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Environmental determinants of leaf-litter ant community composition along an elevational gradient

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Fichaux *et al.*

Environmental Determinants of Ant Community Composition

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3 **1 Environmental determinants of leaf-litter ant community composition along an elevational**
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5 **2 gradient**
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3 **29 Abstract**
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6 30 Ant communities are extremely diverse and provide a wide variety of ecological functions in
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8 31 tropical forests. Here we investigated the abiotic factors driving ant composition turnover across
9
10 32 an elevational gradient at Mont Itoupé, French Guiana. Mont Itoupé is an isolated mountain whose
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12 33 top is covered by cloud forests, a biogeographical rarity that is likely to be threatened according to
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14 34 climate change scenarios in the region. We examined the influence of six soil, climatic and LiDAR-
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16 35 derived vegetation structure variables on leaf-litter ant assembly (267 species) across nine 0.12-ha
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18 36 plots disposed at three elevations (ca. 400, 600 and 800m asl). We tested (a) whether species co-
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20 37 occurring within a same plot or a same elevation were more similar in terms of taxonomic,
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22 38 functional and phylogenetic composition, than species from different plots/elevations, and (b)
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24 39 which environmental variables significantly explained compositional turnover among plots. We
25
26 40 found that the distribution of species and traits of ant communities along the elevational gradient
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28 41 was significantly explained by a turnover of environmental conditions, particularly in soil
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30 42 phosphorus and sand content, canopy height and mean annual relative humidity of soil. Our results
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32 43 shed light on the role exerted by environmental filtering in shaping ant community assembly in
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34 44 tropical forests. Identifying the environmental determinants of ant species distribution along
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36 45 tropical elevational gradients could help predicting the future impacts of global warming on
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38 46 biodiversity organization in vulnerable environments such as cloud forests.
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47 48 *Key words:* ants; climate; elevation; environmental filtering; French Guiana; functional traits; soil
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49 49 composition.
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1. INTRODUCTION

Determining how environmental factors drive biodiversity patterns is one of the fundamental goals in ecology. Predictable changes in diversity and composition of plant and animal communities are observed along broad elevational or latitudinal gradients (Willig *et al.* 2003, Hillebrand 2004, McCain & Grytnes 2010). Elevational gradients are particularly valuable to study biodiversity patterns, given that they often span sharp gradients in abiotic conditions even over small spatial scales (e.g. Hodkinson 2005, Kraft *et al.* 2011, Hoiss *et al.* 2012). For instance, recurrent patterns observed with increasing elevation involve a continuous decrease of temperature (McCain & Grytnes 2010), or an increase in soil moisture and organic carbon content (He *et al.* 2016).

Niche models predict that environmental conditions select species with particular traits to establish and persist within an area (Keddy 1992). The effect of environmental filtering may be studied by comparing observed functional or phylogenetic diversity of communities with those expected under nulls models generated by drawing species at random from a regional species pool (e.g. Gotelli 2000). At local to landscape scales, homogeneous environmental conditions should generate assemblages of species that are functionally and phylogenetically (if traits are conserved) more similar than expected by chance (i.e. functional/phylogenetic clustering, respectively). Several studies examining biodiversity patterns along elevational gradients reported a functional or phylogenetic overdispersion of species in lowland assemblages, shifting to a functional or phylogenetic clustering of species in highland assemblages (Graham *et al.* 2009, Machac *et al.* 2011, Dehling *et al.* 2014). These results can be interpreted as the effect of increasing strength of environmental filtering on shaping communities (Purschke *et al.* 2013), which may be caused by the reduction of temperatures with increasing elevation.

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3 75 Here we aim to measure the variations in ant community composition and to determine the
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5 76 environmental factors that shape these variations along a Neotropical altitudinal gradient. Ants
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7 77 (Hymenoptera: Formicidae) represent an ideal model for studying the determinants of species
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9 78 distribution and coexistence because they are abundant and ecologically dominant in terrestrial
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11 79 ecosystems (Hölldobler & Wilson 1990) and they perform a wide variety of ecological functions
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13 80 such as predation, scavenging and seed dispersal (Folgarait 1998, Del Toro *et al.* 2012).
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15 81 Furthermore, previous studies have shown that ant community composition can change markedly
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17 82 along environmental gradients (e.g. Bihn *et al.* 2010, Yates *et al.* 2011, Arnan *et al.* 2014, Groc *et*
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19 83 *al.* 2014, Silva & Brandão 2014, Smith *et al.* 2014, Bishop *et al.* 2015, Fontanilla *et al.* 2019).
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21 84 Nevertheless, few studies have investigated changes in ant community composition along
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23 85 elevational gradients in tropical regions (Brühl *et al.* 1999, Dunn *et al.* 2009, Smith *et al.* 2014,
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25 86 Nowrouzi *et al.* 2016). Elevational gradients deserve a special attention because they are
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27 87 characterized by a sharp change of various abiotic conditions, especially temperature and
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29 88 humidity, which are predicted to shape ant species distribution. For instance, Nowrouzi *et al.*
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31 89 (2016) have emphasized marked species turnovers between 600 and 800m, which in their study
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33 90 site corresponded to a transition between lowland and cloud forests. Considering the rise of the
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35 91 cloud layers that is predicted by climate change scenarios and associated increases in temperature
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37 92 and decreases in relative humidity (Helmer *et al.* 2019, Los *et al.* 2019), it is urgent to
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39 93 characterize species distributions in these environments to assess threats to their persistence.
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47 94 To address this gap, we assess how taxonomic, functional and phylogenetic composition of
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49 95 Neotropical ant assemblages are shaped by different environmental parameters along an
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51 96 elevational gradient. We focused on leaf-litter ants because they are easily sampled with a
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53 97 standardized and generalizable collection protocol and their taxonomy has been well described in
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55 98 the region (Groc *et al.* 2009, Fichaux *et al.* 2019). We collected leaf-litter ants at Mont Itoupé
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3 99 (French Guiana), a mountain which represents a particular biogeographic interest, because of its
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5 100 isolation and its relatively high elevation (ca. 800m) in the eastern Guiana Shield. The top of the
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7 101 mountain is covered by cloud forests, a biogeographic rarity that is likely to be threatened
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10 102 according to scenarios of climate change in this region. Climatic parameters, such as temperature
11
12 103 and humidity, may represent major drivers of ant species distributions (e.g. Sanders *et al.* 2007,
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14 104 Dunn *et al.* 2009, Silva & Brandão 2014, Arnan *et al.* 2015). Variation in habitat characteristics
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17 105 such as nutrient availability, vegetation cover as well as soil texture may also play an important
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19 106 role (Vasconcelos *et al.* 2003, Chen *et al.* 2015, Blatrix *et al.* 2016, Schmidt *et al.* 2016).

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21 107 We sampled along these gradients to address two main objectives. First, we assessed if ant
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23 108 community structure differed from a random distribution of species along the elevational
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26 109 gradient. A stronger effect of environmental filtering is generally observed at highest elevations,
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28 110 leading to a clustered assemblage structure (Graham *et al.* 2009, Machac *et al.* 2011, Dehling *et*
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30 111 *al.* 2014, Smith *et al.* 2014). Thus, we expected to observe clustered patterns among the leaf-litter
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33 112 assemblages at Mont Itoupé, as a result of the effects of the environmental filtering particularly at
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35 113 high altitude. Second, we identified the main environmental determinants (soil, climate and
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37 114 vegetation structure as measured by LiDAR) of the taxonomic, functional and phylogenetic
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39 115 composition of ant assemblages. A decrease in ant diversity along elevational gradients is a
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42 116 common pattern (Brühl *et al.* 1999, Machac *et al.* 2011, Longino *et al.* 2014, Fontanilla *et al.*
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44 117 2019) which may be explained by the variation in climatic or soil parameters. We therefore
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46 118 expected both climate and soil variables to be strongly correlated with variation in leaf-litter ant
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48 119 assemblages' composition. Moreover, ant species turnover has been shown to be highly
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51 120 coordinated with tree species turnover in the region, independently from environmental gradients
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53 121 (Vleminckx *et al.* 2019). We may therefore expect a change of ant species composition with
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3 122 elevation considering previous evidence that forest structure and composition change along
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5 123 elevational gradients (Swenson *et al.* 2011).
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10 125 **2. METHODS**

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14 127 **2.1. Experimental design**

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17 128 We collected ants during the dry season in November 2014, at Mont Itoupé (3°01'10.32"N,
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19 129 53°04'45.90"W), French Guiana. Mont Itoupé, located in the heart of the National Park of the
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21 130 Amazon in French Guiana, peaks at an altitude of 830m asl, representing one of the highest peaks
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23 131 within 250km. A total of nine 0.12-ha plots were established at approximately 400m, 600m and
24
25 132 800m asl, with three plots per elevation range, spanning a total area of ca. 10km² (Figure 1). The
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27 133 plots were chosen to span the range of variation in both climatic and soil conditions across the
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29 134 site. Mean annual rainfall in the area reached 2584 mm (< 140 mm of difference across
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31 135 elevations) while mean annual temperature ranged from 23.0 at 400m to 21.6°C at 800m
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33 136 (worldclim.com).
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38 137 Each plot represented an area of 30m x 40m, within which we established a grid system of
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40 138 20 sampling points separated by at least 10m, according to the Ants of Leaf Litter Protocol
41
42 139 described in Agosti & Alonso (2000). At each sampling point, we collected leaf-litter ants using
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44 140 pitfall traps and the mini-Winkler method (for more details, see Bestelmeyer *et al.* 2000). Pitfall
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46 141 traps were left in the ground for 72 hours while the mini-Winkler extractors were installed for 48
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48 142 hours. Because pitfall traps and mini-Winkler extractors were used as complementary traps, we
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50 143 pooled data from both methods in our analyses. Thus, only a single occurrence was reported for a
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52 144 species collected in both traps at the same sampling point.
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146 2.2. Ant identification

147 Ants were identified at the species level whenever possible, or assigned to a morpho-species
148 code. Species identification was mainly based on online identification keys published on Antwiki
149 (http://www.antwiki.org/wiki/Category:Identification_key) and keys developed by John T.
150 Longino (<http://ants.biology.utah.edu/AntsofCostaRica.html>). We also used the reference
151 collection of the Laboratory Ecofog (Kourou, French Guiana). For the morphospecies with
152 problematic morphological identification (i.e. species from the genera *Hypoponera*, *Nylanderia*,
153 *Pheidole* and *Solenopsis*), we also sequenced the 16S rRNA barcode (at least three specimens per
154 morphospecies) using the protocol developed by Kocher *et al.* (2016). DNA sequences were
155 compared to a local reference barcode library for the ant species of French Guiana (under
156 development; unpublished data). Samples are housed in the Laboratory Ecofog, with voucher
157 specimens deposited in the Laboratorio de Mirmecologia, Cocoa Research Centre
158 CEPEC/CEPLAC (Itabuna, BA, Brazil) under the references #5761 (mini-Winkler traps) and
159 #5762 (pitfall traps).

160

161 2.3. Morphological data

162 We measured nine morphological attributes (Table 1) using an ocular micrometer accurate to
163 0.01mm mounted on a Leica M80 dissecting microscope (Leica Microsystems, Heerbrugg,
164 Switzerland). Traits were selected based on their expected link with ecological strategies related
165 to resource use (Table 1). Measures were performed for all the species collected (i.e. 267
166 species), using at least six randomly selected (minor-caste) workers per species whenever
167 possible (Table S1).

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169 2.4. Phylogenetic data

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3 170 We produced a genus-level phylogenetic tree and calculated phylogenetic distances among all
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5 171 inventoried genera (n = 56) using the phylogenetic tree produced in a recent publication
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7 172 (Blanchard & Moreau 2016). Because two genera sampled in this study (*Gigantiops* and
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9 173 *Rasopone*) were missing in the tree of Blanchard & Moreau (2016), our resulting tree contained
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11 174 54 genera (Figure S1).
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176 **2.5. Environmental data**

177 We measured environmental parameters from soil, climatic and LiDAR data.

178 2.5.1. Soil data

179 In each plot, soil samples were collected at ten locations from three different soil layers (0-10,
180 10-20, 20-30cm), following the procedure described in Baraloto *et al.* (2011). The 10 samples for
181 each depth were then bulked into a single composite sample of ca. 500g of soil. Composite
182 sample were then transported to the Laboratory Ecofog and dried to reach constant weight at
183 25°C, sieved to 2mm and sent to the INRA Arras soil analysis laboratory (Arras, France) for
184 physical and chemical analyses. A set of nine physico-chemical properties were measured (Table
185 S2): the percentage of sand, silt and clay, soil pH, the percentage of organic matter (OM), the
186 carbon-to-nitrogen ratio (C/N), and the soil P, Na and K contents. Particle size analysis of sand,
187 silt and clay were quantitatively performed by their settling rates in an aqueous solution using a
188 hydrometer. Soil pH was measured in 1 M potassium chloride solution. The organic matter
189 content was determined based on the loss of gases after ignition for 2h at 360°C. The total
190 amount of nitrogen (N) and carbon (C) in all forms in soil were quantitatively analyzed using a
191 dynamic flash combustion system coupled with a gas chromatographic separation system and
192 thermal conductivity detection system. Extractable Phosphorus (P) was assayed using the Olsen
193 method (Olsen *et al.* 1954) based on the extraction of phosphate from the soil by 0.5 N sodium

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3 194 bicarbonate solution adjusted to pH 8.5. A semi-quantitative method was used to determine the
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5 195 amount of soil exchangeable sodium (Na) and potassium (K) residing on the soil colloid
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7 196 exchange sites by displacement with ammonium acetate solution buffered to pH 7.0.
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11 12 198 2.5.2. Climatic data

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14 199 Air temperature (in °C) and relative humidity (in %) were measured in all plots using micro-
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16 200 environmental sensors (HOBO U23-001) as described in Tymen *et al.* (2017). The weather
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18 201 sensors were placed within the area of each plot except for Plot 6, for which the sensor was
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20 202 placed halfway between Plot 5 and 6 because of a logistical issue. Since this sensor was not far
21
22 203 away for the sampled area and at the same elevation, the climatic data were used as a proxy for
23
24 204 environmental data of this plot (see Figure 1).
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28 205 The two parameters (air temperature and relative humidity) were monitored for one year,
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30 206 from 1 January 2015 to 31 December 2015 with one measurement every 30 minutes. Using the
31
32 207 local micro-environmental data, we defined four climatic variables for each plot (Table S2):
33
34 208 T_{MEAN} – mean annual Temperature, RH_{MEAN} – mean annual Relative Humidity, T_{MIN} – minimum
35
36 209 temperature of the coldest month, RH_{MIN} – minimum Relative Humidity of the driest month.
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41 42 211 2.5.3. LiDAR data

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44 212 LiDAR data were acquired in early August 2014 using a LMS-Q560 RIEGL laser range finder
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46 213 (wave length 1550nm) on board an aircraft flying at ca. 600m above the ground. A total of 64
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48 214 km² were covered with a scan angle ranging from $\pm 25^\circ$. Point density slightly exceeded 20
49
50 215 pts/m² (pulse density ca. 13 pulses/m²), with a ground point density of 0.31 pts/m². Digital
51
52 216 Elevation Model (DEM) at 1m resolution was interpolated from ground LiDAR points using
53
54 217 Lastools (Insenburg n.d.). Digital Surface Model (DSM) was built using Quick Terrain Modeler
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3 218 (free trial version, <http://appliedimagery.com>) at the same resolution. Canopy Height Model
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5 219 (CHM) was then calculated as the difference between DSM and DEM. When we ground-
6
7 220 surveyed our plots, multiple GPS point positions were acquired for each plot using a hand-held
8
9 221 GPS (accuracy 5–10m). To further improve plot geo-referencing, we adjusted plot locations
10
11 222 against LiDAR CHM as in Réjou-Méchain *et al.* (2015): the location of all surveyed trees (DBH
12
13 223 $\geq 30\text{cm}$) inferred from ground positioning was first compared to that deduced from CHM. Tree
14
15 224 GPS coordinates were then shifted until best match with the CHM, resulting in horizontal shifts
16
17 225 typically of less than 15m. With the improved plot locations, we then derived three variables for
18
19 226 the plots from LiDAR data (Table S2): canopy height (C_H), canopy cover (C_{COV}) and the gap
20
21 227 fraction (gap). Canopy height was calculated as the mean value of CHM pixels inside each plot.
22
23 228 Canopy cover was calculated using LAStools (*lascanopy -cov*), with the height threshold set at
24
25 229 5m for separating canopy and non-canopy points. Gap fraction was also calculated following the
26
27 230 approach of Morsdorf *et al.* (2006), which was defined as the percent of vegetation echoes to all
28
29 231 (ground and vegetation) echoes.
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37 233 **2.6. Data analysis**

38
39 234 All analyses were conducted using R 3.5.1 statistical software (R Core Team 2018). The
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41 235 taxonomic, functional and environmental datasets are available in supplementary material (Tables
42
43 236 S1, S2 and S3).
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49 238 **2.6.1. Functional heterogeneity among species**

50
51 239 The mean value of traits ($n = 9$) per species were normalized by using a Box-Cox transformation,
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53 240 then all traits (except Weber's length) were standardized by dividing their values by Weber's
54
55 241 length to correct for individual body size (see Table 1). A Principal Component Analysis (PCA)
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3 242 on the species \times traits matrix (hereafter, PCA_{TRAITS}) was then performed to eliminate trait
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5 243 redundancy (see Figure S2), using the R package “FactoMineR” (Lê *et al.* 2008). Subsequent
6
7 244 analyses were based on the first three principal components (except for the fourth-corner analysis
8
9
10 245 for which we also used individual traits; see below), which jointly explained 77% of the overall
11
12 246 trait inertia (Table S4).

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15 247

16 248 **2.6.2. Environmental heterogeneity among plots**

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18
19 249 Environmental variables were normalized (using Box-Cox transformation) and standardized (z-
20
21 250 score transformation) prior to analyses, using the R package “forecast” (Hyndman & Khandakar
22
23 251 2008, Hyndman *et al.* 2019). We then performed a PCA on all environmental variables ($n = 17$),
24
25
26 252 hereafter the PCA_{ENV} , to examine associations among variables and characterize environmental
27
28 253 differences among plots. The difference among the three elevations for each environmental
29
30 254 variable was tested using a Kruskal-Wallis test.

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33 255

34 256 **2.6.3. Community-wide taxonomic, functional and phylogenetic structure**

35
36
37 257 A community that is taxonomically, functionally or phylogenetically clustered within plot
38
39 258 corresponds to a situation where species co-occurring within these plots share more similar taxa,
40
41 259 traits, or are phylogenetically closer-related, respectively, than species from different plots. This
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43
44 260 clustering was quantified using the I_{ST} , τ_{ST} and Π_{ST} statistics which calculate the taxonomic,
45
46 261 functional and phylogenetic turnover among plots, respectively (Hardy & Senterre 2007). The
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48
49 262 three indices are calculated as followed:

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51
52 263 $I_{\text{ST}} = 1 - TD_w/TD_a$ (Taxonomic turnover) eq. 1
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55 264 $\tau_{\text{ST}} = 1 - FD_w/FD_a$ (Functional turnover) eq. 2
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3 265 $\Pi_{ST} = 1 - PD_w/PD_a$ (Phylogenetic turnover) eq. 3
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5

6 266 where TD corresponds to the Taxonomic Diversity calculated using Simpson index with species
7
8 267 occurrence data; FD and PD correspond, respectively, to the mean Functional Dissimilarity (here,
9
10 268 Euclidean) between distinct species and the mean Phylogenetic Distance (mean divergence time
11
12 269 based on the phylogenetic tree) between distinct genera (thus FD and PD are based on
13
14 270 species/genus presence-absence), within (w) and among (a) plots. τ_{ST} and Π_{ST} thus quantify the
15
16 271 relative increase of the mean functional divergence and phylogenetic distance between species
17
18 272 sampled among plots versus within plots, respectively. Species, trait and phylogenetic clustering
19
20 273 is observed if I_{ST} , τ_{ST} or $\Pi_{ST} > 0$, respectively, while negative values indicate overdispersion
21
22 274 (Hardy & Senterre 2007). The overall clustering within plot was calculated using the mean I_{ST} ,
23
24 275 τ_{ST} and Π_{ST} values among all pairs of plots. These mean values were tested by comparing their
25
26 276 observed value with 999 null values obtained under a null model where species occurrences are
27
28 277 randomized across plots (Hardy 2008). We then used the pairwise values of these statistics
29
30 278 among all pairs ($n = 36$) of different plots in regression models to test the effect of environmental
31
32 279 dissimilarity on taxonomic, functional and phylogenetic turnover (see next section). Turnover
33
34 280 values were also quantified and tested among pairs of altitudes (three comparisons, 400-600m,
35
36 281 400-800m and 600-800m). These indices were calculated using the R package “spacodiR”
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38 282 (Eastman *et al.* 2013).
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48 284 **2.6.4. Environmental determinants of taxonomic, functional and phylogenetic composition**

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50 285 We used Multiple Regression on distance Matrices (MRM; Lichstein 2007) to quantify and test
51
52 286 the association between environmental dissimilarity and taxonomic (I_{ST}), phylogenetic (Π_{ST}) and
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54 287 functional (τ_{ST}) turnover of ant assemblages among plots, using the R package “ecodist” (Goslee
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3 288 & Urban 2007). Statistical significance of each regression coefficient was assessed through
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5 289 residuals permutation tests ($n = 9,999$ permutations). Pairwise τ_{ST} values corresponded more
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7 290 exactly to the functional turnover among plots calculated using the three first axes of the
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9 291 PCA_{TRAITS} together, as well as each of these axes individually. Analyzing the functional turnover
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11 292 based on individual PCA axes can help identifying significant effects on traits that may be
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13 293 obscured when all traits are taken into account in the analysis. The examination of trait loadings
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15 294 on the PCA axes can help identifying those traits (Figure 2). It is worth noting that all of our tests
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17 295 may suffer from a limited statistical power due to the number of pairwise turnover values ($n = 36$)
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19 296 investigated in the MRM. Thus, while the significant signals observed may reflect some
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21 297 ecological reality, the absence of signals should also be taken with caution as they could mean
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23 298 that our sampling design did not allow capturing a significant association.
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28 299 Three types of MRM models were used for each of the six response variable (I_{ST} , τ_{ST}
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30 300 calculated over the three first axes of the PCA_{TRAITS} , τ_{ST} calculated for each of these three axes,
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32 301 and Π_{ST}). The first model (Model 1) corresponded to a simple regression testing the effect of the
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34 302 overall environmental (Euclidean) dissimilarity (calculated over the 17 environmental variables)
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36 303 on each response variable. Model 2 corresponded to a multiple regression model where we tested
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38 304 the relative effects (regression coefficients) of the dissimilarity of several environmental
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40 305 variables, using a reduced set of variables with limited collinearity to limit the number of tests.
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42 306 To do so, we retained ecologically relevant variables with r -Spearman correlation ≤ 0.6 for
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44 307 climate and soil variables separately (Figures S3-4). In doing so, four soil variables (the
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46 308 percentage of sand, OM, soil pH and P) and one climatic variable (RH_{MEAN}) were retained for
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48 309 analyses. For LiDAR data, because the variation in the variables “canopy cover” and “gap
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50 310 fraction” remained virtually unchanged across plots (see Table S2), we only retained the variable
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52 311 “canopy height” (C_H) for analyses. This latter variable was positively correlated to the variables
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3 312 “canopy cover” and “gap fraction” (Figure S5). In Model 3, we tested the relative effects of the
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5 313 dissimilarity in the scores of the two first axes of the PCA_{ENV}. In each of the three models, the
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7 314 spatial dependence among plots was taken into account by including spatial distance (Euclidean,
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9 315 untransformed) among the explanatory variables.

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12 316 Finally, to have more accurate insights regarding the associated pairs of environmental
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14 317 variables and traits, we performed a fourth-corner analysis (Legendre *et al.* 1997), using the R
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16 318 packages “ade4” (Dray & Dufour 2007) and “adespatial” (Dray *et al.* 2019). The fourth-corner
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18 319 analysis combines three matrices – plots × environmental variables (R), plots × species
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20 320 occurrences (L) and species × traits (Q) – into a matrix of trait-environment associations. The
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22 321 latter is then used to quantify and test pairwise associations between traits and environmental
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24 322 variables, using 9,999 randomizations with the so-called model “6” which combines models “2”
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26 323 and “4” as described in Dray *et al.* (2014), in order to avoid type-I error inflation.
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325 3. RESULTS

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37 327 We collected a total of 31,865 ant individuals belonging to 267 species, 56 genera and 11
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39 328 subfamilies along the elevational gradient at Mont Itoupé (Table S3). The total number of species
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41 329 slightly decreased with increasing elevation (resp. 198, 176 and 161 species at 400m, 600m and
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43 330 800m asl.). Across plots, the number of observed species ranged from 85 (P6; 600m asl.) to 129
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45 331 (P9; 400m asl.). The average number of species per sample was higher at the lowest elevations
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47 332 (400m: mean ± sd = 25.45 ± 2.69; 600m: mean ± sd = 20.38 ± 4.48; 800m: mean ± sd = 20.63 ±
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49 333 1.60). We also calculated the Simpson’s index and found very similar values along the
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51 334 elevational gradient (mean ± sd = 0.98 ± <0.01 for each elevation).
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3.1. Functional heterogeneity

The PCA performed on species traits (PCA_{TRAITS}) showed that the first three axes jointly explained 77% of the overall trait inertia (38%, 26% and 13%, respectively; Figures 2 and S6; Table S4). Plot scores on the first axis were highly positively correlated to HL, HW, PW and negatively to WL. The second axis was mostly associated with FL, SL and EL which were highly positively correlated to each other; the third axis was negatively associated to ML (Figures 2 and S6, Table S4).

3.2. Environmental heterogeneity

The PCA performed on the matrix of environmental data (hereafter, PCA_{ENV}) revealed that axes 1 and 2 explained 60.5% and 20.7% of the overall environmental inertia across the nine plots, respectively (Figure 3; Table S5). Among the variables retained for analyses, PCA scores indicated that relative humidity (RH_{MEAN}) and canopy height (C_H) were strongly correlated to axis 1 (resp. $r = 0.93$ and $r = -0.90$), while pH was strongly correlated to axis 2 ($r = 0.85$).

We found that the following variables significantly (or almost) varied across elevations (Kruskal-Wallis rank tests): OM ($X^2 = 7.20$, $p = 0.03$), C_H ($X^2 = 6.00$, $p = 0.05$), P ($X^2 = 2.40$, $p = 0.06$) and RH_{MEAN} ($X^2 = 5.42$, $p = 0.07$). In contrast, no significant variation was found in sand ($X^2 = 2.40$, $p = 0.30$) and soil pH ($X^2 = 0.61$, $p = 0.74$) across elevations.

3.3. Taxonomic, functional and phylogenetic structure of ant assemblages

The leaf-litter ant assemblages displayed significant taxonomic and trait clustering at the plot level (Table 2). Trait clustering was mostly explained by a significant clustering observed for the scores of the second axis of the PCA_{TRAITS} (Table 2), which accounted for 26% of the overall functional inertia. The latter axis (i.e. axis 2 of the PCA_{TRAITS}) was mostly associated to relative

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3 360 femur and scape length (Figure 2; Table S4). In contrast, we did not find any significant
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5 361 phylogenetic clustering (Table 2). We further found that the taxonomic clustering was mostly due
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7 362 to differences in species composition between 800 and 600m-elevated plots, and that the
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10 363 functional clustering was mostly due to differences in trait composition between the most
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12 364 elevated plots (800m) and the other plots (Table 2). No phylogenetic clustering signal was found
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15 365 at the plot or the elevation level.
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19 367 **3.4. Effect of environmental variables on taxonomic, functional and phylogenetic** 20 21 368 **composition**

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24 369 To facilitate the reading hereafter, we will sometimes omit to use the term “dissimilarity” when
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26 370 describing that the “dissimilarity of A significantly explains the dissimilarity of B”, and will
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28 371 simply write that “A significantly explains B” but we must keep in mind that we only deal with
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30 372 dissimilarity values among plots in our regression models. The overall environmental
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33 373 dissimilarity significantly explained the taxonomic (I_{ST}) and the overall functional (τ_{ST}) turnover
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35 374 among plots (Table 3) but not the phylogenetic (Π_{ST}) turnover. Moreover, the scores of the first
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37 375 axis (strongly associated to the Weber’s length, the relative head length, the relative head width
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39 376 and the pronotum width) and second axis (strongly associated to the relative scape and the
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42 377 relative femur lengths) of the PCA_{TRAITS} were significantly explained by the overall
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44 378 environmental dissimilarity.

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47 379 Meanwhile, the plot scores of the first axis of the PCA_{ENV} (which was strongly associated
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49 380 with temperature, relative humidity and vegetation structure; Table S5) significantly explained
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51 381 the variation in the overall taxonomic and functional composition, as well as the variation in the
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54 382 plot scores of axes 1 and 2 of the PCA_{TRAITS} (Table 3). When examining the relative effects of
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56 383 each of the six selected environmental variable (sand, pH, OM, P, RH_{MEAN} and C_H), we found

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3 384 that soil phosphorus content and canopy height significantly explained the taxonomic
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5 385 composition (I_{ST}) but not the overall functional composition (τ_{ST}), the latter being only explained
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7 386 by the percentage of sand (with a marginal significance; $p = 0.081$). Although the second axis of
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10 387 the PCA_{TRAITS} displayed the strongest association with environment and with the first axis of the
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12 388 PCA_{ENV} , it was not significantly explained by any individual environmental variable, despite a
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14 389 relatively high coefficient value obtained with C_H , which may result from a lack of power. Axis 1
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17 390 and 3 of the PCA_{TRAITS} , however, were both significantly explained by soil phosphorus, while
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19 391 axis 1 was also significantly explained by pH and axis 3 by the percentage of sand. The
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21 392 phylogenetic (Π_{ST}) turnover was (marginally) significantly explained by soil pH only.

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24 393 The fourth-corner analysis indicated that the percentage of sand was negatively related to
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26 394 the relative scape, eye and femur lengths, and to the second and third axes of the PCA_{TRAITS}
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28 395 (Table 4) which were highly associated to the variation of these three traits, while the third axis
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30 396 was also strongly correlated to the relative mandible length (Table S4). Phosphorus concentration
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32 397 was positively related to relative head length, whereas it was negatively related to Weber's length
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34 398 and the first axis of the PCA_{TRAITS} . Mean annual relative humidity was negatively related to
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36 399 relative scape, eye and femur lengths of ants (Table 4).
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401 **4. DISCUSSION**

403 This study highlights the existence of associations between key abiotic environmental variables
404 and the distribution of species and functional traits among Neotropical ant assemblages at a local
405 (i.e. 10km²) scale. Ant species and functional composition were mostly explained by canopy
406 height and the first axis of the PCA_{ENV} which was strongly associated to the relative humidity
407 and temperature (and thus elevation), and to a lesser extent by soil phosphorus concentration,

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3 408 sand and pH (Table 3). The observed within-plot and within-elevation functional clustering
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5 409 (Table 2) likely arose from the filtering of these environmental conditions.
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8 410 Climate represents a major environmental filter and restricts the number and identity of
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10 411 species that can survive and establish at different locations. Among climatic filters, temperature
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12 412 has been shown to be a key parameter influencing patterns of ant species distributions (e.g.
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14 413 Sanders *et al.* 2007, Dunn *et al.* 2009, Silva & Brandão 2014). Other studies have also reported a
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16 414 relationship between temperature and ant functional composition (Stuble *et al.* 2013, Arnan *et al.*
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18 415 2014). Relative humidity may be even more constraining for leaf-litter ants than temperature
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20 416 (Kaspari & Weiser 2000, Menke & Holway 2006). These studies reported results that were
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22 417 consistent with our findings. Indeed, we found that the variation in the dissimilarity of plot scores
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24 418 along the first axis of the PCA_{ENV}, which was highly explained by variation in soil relative
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26 419 humidity, temperature and elevation (Figure 3; Table S5), significantly explained the taxonomic
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28 420 and functional turnover. As highlighted by the PCA generated on environmental data (PCA_{ENV};
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30 421 Figure 3), the top of the mountain (ca. 800m asl), which is covered by cloud forests, is
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32 422 characterized by slightly higher levels of humidity (mean_{RH} = 99.3%) compared to lower
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34 423 elevations (between ca. 400 and 600m asl; mean_{RH} = 96.5%). The top forests may therefore
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36 424 provide a refuge area for certain species preferring relatively colder and more humid conditions.
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38 425 Changes in species and functional composition may thus reflect the presence of climate-
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40 426 specialists at higher elevations. More specifically, our results suggest that smaller ant species, as
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42 427 well as species with relative smaller eyes or smaller legs, were found in sites with higher levels of
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44 428 humidity (thus at higher elevation). These traits are characteristics of hypogaeic ant species, i.e.
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46 429 ant species that nest and forage within the litter or into the soil (Weiser & Kaspari 2006).
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54 430 Along Mont Itoupé, turnovers in species and functional composition were also associated to
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56 431 variation in phosphorus concentration (Table 3). Phosphorus limitation may explain variation in
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3 432 plant diversity (Wright *et al.* 2011, Vleminckx *et al.* 2017), which in turn is likely to influence the
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5 433 diversity and density of leaf-litter associated invertebrates (McGlynn & Salinas 2007, Vleminckx
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7 434 *et al.* 2019). In their study, McGlynn and Salinas (2007) found that environments richer in
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9 435 phosphorus had greater litter invertebrate densities (mostly detritivores). Thus, the association
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11 436 between phosphorus availability and the species and functional composition of ant communities
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13 437 may be indirectly explained by the variation in the density of prey for predatory ant species. The
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15 438 fourth-corner analysis performed in this study reveal that phosphorus concentration was
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17 439 positively related to the relative head length and negatively related to body length (i.e. Weber's
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19 440 length), features that are characteristics of small hypogaecic ant species belonging to genera such
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21 441 as *Carebara*, *Solenopsis* and *Strumigenys*. Those predatory ant genera may thus benefit from the
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23 442 higher phosphorus concentrations that may favor the abundance of small prey. Such results
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25 443 contrast with those obtained in a study conducted by Jacquemin *et al.* (2012) in which they found
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27 444 a decrease of predatory ant species in plots enriched in Carbon, Nitrogen and Phosphorus. In their
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29 445 study, predatory ants seemed to be limited by habitat loss due to the increased litter
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31 446 decomposition. The positive effect of higher levels of phosphorus for small predatory ant species
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33 447 found in our study may have been counterbalanced by habitat loss in their study, since the
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35 448 amount of leaf litter at the highest elevation, i.e. at high levels of phosphorus, was much more
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37 449 important than at the lowest ones.

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40 450 In addition to climatic factors, nutrient availability and soil texture can also influence
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42 451 invertebrate composition by imposing constraints on species living in ground habitats
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44 452 (Vasconcelos *et al.* 2003, Schmidt *et al.* 2016, Costa-Milanez *et al.* 2017), but also indirectly via
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46 453 an effect of these variables on tree community assembly (Vleminckx *et al.* 2019). In our study, a
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48 454 significant association was found between the functional composition and the soil texture
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50 455 (percentage of sand) turnover across plots (Table 3), especially for the third axis of the PCA_{TRAITS}

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3 456 which was mostly associated with the relative mandible length (Table S4). We lack hypotheses to
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5 457 explain that result. In addition, the percentage of sand was negatively related to individual
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7 458 functional traits of ants (i.e. the relative scape and femur lengths). Particular functional traits of
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9
10 459 ant species rather than the global functional space of ant assemblages may thus be linked to soil
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12 460 texture. Short scape and eye, relative to body size, are typical of hypogaeic ant species (Brandão
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14 461 *et al.* 2012), foraging and nesting inside the leaf-litter. Sandy soils may thus favor movements
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17 462 and nest establishment of hypogaeic species within the litter, compared to clay-rich soils.
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20 21 464 **CONCLUSIONS**

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26 466 Elevational gradients stretching from lowland forests to lower mountain cloud forests represent a
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28 467 major source of environmental variation in tropical regions which, in our study, has been shown
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30 468 to influence the distribution of leaf-litter ants. In particular, the taxonomic and functional
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32 469 turnover of ant communities were mostly explained by soil phosphorus content, climatic
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34 470 (temperature, relative humidity) variables and vegetation structure, while trait variation seemed to
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36 471 be also influenced by soil texture and pH. Our results shed light on the unique biodiversity value
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38 472 of cloud forests, a particularly rare ecosystem in the eastern Guiana Shield, likely to be threatened
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40 473 by climate change, with scenarios predicting an intensification of drought events and an increase
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42 474 of temperature across the region (Esquivel-Muelbert *et al.* 2019). Indeed, the congruence between
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44 475 species and functional turnover along the humidity gradient highlights that a loss of species and
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46 476 functional diversity represent real threats in this regional biodiversity hotspot.
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52 53 478 **ACKNOWLEDGMENTS**

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15 Approach) and DIAMOND (Dissecting And MONitoring amazonian Diversity) projects, by the
16
17 486 *Programme Convergence* 2007-2013, *Région Guyane* from the European community (BREGA,
18
19 487 757/2014/SGAR/DE/BSF) and by the PO-FEDER 2014-2020, *Région Guyane* (BiNG,
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21 488 GY0007194).
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28 491 **DATA AVAILABILITY**

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30 492 Data available from the Dryad Digital Repository: <https://doi.org/10.5061/dryad.00000> (Fichaux
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32 493 *et al.* 2020).
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3 723 TABLE 1. List of morphological traits measured and their hypothesized ecological functions. WL
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5 724 = Weber's length; HW = head width; HL = head length; PW = pronotum width; FL = femur length;
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7 725 SL = scape length; EL = eye length; CL = clypeus length; ML = mandible length.
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Traits	Hypothesized ecological functions
WL	Proxy for body size, related to several physiological and ecological traits, such as habitat use (Weber 1938, Kaspari & Weiser 1999).
HW	Indicator of mandibular musculature, related to trophic position (Kaspari 1993, Weiser & Kaspari 2006).
HL	Indicator of body size (Kaspari & Weiser 1999) and body mass which determines the quantity of resources consumed.
PW	Predictor of body mass (Kaspari & Weiser 1999).
FL	Indicator of foraging speed, related to habitat complexity (Feener Jr. <i>et al.</i> 1988).
SL	Related to sensory abilities (Weiser & Kaspari 2006), indicative of an ant's ability to navigate and move through its surroundings (Yates <i>et al.</i> 2014).
EL	Indicator of feeding behavior (predatory ants have smaller eyes); hypogaeic ant species have smaller eyes compared to epigaeic ant species (Weiser & Kaspari 2006, Yates <i>et al.</i> 2014).
CL	Related to liquid absorption abilities (Davidson <i>et al.</i> 2004); clypeus length is here used as a surrogate for liquid feeding habits in ants.

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4 ML Longer mandibles are associated with larger prey consumption (Fowler *et al.* 1991). In
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6 some cases (i.e. trap-jaw ants), sublinear to linear and long mandibles are used as
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8 extremely rapid trap for hunting and killing fast preys (Gronenberg *et al.* 1993).
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728 TABLE 2. Taxonomic, functional and phylogenetic turnover of ant assemblages, averaged over all
 729 pairs of plots (Global turnover) or for each pair of elevations (in m: 800-600, 800-400, 600-400).
 730 I_{ST} = taxonomic turnover (species level); τ_{ST} = functional turnover (species level); Π_{ST} =
 731 phylogenetic turnover (genus level). The functional turnover was calculated using the three first
 732 axes of PCA_{TRAITs} (τ_{ST}) and each of these axes separately ($\tau_{ST}PC1$; $\tau_{ST}PC2$; $\tau_{ST}PC3$). Turnover
 733 values were multiplied by 10^4 to facilitate the reading. Significant values are emphasized in bold
 734 and with asterisks (*** $p \leq 0.001$; ** $p \leq 0.01$; * $p \leq 0.05$).

	Global turnover	800-600	800-400	600-400
I_{ST}	40.98***	36.31*	31.83	17.26
τ_{ST}	19.31**	14.51**	30.88*	-5.46
$\tau_{ST}PC1$	10.18	-10.44	-9.28	-7.79
$\tau_{ST}PC2$	36.24**	39.62**	92.41*	0.76
$\tau_{ST}PC3$	3.20	-9.20	-2.01	-9.44
Π_{ST}	1.05	9.10	7.52	-4.68

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737 TABLE 3. Regression coefficients quantifying the effect on the turnover in community
 738 composition (I_{ST} = taxonomic turnover; τ_{ST} = functional turnover; Π_{ST} = phylogenetic turnover),
 739 of the overall environmental dissimilarity (Model 1), the dissimilarity of individual environmental
 740 variables (Model 2) and the dissimilarity in the scores of the two first axes of the PCA_{ENV} (PC1,
 741 PC2; Model 3). For the functional turnover, the effect of environmental variables was evaluated
 742 for the three first axes of PCA_{TRAITS} (τ_{ST}) together and for each of these axes separately ($\tau_{ST}PC1$;
 743 $\tau_{ST}PC2$; $\tau_{ST}PC3$). Sand = percentage of sand; pH = soil pH; OM = percentage of organic matter; P
 744 = Olsen-phosphorus concentration; RH_{MEAN} = mean annual relative humidity; C_H = canopy height).
 745 Regression coefficients are multiplied by 10^4 to facilitate the reading as they sometimes reach very
 746 low yet significant values. Significant coefficients are emphasized in bold (** $p \leq 0.01$; * $p \leq 0.05$;
 747 † $p \leq 0.1$). The regression coefficients were obtained by including the spatial distance in
 748 each of the three models in order to remove spatial effects (see methods).

	I_{ST}	τ_{ST}	$\tau_{ST}PC1$	$\tau_{ST}PC2$	$\tau_{ST}PC3$	Π_{ST}
Model 1						
Global env. effect	0.08*	0.20***	0.17*	0.47***	-0.06	-0.02
Model 2						
sand	1.55	10.17†	-0.54	17.08	14.55*	-2.83
pH	-6.95	0.22	14.59†	-14.40	-1.03	10.41†
OM	0.91	-2.08	-0.32	4.93	-7.64	-5.90

P	7.90†	9.42	35.61**	3.22	-13.59†	2.14
RH _{MEAN}	-7.62	7.75	21.61	11.26	-11.51	13.15
C _H	21.99*	15.34	-8.14	43.75	3.40	-13.49
<i>Model 3</i>						
PC1	34.18†	96.57**	67.75†	233.89***	-24.70	-8.90
PC2	9.82	-7.09	28.34	-53.53	-2.23	-0.37

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752 TABLE 4. Results from the fourth-corner analysis quantifying the strength of pairwise trait-
 753 environment associations. Significant relationships are highlighted in bold (** $p \leq 0.01$; * $p \leq 0.05$;
 754 † $p \leq 0.07$). HL = relative head length; HW = relative head width; ML = relative mandible length;
 755 CL = relative clypeus length; SL = relative scape length; EL = relative eye length; WL = Weber's
 756 length; FL = relative femur length; PW = relative pronotum width; PC1/PC2/PC3: axes 1, 2 and 3
 757 of the PCA_{TRAITS}; sand = percentage of sand; pH = soil pH; OM = percentage of organic matter; P
 758 = Olsen-phosphorus concentration; RH_{MEAN} = mean annual relative humidity; C_H = canopy height.

	sand	pH	OM	P	RH _{MEAN}	C _H
HL	0.03	0.05	-0.02	0.07*	0.04	-0.00
HW	0.01	0.04	-0.02	0.05	0.01	-0.02
ML	0.03	0.04	-0.01	0.02	0.01	-0.01
CL	-0.03	0.02	-0.03	0.01	-0.02	0.03
SL	-0.07*	0.02	-0.05	-0.05	-0.07*	0.07
EL	-0.10**	0.00	-0.06	-0.08	-0.10*	0.09
WL	-0.03	-0.04	0.01	-0.08**	-0.05	0.00
FL	-0.08†	0.01	-0.05	-0.10	-0.10**	0.09
PW	0.01	0.04	-0.02	0.05	0.01	-0.01
PC1	-0.04	-0.04	0.01	-0.08*	-0.05	0.01

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PC2	-0.08*	0.03	-0.06	-0.06	-0.08	0.09
PC3	-0.05*	-0.02	-0.02	-0.02	-0.02	0.02

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3 761 FIGURE 1. Location of the study area and the nine sampling plots and environmental sensors at
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5 762 Mont Itoupé. The weather sensor of Plot 6 was located halfway between Plot 5 and Plot 6 (for more
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7 763 details, see section 2.5.2).
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12 765 FIGURE 2. Principal Component Analysis of trait data in each plot. HL = relative head length;
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14 766 HW = relative head width; ML = relative mandible length; CL = relative clypeus length; SL =
15
16 767 relative scape length; EL = relative eye length; WL = Weber's length; FL = relative femur length;
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19 768 PW = relative pronotum width.
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24 770 FIGURE 3. Principal Component Analysis of environmental data in each plot. Plots of the same
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26 771 elevational band are represented by green circles (800m), red squares (600m) and orange triangles
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28 772 (400m). elev = elevation (m); sand = percentage of sand; silt = percentage of silt; clay = percentage
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30 773 of clay; pH = soil pH; OM = percentage of organic matter; C/N = carbon-to-nitrogen ratio; P =
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32 774 Olsen-phosphorus concentration; Na = sodium concentration; K = potassium concentration; T_min
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34 775 = minimum temperature of the coldest month; T_mean = mean annual temperature; RH_min =
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36 776 minimum relative humidity of the driest month; RH_mean = mean annual relative humidity; C_cov
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38 777 = canopy cover; C_h = canopy height; gap = gap fraction. Variables retained for analyses are
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40 778 highlighted in blue.
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SUPPORTING INFORMATION

Environmental determinants of leaf-litter ant community composition along an elevational gradient

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FIGURE S1. Phylogenetic tree of ant genera collected along Mont Itoupé.

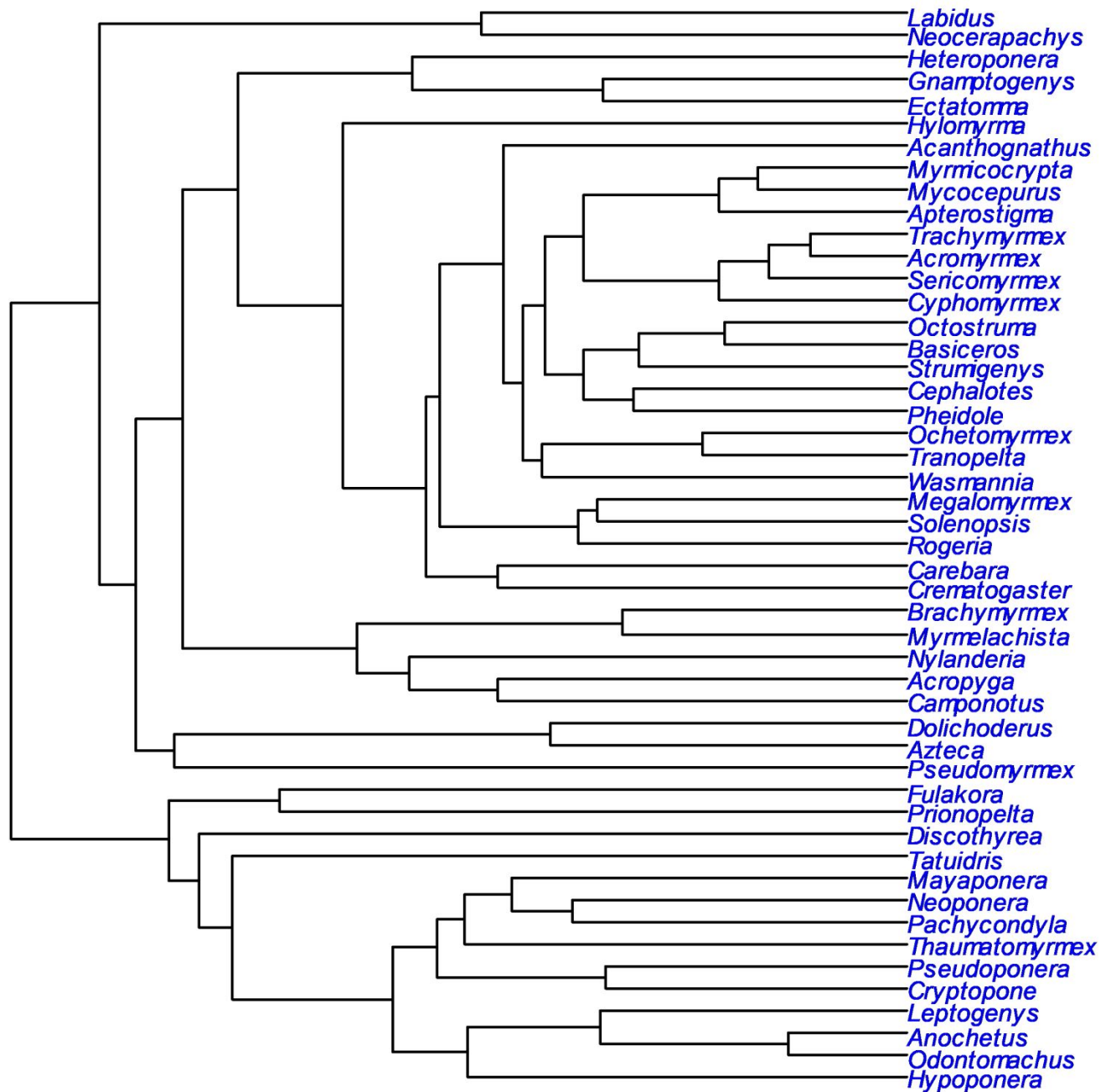


FIGURE S2. Correlation plots showing correlations between the nine morphological traits.

ML = relative mandible length; CL = relative clypeus length; HL = relative head length; HW = relative head width; PW = relative pronotum width; WL = Weber's length; EL = relative eye length; SL = relative scape length; FL = relative femur length.

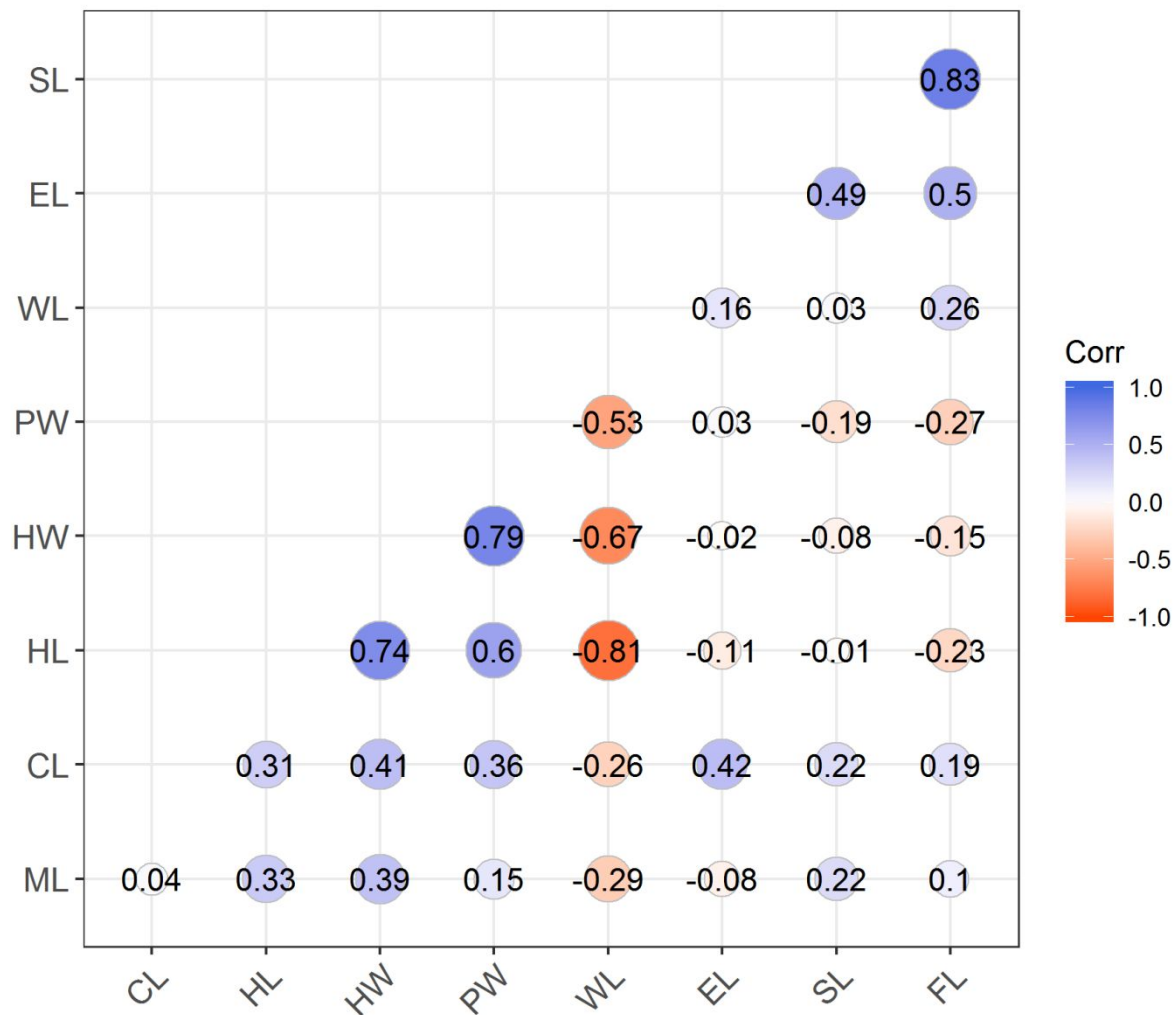


FIGURE S3. Correlation plots showing correlations between the nine soil variables. Clay = percentage of clay; sand = percentage of sand; silt = percentage of silt; P = Olsen-phosphorus concentration; K = potassium concentration; Na = sodium concentration; C/N = carbon-to-nitrogen ratio; OM = percentage of organic matter; pH = soil pH.

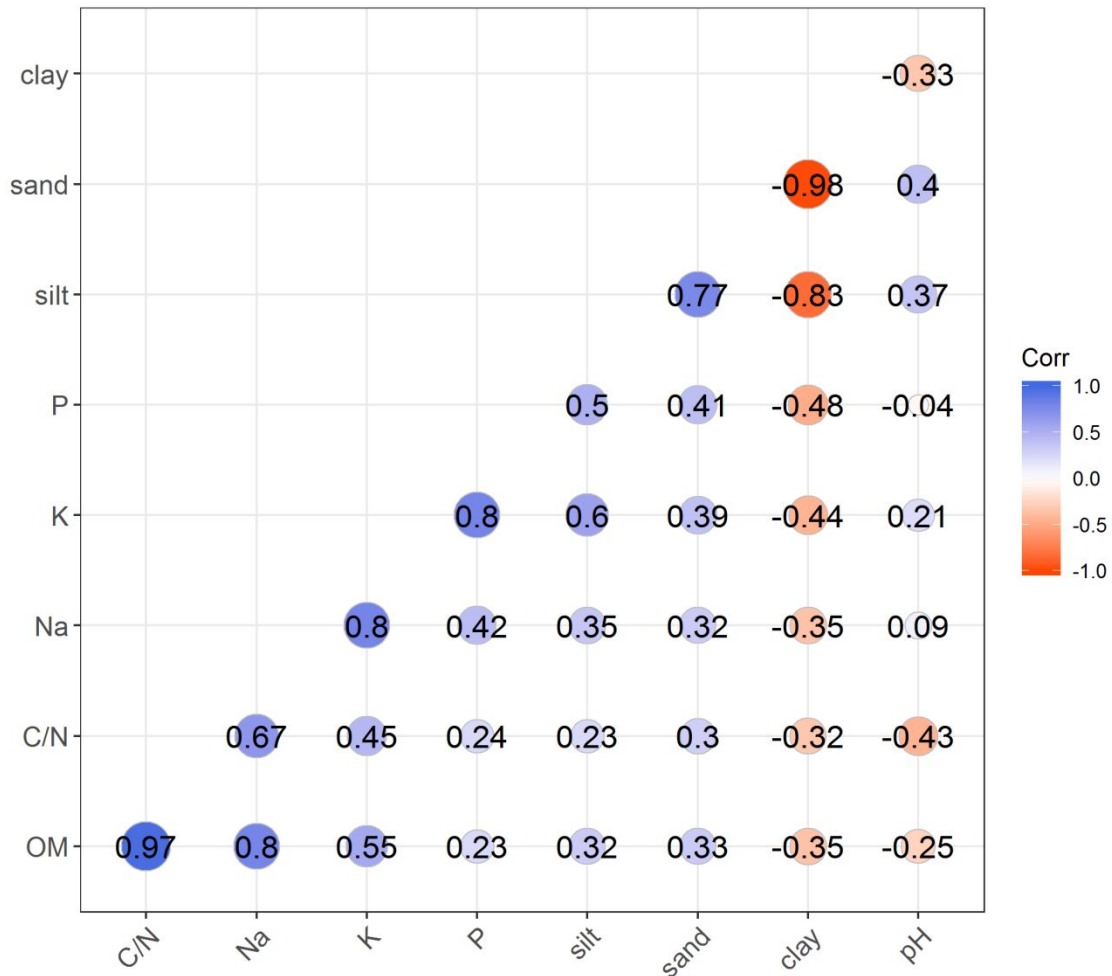


FIGURE S4. Correlation plots showing correlations between the four climatic variables.

T_{MIN} = minimum temperature of the coldest month; T_{MEAN} = mean annual temperature; RH_{MIN} = minimum relative humidity of the driest month; RH_{MEAN} = mean annual relative humidity.

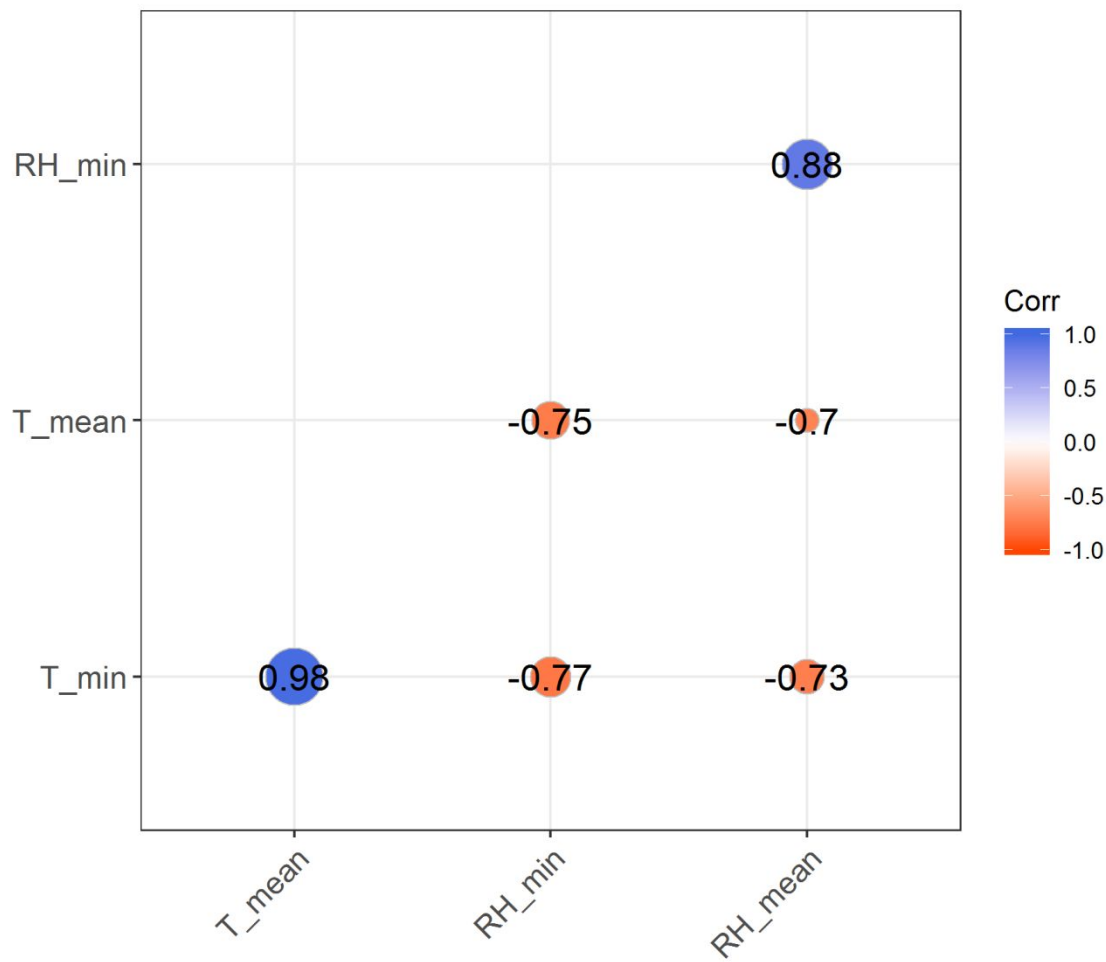
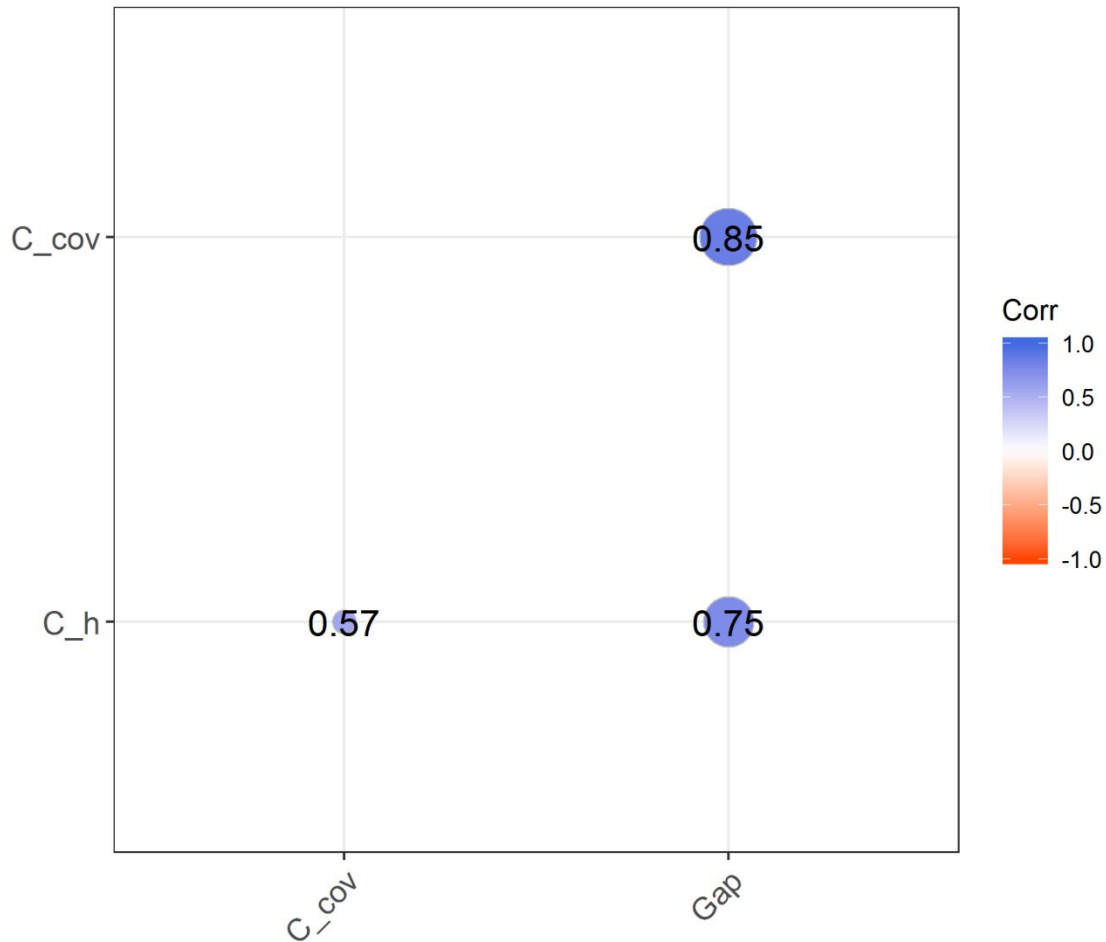


FIGURE S5. Correlation plots showing correlations between the three LiDAR-derived variables. C_{COV} = Canopy cover; C_H = Canopy height; Gap = Gap fraction.



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3 **FIGURE S6. Third and fourth axis of a principal component analysis of trait data.** HL =
4 relative head length; HW = relative head width; ML = relative mandible length; CL = relative
5 clypeus length; SL = relative scape length; EL = relative eye length; WL = Weber's length; FL =
6 relative femur length; PW = relative pronotum width.
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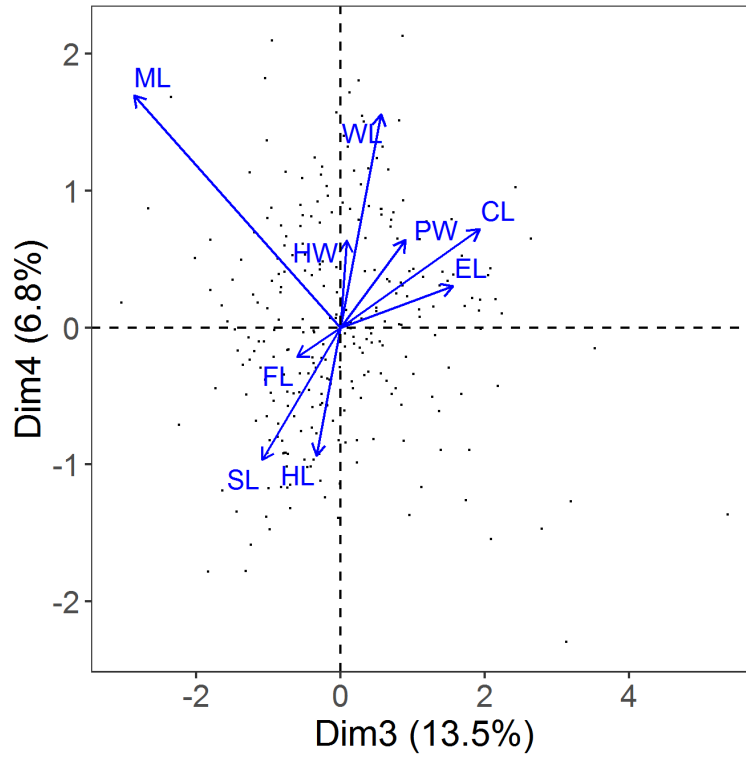


TABLE S1. Mean value of traits per species (HL = head length; HW = head width; ML = mandible length; CL = clypeus length; SL = scape length; EL = eye length; WL = Weber's length; FL = femur length; PW = pronotum width).

Species	HL	HW	ML	CL	SL	EL	WL	FL	PW
<i>Acanthognathus brevicornis</i>	0.83	0.64	0.94	0.26	0.63	0.15	0.79	0.69	0.41
<i>Acanthognathus ocellatus</i>	0.77	0.59	0.76	0.24	0.74	0.13	0.76	0.69	0.39
<i>Acanthognathus</i> sp.IT14.01	0.80	0.65	0.67	0.24	0.68	0.15	0.81	0.75	0.42
<i>Acromyrmex hystrix</i>	1.91	2.30	1.46	0.57	2.64	0.38	3.20	4.26	1.40
<i>Acromyrmex subterraneus brunneus</i>	1.44	1.64	1.11	0.50	1.86	0.27	2.30	2.71	1.02
<i>Acropyga decedens</i>	0.56	0.53	0.31	0.11	0.45	0.03	0.59	0.46	0.35
<i>Acropyga exsanguis</i>	0.48	0.51	0.29	0.10	0.38	0.03	0.51	0.42	0.33
<i>Acropyga fuhrmanni</i>	0.48	0.50	0.28	0.10	0.36	0.04	0.47	0.38	0.31
<i>Acropyga guianensis</i>	0.55	0.50	0.30	0.12	0.45	0.03	0.54	0.45	0.34
<i>Acropyga smithii</i>	0.41	0.40	0.22	0.07	0.26	0.03	0.41	0.25	0.26
<i>Anochetus horridus</i>	1.18	1.02	1.16	0.24	1.41	0.22	1.89	1.49	0.62
<i>Anochetus inermis</i>	1.00	0.95	0.73	0.26	1.03	0.16	1.52	1.12	0.58
<i>Anochetus mayri</i>	0.75	0.76	0.49	0.20	0.66	0.09	1.05	0.72	0.46
<i>Anochetus targionii</i>	0.98	1.02	0.71	0.15	0.95	0.16	1.32	0.96	0.57
<i>Apterostigma acre</i>	0.81	0.65	0.46	0.16	0.71	0.13	1.13	0.91	0.53
<i>Apterostigma auriculatum</i>	1.19	0.85	0.70	0.31	1.16	0.25	1.96	2.05	0.74
<i>Apterostigma avium</i>	1.06	0.72	0.57	0.28	1.40	0.21	1.91	2.14	0.64
<i>Apterostigma chochoense</i>	1.00	0.71	0.53	0.27	1.18	0.19	1.63	1.54	0.59
<i>Apterostigma ierense</i>	0.97	0.69	0.51	0.27	0.92	0.18	1.28	1.32	0.73
<i>Apterostigma pilosum</i>	0.91	0.66	0.48	0.20	0.82	0.15	1.29	1.18	0.55
<i>Apterostigma robustum</i>	1.18	0.86	0.63	0.35	1.12	0.19	1.72	1.62	0.80
<i>Azteca</i> sp.IT14.01	0.65	0.68	0.33	0.19	0.57	0.17	0.77	0.79	0.44
<i>Basiceros manni</i>	1.50	1.18	0.85	0.47	1.34	0.23	2.38	1.98	1.11
<i>Basiceros militaris</i>	1.48	1.39	0.52	0.44	0.81	0.11	1.58	1.13	0.83
<i>Brachymyrmex cavernicola</i>	0.56	0.48	0.28	0.19	0.59	0.09	0.62	0.58	0.34
<i>Brachymyrmex pictus</i>	0.43	0.39	0.21	0.13	0.44	0.10	0.47	0.52	0.27
<i>Brachymyrmex</i> sp.JTL07	0.34	0.29	0.15	0.08	0.32	0.08	0.34	0.33	0.20
<i>Camponotus atriceps</i>	1.97	1.62	0.86	0.62	2.38	0.53	2.86	2.68	1.30
<i>Camponotus excisus</i>	0.98	0.96	0.42	0.30	1.05	0.33	1.25	1.09	0.82
<i>Camponotus fastigatus</i>	1.39	1.17	0.60	0.43	1.78	0.36	2.01	1.84	1.03
<i>Camponotus latangulus</i>	1.08	1.13	0.44	0.32	1.15	0.31	1.46	1.31	0.92
<i>Camponotus linnaei</i>	1.34	1.17	0.54	0.46	1.73	0.36	2.04	1.74	1.22
<i>Camponotus novogranadensis</i>	1.22	1.08	0.58	0.39	1.37	0.32	1.54	1.43	0.84
<i>Camponotus rapax</i>	2.36	1.92	1.09	0.78	3.04	0.46	3.61	3.72	1.55
<i>Camponotus salvini</i>	1.31	1.12	0.64	0.42	1.94	0.34	1.90	2.14	1.04
<i>Camponotus simillimus</i>	2.11	1.56	0.89	0.61	3.07	0.57	3.36	3.66	1.29
<i>Camponotus</i> gp. <i>Tanaemyrmex</i> sp.3	1.52	0.99	0.57	0.50	2.00	0.46	2.50	2.17	0.98
<i>Carebara brevipilosa</i>	0.46	0.42	0.26	0.05	0.29	0.02	0.48	0.37	0.26

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<i>Carebara reina</i>	0.34	0.29	0.14	0.06	0.17	0.02	0.31	0.18	0.20
<i>Carebara</i> sp.KW14.01	0.29	0.25	0.14	0.03	0.16	0.01	0.29	0.18	0.15
<i>Carebara urichi</i>	0.42	0.41	0.26	0.09	0.29	0.02	0.49	0.33	0.25
<i>Crematogaster brasiliensis</i>	0.63	0.66	0.33	0.20	0.66	0.15	0.79	0.79	0.39
<i>Crematogaster carinata</i>	0.56	0.60	0.29	0.17	0.57	0.14	0.68	0.71	0.37
<i>Crematogaster curvispinosa</i>	0.58	0.56	0.29	0.20	0.51	0.14	0.63	0.57	0.37
<i>Crematogaster flavosensitiva</i>	0.49	0.47	0.26	0.17	0.48	0.14	0.52	0.49	0.30
<i>Crematogaster levior</i>	0.55	0.54	0.28	0.18	0.56	0.13	0.66	0.64	0.34
<i>Crematogaster limata</i>	0.70	0.72	0.36	0.22	0.73	0.17	0.83	0.85	0.43
<i>Crematogaster sotobosque</i>	0.49	0.47	0.27	0.17	0.52	0.14	0.58	0.59	0.33
<i>Crematogaster tenuicula</i>	0.55	0.52	0.29	0.17	0.60	0.13	0.68	0.73	0.35
<i>Crematogaster torosa</i>	0.74	0.81	0.36	0.22	0.53	0.18	0.85	0.70	0.47
<i>Cryptopone holmgreni</i>	0.94	0.95	0.64	0.19	0.58	0.00	1.34	0.70	0.64
<i>Cyphomyrmex peltatus</i>	0.51	0.56	0.30	0.18	0.51	0.12	0.74	0.57	0.37
<i>Cyphomyrmex rimosus</i>	0.56	0.57	0.33	0.20	0.57	0.13	0.80	0.69	0.37
<i>Discothyrea denticulata</i>	0.43	0.37	0.18	0.10	0.22	0.01	0.43	0.25	0.26
<i>Discothyrea sexarticulata</i>	0.39	0.35	0.17	0.05	0.20	0.02	0.38	0.23	0.24
<i>Dolichoderus bidens</i>	1.62	1.42	0.75	0.45	1.81	0.38	2.40	2.62	1.06
<i>Dolichoderus bispinosus</i>	1.31	1.47	0.57	0.37	1.35	0.30	1.72	1.75	0.93
<i>Dolichoderus gagates</i>	0.85	0.94	0.43	0.27	0.85	0.21	1.12	1.08	0.62
<i>Dolichoderus imitator</i>	1.37	0.91	0.74	0.48	2.05	0.40	2.59	2.32	0.88
<i>Dolichoderus lutosus</i>	1.16	1.08	0.48	0.38	1.04	0.28	1.54	1.20	0.62
<i>Dolichoderus smithi</i>	1.07	1.03	0.46	0.39	0.87	0.29	1.24	1.20	0.86
<i>Ectatomma edentatum</i>	1.82	1.48	1.21	0.73	1.78	0.35	2.94	2.51	1.20
<i>Ectatomma lugens</i>	2.21	1.77	1.52	0.72	2.27	0.58	3.93	3.40	1.49
<i>Ectatomma tuberculatum</i>	2.40	1.94	1.75	0.97	2.43	0.57	3.75	3.13	1.59
<i>Eurhopalothrix bolau</i>	0.61	0.66	0.24	0.21	0.36	0.08	0.72	0.55	0.41
<i>Fulakora orizabana</i>	0.57	0.52	0.46	0.09	0.35	0.00	0.72	0.36	0.33
<i>Gigantiops destructor</i>	2.18	2.16	1.21	0.90	2.52	1.56	3.25	4.46	1.12
<i>Gnamptogenys acuminata</i>	1.02	0.94	0.66	0.26	0.85	0.29	1.61	1.21	0.83
<i>Gnamptogenys annulata</i>	1.26	1.14	0.86	0.34	0.88	0.27	2.00	1.29	1.03
<i>Gnamptogenys haenschii</i>	1.80	1.76	1.30	0.57	1.45	0.16	2.68	1.98	1.46
<i>Gnamptogenys horni</i>	0.73	0.61	0.42	0.19	0.48	0.14	0.98	0.62	0.54
<i>Gnamptogenys interrupta</i>	0.97	0.83	0.63	0.25	0.60	0.17	1.33	0.79	0.64
<i>Gnamptogenys mecotyle</i>	1.19	1.12	0.88	0.32	1.17	0.29	1.93	1.36	1.05
<i>Gnamptogenys moelleri</i>	1.19	1.00	0.65	0.36	1.29	0.21	1.72	1.63	0.75
<i>Gnamptogenys regularis</i>	0.74	0.69	0.45	0.20	0.52	0.19	1.04	0.70	0.59
<i>Gnamptogenys relict</i>	0.67	0.55	0.35	0.18	0.49	0.08	0.85	0.57	0.44
<i>Gnamptogenys sulcata</i>	1.14	1.12	0.76	0.31	1.01	0.39	1.90	1.56	0.86
<i>Gnamptogenys tortuolosa</i>	1.68	1.51	1.08	0.46	1.52	0.43	2.58	2.02	1.25
<i>Heteroponera flava</i>	0.86	0.74	0.44	0.28	0.52	0.19	1.15	0.68	0.58
<i>Hylomyrma blandiens</i>	0.83	0.80	0.54	0.25	0.61	0.22	1.12	0.78	0.58
<i>Hylomyrma immanis</i>	1.18	1.15	0.79	0.41	0.90	0.28	1.61	1.25	0.83

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3	<i>Hylomyrma reginae</i>	1.04	1.02	0.67	0.29	0.76	0.23	1.43	1.07	0.74
4	<i>Hypoponera foreli</i>	0.58	0.52	0.32	0.10	0.43	0.03	0.77	0.47	0.37
5	<i>Hypoponera</i> sp.02.FGSGt	0.73	0.65	0.39	0.19	0.65	0.04	1.03	0.70	0.50
6	<i>Hypoponera</i> sp.12.FGSGt	0.46	0.36	0.24	0.08	0.30	0.02	0.56	0.31	0.26
7	<i>Hypoponera</i> sp.13.FGSGt	0.51	0.44	0.27	0.09	0.33	0.04	0.64	0.40	0.32
8	<i>Hypoponera</i> sp.B	0.89	0.78	0.51	0.22	0.77	0.04	1.30	0.84	0.61
9	<i>Hypoponera</i> sp.IT14.01	0.64	0.54	0.35	0.18	0.58	0.05	0.88	0.65	0.40
10	<i>Hypoponera</i> sp.IT14.02	0.74	0.69	0.41	0.18	0.70	0.04	1.06	0.72	0.50
11	<i>Hypoponera</i> sp.IT14.04	0.46	0.39	0.21	0.08	0.33	0.04	0.58	0.34	0.30
12	<i>Hypoponera</i> sp.IT14.05	0.59	0.51	0.32	0.14	0.47	0.03	0.82	0.47	0.40
13	<i>Hypoponera</i> sp.MI15.02	0.62	0.49	0.32	0.11	0.45	0.03	0.83	0.59	0.38
14	<i>Hypoponera</i> sp.MI15.05	0.82	0.75	0.46	0.12	0.70	0.05	1.17	0.85	0.55
15	<i>Labidus coecus</i>	1.04	0.96	0.71	0.18	0.77	0.04	1.42	1.41	0.63
16	<i>Leptogenys gaigei</i>	1.44	0.97	0.65	0.52	1.58	0.33	2.39	1.85	0.75
17	<i>Leptogenys langi</i>	0.88	0.60	0.46	0.27	0.79	0.16	1.30	0.88	0.49
18	<i>Leptogenys</i> sp.05.FGSGt	0.96	0.57	0.41	0.36	0.90	0.22	1.47	1.03	0.52
19	<i>Leptogenys</i> sp.IT14.04	1.14	0.94	0.74	0.36	1.17	0.26	1.83	1.22	0.73
20	<i>Mayaponera constricta</i>	1.48	1.23	1.03	0.42	1.56	0.26	2.47	1.88	0.95
21	<i>Megalomyrmex balzani</i>	1.97	1.61	0.99	0.52	2.66	0.43	2.81	3.31	1.18
22	<i>Megalomyrmex drifti</i>	0.54	0.44	0.28	0.13	0.44	0.14	0.69	0.48	0.34
23	<i>Megalomyrmex incisus</i>	0.64	0.54	0.36	0.17	0.59	0.20	0.89	0.78	0.43
24	<i>Megalomyrmex silvestrii</i>	0.56	0.46	0.30	0.16	0.73	0.18	0.77	0.71	0.36
25	<i>Megalomyrmex</i> sp.MI15.01	0.78	0.62	0.42	0.25	0.79	0.22	1.18	0.98	0.52
26	<i>Mycetophylax faunulus</i>	0.74	0.78	0.46	0.19	0.64	0.13	1.01	1.08	0.49
27	<i>Mycetophylax morschi</i>	0.50	0.50	0.32	0.13	0.40	0.09	0.66	0.53	0.37
28	<i>Mycetophylax strigatus</i>	0.66	0.73	0.41	0.20	0.65	0.11	1.01	0.89	0.45
29	<i>Mycocepurus smithii</i>	0.60	0.62	0.40	0.15	0.52	0.12	0.84	0.63	0.40
30	<i>Myrmelachista guyanensis</i>	0.47	0.47	0.17	0.11	0.26	0.10	0.54	0.32	0.30
31	<i>Myrmicocrypta</i> sp.IT14.01	0.68	0.64	0.48	0.22	0.63	0.07	0.92	0.68	0.44
32	<i>Myrmicocrypta</i> sp.IT14.02	0.62	0.53	0.37	0.12	0.55	0.06	0.77	0.62	0.34
33	<i>Myrmicocrypta</i> sp.IT14.03	0.64	0.53	0.39	0.19	0.64	0.07	0.78	0.66	0.36
34	<i>Neocerapachys splendens</i>	0.77	0.58	0.31	0.15	0.40	0.04	0.99	0.56	0.43
35	<i>Neoponera apicalis</i>	2.74	2.32	2.16	0.77	3.08	0.93	4.47	4.19	1.62
36	<i>Neoponera commutata</i>	3.75	3.24	2.96	1.07	3.81	0.98	5.64	5.02	2.46
37	<i>Neoponera crenata</i>	2.34	1.96	1.29	0.85	2.29	0.57	3.58	2.00	1.51
38	<i>Neoponera foetida</i>	2.55	2.28	1.98	1.04	2.36	0.69	4.22	3.46	0.69
39	<i>Neoponera procidua</i>	2.86	2.80	2.28	0.65	2.41	0.33	4.12	3.02	1.90
40	<i>Neoponera verena</i>	2.27	1.79	1.58	0.88	2.63	0.82	3.75	3.03	1.47
41	<i>Nylanderia fulva</i>	0.69	0.57	0.35	0.16	0.89	0.15	0.88	0.96	0.43
42	<i>Nylanderia guatemalensis</i>	0.64	0.56	0.33	0.20	0.78	0.15	0.81	0.77	0.41
43	<i>Nylanderia</i> sp.IT14.01	0.63	0.52	0.33	0.15	0.78	0.10	0.78	0.80	0.39
44	<i>Nylanderia</i> sp.SL13.03	0.69	0.58	0.37	0.17	0.85	0.16	0.87	0.89	0.42
45	<i>Nylanderia steinheili</i>	0.54	0.49	0.26	0.15	0.69	0.14	0.69	0.65	0.35
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<i>Ochetomyrmex neopolitus</i>	0.54	0.51	0.29	0.17	0.42	0.13	0.65	0.49	0.32
<i>Ochetomyrmex semipolitus</i>	0.51	0.47	0.29	0.16	0.35	0.11	0.55	0.39	0.30
<i>Octostruma balzani</i>	0.48	0.54	0.18	0.17	0.27	0.04	0.54	0.35	0.33
<i>Octostruma betschi</i>	0.46	0.53	0.20	0.16	0.28	0.04	0.54	0.37	0.33
<i>Octostruma iheringi</i>	0.60	0.73	0.23	0.23	0.36	0.04	0.74	0.50	0.42
<i>Octostruma obtusidens</i>	0.58	0.70	0.23	0.18	0.35	0.05	0.78	0.53	0.47
<i>Octostruma</i> sp.JTL035	0.52	0.64	0.21	0.18	0.31	0.04	0.69	0.43	0.37
<i>Odontomachus caelatus</i>	3.22	2.72	1.95	0.61	3.09	0.52	3.81	3.55	1.56
<i>Odontomachus chelifer</i>	3.84	2.63	2.32	0.60	3.96	0.66	4.71	4.71	1.51
<i>Odontomachus haematodus</i>	2.42	1.93	1.47	0.41	2.28	0.42	2.87	2.44	1.09
<i>Odontomachus laticeps</i>	2.39	1.86	1.45	0.42	2.11	0.39	3.01	2.61	1.01
<i>Odontomachus meinerti</i>	1.94	1.53	1.16	0.32	1.82	0.30	2.14	1.87	0.91
<i>Odontomachus scalptus</i>	2.66	2.14	1.59	0.45	2.64	0.47	3.24	2.91	1.14
<i>Pachycondyla crassinoda</i>	3.79	3.70	2.64	0.87	3.42	0.74	5.67	4.21	2.68
<i>Pachycondyla harpax</i>	1.70	1.73	1.08	0.38	1.43	0.31	2.54	1.71	1.24
<i>Pachycondyla impressa</i>	2.91	2.80	1.94	0.61	2.46	0.52	4.15	2.95	2.08
<i>Pachycondyla</i> nr. <i>lenkoi</i>	2.13	2.00	1.33	0.50	1.73	0.31	2.79	1.92	1.41
<i>Pheidole aenescens</i>	0.65	0.55	0.38	0.17	0.92	0.16	0.87	1.01	0.38
<i>Pheidole alienata</i>	0.63	0.59	0.40	0.18	0.89	0.14	0.79	1.07	0.38
<i>Pheidole allarmata</i>	0.54	0.57	0.45	0.13	0.61	0.08	0.74	0.61	0.38
<i>Pheidole araneoides</i>	0.89	0.68	0.53	0.25	1.35	0.18	1.36	1.59	0.53
<i>Pheidole biconstricta</i>	0.82	0.73	0.52	0.24	1.00	0.16	1.09	1.18	0.48
<i>Pheidole bruesi</i>	0.56	0.51	0.33	0.18	0.66	0.12	0.70	0.68	0.34
<i>Pheidole bulliceps</i>	0.72	0.62	0.46	0.20	0.94	0.16	1.00	1.08	0.43
<i>Pheidole cataractae</i>	0.51	0.48	0.31	0.16	0.69	0.11	0.67	0.74	0.29
<i>Pheidole coffeicola</i>	0.60	0.49	0.34	0.16	0.86	0.14	0.83	0.96	0.35
<i>Pheidole cramptoni</i>	0.54	0.51	0.32	0.16	0.48	0.11	0.65	0.65	0.34
<i>Pheidole cursor</i>	0.60	0.48	0.36	0.17	0.84	0.14	0.82	0.90	0.35
<i>Pheidole deima</i>	0.72	0.80	0.51	0.22	0.70	0.15	0.98	1.00	0.53
<i>Pheidole embolopyx</i>	0.57	0.49	0.33	0.16	0.71	0.13	0.75	0.77	0.34
<i>Pheidole fissiceps</i>	0.61	0.49	0.35	0.16	0.89	0.15	0.85	0.95	0.35
<i>Pheidole flavens</i>	0.40	0.38	0.24	0.12	0.35	0.08	0.44	0.35	0.25
<i>Pheidole fracticeps</i>	0.41	0.41	0.23	0.13	0.33	0.09	0.49	0.40	0.23
<i>Pheidole gemmula</i>	0.42	0.41	0.24	0.14	0.33	0.08	0.42	0.36	0.25
<i>Pheidole</i> gp. <i>fallax</i> sp.D	0.59	0.56	0.44	0.16	0.80	0.12	0.84	0.94	0.38
<i>Pheidole</i> gp. <i>fallax</i> sp.F	0.64	0.58	0.37	0.18	0.88	0.16	0.88	0.98	0.39
<i>Pheidole</i> gp. <i>tristis</i> sp.B3	0.53	0.52	0.34	0.13	0.49	0.09	0.62	0.60	0.32
<i>Pheidole</i> gp. <i>tristis</i> sp.C	0.45	0.41	0.28	0.13	0.46	0.09	0.56	0.47	0.27
<i>Pheidole</i> gp. <i>tristis</i> sp.D	0.61	0.56	0.43	0.17	0.81	0.11	0.85	0.88	0.38
<i>Pheidole</i> gp. <i>tristis</i> sp.H1	0.52	0.51	0.34	0.14	0.52	0.10	0.68	0.58	0.33
<i>Pheidole guajirana</i>	0.39	0.37	0.22	0.13	0.33	0.08	0.46	0.36	0.23
<i>Pheidole jeannei</i>	0.57	0.56	0.37	0.17	0.64	0.12	0.68	0.73	0.34
<i>Pheidole lattkei</i>	0.59	0.48	0.34	0.14	0.91	0.14	0.85	1.02	0.34

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3	<i>Pheidole longiseta</i>	0.63	0.57	0.37	0.18	0.81	0.15	0.81	0.89	0.39
4	<i>Pheidole lovejoyi</i>	0.62	0.49	0.36	0.17	0.99	0.15	0.94	1.10	0.36
5	<i>Pheidole meinertopsis</i>	0.44	0.45	0.27	0.13	0.42	0.09	0.53	0.46	0.29
6	<i>Pheidole microps</i>	0.52	0.51	0.35	0.13	0.46	0.05	0.64	0.51	0.34
7	<i>Pheidole midas</i>	0.61	0.56	0.35	0.19	0.71	0.12	0.73	0.72	0.36
8	<i>Pheidole nana</i>	0.52	0.50	0.33	0.13	0.49	0.07	0.61	0.59	0.33
9	<i>Pheidole neoschultzi</i>	0.34	0.33	0.18	0.09	0.29	0.08	0.36	0.30	0.21
10	<i>Pheidole nitella</i>	0.36	0.34	0.21	0.11	0.31	0.08	0.41	0.31	0.22
11	<i>Pheidole</i> nr. <i>araneoides</i>	0.74	0.59	0.45	0.20	1.51	0.17	1.18	1.67	0.44
12	<i>Pheidole</i> nr. <i>cramptoni</i>	0.53	0.50	0.32	0.14	0.46	0.11	0.64	0.53	0.33
13	<i>Pheidole</i> nr. <i>fimbriata</i> sp.A	0.68	0.67	0.53	0.18	0.74	0.14	0.98	0.85	0.46
14	<i>Pheidole</i> nr. <i>fimbriata</i> sp.C	0.58	0.59	0.42	0.16	0.58	0.13	0.73	0.71	0.39
15	<i>Pheidole</i> nr. <i>fimbriata</i> sp.D	0.42	0.41	0.26	0.12	0.40	0.08	0.49	0.46	0.26
16	<i>Pheidole</i> nr. <i>sagax</i>	0.61	0.59	0.34	0.17	0.71	0.14	0.79	0.78	0.38
17	<i>Pheidole</i> nr. <i>seeldrayersii</i>	0.60	0.57	0.35	0.17	0.80	0.15	0.81	0.87	0.37
18	<i>Pheidole</i> nr. <i>subarmata</i>	0.38	0.36	0.23	0.11	0.32	0.09	0.44	0.34	0.23
19	<i>Pheidole</i> nr. <i>tristis</i>	0.59	0.59	0.44	0.17	0.62	0.12	0.81	0.79	0.39
20	<i>Pheidole pedana</i>	0.37	0.37	0.21	0.12	0.27	0.08	0.41	0.30	0.24
21	<i>Pheidole rugiceps</i>	0.52	0.46	0.32	0.14	0.70	0.11	0.66	0.78	0.30
22	<i>Pheidole sagax</i>	0.56	0.52	0.33	0.17	0.68	0.13	0.73	0.72	0.34
23	<i>Pheidole sculptor</i>	0.43	0.40	0.27	0.12	0.41	0.09	0.47	0.45	0.27
24	<i>Pheidole</i> sp.IT14.01	0.75	0.75	0.52	0.23	0.75	0.13	1.00	0.98	0.47
25	<i>Pheidole</i> sp.IT14.08	0.42	0.43	0.23	0.12	0.34	0.08	0.43	0.34	0.25
26	<i>Pheidole</i> sp.MI15.06	0.44	0.41	0.25	0.14	0.41	0.09	0.49	0.49	0.25
27	<i>Pheidole subarmata</i>	0.43	0.41	0.28	0.13	0.43	0.09	0.55	0.47	0.27
28	<i>Pheidole terribilis</i>	0.74	0.82	0.64	0.19	0.87	0.16	1.15	0.95	0.56
29	<i>Pheidole tristis</i>	0.73	0.68	0.47	0.23	0.73	0.13	0.96	0.91	0.44
30	<i>Pheidole zelata</i>	0.66	0.63	0.39	0.19	0.86	0.15	0.86	1.04	0.41
31	<i>Pheidole zeteki</i>	0.42	0.42	0.20	0.12	0.29	0.08	0.40	0.29	0.23
32	<i>Platythyrea pilosula</i>	1.51	1.23	0.76	0.41	1.11	0.42	2.31	1.61	1.09
33	<i>Prionopelta amabilis</i>	0.53	0.46	0.26	0.09	0.29	0.03	0.67	0.33	0.31
34	<i>Procryptocerus scabriusculus</i>	1.30	1.40	0.49	0.35	0.86	0.33	1.68	1.04	1.08
35	<i>Procryptocerus schmitti</i>	0.87	0.88	0.27	0.27	0.57	0.27	1.11	0.61	0.64
36	<i>Procryptocerus</i> sp.IT14.01	1.50	1.52	0.30	0.43	0.87	0.40	1.89	1.11	1.12
37	<i>Pseudomyrmex tenuis</i>	1.27	1.13	0.52	0.20	0.60	0.83	1.78	1.18	0.72
38	<i>Pseudoponera stigma</i>	1.01	0.99	0.65	0.24	0.75	0.09	1.48	0.85	0.71
39	<i>Pseudoponera succedanea</i>	0.86	0.81	0.53	0.24	0.60	0.10	1.23	0.69	0.58
40	<i>Rasopone arhuaca</i>	1.28	1.13	0.86	0.23	1.03	0.16	1.85	1.27	0.88
41	<i>Rasopone</i> sp.JTL047	1.29	1.23	0.82	0.21	0.95	0.14	1.82	1.06	0.95
42	<i>Rhopalothrix</i> sp.JTL014	0.34	0.41	0.16	0.12	0.20	0.01	0.46	0.29	0.28
43	<i>Rogeria besucheti</i>	0.69	0.64	0.36	0.21	0.47	0.08	0.75	0.49	0.46
44	<i>Rogeria blanda</i>	0.81	0.74	0.42	0.25	0.55	0.14	1.05	0.70	0.57
45	<i>Rogeria germaini</i>	0.76	0.67	0.35	0.16	0.53	0.08	0.84	0.63	0.49
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<i>Rogeria innotabilis</i>	0.60	0.52	0.28	0.08	0.40	0.08	0.62	0.52	0.35
<i>Rogeria scobinata</i>	0.55	0.48	0.27	0.16	0.35	0.08	0.59	0.41	0.35
<i>Rogeria</i> sp.IT14.01	0.45	0.38	0.22	0.10	0.30	0.03	0.47	0.33	0.29
<i>Rogeria</i> sp.IT14.06	0.50	0.44	0.25	0.10	0.33	0.03	0.51	0.35	0.31
<i>Rogeria</i> sp.SL13.01	0.54	0.49	0.26	0.09	0.36	0.07	0.56	0.43	0.34
<i>Rogeria subarmata</i>	0.77	0.67	0.34	0.16	0.50	0.15	0.88	0.66	0.50
<i>Sericomyrmex bondari</i>	0.96	1.27	0.69	0.32	0.86	0.18	1.53	1.28	0.80
<i>Sericomyrmex mayri</i>	1.11	1.48	0.79	0.33	0.90	0.20	1.65	1.55	0.98
<i>Sericomyrmex parvulus</i>	0.78	0.97	0.56	0.24	0.62	0.15	1.15	0.93	0.63
<i>Solenopsis bicolor</i>	0.52	0.45	0.23	0.10	0.31	0.05	0.56	0.41	0.30
<i>Solenopsis</i> sp.01	0.49	0.42	0.26	0.09	0.40	0.05	0.57	0.46	0.29
<i>Solenopsis</i> sp.02	0.47	0.40	0.23	0.07	0.34	0.05	0.57	0.44	0.26
<i>Solenopsis</i> sp.03	0.46	0.39	0.24	0.07	0.28	0.04	0.50	0.31	0.26
<i>Solenopsis</i> sp.09	0.59	0.54	0.25	0.11	0.36	0.05	0.67	0.48	0.36
<i>Solenopsis</i> sp.11	0.34	0.30	0.15	0.06	0.18	0.04	0.35	0.18	0.20
<i>Solenopsis</i> sp.12	0.40	0.34	0.21	0.07	0.26	0.04	0.44	0.27	0.23
<i>Solenopsis</i> sp.13	0.39	0.33	0.17	0.06	0.22	0.04	0.42	0.25	0.22
<i>Solenopsis</i> sp.14	0.35	0.30	0.18	0.04	0.24	0.04	0.40	0.27	0.20
<i>Solenopsis</i> sp.15	0.38	0.31	0.19	0.07	0.26	0.04	0.42	0.28	0.21
<i>Solenopsis</i> sp.17	0.42	0.35	0.19	0.08	0.27	0.04	0.45	0.30	0.23
<i>Solenopsis</i> sp.21	0.34	0.28	0.16	0.05	0.22	0.03	0.35	0.23	0.19
<i>Solenopsis</i> sp.23	0.41	0.34	0.21	0.06	0.29	0.03	0.42	0.34	0.22
<i>Solenopsis</i> sp.24	0.34	0.27	0.15	0.06	0.17	0.04	0.34	0.19	0.18
<i>Solenopsis</i> sp.25	0.30	0.24	0.14	0.04	0.16	0.03	0.30	0.18	0.15
<i>Solenopsis</i> sp.28	0.48	0.41	0.22	0.09	0.34	0.05	0.52	0.38	0.26
<i>Solenopsis virulens</i>	0.83	0.78	0.44	0.24	0.74	0.12	1.08	0.99	0.50
<i>Strumigenys auctidens</i>	0.47	0.36	0.19	0.15	0.17	0.05	0.48	0.27	0.25
<i>Strumigenys beebei</i>	0.55	0.39	0.14	0.16	0.26	0.08	0.57	0.33	0.26
<i>Strumigenys borgmeieri</i>	0.69	0.48	0.48	0.21	0.57	0.09	0.77	0.72	0.34
<i>Strumigenys cincinnata</i>	0.45	0.33	0.10	0.15	0.22	0.04	0.45	0.31	0.21
<i>Strumigenys cosmoptela</i>	0.48	0.44	0.32	0.11	0.32	0.05	0.57	0.39	0.28
<i>Strumigenys crassicornis</i>	0.48	0.40	0.20	0.15	0.24	0.05	0.49	0.36	0.27
<i>Strumigenys denticulata</i>	0.41	0.35	0.36	0.12	0.27	0.04	0.46	0.30	0.24
<i>Strumigenys diabola</i>	0.73	0.70	1.11	0.23	0.75	0.09	0.89	0.83	0.42
<i>Strumigenys dyseides</i>	0.38	0.32	0.24	0.09	0.25	0.02	0.38	0.29	0.21
<i>Strumigenys elongata</i>	0.54	0.48	0.41	0.13	0.47	0.05	0.61	0.46	0.30
<i>Strumigenys perparva</i>	0.36	0.33	0.22	0.10	0.24	0.04	0.39	0.26	0.21
<i>Strumigenys schulzi</i>	0.46	0.38	0.12	0.17	0.24	0.06	0.50	0.32	0.25
<i>Strumigenys smithii</i>	0.59	0.58	0.43	0.16	0.49	0.08	0.75	0.62	0.37
<i>Strumigenys spathula</i>	0.52	0.49	0.36	0.12	0.42	0.05	0.59	0.44	0.27
<i>Strumigenys subedentata</i>	0.46	0.44	0.32	0.11	0.21	0.06	0.53	0.39	0.27
<i>Strumigenys trinidadensis</i>	0.67	0.65	0.55	0.18	0.59	0.11	0.85	0.73	0.38
<i>Strumigenys tridifera</i>	0.65	0.51	0.77	0.18	0.57	0.04	0.70	0.65	0.32

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3	<i>Strumigenys villiersi</i>	0.48	0.35	0.16	0.15	0.25	0.05	0.57	0.37	0.22
4	<i>Strumigenys waiwai</i>	0.31	0.27	0.20	0.07	0.22	0.03	0.36	0.22	0.18
5	<i>Tatuidris tatusia</i>	0.67	0.86	0.37	0.18	0.33	0.05	0.72	0.41	0.55
6	<i>Thaumatomyrmex soesilae</i>	0.65	0.80	0.79	0.17	0.59	0.19	1.04	0.76	0.53
7	<i>Trachymyrmex cornetzi</i>	0.73	0.79	0.50	0.21	0.75	0.14	1.11	1.00	0.52
8	<i>Trachymyrmex farinosus</i>	1.01	1.23	0.77	0.32	0.92	0.21	1.63	1.48	0.81
9	<i>Trachymyrmex mandibularis</i>	1.02	1.34	0.78	0.30	1.21	0.22	1.57	1.61	0.78
10	<i>Trachymyrmex nr. farinosus</i>	1.22	1.34	0.87	0.40	1.11	0.25	1.48	1.64	0.88
11	<i>Trachymyrmex sp.A</i>	1.27	1.50	0.92	0.38	1.14	0.26	2.06	1.90	1.02
12	<i>Trachymyrmex sp.B</i>	0.94	1.01	0.71	0.27	0.89	0.19	1.51	1.39	0.68
13	<i>Tranopelta gilva</i>	0.64	0.63	0.38	0.19	0.42	0.06	0.76	0.52	0.42
14	<i>Typhlomyrmex pusillus</i>	0.43	0.36	0.22	0.11	0.27	0.01	0.57	0.27	0.26
15	<i>Wasmannia auropunctata</i>	0.45	0.40	0.20	0.14	0.37	0.11	0.46	0.44	0.27
16	<i>Wasmannia rochai</i>	0.49	0.49	0.24	0.17	0.40	0.11	0.55	0.44	0.33
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TABLE S2. Leaf-litter ant sampling plots, coordinates, elevation and environmental parameters measured in the study. Lat. = latitude; long. = longitude; elev. = elevation (m); sand = percentage of sand; silt = percentage of silt; clay = percentage of clay; pH = soil pH; OM = percentage of organic matter; C/N = carbon-to-nitrogen ratio; P = Olsen-phosphorus concentration; Na = sodium concentration; K = potassium concentration; T_{MIN} = minimum temperature of the coldest month; T_{MEAN} = mean annual temperature; RH_{MIN} = minimum relative humidity of the driest month; RH_{MEAN} = mean annual relative humidity; C_{COV} = canopy cover; C_H = canopy height; gap = gap fraction. Variables retained for analyses are highlighted in bold.

Plot	lat.	long.	elev.	sand	silt	clay	pH	OM	C/N	P	Na	K	T _{MIN}	T _{MEAN}	RH _{MIN}	RH_{MEAN}	C _{COV}	C_H	gap
IT-01	-53.08	3.03	818.85	22.47	32.77	44.76	4.54	8.16	12.96	2.27	3.66	0.12	17.44	21.08	69.34	99.54	0.98	21.05	0.85
IT-02	-53.08	3.02	822.86	29.42	29.77	40.81	4.60	9.35	13.07	2.53	4.15	0.13	17.65	20.99	64.77	99.18	1.00	22.69	0.91
IT-03	-53.09	3.02	801.74	28.57	9.00	62.44	4.74	6.13	12.87	1.73	2.77	0.09	17.68	21.18	71.13	99.27	0.99	20.36	0.88
IT-04	-53.10	3.03	581.82	13.39	8.36	78.25	5.54	5.59	12.24	1.27	2.66	0.07	19.37	22.35	59.74	97.53	1.00	30.82	0.95
IT-05	-53.10	3.02	578.16	15.78	9.31	74.91	4.73	5.68	12.13	1.20	2.72	0.08	19.72	22.67	54.38	95.41	1.00	32.53	0.96
IT-06	-53.10	3.01	623.70	8.98	11.83	79.92	4.61	5.83	12.61	1.53	2.69	0.09	19.32	22.27	58.23	96.56	1.00	34.20	0.95
IT-07	-53.11	3.03	464.55	6.70	6.44	86.85	4.47	4.66	12.11	1.80	2.24	0.08	20.34	23.21	57.53	96.86	0.99	32.15	0.94
IT-08	-53.11	3.02	434.11	36.61	48.44	14.96	6.22	3.83	9.18	2.00	2.43	0.09	19.77	23.14	58.57	96.78	1.00	39.11	0.95
IT-09	-53.11	3.02	422.30	8.16	8.64	83.21	5.66	5.14	9.77	1.80	3.06	0.10	20.44	23.36	58.08	95.83	1.00	37.09	0.97

TABLE S3. Number of occurrences of species collected at each elevation (between 0 and 60 per elevation), according to their classification. A dash indicates the absence of a species at an elevation.

Species occurrences at each elevation	400m	600m	800m
Subfamily AGROECOMYRMECINAE Carpenter, 1930			
Tribe Agroecomyrmecini Carpenter, 1930			
<i>Tatuidris tatusia</i> Brown & Kempf, 1968	1	2	-
Subfamily AMBLYOPONINAE Forel, 1893			
Tribe Amblyoponini Forel, 1893			
<i>Fulakora orizabana</i> (Brown, 1960)	1	-	-
<i>Prionopelta amabilis</i> Borgmeier, 1949	8	5	26
Subfamily DOLICHODERINAE Forel, 1878			
Tribe Dolichoderini Forel, 1878			
<i>Azteca</i> sp.IT14.01	1	-	-
<i>Dolichoderus bidens</i> (Linnaeus, 1758)	1	-	-
<i>Dolichoderus bispinosus</i> (Olivier, 1792)	1	1	-
<i>Dolichoderus gagates</i> Emery, 1890	-	2	-
<i>Dolichoderus imitator</i> Emery, 1894	1	1	-
<i>Dolichoderus lutosus</i> (Smith, 1858)	1	-	-
<i>Dolichoderus smithi</i> MacKay, 1993	-	1	-
Subfamily DORYLINAE Leach, 1815			
Tribe Cerapachyini Forel, 1893			
<i>Neocerapachys splendens</i> (Borgmeier, 1957)	-	2	1
Tribe Ecitonini Forel, 1893			
<i>Labidus coecus</i> (Latreille, 1802)	5	5	3
Subfamily ECTATOMMINAE Emery, 1895			
Tribe Ectatommini Emery, 1895			
<i>Ectatomma edentatum</i> Roger, 1863	12	5	3
<i>Ectatomma lugens</i> Emery, 1894	21	20	-
<i>Ectatomma tuberculatum</i> (Olivier, 1792)	1	1	-
<i>Gnamptogenys acuminata</i> (Emery, 1896)	-	1	2
<i>Gnamptogenys annulata</i> (Mayr, 1887)	-	-	1
<i>Gnamptogenys haenschi</i> (Emery, 1902)	1	2	3
<i>Gnamptogenys horni</i> (Santschi, 1929)	13	12	11
<i>Gnamptogenys interrupta</i> (Mayr, 1887)	1	-	-
<i>Gnamptogenys mecotyle</i> Brown, 1958	1	-	1
<i>Gnamptogenys moelleri</i> (Forel, 1912)	1	5	9
<i>Gnamptogenys regularis</i> Mayr, 1870	-	1	-
<i>Gnamptogenys relicta</i> (Mann, 1916)	-	-	1
<i>Gnamptogenys sulcata</i> (Smith, 1858)	1	-	-
<i>Gnamptogenys tortuolosa</i> (Smith, 1858)	-	1	-
Tribe Typhlomyrmecini Emery, 1911			

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4	<i>Typhlomyrmex pusillus</i> Emery, 1894	-	-	2
5	<hr/> Subfamily FORMICINAE Latreille, 1809 <hr/>			
6	Tribe Camponotini Forel, 1878			
7	<i>Camponotus atriceps</i> (Smith, 1858)	15	23	1
8	<i>Camponotus excisus</i> Mayr, 1870	1	-	-
9	<i>Camponotus fastigatus</i> Roger, 1863	1	2	2
10	<i>Camponotus latangulus</i> Roger, 1863	-	1	-
11	<i>Camponotus linnaei</i> Forel, 1886	1	1	-
12	<i>Camponotus novogranadensis</i> Mayr, 1870	24	12	-
13	<i>Camponotus rapax</i> (Fabricius, 1804)	1	4	-
14	<i>Camponotus salvini</i> Forel, 1899	1	-	-
15	<i>Camponotus simillimus</i> (Smith, 1862)	-	-	2
16	<i>Camponotus</i> gp. <i>Tanaemyrmex</i> sp.3	1	-	-
17	Tribe Gigantiopini Ashmead, 1905			
18	<i>Gigantiops destructor</i> (Fabricius, 1804)	1	-	-
19	Tribe Lasiini Ashmead, 1905			
20	<i>Acropyga decedens</i> (Mayr, 1887)	-	1	2
21	<i>Acropyga exsanguis</i> (Wheeler, 1909)	1	-	-
22	<i>Acropyga fuhrmanni</i> (Forel, 1914)	-	1	1
23	<i>Acropyga guianensis</i> Weber, 1944	-	1	-
24	<i>Acropyga smithii</i> Forel, 1893	8	2	-
25	Tribe Myrmelachistini Forel, 1912			
26	<i>Myrmelachista guyanensis</i> Wheeler, 1934	-	1	-
27	Tribe Plagiolepidini Forel, 1886			
28	<i>Brachymyrmex cavernicola</i> Wheeler, 1938	8	7	4
29	<i>Brachymyrmex pictus</i> Mayr, 1887	1	-	-
30	<i>Brachymyrmex</i> sp.JTL07	4	2	2
31	<i>Nylanderia fulva</i> (Mayr, 1862)	1	-	-
32	<i>Nylanderia guatemalensis</i> (Forel, 1885)	10	2	15
33	<i>Nylanderia</i> sp.IT14.01	3	1	-
34	<i>Nylanderia</i> sp.SL13.03	1	1	2
35	<i>Nylanderia steinheili</i> (Forel, 1893)	27	24	8
36	<hr/> Subfamily HETEROPONERINAE Bolton, 2003 <hr/>			
37	Tribe Heteroponerini Bolton, 2003			
38	<i>Heteroponera flava</i> Kempf, 1962	-	-	2
39	<hr/> Subfamily MYRMICINAE Lepeletier de Saint-Fargeau, 1835 <hr/>			
40	Tribe Attini Smith, 1858			
41	<i>Acanthognathus brevicornis</i> Smith, 1944	-	-	1
42	<i>Acanthognathus ocellatus</i> Mayr, 1887	2	-	2
43	<i>Acanthognathus</i> sp.IT14.01	-	-	1
44	<i>Acromyrmex hystrix</i> (Latreille, 1802)	-	-	1
45	<i>Acromyrmex subterraneus brunneus</i> (Forel, 1912)	2	2	1
46	<i>Apterostigma acre</i> Latkze, 1997	5	5	4
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4	<i>Apterostigma auriculatum</i> Wheeler, 1925	2	-	1
5	<i>Apterostigma avium</i> Lattke, 1997	-	1	-
6	<i>Apterostigma chocoense</i> Lattke, 1997	1	3	1
7	<i>Apterostigma ierense</i> Weber, 1937	1	-	-
8	<i>Apterostigma pilosum</i> Mayr, 1865	21	6	8
9	<i>Apterostigma robustum</i> Emery, 1896	2	2	1
10				
11	<i>Basiceros manni</i> Brown & Kempf, 1960	-	-	1
12	<i>Basiceros militaris</i> (Weber, 1950)	-	1	1
13	<i>Cyphomyrmex peltatus</i> Kempf, 1966	10	13	2
14	<i>Cyphomyrmex rimosus</i> (Spinola, 1851)	26	11	14
15				
16	<i>Eurhopalothrix bolai</i> (Mayr, 1870)	-	-	1
17	<i>Mycetophylax faunulus</i> (Wheeler, 1925)	1	-	-
18	<i>Mycetophylax morschi</i> (Emery, 1888)	1	-	-
19	<i>Mycetophylax strigatus</i> (Mayr, 1887)	2	-	-
20				
21	<i>Mycocepurus smithii</i> (Forel, 1893)	-	2	-
22	<i>Myrmicocrypta</i> sp.IT14.01	-	-	1
23	<i>Myrmicocrypta</i> sp.IT14.02	1	1	-
24	<i>Myrmicocrypta</i> sp.IT14.03	11	2	1
25				
26	<i>Octostruma balzani</i> (Emery, 1894)	16	5	19
27	<i>Octostruma betschi</i> Perrault, 1988	13	15	21
28	<i>Octostruma iheringi</i> (Emery, 1888)	1	-	-
29	<i>Octostruma obtusidens</i> Longino, 2013	2	1	1
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31	<i>Octostruma</i> sp.JTL035	-	1	2
32	<i>Procryptocerus scabriusculus</i> Forel, 1899	1	-	-
33	<i>Procryptocerus schmitti</i> Forel, 1901	-	-	1
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35	<i>Procryptocerus</i> sp.IT14.01	1	-	-
36	<i>Rhopalothrix</i> sp.JTL014	1	-	-
37	<i>Sericomyrmex bondari</i> Borgmeier, 1937	1	2	5
38	<i>Sericomyrmex mayri</i> Forel, 1912	2	-	-
39	<i>Sericomyrmex parvulus</i> Forel, 1912	-	-	1
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41	<i>Trachymyrmex cornetzi</i> (Forel, 1912)	2	-	-
42	<i>Trachymyrmex farinosus</i> (Emery, 1894)	5	3	-
43	<i>Trachymyrmex mandibularis</i> Weber, 1938	1	-	1
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45	<i>Trachymyrmex</i> nr. <i>farinosus</i>	-	1	-
46	<i>Trachymyrmex</i> sp.A	3	3	-
47	<i>Trachymyrmex</i> sp.B	1	1	-
48	<i>Tranopelta gilva</i> Mayr, 1866	1	-	3
49	<i>Wasmannia auropunctata</i> (Roger, 1863)	13	8	3
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51	<i>Wasmannia rochai</i> Forel, 1912	2	1	-
52	Tribe Crematogastrini Forel, 1893			
53	<i>Crematogaster brasiliensis</i> Mayr, 1878	17	12	3
54	<i>Crematogaster carinata</i> Mayr, 1862	-	1	-
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56	<i>Crematogaster curvispinosa</i> Mayr, 1862	1	1	-
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11	Tribe Dacetini Forel, 1892			
12	<i>Strumigenys auctidens</i> (Bolton, 2000)	17	8	3
13	<i>Strumigenys beebei</i> (Wheeler, 1915)	5	-	1
14	<i>Strumigenys borgmeieri</i> Brown, 1954	1	-	-
15	<i>Strumigenys cincinnata</i> (Kempf, 1975)	-	5	-
16	<i>Strumigenys cosmostela</i> Kempf, 1975	4	2	-
17	<i>Strumigenys crassicornis</i> Mayr, 1887	1	-	3
18	<i>Strumigenys denticulata</i> Mayr, 1887	54	47	55
19	<i>Strumigenys diabola</i> Bolton, 2000	1	-	-
20	<i>Strumigenys dyseides</i> Bolton, 2000	2	-	4
21	<i>Strumigenys elongata</i> Roger, 1863	21	4	17
22	<i>Strumigenys perparva</i> Brown, 1958	3	4	17
23	<i>Strumigenys schulzi</i> Emery, 1894	3	5	14
24	<i>Strumigenys smithii</i> Forel, 1886	1	4	7
25	<i>Strumigenys spathula</i> Lattke & Goitía, 1997	1	-	-
26	<i>Strumigenys subedentata</i> Mayr, 1887	2	1	4
27	<i>Strumigenys trinidadensis</i> Wheeler, 1922	1	-	6
28	<i>Strumigenys trudifera</i> Kempf & Brown, 1969	10	2	-
29	<i>Strumigenys villiersi</i> (Perrault, 1986)	1	-	2
30	<i>Strumigenys waiwai</i> (Sosa-Calvo <i>et al.</i> , 2010)	-	1	-
31	Tribe Formicoxenini Forel, 1893			
32	<i>Ochetomyrmex neopolitus</i> Fernández, 2003	16	21	11
33	<i>Ochetomyrmex semipolitus</i> Mayr, 1878	7	5	2
34	Tribe Pheidolini Emery, 1877			
35	<i>Pheidole aenescens</i> Wilson, 2003	1	2	3
36	<i>Pheidole alienata</i> Borgmeier, 1929	-	1	-
37	<i>Pheidole allarmata</i> Wilson, 2003	20	16	25
38	<i>Pheidole araneoides</i> Wilson, 2003	13	11	1
39	<i>Pheidole biconstricta</i> Mayr, 1870	2	2	29
40	<i>Pheidole bruesi</i> Wheeler, 1911	-	1	4
41	<i>Pheidole bulliceps</i> Wilson, 2003	3	1	2
42	<i>Pheidole cataractae</i> Wheeler, 1916	1	-	-
43	<i>Pheidole coffeicola</i> Borgmeier, 1934	1	-	-
44	<i>Pheidole cramptoni</i> Wheeler, 1916	-	2	-
45	<i>Pheidole cursor</i> Wilson, 2003	9	5	1
46	<i>Pheidole deima</i> Wilson, 2003	-	14	1
47	<i>Pheidole embolopyx</i> Brown, 1968	4	1	3
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4	<i>Pheidole fissiceps</i> Wilson, 2003	1	-	-
5	<i>Pheidole flavens</i> Roger, 1863	37	20	47
6	<i>Pheidole fracticeps</i> Wilson, 2003	1	1	-
7	<i>Pheidole gemmula</i> Wilson, 2003	-	-	4
8	<i>Pheidole</i> gp. <i>fallax</i> sp.D	10	13	-
9	<i>Pheidole</i> gp. <i>fallax</i> sp.F	1	15	5
10	<i>Pheidole</i> gp. <i>tristis</i> sp.B3	-	-	3
11	<i>Pheidole</i> gp. <i>tristis</i> sp.C	9	20	5
12	<i>Pheidole</i> gp. <i>tristis</i> sp.D	1	3	-
13	<i>Pheidole</i> gp. <i>tristis</i> sp.H1	-	1	1
14	<i>Pheidole guajirana</i> Wilson, 2003	40	23	12
15	<i>Pheidole jeannei</i> Wilson, 2003	2	4	3
16	<i>Pheidole lattkei</i> Wilson, 2003	1	1	-
17	<i>Pheidole longiseta</i> Wilson, 2003	4	3	3
18	<i>Pheidole lovejoyi</i> Wilson, 2003	6	6	2
19	<i>Pheidole meinertopsis</i> Wilson, 2003	3	-	-
20	<i>Pheidole microps</i> Wilson, 2003	3	1	9
21	<i>Pheidole midas</i> Wilson, 2003	4	-	-
22	<i>Pheidole nana</i> Emery, 1894	1	1	-
23	<i>Pheidole neoschultzi</i> LaPolla, 2006	18	11	1
24	<i>Pheidole nitella</i> Wilson, 2003	51	48	43
25	<i>Pheidole</i> nr. <i>araneoides</i>	-	-	3
26	<i>Pheidole</i> nr. <i>cramptoni</i>	-	5	5
27	<i>Pheidole</i> nr. <i>fimbriata</i> sp.A	1	-	-
28	<i>Pheidole</i> nr. <i>fimbriata</i> sp.C	3	2	3
29	<i>Pheidole</i> nr. <i>fimbriata</i> sp.D	5	-	-
30	<i>Pheidole</i> nr. <i>sagax</i>	1	3	-
31	<i>Pheidole</i> nr. <i>seeldrayersii</i>	2	-	-
32	<i>Pheidole</i> nr. <i>subarmata</i>	-	-	1
33	<i>Pheidole</i> nr. <i>tristis</i>	-	1	-
34	<i>Pheidole pedana</i> Wilson, 2003	27	15	9
35	<i>Pheidole rugiceps</i> Wilson, 2003	5	4	18
36	<i>Pheidole sagax</i> Wilson, 2003	2	6	2
37	<i>Pheidole sculptior</i> Forel, 1893	1	1	1
38	<i>Pheidole</i> sp.IT14.01	1	-	-
39	<i>Pheidole</i> sp.IT14.08	1	-	-
40	<i>Pheidole</i> sp.MI15.06	-	1	-
41	<i>Pheidole subarmata</i> Mayr, 1884	3	32	11
42	<i>Pheidole terribilis</i> Wilson, 2003	3	6	-
43	<i>Pheidole tristis</i> (Smith, 1858)	-	-	1
44	<i>Pheidole zelata</i> Wilson, 2003	3	3	-
45	<i>Pheidole zeteki</i> Smith, 1947	1	-	-
46	Tribe Pogonomyrmecini Ward <i>et al.</i> , 2015			
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4		<i>Hylomyrma blandiens</i> Kempf, 1961	11	6	1
5		<i>Hylomyrma immanis</i> Kempf, 1973	2	8	20
6		<i>Hylomyrma reginae</i> Kutter, 1977	-	3	21
7	Tribe Solenopsidini Forel, 1893				
8		<i>Carebara brevopilosa</i> Fernández, 2004	2	2	-
9		<i>Carebara reina</i> Fernández, 2004	8	5	9
10		<i>Carebara</i> sp.KW14.01	7	6	17
11		<i>Carebara urichi</i> (Wheeler, 1922)	8	6	4
12		<i>Megalomyrmex balzani</i> Emery, 1894	3	-	2
13		<i>Megalomyrmex drifti</i> Kempf, 1961	2	-	1
14		<i>Megalomyrmex incisus</i> Smith, 1947	-	1	1
15		<i>Megalomyrmex silvestrii</i> Wheeler, 1909	2	3	2
16		<i>Megalomyrmex</i> sp.MI15.01	1	-	-
17		<i>Rogeria besucheti</i> Kugler, 1994	-	-	1
18		<i>Rogeria blanda</i> (Smith, 1858)	1	-	1
19		<i>Rogeria germaini</i> Emery, 1894	-	-	2
20		<i>Rogeria innotabilis</i> Kugler, 1994	1	-	2
21		<i>Rogeria scobinata</i> Kugler, 1994	5	-	-
22		<i>Rogeria</i> sp.IT14.01	3	-	-
23		<i>Rogeria</i> sp.IT14.06	1	-	-
24		<i>Rogeria</i> sp.SL13.01	10	-	-
25		<i>Rogeria subarmata</i> (Kempf, 1961)	-	1	-
26		<i>Solenopsis bicolor</i> (Emery, 1906)	7	2	-
27		<i>Solenopsis</i> sp.01	7	21	23
28		<i>Solenopsis</i> sp.02	1	4	2
29		<i>Solenopsis</i> sp.03	15	26	7
30		<i>Solenopsis</i> sp.09	4	2	1
31		<i>Solenopsis</i> sp.11	32	2	23
32		<i>Solenopsis</i> sp.12	23	3	5
33		<i>Solenopsis</i> sp.13	37	38	20
34		<i>Solenopsis</i> sp.14	7	3	17
35		<i>Solenopsis</i> sp.15	46	50	54
36		<i>Solenopsis</i> sp.17	13	5	1
37		<i>Solenopsis</i> sp.21	21	12	12
38		<i>Solenopsis</i> sp.23	4	3	4
39		<i>Solenopsis</i> sp.24	7	5	2
40		<i>Solenopsis</i> sp.25	5	-	-
41		<i>Solenopsis</i> sp.28	1	2	-
42		<i>Solenopsis virulens</i> (Smith, 1858)	7	2	9
43	Subfamily PONERINAE Lepeletier de Saint-Fargeau, 1835				
44	Tribe Ponerini Lepeletier de Saint-Fargeau, 1835				
45		<i>Anochetus horridus</i> Kempf, 1964	11	7	6
46		<i>Anochetus inermis</i> André, 1889	2	2	15
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3	<i>Anochetus mayri</i> Emery, 1884	-	-	1
4	<i>Anochetus targionii</i> Emery, 1894	2	2	1
5	<i>Cryptopone holmgreni</i> (Wheeler, 1925)	-	1	2
6	<i>Hypoponera foreli</i> (Mayr, 1887)	12	8	24
7	<i>Hypoponera</i> sp.02.FGSGt	10	-	5
8	<i>Hypoponera</i> sp.12.FGSGt	14	6	19
9	<i>Hypoponera</i> sp.13.FGSGt	5	5	12
10	<i>Hypoponera</i> sp.B	14	9	3
11	<i>Hypoponera</i> sp.IT14.01	3	4	8
12	<i>Hypoponera</i> sp.IT14.02	8	8	24
13	<i>Hypoponera</i> sp.IT14.04	-	-	2
14	<i>Hypoponera</i> sp.IT14.05	9	2	-
15	<i>Hypoponera</i> sp.MI15.02	-	1	-
16	<i>Hypoponera</i> sp.MI15.05	-	-	1
17	<i>Leptogenys gaigei</i> Wheeler, 1923	-	3	1
18	<i>Leptogenys langi</i> Wheeler, 1923	1	1	2
19	<i>Leptogenys</i> sp.05.FGSGt	2	1	7
20	<i>Leptogenys</i> sp.IT14.04	-	-	1
21	<i>Mayaponera constricta</i> (Mayr, 1884)	8	4	6
22	<i>Neoponera apicalis</i> (Latreille, 1802)	1	5	2
23	<i>Neoponera commutata</i> (Roger, 1860)	-	3	1
24	<i>Neoponera crenata</i> (Roger, 1861)	-	-	1
25	<i>Neoponera foetida</i> (Linnaeus, 1758)	-	1	-
26	<i>Neoponera prociua</i> (Emery, 1890)	-	1	-
27	<i>Neoponera verena</i> Forel, 1922	3	5	-
28	<i>Odontomachus caelatus</i> Brown, 1976	2	2	-
29	<i>Odontomachus chelifer</i> (Latreille, 1802)	5	9	10
30	<i>Odontomachus haematodus</i> (Linnaeus, 1758)	1	5	-
31	<i>Odontomachus laticeps</i> Roger, 1861	4	2	1
32	<i>Odontomachus meinerti</i> Forel, 1905	8	9	11
33	<i>Odontomachus scalptus</i> Brown, 1978	4	-	4
34	<i>Pachycondyla crassinoda</i> (Latreille, 1802)	5	9	-
35	<i>Pachycondyla harpax</i> (Fabricius, 1804)	21	22	15
36	<i>Pachycondyla impressa</i> (Roger, 1861)	1	-	2
37	<i>Pachycondyla</i> nr. <i>lenkoi</i>	1	-	-
38	<i>Platythyrea pilosula</i> (Smith, 1858)	-	1	-
39	<i>Pseudoponera stigma</i> (Fabricius, 1804)	-	4	2
40	<i>Pseudoponera succedanea</i> (Roger, 1863)	-	-	6
41	<i>Rasopone arhuaca</i> (Forel, 1901)	-	-	1
42	<i>Rasopone</i> sp.JTL047	-	-	3
43	<i>Thaumatomyrmex soesilae</i> Makhan, 2007	-	1	-

Subfamily PROCERATIINAE Emery, 1895

Tribe Proceratiini Emery, 1895

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3	<i>Discothyrea denticulata</i> Weber, 1939	1	1	1
4	<i>Discothyrea sexarticulata</i> Borgmeier, 1954	11	1	7
5	<hr/>			
6	Subfamily PSEUDOMYRMECINAE Smith, 1952			
7	<hr/>			
8	Tribe Pseudomyrmecini Smith, 1952			
9	<i>Pseudomyrmex tenuis</i> (Fabricius, 1804)	3	3	-
10	<hr/>			

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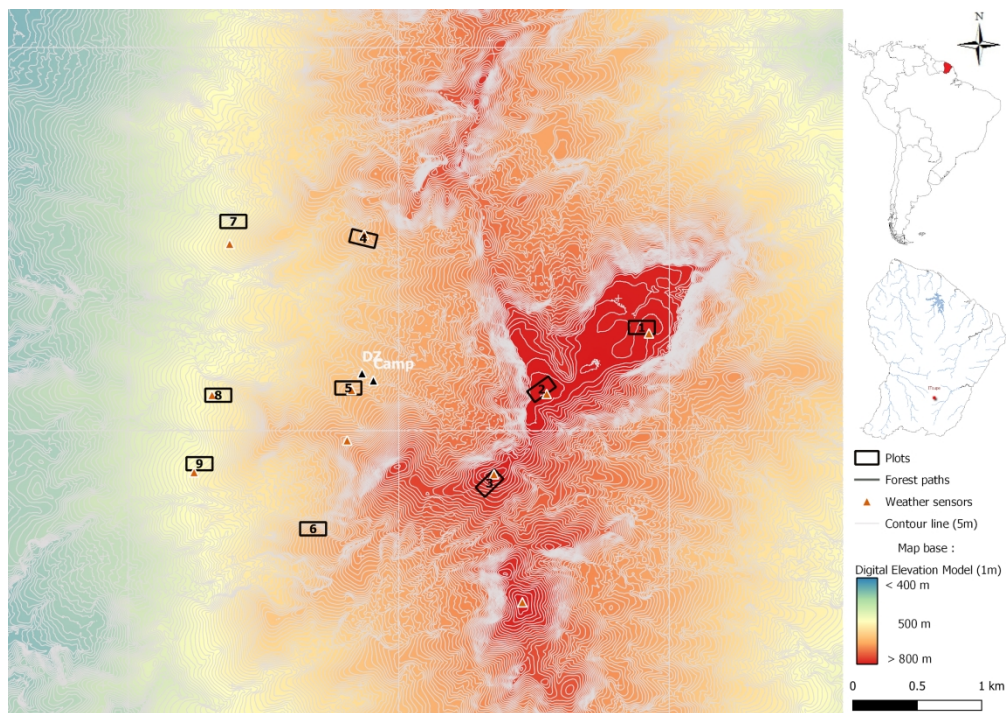
TABLE S4. Eigenvalues and trait loadings of the three first axes of a PCA performed on the matrix of mean trait values for each species (PCA_{TRAITS}).

	Axis 1	Axis 2	Axis 3
Eigenvalue	3.46	2.33	1.21
Percentage of variance	38.38	25.58	13.48
Cumulative percentage of variance	38.38	63.96	77.44
Trait loadings			
- Weber's length	-0.83	-0.08	0.15
- Relative head width	0.89	0.21	0.02
- Relative head length	0.88	0.17	-0.09
- Relative pronotum width	0.80	0.10	0.24
- Relative femur length	-0.44	0.81	-0.17
- Relative scape length	-0.27	0.83	-0.29
- Relative eye length	-0.27	0.70	0.42
- Relative clypeus length	0.35	0.55	0.52
- Relative mandible length	0.30	0.28	-0.76

TABLE S5. Eigenvalues and trait loadings of the two first axes of a PCA performed on the matrix of the 17 environmental variables measured at each plot (PCA_{ENV}). T_{MIN} = minimum temperature of the coldest month; T_{MEAN} = mean annual temperature; Gap = Gap fraction; C_{H} = Canopy height; C_{COV} = Canopy cover; Clay = percentage of clay; pH = soil pH; Silt = percentage of silt; Phosphorus = Olsen-phosphorus concentration; sand = percentage of sand; K = potassium concentration; C/N = carbon-to-nitrogen ratio; Na = sodium concentration; OM = percentage of organic matter; RH_{MIN} = minimum relative humidity of the driest month; RH_{MEAN} = mean annual relative humidity. The variables retained for analyses are highlighted in bold.

	Axis 1	Axis 2
Eigenvalue	10.28	3.52
Percentage of variance	60.45	20.70
Cumulative percentage of variance	60.45	81.15
Trait loadings		
- T_{MIN}	-0.98	0.01
- T_{MEAN}	-0.97	0.15
- Gap	-0.92	0.01
- C_{H}	-0.90	0.38
- C_{COV}	-0.86	-0.04
- Clay	-0.58	-0.73
- pH	-0.42	0.85
- Silt	0.54	0.70
- Phosphorus	0.59	0.54
- Sand	0.60	0.57
- K	0.63	0.48
- C/N	0.68	-0.69
- Na	0.72	0.12
- OM	0.77	-0.43
- RH_{MIN}	0.89	0.07
- Elevation	0.91	-0.30
- RH_{MEAN}	0.93	0.00

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