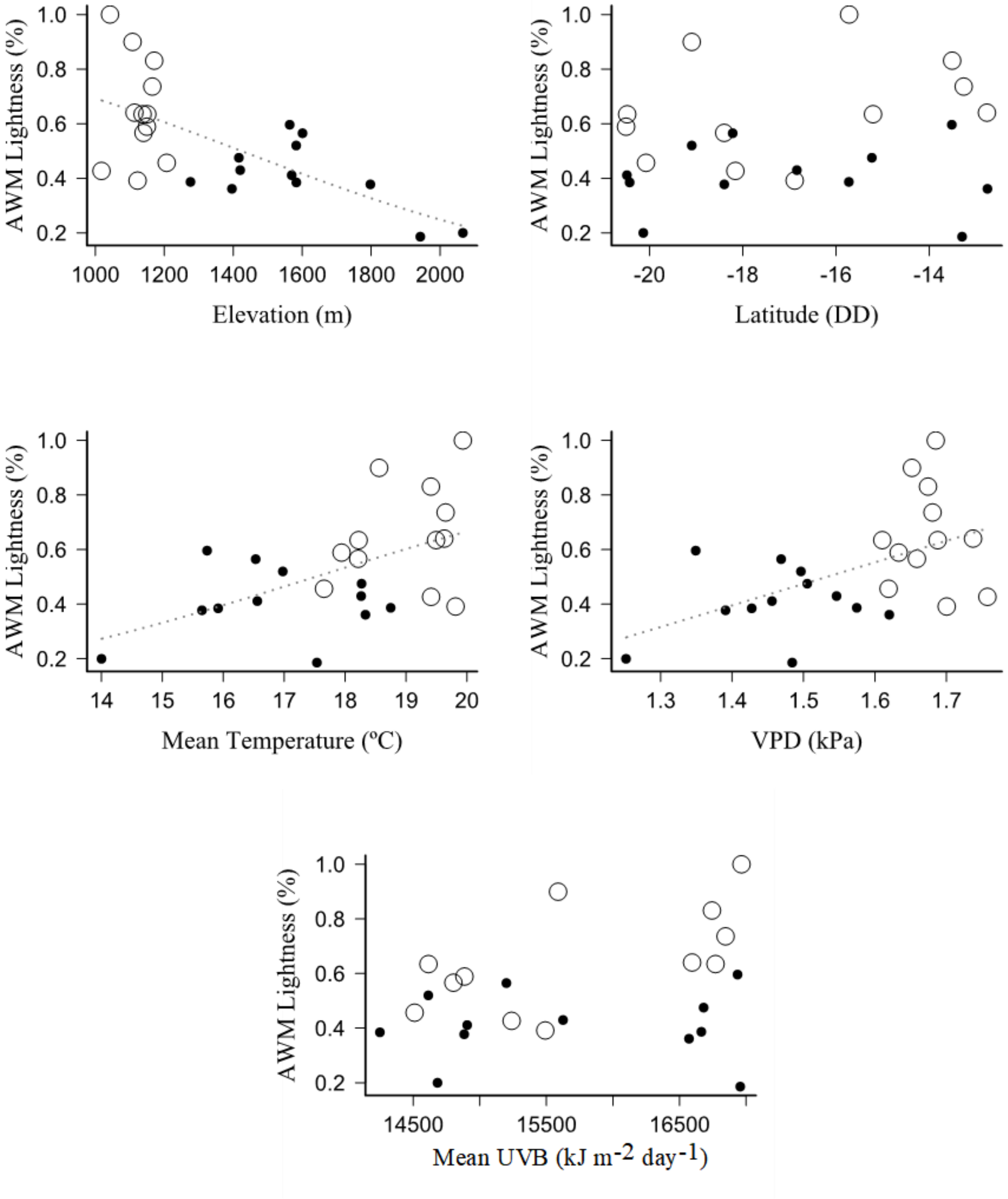

Fig. 6. Results of generalized linear models between cuticle lightness and both spatial and environmental variables testing the hypotheses of TMH, MDH, and PPH for patterns in cuticle colour Legend: TMH –

Thermal Melanism Hypothesis; MDH - -Melanism Desiccation Hypothesis; PPH - -Photo-Protection Hypothesis; AWM V – assembly weight means of cuticle lightness; VPD – Vapor Pressure Deficit (kPa - kilo Paschal); Elevation: meters above sea level (m a.s.l.); Latitude: decimal degrees. Colour and size dots: black tiny dots – upper sites; white big dots – lower sites.

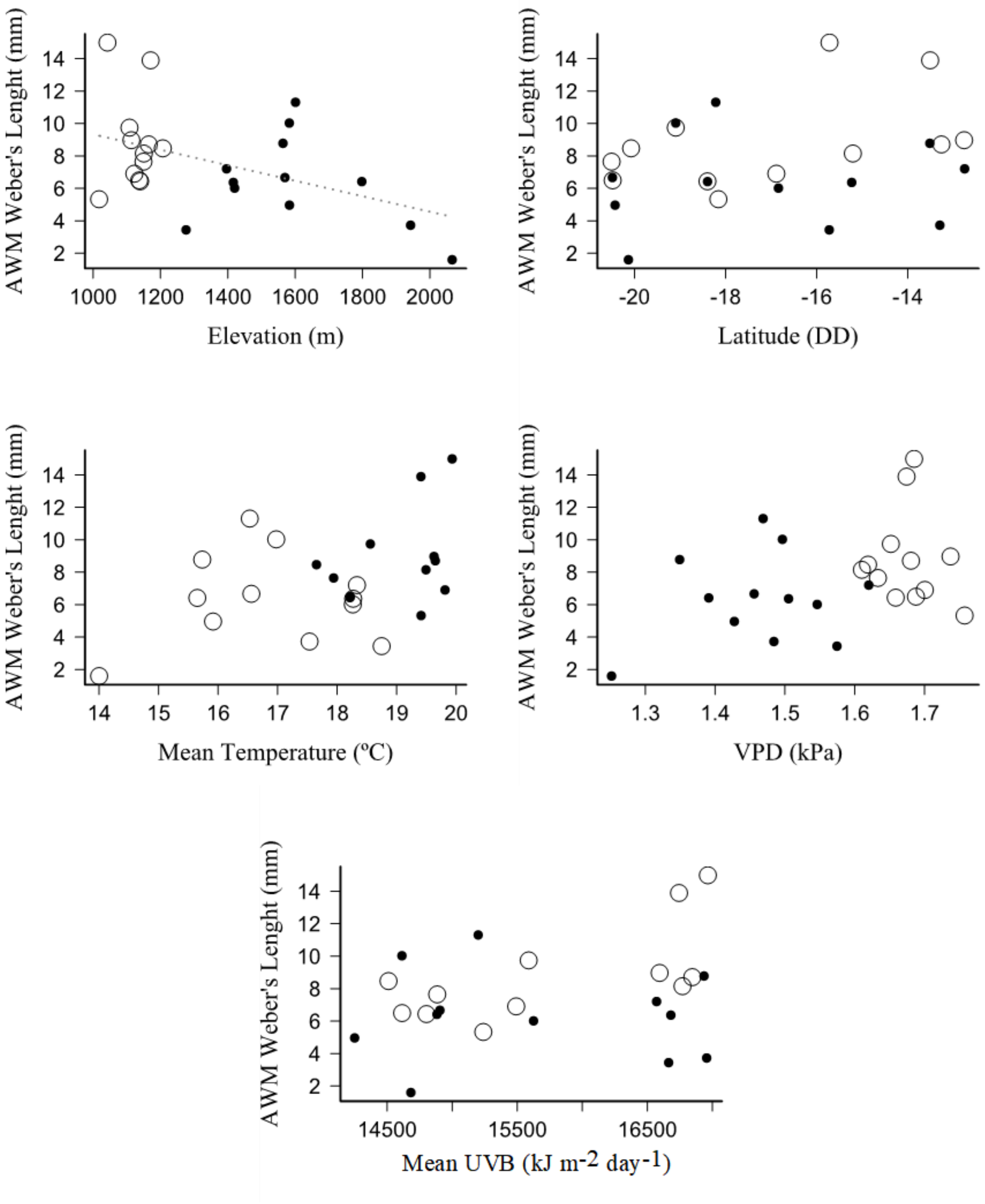

Fig. 7. Results of generalized linear models between body size and both spatial and environmental variables testing the hypotheses of TMH, MDH, and PPH for patterns in cuticle colour. Legend: TMH –

Thermal Melanism Hypothesis; MDH - -Melanism Desiccation Hypothesis; PPH - -Photo-Protection Hypothesis; AWM WL – assembly weight means of body size; VPD – Vapor Pressure Deficit (kPa - kilo Paschal); Elevation: meters above sea level (m a.s.l.); Latitude: decimal degrees. Colour and size dots: black tiny dots – upper sites; white big dots – lower sites.

For the GLM models in which we tested the TMH hypothesis, we observed an increase in cuticle lightness due to average temperature increase, together with the negative effect of the elevation increase revealing a darker ant community in the upper sites than lower ones (Model 5, Table 4; Figure 6). We also observed an increase in cuticle lightness as a function of vapor pressure deficit (VPD) when we tested the MDH hypothesis and, similarly, we found the same pattern of the negative effect of increased elevation indicating the occurrence of a darker community in environments with most moisture or with lower VPD values (Model 6, Table 4; Figure 6). When we tested the PPH hypothesis, no effects of UV-B radiation on cuticle colour were observed.

We found no effects of the environmental variables in the models generated to test the relationship of body size to the three melanisation hypotheses (Table 4; Figure 7). However, we observed that ants are tiny in upper sites than lower sites (Model 10, Table 4).

Discussion

In the latitudinal gradient where the Espinhaço mountain range occurs, ant species tend to be tinier and darker on mountaintops than ants of lower sites in the *campo rupestre* regardless of the latitude. Despite the redundant pattern of functional diversity found in the latitudinal gradient (as found by Silva & Brandão, 2014), there is a strong and positive relationship between cuticle colour brightness and body size for snow-free mountaintops ants' communities in the elevational gradient. Beyond the elevational effects, the main drivers of functional ant diversity that act as environmental filters were the decrease in mean temperature and vapor pressure deficit (VPD) values. Generally, ants are considered thermophilic organism, being this variable important to ants' community structuring (Kaspari *et al.*, 2015; Bishop *et al.*, 2017), including *campo rupestre* ants' communities (Costa *et al.*, 2018). Nevertheless, we presented here the first study relating changes in distribution and diversity patterns of ant communities to colour attribute and to body size variation (i.e., shifts on functional diversity by also considering other traits) in a tropical elevational and latitudinal geo-climatic gradient.

Contrary to our expectations, we find a redundant pattern of functional diversity across the latitudinal gradient, the same pattern was found for ants in the Atlantic Forest by Silva & Brandão (2014). As we expected, we found ants' communities with lower functional richness (FRic) in upper sites than lower ones of *campo rupestre*, as a direct effect of the decrease in taxonomic α-diversity due to elevation increasing. The species richness decrease due to the increasing elevation is a recurrent pattern on *campo rupestre*'s ant communities (Castro *et al.* in prep.; Perillo *et al.*, in prep.). Ants' functional diversity in *campo rupestre* shows redundant functional patterns in the elevational gradient (Castro et al. in prep), even with the high species turnover found between the elevation bands. However, unlike this study, the highest elevation in Castro *et al.* (in prep) did not exceed 1400 m, which makes it difficult to report these functional diversity patterns directly to our results, especially for upper site communities' patterns, since we have sites up to 2000 m a.s.l. across the Espinhaço range.

In addition, according to our expectations, regardless of the elevation or latitude range, the functional evenness (FEve) index was high in the whole system and negative related to mean temperature (as seen by Silva & Brandão, 2014). Since the FEve is dependent of abundance distribution (in our case based on species incidence) (Mason *et al.*, 2005; Mouillot *et al.*, 2013), we found high FEve in upper sites than lower sites, as seen as by Silva & Brandão (2014) for ants in Atlantic Forest. In all mountains surveyed on the Espinhaço mountain range, the mean temperature decreases with elevation increase (Fernandes *et al.*, 2016; Ferrari *et al.*, 2016). This FEve pattern evidenced higher evenness in incidence of mountaintops' ants (upper sites) in the functional space, especially on mountains with greater geographical distance between upper and lower sites (such as Caraça, Pico do Breu, Pico das Almas e Barbado), whereas the mean temperature and vapor pressure deficit varies more. Additionally, no effects were observed on functional divergence (FDiv) and functional originality (FOri). Since functional divergence and functional originality are low and not driven by variables related to elevation and latitude (Mouillot *et al.,* 2013). These results evidencing the functional redundancy pattern on these ants' communities across the Espinhaço mountain range. The high number of epigeic omnivores ants in the whole system (like *Pheidole* spp., *Linepithema* spp and *Ectatomma* spp.) and the recurrent decrease in occurrence of predators' species due to the increased elevation may have contributed to these results. In all mountains, there was a decreased occurrence in mountaintop of Ponerinae, a taxon with predominant predators' species, and the absence of Dorylinae, exclusively formed by predators' species, in all upper sites surveyed. At high elevations Ponerinae's species richness, and their incidence as well, tend to be lower than in lowland communities in a tropical mountains range in South America and Meso America (Tiede *et al.*, 2017; Longino & Branstetter, 2019). In the same way, most Dorylinae species were related to the forest habitats and only the *Neivamyrmex* spp. were related to the montane habitat, while the others species of this subfamily were not sampled beyond 1400 m.a.s.l (Tiede *et al.*, 2017; Longino & Branstetter, 2019) including the *campo rupestre* (Anjos *et al.*, 2015; Costa *et al.*, 2015, 2018; Castro *et al*. in prep).

As seen by Tiede *et al.* (2017), we also found that the species richness and incidence of ants were important drivers of ant functional diversity. Different from these authors, we found a negative effect of elevation and mean temperature on ants' incidence and species richness, consequently in functional evenness and functional richness. As a consequence, a species poor community dominated by tinier and darker ants was selected due to their adaptation to harsh environmental conditions at high elevations (Machac *et al.*, 2011; Smith, 2015; Bishop *et al.*, 2016; Castro *et al.*, in prep) under effects of environmental filters such as the increase in elevation and hence decrease in mean temperature and vapor pressure deficit.

Our findings confirm, only across the elevational gradient independently of latitude, the thermal melanism hypothesis (TMH) in *campo rupestre*'s ant communities and refute the melanism desiccation hypothesis (MDH). This last pattern was found in temperate mountains with snow-mountaintops, whereas ants were darker and bigger as the mean temperature decreased with elevation increase (Bishop *et al.*, 2016). Also, in forest canopy, which presents darker ants in high strata as a function of temperature, vapor pressure deficit and UV-B radiation rates arisen (Law *et al.*, 2019). We did not find any relationship between UV-B radiation and colour brightness and body size with the photo-protection hypothesis (PPH). However, due to the constantly lower temperature in temperate mountains along the day, Bishop *et al.*(2016) found a negative relationship between brightness and body size. On the other hand, Law *et al.* (2019), despite encountering darker ants in the hotter forest strata, did not find any relationship between colour brightness and body size. In our study, we found a positively correlation between colour brightness and body size, an important trade-off found in ectothermic species (Clusella Trullas *et al.*, 2007; Clusella-Trullas *et al.*, 2008; Schweiger & Beierkuhnlein, 2016), where large-sized ants are brighter than small-sized ones. In upper sites we found smaller ant communities predominantly tinier and darker. Habitat filtering species unable to tolerate abiotic conditions of a given habitat, which limiting the establishment, and resulting in co-occurring species with similar ecological attributes (Keddy, 1992). These findings were driven for example, by the distribution of *Ectatomma* spp. found in the *campo rupestre.* We sampled five *Ectatomma* spp. and, one of them was one of two species that occurred on all sampled mountains and the only species of the genus sampled in upper sites: *E. edentatum*, the tinier and darker *Ectatomma* surveyed in this study. The other species found only in lower sites, like *E. tuberculatum* and *E. opaciventre,* were bigger ants with brighter colour.

In this way, we can directly relate the decrease in temperature, and the vapor pressure deficit (moisture rise) as important environmental filters due to the increase in elevation, revealing a trade-off pattern in the relationship among body size and colour brightness in ants' communities of *campo rupestre* inhabiting the Espinhaço mountain range. In general, small ectothermic organism could take heat faster and have a greater convective heat-transfer capacity with the environment compared to large ones. These characteristics improve the fitness of small ectothermic species under low temperatures (e.g. small lizards) and they are more melanic to catch more heat from the environment since they can dissipate heat faster in windy conditions (Clusella-Trullas *et al.*, 2008), like a "bio-radiator", adjusting more efficiently body temperature than lighter and bigger individuals. During the cool early-morning periods typical of *campo rupestre* (Fernandes *et al.*, 2016; Ferrari *et al.*, 2016) tiny darker ants could benefit from heating faster than big lighter ones, because with their small size, rapid heat loss occurs during warm periods of the day as seen for tiny and black beetles in Namibia desert (Turner & Lombard, 1990).

In conclusion, we found a redundant pattern of functional diversity across the latitudinal gradient and a decrease in functional richness in the elevational gradient. Thus, we show evidences for the vertical stratification of cuticle lightness and body size in the tropical ant communities of snow-free mountains as a response to the increase in elevation, following by a decrease in mean temperature and vapor pressure deficit. This can be interpreted by the thermal melanism hypothesis (TMH), which occurs in old mountains of an OCBIL but not in new mountains in landscapes characterised by fertile soils (young, often disturbed, fertile landscapes - YODFEL). These findings highlight the importance of the climatic variables on ants' community structuring and enhanced the importance of understanding and preserve them, reaffirming the importance to monitoring ant communities in a global warming crisis. Changes to climate on mountains, like temperature enhanced, was predicted by IPPC World Climatic panel (Minx *et al.*, 2017). Shifts in the relative abundance or species incidence, and consequently in the functional structure of mountain communities, could be a result of changes in environmental conditions that act as filters for species distributions.

Acknowledgments

We thank all friends involved in data collection during fieldwork and processing material in lab, specially LEI Team (Lab. Ecology of Insects - years 2013 to these days). We also thanks Nubia Campos, Rayana Melo, Daniela Melo, Luiza Azevedo, Jéssica Martins, Matteus Carvalho, André Araújo, Heron Hilário and Ivan Monteiro for help us in the field and laboratory work as well. We also thank Flávio Camarota and Scott Powel (*Cephalotes*) and Rodrigo Feitosa for ant identification. We also thank all the Espinhaço's people, like " Seo" José Camilo (Alitota from Monte Azul - MG), Sinval, Zé do Pilão and Dona Maria (Rio de Contas – BA), for kindly received us in their home and their accepting we maked our "madness" to look up the ants, wasps and bees at the highlands! We thank the Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG - CRA - APQ-00311-15) for financial support. FSN received a Research Productivity Fellowship from CNPq. RRCS is supported by Pesquisa & Desenvolvimento of Agência Nacional de Energia Elétrica and Companhia Energética de Minas Gerais (P&D ANEEL/CEMIG, PROECOS project GT-599), FAPEMIG (APQ-00288-17) and CNPq (428298/2018-4) research project grants. This study was financed in part by the Coordenação de

Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001. FSN, PGdS, and FSC thank the CAPES for grants. We are also grateful to Instituto Estadual de Florestas (IEF-MG), Instituto Chico Mendes para Biodiversidade (ICMBio-MG and ICMBio-BA) and GSG for logistical support. The author(s) declare(s) that there is no conflict of interest regarding the publication of this article.

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Appendix 1 - Supplementary Information

A.1. Information of the 12 *campo rupestre* mountains across Espinhaço Mountain Range, southeast Brazil.

Locality (Abbreviation)	**Lower elevation sites**			**Upper elevation sites**		
	Latitude	**Longitude**	**Elevation**	**Latitude**	**Longitude**	**Elevation**
P.E. Serra do Ouro Branco (OB)	20º 30' 20.10" S	43º 37' 23.21 " W	1150	20º 29' 12.37" S	43º 42' 43.96" W	1569
P.E. Pico do Itacolomi (OP)	20º 28' 53.04" S	43º 27' 48.14" W	1137	20º 25' 40.44' S	43º 28' 50.96" W	1583
RPPN Santuário do Caraça (CA)	20º 04' 37.99" S	43º 29' 37.90" W	1207	20º 08' 07.19" S	43º 27' 08.87" W	2066
Pico do Breu - Serra do Cipó (PB)	19º 05' 46.00" S	43º 41' 14.89" W	1108	19º 05' 44.02" S	43º 39' 56.42" W	1583
P.E. Pico do Itambé (IT)	18º 24' 00.45" S	43º 18' 05.42" W	1140	18º 23' 52.59" S	43º 20' 11.85" W	1798
P.E. do Rio Preto (RP)	18º 09' 35.89" S	43º 19' 14.18" W	1018	18º 13' 05.21" S	43º 18' 56.35" W	1601
Botumirim (BO)	16º 53' 15.06" S	43º 01' 50.16" W	1122	16º 50' 27.23" S	43º 04' 15.56" W	1420
P.E. Serra Nova (SN)	15º 43' 11.67" S	42º 50' 10.32" W	1043	15º 43' 33.77" S	42º 49' 42.76" W	1276
Pico da Formosa - Monte Azul (PF)	15º 12' 25.39" S	42º 48' 04.10" W	1151	15 º 13' 54.52" S	42º 48' 54.52" W	1416
Pico das Almas (AL)	13º 30' 33.86" S	41º 53' 29.94" W	1171	13º 31' 01.16" S	41º 57' 29.63" W	1564
Pico do Barbado (BA)	13º 15' 43.80" S	41º 52' 37.72" W	1165	13º 17' 47.70" S	41º 54' 13.08" W	1943
P.N. Chapada Diamantina – Guiné (GU)	12º 45' 48.28" S	41º 30' 40.05" W	1114	12º 45' 10.47" S	41º 30' 20.59" W	1396

A.2. Environmental variables extracted from WorldClim data (version 2, 1970-2000). Units: Wind (Mean and variance): m s^{-1}; VPD (vapor pressure deficit) (Mean and variance): kPa; UV-B (Mean and variance): kJ m^{-2} day^{-1}; Precipitation (Mean and variance): mm; TMax (Mean and variance): ºC; Temperature (Mean and variance): ºC; Elevation: m a.s.l. (above sea level); Longitude and Latitude: decimal degrees (DD). Bold columns represent the variables selected for GDM and GLM's (with *) models after Pearson's correlation multicollinearity test.

Site	**Wind (Mean)**	***VPD (Mean)**	***UV-B (Mean)**	**Precipitation (Mean)**	**TMax (Mean)**	***Temperature (Mean)**	**Wind (variance)**	VPD (variance)	**UV-B (variance)**	**Precipitation (variance)**	TMax (variance)	Temperatur (variance)	***Elevation**	Longitude	***Latitude**
OB Lower	1.63	1.63	14884.93	123.97	23.44	17.94	0.23	0.43	2623531.80	10775.53	5.26	4.23	1149.61	-43.6231147	-20.5055833
OB Upper	1.86	1.46	14905.33	132.83	21.92	16.56	0.24	0.36	2227368.24	12114.70	4.81	3.91	1569.47	-43.7122106	-20.4867697
OP Lower	1.57	1.69	14614.72	122.20	24.02	18.22	0.23	0.45	3907401.20	9867.01	6.17	4.66	1137.12	-43.4633711	-20.4814008
OP Upper	1.91	1.43	14250.02	137.45	21.13	15.91	0.22	0.35	3760208.77	11471.25	4.96	4.03	1582.92	-43.4808217	-20.4279011
CA Lower	1.58	1.62	14510.32	132.45	23.12	17.65	0.20	0.40	4009626.69	11461.68	5.06	3.92	1207.00	-43.4938572	-20.0772203
CA Upper	2.11	1.25	14682.25	143.58	18.79	14.00	0.22	0.27	2509313.84	12874.27	4.35	3.76	2066.00	-43.4524625	-20.1353306
PB Lower	1.37	1.65	15587.92	122.58	24.23	18.56	0.14	0.37	2801926.45	12010.81	5.36	4.08	1108.00	-43.6874689	-19.0961119
PB Upper	1.54	1.50	14613.45	135.03	22.28	16.98	0.16	0.31	3056712.32	12400.66	4.44	3.53	1582.60	-43.6656711	-19.0955617
IT Lower	1.29	1.66	14801.87	123.58	23.41	18.22	0.16	0.30	3878510.71	10760.49	4.61	3.76	1139.76	-43.3015058	-18.4001244
IT Upper	1.62	1.39	14883.00	129.50	20.39	15.65	0.17	0.23	2856372.91	11553.91	3.35	2.85	1797.78	-43.3366247	-18.3979431
RP Lower	1.20	1.76	15239.07	110.48	24.96	19.41	0.16	0.33	4149096.59	9517.74	5.04	3.60	1017.91	-43.3206047	-18.1599686
RP Upper	1.51	1.47	15199.88	121.97	21.88	16.53	0.17	0.24	3908683.17	10880.80	3.71	2.90	1600.95	-43.3156525	-18.2181147
BO Lower	1.35	1.70	15491.68	87.60	25.67	19.81	0.16	0.22	4172134.97	6657.52	3.33	2.74	1122.46	-43.0306000	-16.8875178
BO Upper	1.53	1.55	15625.25	89.77	23.84	18.26	0.18	0.19	3620895.62	7109.12	2.91	2.49	1420.22	-43.0709894	-16.8408969
SN Lower	1.58	1.69	16965.08	74.67	25.70	19.93	0.19	0.18	2785448.08	5599.33	2.87	2.73	1042.62	-42.8361989	-15.7199089
SN Upper	1.72	1.57	16663.75	75.25	24.32	18.75	0.23	0.16	3288265.07	5553.69	2.72	2.60	1276.03	-42.8285450	-15.7260461
PF Lower	1.79	1.61	16770.15	75.00	24.96	19.49	0.24	0.19	3418514.43	5193.71	2.04	1.95	1150.70	-42.8011381	-15.2070519
PF Upper	1.92	1.51	16680.88	76.72	23.55	18.27	0.28	0.17	3338734.19	5257.14	2.02	1.93	1416.27	-42.8151450	-15.2318111
AL Lower	2.18	1.67	16743.42	92.42	25.23	19.41	0.21	0.09	3732885.17	4040.45	1.48	1.41	1170.76	-41.8916511	-13.5094061
AL Upper	2.54	1.35	16935.75	92.08	20.87	15.73	0.25	0.08	3073133.48	3081.72	1.41	1.36	1563.67	-41.9582300	-13.5169889
BA Lower	2.17	1.68	16845.58	78.68	25.37	19.65	0.21	0.10	3632592.00	3474.26	1.67	1.61	1165.18	-41.8771439	-13.2621669
BA Upper	2.39	1.48	16955.82	88.00	22.76	17.54	0.26	0.09	3153682.19	3775.27	1.58	1.51	1942.59	-41.9036339	-13.2965831
GU Lower	2.12	1.74	16594.23	70.02	25.34	19.63	0.14	0.08	3559622.99	1902.33	1.65	1.60	1113.67	-41.5111250	-12.7634100
GU Upper	2.26	1.62	16571.00	78.65	23.88	18.33	0.18	0.08	4152143.79	1565.68	1.66	1.57	1396.29	-41.5057219	-12.7529081

A.3. Species of ants captured and traits used to calculate functional diversity (FD): (1) morphological traits (a) WL: Weber's length (μm); (b) HFL: Hind femur length (μm); (c) V: measure of colour brightness (%); (d) Workers polymorphism: categorical (monomorphic, dimorphic and polymorphic); (e) integument sculpture (ordinal data (smooth/often shine, intermediate and texturized); and (2) ecological traits or life history traits (a): functional groups based on global-scale responses of ants to environmental stress and disturbance AA = Army Ants; AD = Arboreal Dominant; AP = Arboreal Predator; AS = Arboreal Subordinate; CO = Cryptic Omnivores; CP = Cryptic Predators; DD = Dominant Dolichoderinae; EO = Epigeic Omnivores; EP = Epigeic Predators; Hatt = High Attini; Latt = Low Attini; OPP = Opportunist; SC = Subordinate Camponotini SH = Seed Harvester; UT = Underground trophobiont.

Morphospecies	**Polymorphism**	**Sculpturing**	**FG**	**WL**	**HFL**	**V**
Acromyrmex cf. *niger*	polymorphic	intermediate	Hatt	2337.03	1.1170	0.5702
Acromyrmex RPsp.1	polymorphic	intermediate	Hatt	1208.43	0.9377	0.8235
Acromyrmex sp.2	polymorphic	intermediate	Hatt	2325.11	1.0800	0.6856
Acromyrmex sp.4	polymorphic	intermediate	Hatt	2186.92	1.1318	0.6307
Acromyrmex subterraneus	polymorphic	intermediate	Hatt	2000.10	1.2960	0.6327
Acropyga goeldii	monomorphic	smooth	UT	523.92	0.8404	0.9216
Anochetus sp.1	monomorphic	intermediate	EP	2620.73	0.8879	0.7882
Apterostigma gp. *pilosum* sp.1	monomorphic	intermediate	Latt	1381.88	0.9575	0.7660
Apterostigma gp. *pilosum* sp.2	monomorphic	intermediate	Latt	1359.25	1.0274	0.7046
Atta bisphaerica	polymorphic	intermediate	Hatt	3187.84	1.2435	0.7680
Atta sexdens	polymorphic	intermediate	Hatt	2999.99	1.5110	0.6895
Azteca sp.1	polymorphic	smooth	AD	1180.16	1.0282	0.6333
Brachymyrmex cf. *pictus*	monomorphic	smooth	OPP	347.35	0.8303	0.6725
Brachymyrmex cordemoyi	monomorphic	smooth	OPP	491.83	0.8734	0.6797
Camponotus (Tanaemyrmex) sp.3	dimorphic	intermediate	SC	1848.11	0.8847	0.7078
Camponotus atriceps	polymorphic	intermediate	SC	2657.95	1.0252	0.6359
Camponotus bidens	dimorphic	intermediate	SC	1197.02	0.7747	0.8510
Camponotus blandus	dimorphic	intermediate	SC	2180.12	0.9366	0.6765
Camponotus cingulatus	dimorphic	intermediate	SC	2648.08	0.9730	0.6255
Camponotus crassus	dimorphic	intermediate	SC	1741.61	0.8071	0.7621
Camponotus fastigatus	dimorphic	intermediate	SC	1505.01	0.8217	0.8490
Camponotus lespesii	dimorphic	intermediate	SC	4171.45	1.0810	0.6078
Camponotus leydigi	dimorphic	intermediate	SC	2993.01	0.8530	0.6928
Camponotus melanoticus	polymorphic	intermediate	SC	2976.27	1.0032	0.7882
Camponotus novogranadensis	dimorphic	intermediate	SC	1802.05	0.7962	0.7405
Camponotus renggeri	polymorphic	intermediate	SC	3430.93	0.9354	0.7755
Camponotus rufipes	polymorphic	intermediate	SC	2998.64	0.9685	0.6634
Camponotus sp.6	dimorphic	intermediate	SC	1944.56	0.8435	0.8523
Camponotus textor	dimorphic	intermediate	SC	2096.84	0.9408	0.7314
Camponotus vitatus	dimorphic	intermediate	SC	3200.65	0.8942	0.6431
Camponotus westermanni	dimorphic	intermediate	SC	1781.13	0.9258	0.7732
Cephalotes depressus	dimorphic	intermediate	AS	1250.75	0.6224	0.9712
Cephalotes maculatus	dimorphic	intermediate	AS	974.54	0.6177	0.8902
Cephalotes minutus	dimorphic	intermediate	AS	1112.30	0.7101	0.7673

Morphospecies	Polymorphism	Sculpturing	FG	WL	HFL	V
Cephalotes pinelli	dimorphic	intermediate	AS	1011.15	0.6333	0.9412
Cephalotes pusillus	dimorphic	intermediate	AS	1249.10	0.6933	0.8157
Crematogaster acuta	polymorphic	intermediate	AD	1238.96	0.8884	0.9373
Crematogaster BAsp.1	polymorphic	intermediate	AD	843.72	0.8336	0.8010
Crematogaster BOsp.1	polymorphic	intermediate	AD	751.35	0.8796	0.6444
Crematogaster brasiliensis	polymorphic	intermediate	AD	709.58	0.7649	0.8301
Crematogaster cf. *erecta*	polymorphic	intermediate	AD	912.38	0.9013	0.8510
Crematogaster obscurata	polymorphic	intermediate	AD	631.46	0.8671	0.8745
Crematogaster OBsp.1	polymorphic	intermediate	AD	731.79	0.7231	0.6020
Crematogaster PFsp.1	polymorphic	intermediate	AD	840.56	0.8665	0.7349
Crematogaster SNsp.1	polymorphic	intermediate	AD	719.89	0.8525	0.6745
Crematogaster sp.1	polymorphic	intermediate	AD	653.64	0.7660	0.6314
Crematogaster sp.10	polymorphic	intermediate	AD	557.10	0.7844	0.7948
Crematogaster sp.7	polymorphic	intermediate	AD	678.52	0.7722	0.9059
Crematogaster sp.8	polymorphic	intermediate	AD	566.21	0.7182	0.5804
Crematogaster sp.9	polymorphic	intermediate	AD	631.88	1.0087	0.6451
Cyphomyrmex sp.1	monomorphic	intermediate	Latt	896.27	0.8682	0.6569
Cyphomyrmex sp.2	monomorphic	intermediate	Latt	944.99	0.8775	0.7771
Cyphomyrmex sp.6	monomorphic	intermediate	Latt	894.34	0.9035	0.6643
Dorymyrmex brunneus	monomorphic	smooth	OPP	1181.72	1.0537	0.6935
Dorymyrmex goeldii	monomorphic	smooth	OPP	1316.34	0.9711	0.6170
Dorymyrmex piramicus	monomorphic	smooth	OPP	1019.26	1.0432	0.8516
Dorymyrmex sp.5	monomorphic	smooth	OPP	1103.42	0.9810	0.7340
Dorymyrmex sp.6	monomorphic	smooth	OPP	1046.68	0.9757	0.6373
Eciton vagans	polymorphic	intermediate	AA	2167.79	0.9079	0.9059
Ectatomma brunneum	monomorphic	textured	EP	3758.86	0.8571	0.7203
Ectatomma edentatum	monomorphic	textured	EP	2850.07	0.9294	0.7732
Ectatomma opaciventre	monomorphic	textured	EP	4508.32	0.9763	0.7739
Ectatomma permagnum	monomorphic	textured	EP	3887.23	0.7976	0.7418
Ectatomma tuberculatum	monomorphic	textured	EP	3876.18	0.8324	0.9882
Eurhopalothrix bruchi	monomorphic	textured	CP	473.06	0.6214	0.6412
Forelius maranhaoensis	monomorphic	smooth	DD	778.43	1.0943	0.6928
Gnamptogenys cf. *menozzii*	monomorphic	textured	EP	1660.06	0.7318	0.4706
Gnamptogenys gp. *striatula*	monomorphic	textured	EP	1526.58	0.8254	0.7791
Gnamptogenys sp.2	monomorphic	textured	EP	1592.71	0.7780	0.8235
Gnamptogenys sp.3	monomorphic	textured	EP	1266.40	0.7647	0.9503
Gnamptogenys sulcata	monomorphic	textured	EP	1700.09	0.7670	0.5229
Hypoponera distinguenda	monomorphic	smooth	CP	1055.38	0.7148	0.7549
Kalathomyrmex emeryi	monomorphic	intermediate	Latt	901.01	0.7900	0.5882
Kalathomyrmex sp.1	monomorphic	intermediate	Latt	889.14	0.8910	0.9098
Labidus praedator	polymorphic	smooth	AA	1783.46	0.9842	0.6176
Linepithema cerradensis	monomorphic	smooth	EO	741.50	0.7646	0.7484
Linepithema iniqum	monomorphic	smooth	EO	863.79	0.7920	0.6980
Linepithema micans	monomorphic	smooth	EO	864.63	0.7855	0.8353
Linepithema neotropicum	monomorphic	smooth	EO	756.42	0.7582	0.7627

Morphospecies	Polymorphism	Sculpturing	FG	WL	HFL	V
Mycetophylax sp.5	monomorphic	textured	Latt	916.62	0.8726	0.7245
Mycetophylax sp.7	monomorphic	textured	Latt	1035.32	0.8986	0.8137
Mycetophylax sp.8	monomorphic	textured	Latt	675.74	0.8108	0.7592
Mycocepurus goeldii	monomorphic	textured	Latt	1008.20	0.8545	0.6993
Mycocepurus smithii	monomorphic	textured	Latt	721.08	0.7189	0.8235
Myrmelachista ruszkii	monomorphic	intermediate	AS	560.56	0.4227	0.2824
Myrmelachista sp.1	monomorphic	intermediate	AS	599.48	0.5816	0.8608
Myrmicocrypta sp.1	monomorphic	intermediate	Latt	949.19	0.9161	1.0000
Myrmicocrypta sp.2	monomorphic	intermediate	Latt	910.19	0.8981	0.8196
Neivamyrmex pseudops	polymorphic	intermediate	AA	1423.86	0.9358	0.5459
Neivamyrmex sp.2	polymorphic	intermediate	AA	916.45	0.6682	0.3765
Neoponera verenae	monomorphic	intermediate	EP	3666.04	0.8217	0.9000
Nesomyrmex sp.2	monomorphic	textured	AS	NA	NA	NA
Nomamyrmex hartigii	polymorphic	intermediate	AA	2065.72	0.8517	0.7176
Nylanderia sp.1	monomorphic	smooth	OPP	768.83	0.9711	0.6612
Nylanderia steinheili	monomorphic	smooth	OPP	807.71	0.9246	0.7105
Ochetomyrmex semipolitus	monomorphic	intermediate	EO	509.50	0.6875	0.7229
Odontomachus bauri	monomorphic	intermediate	EP	3521.84	0.7690	0.8853
Odontomachus meinerti	monomorphic	intermediate	EP	2505.14	0.8407	0.6000
Oxyepoecus sp.2	monomorphic	intermediate	EP	664.17	0.6242	0.7778
Oxyepoecus sp.5	monomorphic	intermediate	EP	673.24	0.6470	0.7059
Pachycondyla striata	monomorphic	intermediate	EP	4989.69	0.7926	0.8464
Pachycondyla harpax	monomorphic	intermediate	EP	3189.35	0.6839	0.7755
Pheidole capillata	dimorphic	textured	EO	858.38	0.9582	0.8595
Pheidole diligens	dimorphic	intermediate	EO	652.69	0.9257	0.6908
Pheidole diligens sp.2	dimorphic	intermediate	EO	713.50	0.9993	0.7359
Pheidole gp. *flavens* sp.1	dimorphic	intermediate	EO	456.76	0.8902	0.6359
Pheidole gp. *flavens* sp.2	dimorphic	intermediate	EO	462.98	0.8950	0.6712
Pheidole gp. *flavens* sp.3	dimorphic	intermediate	EO	625.07	0.9062	0.8837
Pheidole oxyops	dimorphic	intermediate	EO	826.96	1.0488	0.7268
Pheidole radoszkowskii	dimorphic	intermediate	EO	768.17	1.0651	0.7203
Pheidole sp.1	dimorphic	intermediate	EO	1214.31	1.0727	0.8699
Pheidole sp.10	dimorphic	intermediate	EO	799.29	1.0343	0.8569
Pheidole sp.11	dimorphic	intermediate	EO	849.37	0.7436	0.7314
Pheidole sp.12	dimorphic	intermediate	EO	712.90	0.8446	0.8190
Pheidole sp.13	dimorphic	intermediate	EO	848.68	0.9264	0.2855
Pheidole sp.14	dimorphic	intermediate	EO	769.03	1.0553	0.6000
Pheidole sp.17	dimorphic	intermediate	EO	1229.00	1.2434	0.7908
Pheidole sp.18	dimorphic	intermediate	EO	705.65	0.9362	0.7451
Pheidole sp.19	dimorphic	intermediate	EO	669.13	1.0206	0.6369
Pheidole sp.20	dimorphic	intermediate	EO	806.47	1.0412	0.7209
Pheidole sp.21	dimorphic	intermediate	EO	705.09	0.8181	0.4549
Pheidole sp.22	dimorphic	intermediate	EO	1014.65	1.2990	0.7843
Pheidole sp.23	dimorphic	intermediate	EO	1102.34	1.0660	0.7085
Pheidole sp.24	dimorphic	intermediate	EO	1338.25	1.2973	0.6569

Morphospecies	Polymorphism	Sculpturing	FG	WL	HFL	V
Pheidole sp.25	dimorphic	intermediate	EO	980.23	1.1163	0.8980
Pheidole sp.26	dimorphic	intermediate	EO	654.23	0.8736	0.6059
Pheidole sp.27	dimorphic	intermediate	EO	1371.20	1.0651	0.6275
Pheidole sp.5	dimorphic	intermediate	EO	858.84	0.8645	0.7928
Pheidole sp.6	dimorphic	smooth	EO	976.26	0.9256	0.6752
Pheidole sp.7	dimorphic	intermediate	EO	945.03	1.0890	0.7843
Pheidole sp.9	dimorphic	intermediate	EO	802.47	1.0872	0.6908
Pheidole subarmata	dimorphic	smooth	EO	580.50	0.8749	0.8634
Pheidole vafra	dimorphic	intermediate	EO	845.15	1.0654	0.6451
Platythyrea cf. *angusta*	monomorphic	textured	AP	2777.42	0.7959	0.9804
Pogonomyrmex naegelii	monomorphic	textured	SH	1581.88	0.8488	0.7856
Pseudomyrmex gp. *pallidus* sp.1	monomorphic	intermediate	AS	1042.05	0.5026	0.6346
Pseudomyrmex sp.1	monomorphic	intermediate	AS	2329.55	0.5927	0.8784
Pseudomyrmex sp.2	monomorphic	intermediate	AS	1444.89	0.5267	0.7412
Pseudomyrmex termitarius	monomorphic	intermediate	AS	1795.57	0.6547	0.6706
Pseudoponera sp.1	monomorphic	intermediate	EP	2287.51	0.6513	0.7739
Pseudoponera sp.2	monomorphic	intermediate	EP	2415.93	0.6065	0.7098
Rasopone sp.1	monomorphic	intermediate	EP	736.78	0.5505	0.6627
Rogeria besucheti	monomorphic	textured	CO	757.25	0.7424	0.5255
Sericomyrmex amabilis	monomorphic	intermediate	Hatt	1514.82	0.8861	0.7392
Sericomyrmex sp.1	monomorphic	intermediate	Hatt	1341.57	0.9268	0.1569
Solenopsis globularia sp.1	polymorphic	smooth	CO	648.44	0.6436	0.7876
Solenopsis globularia sp.2	polymorphic	smooth	CO	677.46	0.6618	0.6948
Solenopsis saevissima	polymorphic	smooth	EO	906.83	0.7177	0.8425
Solenopsis sp.1	monomorphic	smooth	CO	416.84	0.5984	0.7281
Solenopsis sp.2	polymorphic	smooth	CO	562.92	0.6815	0.8516
Solenopsis sp.3	polymorphic	smooth	EO	577.03	0.6985	0.7569
Solenopsis sp.7	polymorphic	smooth	EO	491.50	0.6557	0.7993
Solenopsis substituta	polymorphic	smooth	EO	914.39	0.8837	0.8085
Strumigenys cf. *grytava*	monomorphic	textured	CP	500.71	0.5342	0.8235
Strumigenys louisianae	monomorphic	textured	CP	541.94	0.7431	0.7588
Strumigenys subedentata	monomorphic	textured	CP	716.89	0.6806	0.8549
Trachymyrmex ALsp.2	monomorphic	intermediate	Latt	1992.15	1.0158	0.8275
Trachymyrmex ALsp.3	monomorphic	intermediate	Latt	1666.33	0.9331	0.8353
Trachymyrmex RPsp.1	monomorphic	intermediate	Latt	1474.82	0.9021	0.6654
Trachymyrmex sp.1	monomorphic	intermediate	Latt	1486.19	0.8954	0.7405
Trachymyrmex sp.2	monomorphic	intermediate	Latt	1705.35	0.8988	0.7255
Trachymyrmex sp.3	monomorphic	intermediate	Latt	1851.45	0.9483	0.7373
Trachymyrmex sp.4	monomorphic	intermediate	Latt	1051.19	0.8351	0.7634
Trachymyrmex sp.5	monomorphic	intermediate	Latt	1858.54	0.9407	0.7147
Trachymyrmex sp.8	monomorphic	intermediate	Latt	2023.80	0.8932	0.8353
Tranopelta gilva	monomorphic	smooth	CO	644.49	0.6121	0.8627
Wasmannia affinis	monomorphic	textured	EO	583.92	0.7648	0.8752
Wasmannia auropunctata	monomorphic	textured	EO	495.41	0.8352	0.6641
Wasmannia lutzi	monomorphic	textured	EO	549.84	0.7439	0.9049

A.4. Assembly weighted averages of lightness (AWM V) and body size (AWM WL), calculated for each community (N=24).

Site	AWM_V	AWM_WL	Site	AWM_V	AWM_WL
OB Lower	0.59	7.65	BO Lower	0.39	6.91
OB Upper	0.41	6.67	BO Upper	0.43	6.01
OP Lower	0.63	6.50	SN Lower	1.00	14.99
OP Upper	0.38	4.96	SN Upper	0.39	3.44
CA Lower	0.46	8.47	PF Lower	0.63	8.15
CA Upper	0.20	1.60	PF Upper	0.48	6.37
PB Lower	0.90	9.74	AL Lower	0.83	13.90
PB Upper	0.52	10.03	AL Upper	0.60	8.78
IT Lower	0.57	6.43	BA Lower	0.74	8.71
IT Upper	0.38	6.42	BA Upper	0.19	3.73
RP Lower	0.43	5.33	GU Lower	0.64	8.97
RP Upper	0.56	11.31	GU Upper	0.36	7.21

A.5. Records of Formicidae species sampling in *campo rupestre* localities across Espinhaço Mountain Range, southeast Brazil. Legend: 1) Ouro Branco; 2) Ouro Preto; 3) Caraça; 4) Pico do Breu; 5) Pico do Itambé; 6) Rio Preto; 7) Botumirim; 8) Serra Nova; 9) Monte Azul; 10) Pico das Almas; 11) Pico Barbados; 12) P.N. Chapada Diamantina – Guiné; S_{obs}= Taxonomic richness; Records = % Frequency records of specimens on the whole system.

		Lower elevation sites												**Upper elevation sites**											
Subfamily/ Genera	**Morphospecies**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
Dolichoderinae (S_{obs}=11; Records= 12.2%)																									
Azteca	*Azteca* sp.1									X															
Dorymyrmex	*Dorymyrmex brunneus*				X	X	X		X	X		X									X				
	Dorymyrmex goeldii				X		X	X	X		X			X						X	X	X	X		
	Dorymyrmex piramicus				X				X			X													
	Dorymyrmex sp.5				X														X						
	Dorymyrmex sp.6										X														
Forelius	*Forelius maranhaoensis*				X				X			X													
Linepithema	*Linepithema cerradensis*					X		X		X			X							X		X		X	
	Linepithema iniqum																							X	
	Linepithema micans	X	X	X	X		X		X				X	X	X	X	X	X	X	X	X	X	X		X
	Linepithema neotropicum																				X				
Dorylinae (S_{obs}=5; Records= 0.4%)																									
Eciton	*Eciton vagans*		X																						
Labidus	*Labidus praedator*												X												
Neivamyrmex	*Neivamyrmex pseudops*		X						X																
	Neivamyrmex sp.2				X																				
Nomamyrmex	*Nomamyrmex hartigii*								X																
Ectatomminae (S_{obs}=10; Records= 6.8%)																									
Ectatomma	*Ectatomma brunneum*					X	X		X		X		X												

Subfamily/ Genera	Morphospecies	Lower elevation sites												Upper elevation sites											
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
	Ectatomma edentatum	X	X	X	X	X	X	X	X	X	X	X	X	X							X	X	X		X
	Ectatomma opaciventre								X		X														
	Ectatomma permagnum	X																							
	Ectatomma tuberculatum									X															
Gnamptogenys	*Gnamptogenys* cf. *menozzii*																	X							
	Gnamptogenys gp. *striatula*			X	X			X				X					X							X	
	Gnamptogenys sp.2	X																							
	Gnamptogenys sp.3	X			X																				
	Gnamptogenys sulcata				X		X													X					
Formicinae (S_{obs}=24; Records= 26.6%)																									
Acropyga	*Acropyga goeldii*													X											
Brachymyrmex	*Brachymyrmex* cf. *pictus*	X	X	X	X	X		X	X	X	X	X	X		X					X	X	X	X		X
	Brachymyrmex cordemoyi				X	X		X	X	X	X		X	X	X		X	X	X	X	X			X	
Camponotus	*Camponotus atriceps*				X				X		X	X		X											
	Camponotus bidens											X													
	Camponotus blandus								X	X	X	X													
	Camponotus cingulatus		X	X	X		X	X	X	X	X		X	X							X	X		X	
	Camponotus crassus		X	X	X		X	X	X	X	X		X	X	X		X		X	X		X		X	X
	Camponotus fastigatus			X			X	X	X	X	X	X							X		X	X			
	Camponotus lespesii											X													
	Camponotus leydigi								X		X	X													
	Camponotus melanoticus	X	X	X	X	X	X		X	X	X			X	X	X	X	X	X			X	X	X	X
	Camponotus novogranadensis	X								X				X						X					
	Camponotus renggeri		X				X																		
	Camponotus rufipes	X	X	X	X	X				X	X		X	X	X		X	X				X	X		X

		Lower elevation sites												**Upper elevation sites**											
Subfamily/ Genera	**Morphospecies**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
	Camponotus sp.6			X	X				X					X					X						
	Camponotus Tanaemyrmex sp.3											X													
	Camponotus textor									X	X														
	Camponotus vitatus	X							X			X													
	Camponotus westermanni				X	X		X	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X
Myrmelachista	*Myrmelachista ruszkii*																				X				
	Myrmelachista sp.1		X			X									X	X					X				
Nylanderia	*Nylanderia* sp.1	X				X																			
	Nylanderia steinheili							X	X		X	X	X				X				X		X	X	X
Myrmicinae (S_{obs}=104; Records= 47.0%)																									
Acromyrmex	*Acromyrmex* cf. *niger*														X										
	Acromyrmex RPsp.1						X																		
	Acromyrmex sp.2				X	X																			
	Acromyrmex sp.4				X						X		X				X		X	X			X		
	Acromyrmex subterraneus			X			X					X									X	X			
Apterostigma	*Apterostigma* gp. *pilosum* sp.1				X																				
	Apterostigma gp. *pilosum* sp.2											X													
Atta	*Atta bisphaerica*								X			X													
	Atta sexdens			X																					
Cephalotes	*Cephalotes depressus*								X																
	Cephalotes maculatus																X								
	Cephalotes minutus								X	X		X													
	Cephalotes pinelli																X								
	Cephalotes pusillus		X		X				X	X	X										X	X			
Crematogaster	*Crematogaster acuta*	X																							

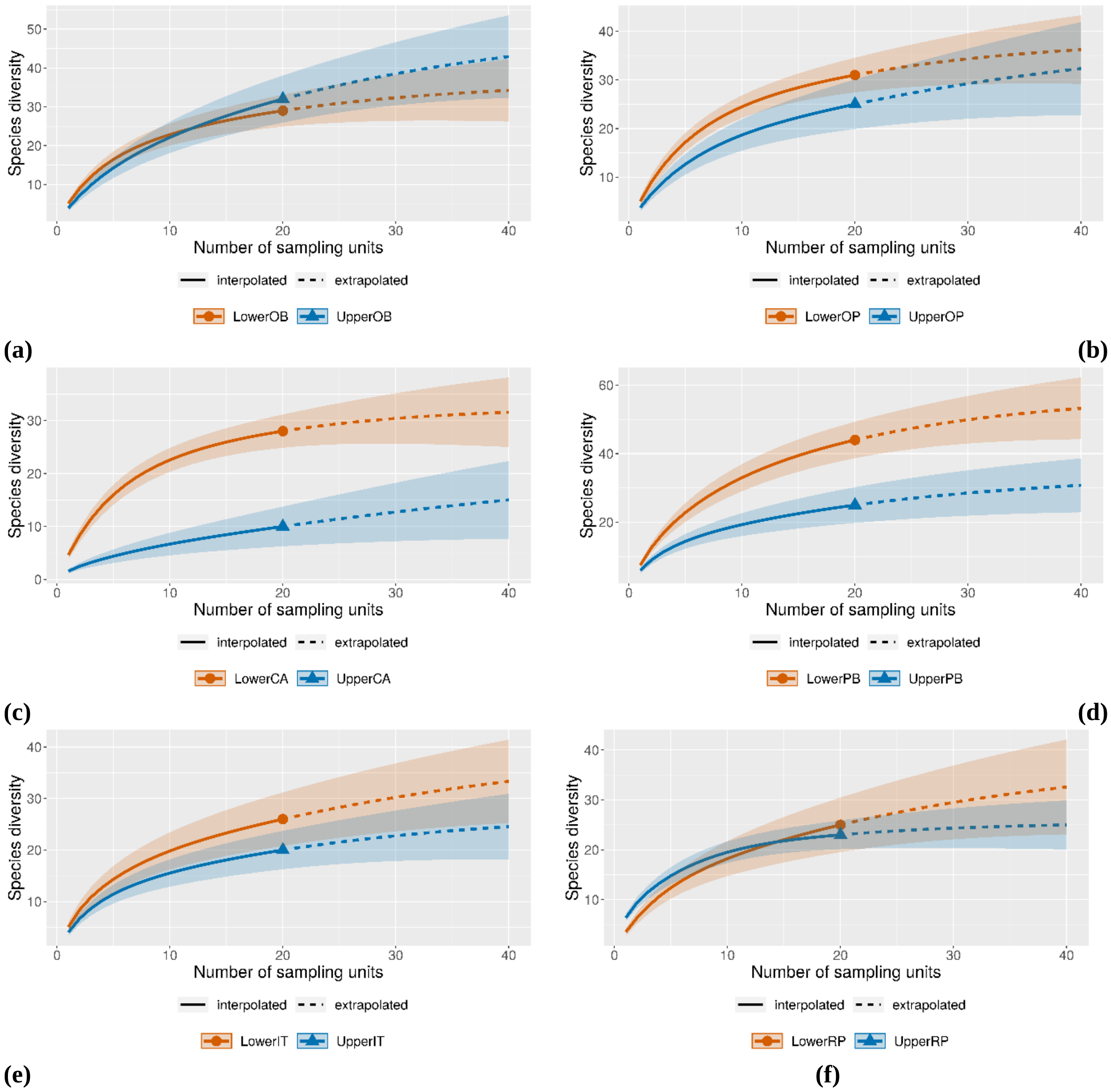
		Lower elevation sites												Upper elevation sites											
Subfamily/ Genera	**Morphospecies**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
	Crematogaster BAsp.1																							X	
	Crematogaster BOsp.1																			X					
	Crematogaster brasiliensis				X	X								X											
	Crematogaster cf. *erecta*	X																							
	Crematogaster obscurata						X																		
	Crematogaster OBsp.1													X					X						
	Crematogaster PFsp.1																					X			
	Crematogaster SNsp.1								X																
	Crematogaster sp.1		X												X										
	Crematogaster sp.10										X														
	Crematogaster sp.7			X																					
	Crematogaster sp.8																						X		
	Crematogaster sp.9										X														
Cyphomyrmex	*Cyphomyrmex* sp.1										X												X		X
	Cyphomyrmex sp.2		X	X										X			X				X		X		
	Cyphomyrmex sp.6	X																							
Eurhopalothrix	*Eurhopalothrix bruchi*											X													
Kalathomyrmex	*Kalathomyrmex emeryi*				X																				
	Kalathomyrmex sp.1											X													
Mycetophylax	*Mycetophylax* sp.5			X													X								
	Mycetophylax sp.7																	X							
	Mycetophylax sp.8											X													
Mycocepurus	*Mycocepurus goeldii*	X				X						X													
	Mycocepurus smithii								X			X													
Myrmicocrypta	*Myrmicocrypta* sp.1									X															

		Lower elevation sites												Upper elevation sites											
Subfamily/ Genera	**Morphospecies**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
	Myrmicocrypta sp.2											X													
Nesomyrmex	*Nesomyrmex* sp.2			X																					
Ochetomyrmex	*Ochetomyrmex semipolitus*	X			X			X		X												X			
Oxyepoecus	*Oxyepoecus* sp.2				X										X		X	X							
	Oxyepoecus sp.5															X									
Pheidole	*Pheidole capillata*	X	X	X										X								X	X		
	Pheidole diligens		X	X			X	X	X	X	X	X									X	X	X		
	Pheidole diligens sp.2										X														
	Pheidole gp. *flavens* sp.1	X											X										X		X
	Pheidole gp. *flavens* sp.2			X	X	X	X	X	X	X		X					X		X						
	Pheidole gp. *flavens* sp.3										X	X													
	Pheidole oxyops	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X			X			X	X	X
	Pheidole radoszkowskii	X	X	X	X	X		X	X	X	X			X	X		X			X	X	X	X		X
	Pheidole sp.1	X	X		X									X					X	X					
	Pheidole sp.10					X				X	X			X			X	X				X			
	Pheidole sp.11													X											
	Pheidole sp.12						X	X				X									X		X		
	Pheidole sp.13						X												X						
	Pheidole sp.14						X																	X	
	Pheidole sp.17								X		X	X													
	Pheidole sp.18																				X				
	Pheidole sp.19								X																
	Pheidole sp.20					X												X							
	Pheidole sp.21									X															
	Pheidole sp.22										X														

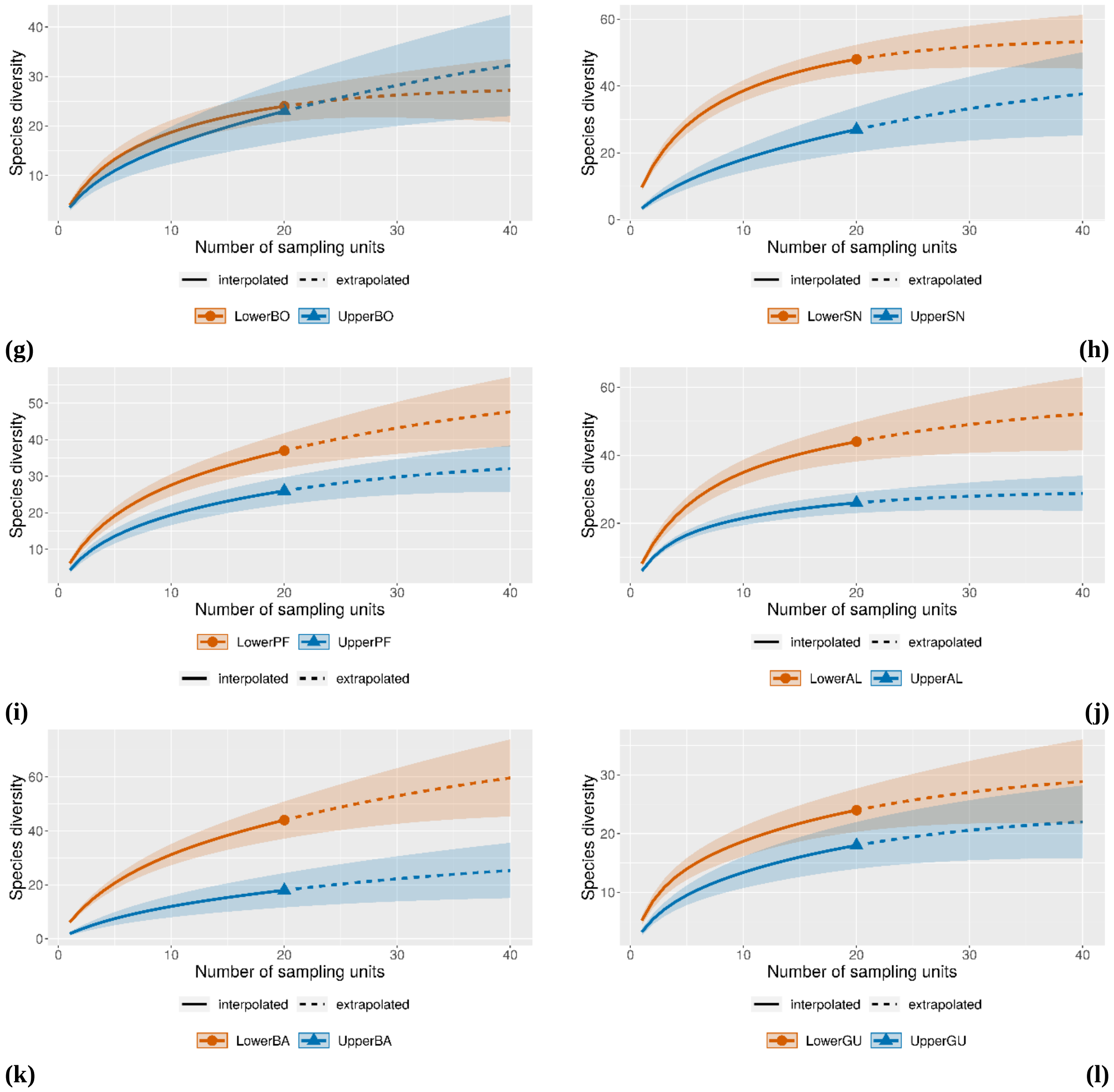
		Lower elevation sites												Upper elevation sites											
Subfamily/ Genera	**Morphospecies**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
	Pheidole sp.23										X												X		
	Pheidole sp.24																						X		
	Pheidole sp.25											X												X	
	Pheidole sp.26				X																				
	Pheidole sp.27									X															
	Pheidole sp.5														X			X							
	Pheidole sp.6														X		X	X	X	X				X	X
	Pheidole sp.7			X																					
	Pheidole sp.9	X												X											
	Pheidole subarmata	X	X		X									X											
	Pheidole vafra		X		X				X											X	X		X		
Pogonomyrmex	*Pogonomyrmex naegelii*		X		X	X		X	X	X		X	X		X				X	X	X	X	X		X
Rogeria	*Rogeria besucheti*											X													
Sericomyrmex	*Sericomyrmex* sp.1				X																				
	Sericomyrmex sp.2								X	X	X	X													
Solenopsis	*Solenopsis globularia* sp.1						X		X	X	X	X							X			X			
	Solenopsis globularia sp.2							X												X					
	Solenopsis saevissima		X		X	X		X	X		X		X					X		X	X	X	X		X
	Solenopsis sp.1	X	X	X	X	X			X	X	X	X		X	X	X	X		X	X		X		X	
	Solenopsis sp.2			X			X		X					X		X					X	X			
	Solenopsis sp.3															X									
	Solenopsis sp.7	X			X	X				X		X		X	X		X	X	X	X		X			
	Solenopsis substituta				X				X		X	X													
Strumigenys	*Strumigenys* cf. *grytava*							X																	
	Strumigenys louisianae	X												X											

		Lower elevation sites												Upper elevation sites											
Subfamily/ Genera	**Morphospecies**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
	Strumigenys subedentata														X										
Trachymyrmex	*Trachymyrmex* ALsp.2										X														
	Trachymyrmex ALsp.3																			X					
	Trachymyrmex RPsp.1																		X						
	Trachymyrmex sp.1																		X						
	Trachymyrmex sp.2		X	X	X					X	X	X	X	X	X		X	X					X		
	Trachymyrmex sp.3	X																							
	Trachymyrmex sp.4									X		X	X												
	Trachymyrmex sp.5										X		X												X
	Trachymyrmex sp.8								X																
Tranopelta	*Tranopelta gilva*						X														X				
Wasmannia	*Wasmannia affinis*			X						X		X					X				X				
	Wasmannia auropunctata	X	X	X	X	X	X		X	X	X	X	X	X	X			X	X				X	X	
	Wasmannia lutzi							X			X				X										
Ponerinae (S_{obs}=11; Hits= 4.7%)																									
Anochetus	*Anochetus* sp.1																								X
Hypoponera	*Hypoponera distinguenda*					X												X							
Neoponera	*Neoponera verenae*		X											X											
Odontomachus	*Odontomachus bauri*						X		X		X														
	Odontomachus meinerti												X												
Pachycondyla	*Pachycondyla striata*			X		X		X						X	X		X	X	X	X		X		X	X
	Pachycondyla harpax		X													X									
Platythyrea	*Platythyrea* cf. *angusta*									X															
Pseudoponera	*Pseudoponera* sp.1														X			X							
	Pseudoponera sp.2																X								

		Lower elevation sites												**Upper elevation sites**											
Subfamily/ Genera	**Morphospecies**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
Rasopone	*Rasopone* sp.1																							X	
Pseudomyrmicinae (S$_{obs}$=4; Records= 2.3%)																									
Pseudomyrmex	*Pseudomyrmex* gp. *pallidus* sp.1				X			X	X				X	X	X				X		X				
	Pseudomyrmex sp.1		X																						
	Pseudomyrmex sp.2		X																						



A.6.a. Rarefaction-extrapolation species accumulation curves of ant richness for each site in the 12 mountains survey: A:(OB) Ouro Branco; B: (OP) Pico do Itacolomi, Ouro Preto; C: (CA) RPPN Santuário do Caraça; D: (PB) Pico do Breu, Serra do Cipó; E: (IT) Parque Estadual Pico do Itambé; F: (RP) Parque Estadual do Rio Preto. Colour code: dark orange = Lower Sites; dark blue = Upper Sites.



A.6.b. Rarefaction-extrapolation species accumulation curves of ant richness for each site in the 12 mountains survey: G: (BO) Botumirim; H: (SN) Parque Estadual Serra Nova; I: (PF) Pico da Formosa, Monte Azul; J: (AL) Pico das Almas; K: (BA) Pico do Barbado; L:. (GU) Parque Nacional Chapada Diamantina, Guiné. Colour code: dark orange = Lower Sites; dark blue = Upper Sites.

A.7. Table with the results of rarefaction-extrapolation accumulation curves of the 24 sites of the 12 mountains in the *Espinhaço* Mountain Range. Sample coverage is expressed by C.*ha* index

Site	S.(obs)	Sample Coverage	Site	S (obs)	Sample Coverage
OB Lower	29	0.9127	BO Lower	24	0.9144
OB Upper	32	0.7969	BO Upper	23	0.8322
OP Lower	31	0.9119	SN Lower	48	0.9384
OP Upper	25	0.8677	SN Upper	27	0.7816
CA Lower	28	0.9251	PF Lower	37	0.8787
CA Upper	10	0.8086	PF Upper	26	0.8851
PB Lower	44	0.8934	AL Lower	44	0.9202
PB Upper	25	0.9243	AL Upper	26	0.9503
IT Lower	26	0.9016	BA Lower	44	0.8301
IT Upper	20	0.9145	BA Upper	18	0.741
RP Lower	25	0.8445	GU Lower	24	0.9238
RP Upper	23	0.9689	GU Upper	18	0.8942

Conclusão Geral

Apesar do elevado *turnover* de espécies de formigas em todas as dimensões espaço-temporais ao longo do gradiente de elevação e de latitude, as comunidades de formigas são funcionalmente redundantes, ou seja, as espécies mudam entre habitats, elevações ou latitudes, mas as principais características funcionais e funções ecológicas permanecem basicamente inalteradas.

Na escala da montanha, diferenças taxonômicas na composição da comunidade como consequência da elevada diversidade β taxonômica ao longo do gradiente em distâncias geográficas curtas enfatizam a importância de conservar toda a montanha, pois a perda de qualquer parte da comunidade pode acarretar perda de diversidade taxonômica e funcional. Como as espécies são restritas, caso as comunidades de topo de montanha não sejam preservadas, haverá uma possível perda das principais funções ecológicas avaliadas neste estudo. As comparações dos padrões taxonômicos e funcionais demonstraram a importância e relevância do uso de diferentes facetas de β diversidade (taxonômico e funcional) em escalas distintas (espaço-tempo). Com essas informações sobre dos padrões das múltiplas facetas da diversidade, podemos relacionar diretamente nossas observações e descobertas sobre biodiversidade à ecologia aplicada. Por exemplo, ao elaborar políticas públicas ou identificar áreas prioritárias para conservação da biodiversidade.

No gradiente latitudinal, as espécies de formigas de campos rupestre tendem a ser menores e mais escuras no topo das montanhas do que comunidades em locais mais baixos, independentemente da latitude. Apesar do padrão redundante de diversidade funcional encontrada no gradiente latitudinal existe uma forte e positiva relação entre o brilho da cor da cutícula e o tamanho do corpo para as comunidades de formigas em montanhas antigas. Além dos efeitos de elevação, a diminuição da temperatura média e déficit de pressão de vapor em função do aumento da elevação atuam como filtros ambientais, sendo os principais fatores estruturadores da diversidade taxonômica e funcional das formigas em gradientes latitudinais. Por serem consideradas organismos termofílicos, essas variáveis são de extrema importância para a estruturação da comunidade das formigas nos ambientes montanos de campo rupestre.

Investigar a relação entre os padrões de diversidade taxonômica e funcional e a distribuição de formigas em ambientes montanos tropicais nos mostrou a grande capacidade adaptativa das comunidades de formigas frente aos diferentes filtros encontrados nesses ambientes, evidenciando a importância do entendimento de como esses organismos tão antigos podem viver e interagir no e com o ambiente natural, bem como as mudanças nesses ambientes podem afetar a estruturação dessas comunidades.