UNIVERSIDAD DE BUENOS AIRES

Facultad de Ciencias Exactas y Naturales

Sistemática y ecología de las hormigas predadoras (Formicidae: Ponerinae) de la Argentina

Tesis presentada para optar al título de Doctor de la Universidad de Buenos Aires en el área CIENCIAS BIOLÓGICAS

PRISCILA ELENA HANISCH

Directores de tesis: Dr. Andrew Suarez y Dr. Pablo L. Tubaro

Consejero de estudios: Dr. Daniel Roccatagliata

Lugar de trabajo: División de Ornitología, Museo Argentino de Ciencias Naturales "Bernardino Rivadavia"

Buenos Aires, Marzo 2018 Fecha de defensa: 27 de Marzo de 2018

Sistemática y ecología de las hormigas predadoras (Formicidae: Ponerinae) de la Argentina

Resumen

Las hormigas son uno de los grupos de insectos más abundantes en los ecosistemas terrestres, siendo sus actividades, muy importantes para el ecosistema. En esta tesis se estudiaron de forma integral la sistemática y ecología de una subfamilia de hormigas, las ponerinas. Esta subfamilia predomina en regiones tropicales y neotropicales, estando presente en Argentina desde el norte hasta la provincia de Buenos Aires. Se utilizó un enfoque integrador, combinando análisis genéticos con morfológicos para estudiar su diversidad, en combinación con estudios ecológicos y comportamentales para estudiar la dominancia, estructura de la comunidad y posición trófica de las Ponerinas. Los resultados sugieren que la diversidad es más alta de lo que se creía, tanto por que se encontraron nuevos registros durante la colecta de nuevo material, como porque nuestros análisis sugieren la presencia de especies crípticas. Adicionalmente, demostramos que en el PN Iguazú, dos ponerinas: *Dinoponera australis* y *Pachycondyla striata* son componentes dominantes en la comunidad de hormigas. Análisis de isótopos estables revelaron que la mayoría de las Ponerinas ocupan niveles tróficos altos, con excepción de algunas especies arborícolas del género *Neoponera* que dependerían de néctar u otros recursos vegetales. Por otro lado, nuestros resultados sugieren que la especie arborícola *Platythyrea pilosula* es un depredador especializado y tiene uno de los mayores valores de δ15N de cualquier especie de hormiga en el PN Iguazú. Finalmente, comprobamos la fidelidad de forrajeo para *D. australis*, una estrategia que le ayudaría a maximizar la obtención de comida. En conclusión, esta tesis brinda una importante información sobre la diversidad, distribución y el papel ecológico de la subfamilia Ponerinae.

Palabras clave: Bosque Atlántico, isotopos estables, Código de barras genético, especies crípticas, fidelidad de rutas, *Dinoponera australis*.

Systematics and ecology of predatory ants (Formicidae: Ponerinae) of Argentina

Abstract

Ants are one of the most abundant insect groups in terrestrial ecosystems, and their activities are very important for the ecosystem. In this thesis, we studied comprehensively, the systematics and ecology of one ant subfamily: Ponerinae. This subfamily predominates in tropical and Neotropical regions, being present in Argentina from the north to Buenos Aires province. We applied an integrative approach, combining genetic and morphological analyzes to study their diversity, in combination with ecologic and behavioral studies to study the dominance, community structure and trophic position of the ponerines. Our results suggest that diversity is higher than previously believed, both because new records were found during the collection of new material and because our analyses suggest the presence of cryptic species. Additionally, we showed that in the Iguazú national park, two ponerines: *Dinoponera australis* and *Pachycondyla striata* were dominant components in the ant community. Stable isotope analysis revealed that most Ponerinae species occupied high trophic levels (primary and secondary predators), but some species overlapped with known insect herbivores. These low trophic level species were primarily arboreal *Neoponera,* and may rely heavily on nectar or other plant based resources in their diet. In contrast, field observations and isotope analysis suggest that the arboreal *Platythyrea pilosula* is a specialized predator, and has one of the highest δ15N value of any ant at Iguazú National Park. Finally, we proved the use of the fidelity of foraging routes for *D. australis*, a strategy that would help her to maximize prey harvesting. In conclusion, this thesis provides important information on the diversity and distribution of the ponerines and the ecological role of this subfamily.

Keywords: Atlantic forest, stable isotopes, DNA-barcoding, cryptic species, route fidelity, *Dinoponera australis*.

Contenido

Agradecimientos

Este trabajo se realizó gracias al financiamiento del CONICET (Consejo Nacional de Investigaciones Científicas y Técnicas), del BIO (Centre for Biodiversity Genomics), la Fundación Williams, la Fundación Temaiken, Andrew Suarez, Wendy Yang y el Department of Entomology and School of Integrative Biology en Illinois.

Agradezco a la Comisión de seguimiento de doctorado, Consejo Directivo y a las autoridades de la FCEyN (Facultad de Ciencias Exactas y Naturales) de la UBA (Universidad de Buenos Aires). Al personal del MACN (Museo de Ciencias Naturales "Bernardino Rivadavia"), del BIO y de los departamentos de Entomología y Biología de Plantas de la Universidad de Illinois en donde trabaje en las distintas etapas de esta tesis. A los curadores de las colecciones de Entomología de MSZP (Museu de Zoologia da Universidade de São Paulo), BMNH (Natural History Museum), IMML (Instituto y Museo de Ciencias Naturales Miguel Lillo) y RBINS (Royal Belgian Institute of Natural Sciences).

A la administración de Parques Nacionales, especialmente Parque Nacional Iguazú, que me dio soporte logístico y los permisos para colectar muestras. Agradezco también al personal del Ministerio de Ecología de Misiones, CIAR (Centro de Investigación Antonia Ramos), Fundación Bosques Nativos Argentinos, CIES (Centro de Investigación de Estudios Tropicales) y de la Reserva Privada Osununú. Gracias a todos los guardaparques de las áreas protegidas donde trabaje por su inmensa labor.

Agradezco a Fabián Gatti, Cristian Grismado, Abel Pérez Gonzáles, Diego Carpintero y Braun Holger por la identificación de muestras destinadas a los análisis de isótopos estables. A la división de aracnología del MACN por facilitar material bycatch. A mis colegas Maurice Leponce, Itanna Fernandes, Rodolfo Proust, John Lattke, Claudia Marcela Ortiz, Andrés Sánchez Restrepo, Ian Traniello, William Mackay y Lina Pedraza por molestarse en responder mis muchas consultas.

En lo personal, quiero agradecer en primer lugar a mis directores, Andy y Pablo, por la paciencia, los consejos, las exigencias y las no exigencias. A Andy, por animarse a dirigirme a la distancia y a Pablo por aventurarse en un mundo de 6 patas. Me siento muy afortunada de haberlos tenido como directores. Aprendí mucho de ustedes, en lo académico y humano durante estos 5 años.

A mi mamá, mi papá y mi hermano Elián. Gracias por el amor y el soporte durante toda la carrera. Gracias a ustedes soy bióloga. El último capítulo de la tesis tuvo muchas versiones y fallidos, les debo a Elián y Federico, haber podido terminar el trabajo de campo a tiempo.

A Fede, mi compañero incondicional durante toda la carrera. Compartimos muchas charlas de hormigas, filosofía y ciencia. Gracias por tanto amor.

Les debo mucho a mis amigas y amigos Marina, Gabriel, Azul, Celeste N., Claudia, Adriana, Marto, Paula, Andrecito, Lucila, Carolina, Agustín, Nacho. A Carolina Paris con quien empecé a mirar hormigas, y seguimos haciéndolo juntas hasta el día de hoy. A mí ahijada Catalina y mi pequeña cuñada Martina por llenarme de alegría. A mis muy queridas primas Verónica y Valeria. A Fufi, la alma mater del MACN. Agradezco especialmente a Damián, Sergio, Iván, Ricardo, Maiten, Daniella, María y Tincho, por los mates, la compañía, la ayuda, las discusiones de análisis, animales y plantas. A mis amigos y compañeros morfométricos: Santiago, Celeste, Dani, Guada y Álvaro. A mis gatas Pelusa y Akira, con quienes comparto la curiosidad por los pequeños bichos.

A mis compañeras y compañeros de laboratorio en el MACN: Laura, Sebastián, Majo, Natalia T, Cecilia E, Natalia G, Ana, Natalí, Pili, Cecilia K, Luciano, Andrés y Emilio. Gracias por el cariño y la compañía de todos los días. Le agradezco especialmente a Yolanda, a Ezequiel por la donación de material, a Darío por responder mis muchas consultas, a Belén que procesó parte del material de las trampas Malaise, a Pablito que me ayudo con los análisis moleculares y a Eli por su ayuda en el laboratorio molecular.

I greatly appreciate the help and moments I shared with my friends and lab mates in Illinois. Thanks to Adrian, Rafael, Michael and Celina. I want to especially thank Josh and Kim with whom I shared a lot of fun. Kim helped me with the isotope analysis and Josh used a lot of his time to help me to overcome problems and made me feel always welcome. Thank you so much, guys! I also want to thank to Janice Jayes and her kids Maddy and Marty, who give me a place to stay during my first visit to Illinois. We shared barbecues, parties… a school play! You were very kind to me.

I spend a wonderful time at the Bio in Guelph, Canada. Especial thanks to the people who make it possible and with whom I shared unforgettable moments, Bio-Bus included: Paul, Jeremy, Kate, Allison, Angela, Monica, Crystal, Graham, Megan, Jaclyn, Jayme, Valerie, Thanushi and Shannon.

A los etceterianos. Mis compañeros, amigos y profesores del curso de Ecología Tropical en Costa Rica por ser fuente de inspiración y seguir acompañándome hasta el día de hoy.

Por último, le agradezco a ellas, las hormigas.

A mis padres

I. Introduction

1.1. Ponerinae ants

Ants are a ubiquitous component of almost all terrestrial communities. They are considered a key component of terrestrial ecosystems, directly or indirectly providing ecological services including seed dispersion, control of herbivore populations, acceleration of forest recovery or plant succession, organic matter decomposition and nutrient cycling in the soil through their nest building and maintenance (Folgarait 1998, Del Toro et al. 2012). Ants are composed of 17 extant (living) subfamilies. In terms of species richness, only 3 subfamilies surpass the 1000 species: Myrmicinae, Formicinae and Ponerinae (Fig 1.1).

The ant subfamily Ponerinae consists primarily of predatory species, many of which retain characters thought to be shared with the common ancestor of all ants, including worker fertility and solitary foraging. To date, the earliest Ponerinae species are known from early Eocene amber (52-55 million-year-old; Aria *et al.*, 2011). Most of the species can be found in warm and temperate regions (Fig 1.2), from several centimeters deep in the soil to the canopy of tall, tropical trees. These ants exhibit an amazing array of variation in size, diet, abundance, and behavior (Fig 1.3). Additionally, this subfamily has been a challenge for taxonomists in terms of determining relationships among genera, placing species in appropriate genera, and estimating diversity in genera with many cryptic species (Ward 2007). Recent progress has been made in understanding the phylogenetic relationship among Ponerinae genera (Schmidt & Shattuck 2014, Larabee et al. 2016). At the species level, given the difficulty of achieving a complete revision of challenging groups as in the case of *Hypoponera*, regional revisions had been proposed in the myrmecological community as an alternative to study these taxa (Jiménez et al. 2008, Bolton & Fisher 2011, Macgown et al. 2014). Additionally, the presence of cryptic species and evidence that several recognized species are actually a complex of species

(Wild 2002, Lucas et al. 2002, Delabie et al. 2008, Ferreira et al. 2010), suggests that the diversity of this group might be higher than currently recognized. In Argentina, Ponerinae have received little attention and due to recent taxonomic changes and new described species, a taxonomic and diversity distribution update is needed, in addition to ecological and behavioral information.

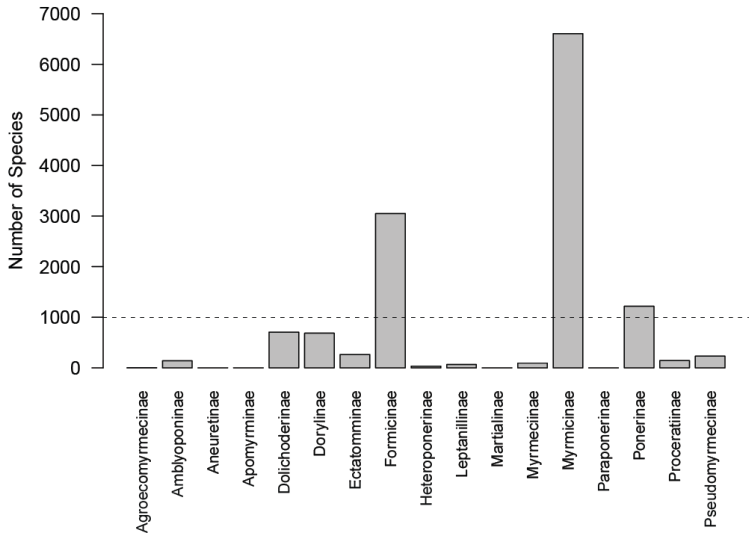


Fig 1.1 Species number by subfamily. Source: http://www.antcat.org, acceded date: 04/04/2017

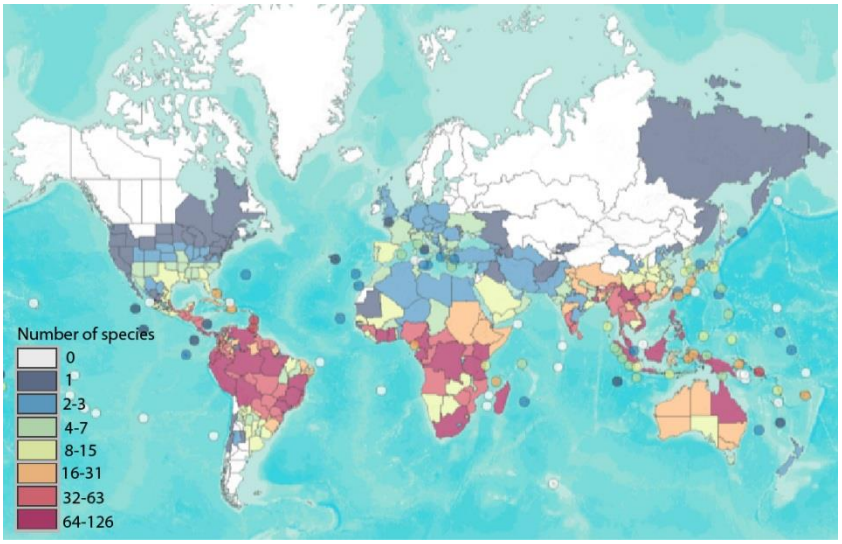


Fig 1.2 Number of Ponerinae species by country. Source: http://antmaps.org/, acceded date: 16/05/2017

Fig 1.3 The biggest Ponerinae ant (*Dinoponera australis*) and the smallest (*Hypoponera parva*) from Argentina. Photo credit: Priscila E. Hanisch

1.2. Colony organization in Ponerinae

All ant species are eusocial defined by colonial living, cooperative brood care, an overlap of generations, and a division of labor into reproductive and non-reproductive groups. In the subfamily Ponerinae, a variety of colony organizations can be found; colonies range from a few (e.g. *Thaumatomyrmex*; Delabie *et al.*, 2000) to tens of thousands of individuals (*Leptogenys*; Witte & Maschwitz, 2000). Some colonies have a single reproductive queen (e.g. *Neoponera apicalis;* Dietemann & Peeters 2000) and others are polygynous (e.g. *Odontomachus chelifer;* Medeiros *et al.* 1992). Moreover, monogynous (one queen) or polygynous (several queens) colonies might be found in the same species along its distribution (e.g. *Pachycondyla striata;* Rodrigues *et al.*, 2010; *Odontomachus hastatus* Oliveira *et al.*, 2011). Additionally, workers can vary in the degree to which they are truly sterile: In many ponerines, workers can lay eggs, and in a few species workers have spematheca and can mate (Peeters 1991a). To distinguish them from true queens, mated workers receive the name of gamergates ("married worker" in ancient Greek). Species where gamergates are present may still have true queens (e.g. *Platythyrea*) or not (e.g. *Dinoponera*) (Fig 1.4). Also, an intermediate between the queen and the workers may occur (inter-caste and ergatoids queens; Peeters, 1991b). But how reproduction is organized in a colony where all individuals have the capacity to reproduce?

This is done by controlling which individuals can reproduce and which do not. Conflicts over reproduction can occur between queens or workers, may involve chemical signals and/or physical aggression, and can result in a dominance hierarchy where only the dominant female reproduces (Monnin & Peeters 1999, Smith et al. 2013a). Additionally, to discourage egg laying or ovarian development in low ranking females, ovarian-active females can be attacked or punished by other nestmates, a behavior known as worker policing (Liebig et al. 1999). Other mechanisms to determine the dominant female includes age or mutilation (Peeters & Higashi 1989, Higashi et al. 1994). For example, in the genus *Diacamma*, inhibition of ovaries development occurs by the mutilation of a particular body of the emerging females by the dominant gamergate. In the absence of a gamergate, the first emerging female will mutilate her sisters and become the gamergate (Peeters & Higashi 1989).

Fig 1.4 Two ponerine colonies at MACN's bioterium. Left: A colony of *Neoponera curvinodis*, the queen is in the center of the image carrying eggs. At the bottom, a worker is feeding the brood. It can be observed that the queen is faintly different from the workers. Right: A colony of *D. australis*, this species lost the queen caste and reproduction is carried by a mated worker. Photo credit: Patrich Cerpa

1.3. Caste morphology in ants

Ant males and queens (alates) are usually winged and their morphology can be very different than that of the more well-known and conspicuous workers. The reduced state of the male mandible is characteristic of all ponerines (with the exception of the genus *Platythyrea*; Bolton, 2003). Usually, alates are sampled with collection methodologies specialized for flying

insects like Malaise or light traps. Ideally, they are collected along with complete colonies during the reproductive period so workers and alates can be directly associated. However, this does not often occur resulting in a lack of association of males and queens with their corresponding worker caste. This lack of association prevents the identification of species based on males and queens alone which can impede ecological studies and species inventories. In the past, male morphology, especially at the species level, has been considered taxonomically irrelevant. Currently, this view is changing, and the focus on males has been increasing in the past years, accompanied with interesting discoveries (Yoshimura & Fisher 2007, Boudinot 2013, Fernandes et al. 2014, Macgown et al. 2014). For example, based on the study of Neartic *Odontomachus* males, Macgown et al. (2014) revived *O. desertorum* from synonymy with *O. clarus*.

1.4. Diet and trophic position of Ponerinae

Most species of ants in the subfamily Ponerinae are assumed to be predatory. Observations of foraging have confirmed this for many species, and both generalist and specialist predators are common in this subfamily (Hölldobler & Wilson 1990). For example, data obtained from stable isotopes and from direct observations of foragers, suggest that the ponerinae ant, *Dinoponera australis*, is among the top predators in the terrestrial invertebrate community (Tillberg et al. 2014). Instead, *Neoponera marginata* is known to feed only from the termite *Neocapritermes opacus* (Leal & Oliveira 1995). In contrast, some ponerine species also feed on nectar, homopteran honeydew, fruits or lipid-rich seeds (Evans & Leston 1971, Holldobler 1985, Devries 1991, Pizo & Oliveira 1998). Remarkably, *Platythyrea conradti* workers collect nectar onto part of their body surface for transport to the nest; the liquid is retained via surface tension (Dejean & Suzzoni 1997). The incorporation of vegetal items in the diet of Ponerine species can help to improve larval development which is related with adult size and health (Bottcher et al. 2014). Furthermore, some Ponerinae species can affect seed distribution and survival of plants. For example, *P. striata* can disperse *Clusia criuva*

seeds up to 10 m, additionally seedling survival is greater near colonies of *P. striata* (Passos & Oliveira 2002). This dispersion may be complementary to dispersion made by vertebrates (Passos & Oliveira 2002, Christianini & Oliveira 2010, Santana et al. 2013). Other negative or positive impact on plants can be found, for example, the predatory behavior of some ponerine species can discourage visiting pollinators or butterflies laying eggs (Oliveira & Freitas 2004). Despite a long history of studying the foraging behavior of key ponerine taxa, the natural history for most species remains unknown. Moreover, diet observations are difficult for small and subterranean species like the genus *Hypoponera*.

1.5. Foraging behavior

Ponerinae strategies to gather food ranges from solitary foraging without nest mate recruitment (e.g. *D. australis*) to varying levels of co-operative foraging or social foraging (e.g. swarm raiding as in some *Leptogenys* species). It has been hypothesized that these different foraging strategies are linked and optimized according the diet and its distribution (Pie 2004, Lanan 2014). Experimental and theorical studies have shown that group-foragers find and exploit clumped and abundant resources more efficiently, whereas solitary foragers are more efficient when resources are scattered and sparse (Lanan 2014).

1.6. General and specific objectives

The main objective of this thesis is to review the diversity and distribution of Ponerinae species and their ecological influence in the ecosystems at a regional level. To achieve these goals, we first studied Ponerinae diversity patterns in Argentina, and we latter focused on the ecology, behavior and structure of the species living in the Atlantic Forest. The specific objectives are:

1- To test the performance for species identification of DNA Barcode for ants in general.

2- To study the diversity and distribution of Ponerinae species in Argentina using DNA Barcode and morphology analysis.

3- To assess Ponerinae diurnal foraging activity and the interactions with other ant species.

4- Define the trophic position of Ponerine species.

5- To study foraging behavior of the giant ant *Dinoponera australis.*

Capítulo I en castellano

Las hormigas son consideradas un importante componente de las comunidades terrestres, directa o indirectamente proveyendo de servicios ecológicos como por ejemplo la dispersión de semillas, control de la población de herbívoros o el ciclado de nutrientes a través del mantenimiento y construcción de las colonias. Las hormigas se componen de 17 familias actuales. En términos de riqueza, solo 3 subfamilias sobrepasan las 1000 especies: Myrmicinae, Formicinae y Ponerinae. La subfamilia Ponerinae consiste mayormente en especies predadoras, compartiendo muchos caracteres posiblemente ancestrales en las hormigas: Por ejemplo la fertilidad de las obreras y el forrajeo en solitario. Adicionalmente esta subfamilia ha sido un desafío para los taxónomos en términos de determinar los límites entre las especies en muchos géneros con presencia de especies crípticas. De hecho, el reconocimiento de que muchas especies son en realidad, complejos de especies (Por ejemplo *Neoponera apicalis*), sugiere que la diversidad de este grupo podría ser más alta.

Todas las hormigas son eusociales, es decir que viven en una colonia, donde individuos de distintas generaciones cooperan para el cuidado de la cría, existiendo una división del trabajo (grupos reproductores y no reproductores). En las ponerinas, se puede encontrar una variedad de tipos de organización de la colonia; desde colonias formadas por unos pocos hasta decenas de miles de individuos e incluyendo una o más reinas. Adicionalmente las obreras pueden ser estériles o fértiles (con o sin espermateca). Algunas especies, como el género *Dinoponera* han perdido la casta reina y solo se reproducen por obreras. Estas obreras reciben el nombre de gamergate por ser morfológicamente diferentes de las reinas.

Los machos y reinas usualmente son alados y su morfología es muy distinta al de las obreras. Los machos de ponerinas se caracterizan por unas mandíbulas reducidas (con excepción de *Platythyrea*). Idealmente, es deseable colectar los alados al muestrear colonias

enteras, asociados a las obreras. Sin embargo, esto no siempre es posible, siendo comúnmente colectados con metodología especializada para insectos voladores (por ejemplo trampas de luz o trampas Malaise). Como resultado, los machos y reinas no pueden ser identificados por su propia morfología, impidiendo estudios ecológicos e inventarios de especies basados en hormigas aladas.

Se asume que la mayoría de las ponerinas son predadoras. Efectivamente, la historia natural de muchas especies las posiciona como especies predadoras generalistas (Por ejemplo *Dinoponera australis*) o especialistas (Por ejemplo *Neoponera marginata*). No obstante, muchas especies se alimentan de néctar de plantas o hemípteros, frutas y semillas. De hecho, se ha encontrado que la incorporación de material vegetal en la dieta de algunas especies puede mejorar el desarrollo de las larvas. Finalmente, aún se desconoce la dieta de muchas especies, especialmente en casos de especies pequeñas y crípticas (por ejemplo el género *Hypoponera*).

Las especies de ponerinas pueden tener distintas estrategias para la obtención de comida, desde forrajeo en solitario sin reclutamiento hasta distintos niveles de forrajeo cooperativo o forrajeo social. Distintos estudios correlacionan el tipo de forrajeo con la distribución de la comida. Por ejemplo se ha encontrado que las hormigas forrajeando en grupos son más eficientes para explotar recursos que se encuentran espacialmente agrupados (Por ejemplo nidos de termitas) mientras hormigas forrajeando en solitario son más eficientes para encontrar recursos que se encuentran distribuidos aleatoriamente en el espacio y tiempo.

El objetivo de esta tesis es revisar la diversidad y distribución de las ponerinas, así como su influencia ecológica en los ecosistemas a nivel regional. Para ello, primero se estudió los patrones de diversidad de las ponerinas en Argentina, y luego se enfocó en la ecología y comportamiento de las especies que habitan el Bosque Atlántico.

Los objetivos específicos son:

1- Poner a prueba el código de barras genético para la identificación de especies de hormigas.

2- Estudiar la diversidad y distribución de las ponerinas en Argentina a través del uso de técnicas moleculares y morfológicas.

3- Estudiar la actividad de diurna de las ponerinas y sus interacciones con otras especies de hormigas.

4- Definir la posición trófica de las ponerinas.

5- Estudiar el comportamiento de forrajeo de la hormiga tigre *Dinoponera australis.*

II. Diversity and distribution of Ponerinae species in Argentina

Abstract

The ant subfamily Ponerinae consists of primarily predatory species many of which retain characters thought to be shared with the common ancestor of all ants including worker fertility and solitary foraging. In addition to their diverse ecology and reproductive behavior, this subfamily has also been a challenge for taxonomists in terms of determining relationships among genera, placing species in appropriate genera, and estimating diversity in genera with many cryptic species (e.g. *Hypoponera*). In this study, we used DNA barcodes to test hypotheses regarding the delineation of currently recognized species, to assess genetic linages among different biogeographic regions, and to link reproductive castes with the worker castes. Additionally, we selected seven species to be studied in more detail with linear morphometry. In total, we processed 530 individuals from 48 species for DNA barcode analysis. We obtained 417 COI sequences belonging to 42 identified species. From our collections and revised material, we found 10 new species records for Argentina. The mean intraspecific sequence divergence was 1.6%, eight times lower than the mean distance to the nearest neighbor (13.4%). We found more Molecular Operational Taxonomic Units (87 MOTUs) than identified species (42), with MOTUs being shared by different species in only one case. Using our database of identified species, more than half of the males and queens were assigned to a species name based on a 1% distance threshold. Four species did not fulfill DNA barcode intra-inter divergence relationship. The morphological analyses were congruent with DNA barcoding results in nearly half of the cases. Our results highlight the advantage of combining DNA barcodes with morphology, both to assess species boundaries and cryptic diversity, and to link reproductive and worker castes.

2.1. Introduction

Cryptic species, two or more morphologically similar species incorrectly placed under the same scientific name, are common in animals. The presence of cryptic species makes ecological and conservation research difficult, and can result in inaccurate measurements of diversity or management recommendations (Bickford et al. 2007). Even well-studied vertebrate taxa are routinely revealed to harbor cryptic species (e.g. Ceballos & Ehrlich, 2009; Saitoh *et al.*, 2015). However, their incidence is particularly high in invertebrates and are likely most common in animals where chemical and tactile senses are more relevant than visual ones, such as ants (Mayr 1970).

Seifert (2009) estimated that more than 40% of the species in three European ant genera cannot be identified with confidence using only morphology. If those numbers can be extrapolated globally, it constitutes a major impediment for diversity studies and taxonomic revisions. The ant subfamily Ponerinae, for example, contains several taxonomic challenging genera and the presence of cryptic species is suspected in several groups. This is well illustrated by recent work on the genus *Neoponera*. By analyzing cuticle hydrocarbons, isozymes, and morphology, Lucas (2002) found that the widespread ant *Neoponera* v*illosa* was three different species living in sympatry. Additional physiological and morphological studies supported this result and recognized two additional undescribed species to this complex (Fernandes et al. 2014, Barcellos et al. 2015). Similarly, Ferreira (2010) analyzed acoustic signals, DNA Barcodes, and morphology of the stridulatory organ in *N*. *apicalis* concluded it consists of a complex of 6-9 species. An additional *Neoponera* suspected to contain cryptic species but not formally tested yet is *N. crenata* (Wild 2002).

DNA Barcoding is based on the amplification and analysis of a standardized short sequence of mitochondrial DNA near the 5’ end of the cytochrome c oxidase subunit I (COI) gene (for the majority of the animal kingdom). Its utility relies on the premise that intraspecific diversity is

predictably lower than interspecific diversity at this locus, even between closely related (i.e. sister) species (Hebert et al., 2003a; Hebert al., 2003b). Moreover, when coupled with different clustering algorithms, DNA barcodes can be used to delimit Molecular Operational Taxonomic Units (MOTUs): clusters of sequences grouped together based on similarity (Floyd et al. 2002). These MOTUs can be used to accelerate specimen identification and species recognition, unveil cryptic diversity, test species delimitation hypothesis (Ramalho et al. 2016a), or to perform fast census of animal diversity that could serve as the basis for subsequent taxonomic work (Smith et al. 2014). The method designated to analyzed DNA Barcode data is the Barcode Index Number System (BIN; Ratnasingham & Hebert 2013). This method uses the Refined Single Linkage (RESL) algorithm, an algorithm whose design was primarily driven by the need for rapid computation to process the nearly 6 M barcode sequence records present on BOLD (a cloud-based data storage and analysis platform; http://v4.boldsystems.org/) and to enable ongoing adjustments in MOTU boundaries linked to the incorporation of new records. Each genetic cluster or BIN is associated with a uniform resource identifier (URI) and a Document Object Identifier (DOI). The BOLD acronym is used as a prefix for the URIs to ensure their discrimination from identifiers employed by other database (e.g. BOLD:AAA0001 is the BIN for *Homo sapiens*; Ratnasingham & Hebert 2013).

In this study, we generated a DNA barcode reference library for the Ponerinae ants of Argentina. Currently, 11 genera, 42 species and 3 subspecies of Ponerinae are found in Argentina, all of them in the center and northern part of the country (Table 2.1). Queens and males are unknown for many of these species (but see recent descriptions by Lenhart *et al.*, 2013; Fernandes *et al.*, 2014). We first investigated the presence of cryptic species by estimating the number of MOTUs using the RESL algorithm and comparing our results to recognized species. In four groups where cryptic species were suspected (and one where different species merged into a single MOTU), we then examined morphological characters to search for supporting evidence for splitting taxa. Finally, we use our DNA barcode reference

library to associate the reproductive caste with the worker caste and describe morphological differences of males and queens for newly associated species.

Table 2.1. Records of the 42 Ponerinae species currently present in Argentina. An additional species, *Dinoponera gigantea,* is reported for Misiones province in several articles all referring to the article "Ameisen aus Guatemala usw., Paraguay und Argentinien (Hym.)" by Forel (1909). This article actually refers to "*Dinoponera grandis* var *australis*", currently recognized as *Dinoponera australis*.

Species	Province	Source
Anochetus altisquamis Mayr, 1887	For; Juj; Sal; Tuc	(Emery 1894, Kempf 1972, Kusnesov 1978)
Anochetus diegensis Forel, 1912	For	(Leponce et al. 2004)
Anochetus emarginatus (Fabricius, 1804)	For	(Kusnesov 1956)
Anochetus mayri Emery, 1884	Córd; Corr; For; Juj; Sal; SanF; Tuc	(Bruch 1915, Pignalberi 1961, Kusnesov 1978, Vittar 2008)
Anochetus miserabilis González-Campero & Elizalde, 2008	Cha, For	(González-Campero & Elizalde 2008)
Anochetus neglectus Emery, 1894	Córd, Ent, Mis, Sal, SanF, Tuc	(Gallardo 1918, Santschi 1922, Kusnesov 1953, Kempf 1972, Hanisch et al. 2015)
Centromyrmex gigas, Forel, 1911	Mis	(Santschi 1933)
Dinoponera australis Emery, 1901	Corr, For, Mis	(Emery 1901, Kusnesov 1956)
Hypoponera argentina (Santschi, 1922)	Córd, SanF	(Santschi 1922, 1929)
Hypoponera clavatula (Emery, 1906)	Bue, Cat, Córd, For, Mis	(Emery 1906, Santschi 1929, Kusnesov 1978, Leponce et al. 2004)
Hypoponera distinguenda (Emery, 1890)	Córd, Juj, Mis, SanF,	(Kusnesov 1978)
Hypoponera distinguenda histrio (Forel, 1912)	Mis	(Bruch 1914)
Hypoponera fenestralis (Gallardo, 1918)	Bue	(Gallardo 1918)
Hypoponera fiebrigi (Forel, 1908)	Bue, Córd, Mis, Sal, Tuc	(Gallardo 1918, Kusnesov 1978)
Hypoponera fiebrigi transiens (Santschi, 1925)	Córd	(Santschi 1925)
Hypoponera foreli (Mayr, 1887)	Mis	(Hanisch et al. 2015)
Hypoponera opaciceps (Mayr, 1887)	Bue, Cat, Cha, Córd, Corr, For, Juj, Mis, Sal, SanF, Tuc	(Bruch 1914, 1915, Kusnesov 1978, Calcaterra et al. 2010)
Hypoponera opaciceps pampana (Santschi, 1925)	Bue, Cat, Córd, Mis, SanF, Tuc	(Santschi 1925)
Hypoponera opacior (Forel, 1893)	Bue, For, Men, Mis, Tuc	(Emery 1906, Leponce et al. 2004)
Hypoponera schmalzi (Emery, 1896)	Mis	(Hanisch et al. 2015)
Hypoponera trigona (Mayr, 1887)	Bue, Cha, For, Juj, Mis, Sal, SanF, Tuc	(Emery 1906, Forel 1913, Santschi 1933, Kempf 1972, Kusnesov 1978)
Leptogenys australis (Emery, 1888)	Bue, SanF	(Emery 1888, Forel 1913)
Leptogenys bohlsi Emery, 1896	For, SanF	(Santschi 1925, Kusnesov 1978)
Leptogenys consanguínea Wheeler 1909	Córd, For	(Leponce et al. 2004, Lattke 2011)
Neoponera agilis Forel, 1901	Mis	(Kusnesov 1969)
Neoponera crenata (Roger, 1961)	Entr, For	(Santschi 1919, Cuezzo 1998)
Neoponera fauveli (Emery, 1895)	Juj, Sal	(Bruch 1914, Badano et al. 2005)
Neoponera fiebrigi Forel, 1912	Mis	(MacKay & Mackay 2010)
Neoponera marginata (Roger 1961)	Cha, Corr, For, Mis, Sal	(Bruch 1914, Borgmeier 1948, Kusnesov 1956, Bestelmeyer & Wiens 1996, Calcaterra et al. 2008)
Neoponera moesta (Mayr, 1870)	Cha, Córd, For, Mis	(Santschi 1919, Kempf 1972)
Neoponera obscuricornis (Emery, 1890)	For	(Theunis et al. 2005)
Neoponera rostrata (Emery, 1890)	Sal	(Bestelmeyer & Wiens 1996)

Neoponera villosa (Fabricius, 1804)	Cha, Corr, For, Juj, Mis, Sal, Tuc	(Gallardo 1918, Santschi 1921, Kusnesov 1953, 1978)
Odontomachus bauri Emery, 1892	For	(Leponce et al. 2004)
Odontomachus chelifer (Latreille, 1802)	Bue, Cha,Corr, Ent, For, Juj, Mis, Sal, SanF, SanE, Tuc	(Emery 1906, Bruch 1914, Gallardo 1918, Santschi 1922, Kusnesov 1957, 1978, Pignalberi 1961)
Odontomachus haematodus (Linnaeus, 1758)	Corr, Ent, Juj, Men, Mis, Sal, SanF, SanE, Tuc	(Emery 1906, Santschi 1925, Kusnesov 1953, 1978)
Odontomachus meinerti Forel, 1905	For, Mis	(Leponce et al. 2004, Hanisch et al. 2015)
Pachycondyla constricticeps Mackay & Mackay, 2010	Mis	(MacKay & Mackay 2010)
Pachycondyla harpax (Fabricius, 1804)	For, Mis, Sal	(Kusnesov 1978, Bestelmeyer & Wiens 1996, MacKay & Mackay 2010)
Pachycondyla striata Smith, 1858	Cat, Cha, Córd, Corr, Entr, For, Juj, Mis, Sal, SanL, SanF	(Emery 1906, Bruch 1914, Santschi 1916, 1919, 1925, Gallardo 1918, Kusnesov 1956, Kempf 1972)
Platythyrea sinuata (Roger, 1860)	For	(Kusnesov 1956)
Pseudoponera stigma (Fabricius, 1804)	For	(Kempf 1960)
Rasopone ferruginea (Smith, 1858)	For	(Leponce et al. 2004)
Rasopone lunaris (Emery, 1896)	Mis	(Hanisch et al. 2015)
Thaumatomyrmex mutilatus Myr, 1887	Mis	(Hanisch et al. 2015)

2.2. Methodology

2.2.1. Museum surveys and material collection

We reviewed Ponerinae type material and additional specimens in the collections of the Museu de Zoologia da Universidade de São Paulo in Brazil (MZSP), the Natural History Museum (BMNH) in London, United Kingdom, the Royal Belgian Institute of Natural Sciences (RBINS) in Brussels, Belgium, the Museo de Ciencias Naturales “Bernardino Rivadavia” (MACN) in Buenos Aires, Argentina and the Instituto y Museo de Ciencias Naturales Miguel Lillo (IMML) in Tucumán, Argentina. A list of all the examined material can be found at Appendix 2.1.

Sampling efforts were focused in the north of Argentina, where most Ponerinae species are found (Table 2.1 and Fig 2.1). A special emphasis was made in Misiones province, were ecological and behavioral studies of ponerines were also conducted (see chapters III, IV and V). Our primary field sites included: Centro de Investigación Antonia Ramos (CIAR; Misiones), Osununú Private Reserve (Misiones), Iguazú National Park (Misiones), Calilegua National Park (Jujuy), Campo de los Alisos National Park (Tucumán) and Copo National Park (Santiago del Estero). Additional small collection events were made and alcohol stored material from the MACN were included from 32 additional localities (Supplementary Table

2.1). The collected material involved overall 1339 hand collection samples, 305 baits, 188 litter samples and 138 pitfall traps. Finally, material from two, year-long Malaise trap located in Oberá (CIAR; Misiones) and El Bagual (Formosa) were included. Collected ants were preserved in 96% ethanol and stored at -20 °C. Specimens were identify to species following current taxonomical knowledge (Brown 1976, Wild 2005, Jiménez et al. 2008, MacKay & Mackay 2010, Dash 2011, Lattke 2011, Lenhart et al. 2013) and reviewed types from museums. If this was not possible , they were assigned to a morphospecies based on morphological differences perceived to be indicators of species boundaries.

All the collected material is deposited in the MACN collection. Although our objectives focused on ponerines from Argentina, alcohol stored museum specimens of *Odontomachus chelifer*, *Odontomachus haematodus* and *Pachycondyla striata* from Brazil and Bolivia were included for comparison to Argentina populations.

2.2.2. DNA Barcoding

Genomic DNA was obtained from a leg (or more than one in cases of really small specimens) following a glass fiber-based extraction protocol developed by Ivanova (2006). A 658bp fragment near the 5' end of the COI gene was amplified following standard protocols developed for DNA barcoding (Wilson 2012) and using two sets of primers: LepF1 and LepR1 (Hebert et al. 2004), and the primer cocktails C_LepFolF [LepF1+LCO1490 (Folmer et al. 1994)] and C_LepFolR [(LepR1+HCO2198 (Folmer et al. 1994)]. The cocktails were implemented to increase the amplification success for the oldest samples and for those specimens that were not preserved under ideal, DNA-friendly conditions (e.g. stored at room temperature). DNA extraction and COI amplification were performed at the MACN, while sequencing was performed bi-directionally at the Canadian Centre for DNA Barcoding (CCDB; University of Guelph, Canada) with the same primers used for amplification. Residual genomic DNA was

deposited, together with backup legs, at the National Ultrafrozen Tissue Collection at the MACN. Photographs and collection data for each specimen was uploaded on BOLD.

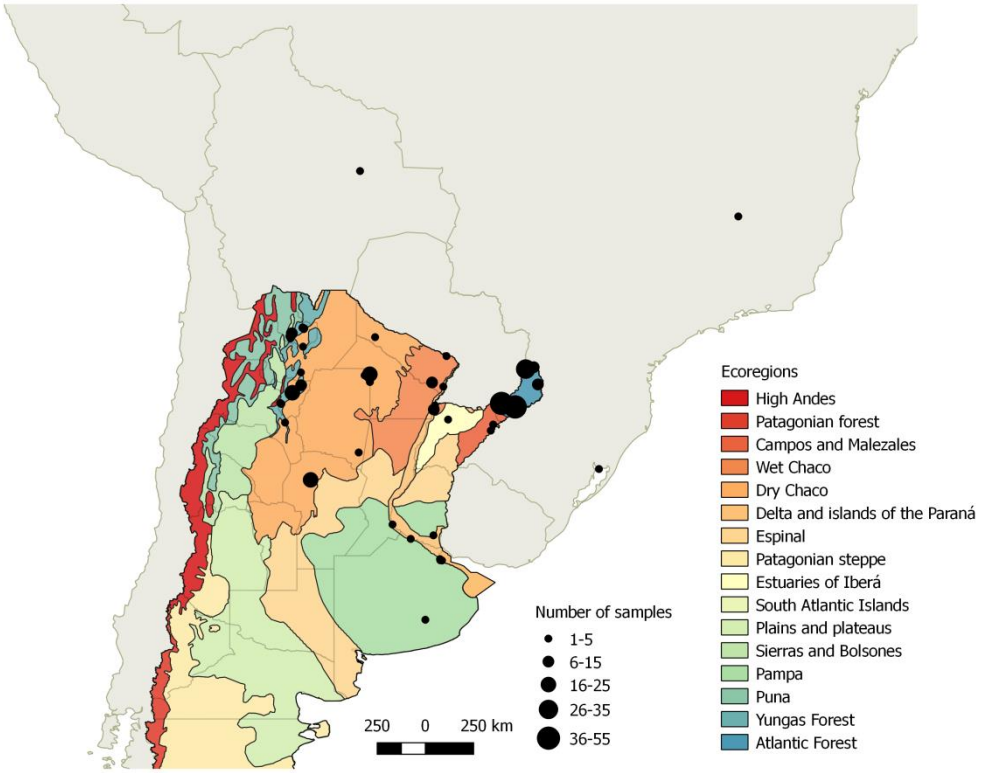


Fig 2.1 Location of the samples processed for DNA barcode. Sizes of the circles represent the number of samples.

Sequences were aligned and translated into amino acid sequence to verify the lack of stop codons within the reading frame. We also looked for presence of indels in the alignment using MEGA 7.0 (Tamura et al. 2011). Genetic distances were computed and compared using the Kimura 2-parameter (K2P) distance model (Kimura 1980). This is the standard model implemented in DNA barcoding therefore enabling a more direct comparison of our results with that of other studies. Missing data were handled using the pairwise deletion approach. The mean intraspecific divergence was obtained with the package SPIDER (Brown et al. 2012) in R 3.3.1 (R Core Team, 2016) for all species represented by two or more individuals, and then averaged to obtain the overall value for the whole dataset. As a measure of interspecific distance, we estimated the mean distance among congeneric species for those genera

represented by at least two species. Values were first averaged within each genus and then for the entire dataset. Interspecific divergence values among congeneric species were obtained using the Distance Summary tool available in the Barcode of Life Data v4 (BOLD; www.v4.boldsystems.org). Because most of the males and queens cannot be identified to species level by their morphology, these specimens were excluded from genetic distance calculations. Finally, we generated a neighbor-joining (NJ) tree in BOLD using the Taxon ID tree tool (K2P and pairwise deletion were used). Node support was computed with 1,000 bootstrap pseudoreplicates performed in MEGA 7.0 program (Tamura et al. 2011).

2.2.3. Estimation of MOTUs

To estimate the number of species we use the RESL algorithm as implemented in BOLD. RESL is the algorithm used to group COI barcode sequences uploaded to BOLD into genetic clusters (MOTUs). This method first divides the sequence alignment into initial MOTUs based on single linkage clustering with a threshold of 2.2% of maximum intra-cluster divergence. These primary MOTUs are then refined using Markov Clustering and the Silhouette Criterion (for more details see Ratnasingham & Hebert 2013). We employed the RESL algorithm exclusively to our dataset using the Cluster Sequences analysis tool available on BOLD (refer in this study as MOTUs), but we compare them with MOTUs generated by using the information of the entire COI barcode library. These clusters are called BINs since they are part of BOLD's Barcode Index Number system (Ratnasingham & Hebert 2013). To facilitate the comparisons among MOTUs and specimens identified by their morphology (worker caste), analysis were applied to a worker data-set (excluding males and queens) in addition to the whole data-set.

2.2.4. Morphological analysis

To explore morphological evidence for cryptic diversity (taxa split into several MOTUs), and to study the most relevant characters for morphological differentiation, we performed a

PCA analysis on a matrix of variance and covariance of the following 9 standard morphological traits and 3 ratios (Fig 2.2):

Head length (HL): In full-face view, the midline distance from level of maximum posterior projection of posterior margin of head to level of most anterior projection of anterior clypeal margin.

Head width (HW): In full-face view, the maximum width of head posterior to compound eyes.

Scape length (SL): In frontal view, measured from apex of first antennal segment to base.

Weber's length (WBL): In lateral view, the distance between anterior margin of pronotum to posterior margin of metapleura.

Nodal height lateral (NHl): In lateral view, the distance from lower edge of petiolar sternite to apex of petiolar tergite (node), taken as a vertical measurement perpendicular to the longitudinal axis of the petiole.

Nodal length lateral (NLl): In lateral view, the maximum longitudinal distance between anterior and posterior extremes of petiolar node, excluding anterior and posterior condyles.

Nodal width dorsal (NWd): In dorsal view, maximum width of petiolar node in dorsal view, measured side to side.

Nodal length dorsal (NLd): In dorsal view, measured from anterior to posterior face of petiole.

Pronotal width (PW): In dorsal view, the maximum width of pronotum, measured from side to side.

Scape Index (SI): SL / HW × 100.

Nodal Index lateral (NIl): (NLl / NHl) × 100.

Nodal index dorsal (NId): (NWd / NLd) × 100.

Measurements were done on a LEICA M165 C attached to a DFC295 camera and using LAS V3.8 software. PCA analyses were performed with Past V. 3.15 (Hammer et al. 2001). Species with more than 6% of maximum intraspecific distance or merged into a single MOTU according

to RESL algorithm were chosen to be studied with linear morphometric analysis (*D. australis, Neoponera crenata, Hypoponera* cf. *opacior, Pachycondyla striata, Neoponera curvinodis* and *Neoponera bactronica*). We also included *N. villosa* (from the same *N. bactronica* and *N. curvinodis* group), for comparison. Other species: *Hypoponera foreli*, *H. trigona*, *Neoponera marginata*, *Hypoponera opaciceps* and *Hypoponera* PEH08 were not included because they were represented by a few specimens.

Fig 2.2 Graphical representation of morphological traits measured for PCA analysis.

2.2.5. Reproductive castes

To match reproductive castes with workers, we queried sequences of males and queens against both our database and BOLD's entire library (as of December 2017 through BOLD's Identification engine). We identified the closest match for each of both libraries and then compared the outcomes. We considered the species assignment to be accurate if the query matched to a species with less than 1% of divergence (BOLD identification criteria). Finally, we used the dates that queens and workers were captured to describe the distribution of flight times for each species.

To obtain additional males for morphological work, we collected colonies of three species and brought them to the lab where they reared males over the course of a year: *N. bactronica* (Iguazú NP, Misiones), *O. chelifer* (Copo NP, Santiago del Estero, worker MACN-bar-ins-07558), *Odontomachus* PEH01 (Osununú PR, Misiones, workers MACN-bar-ins-07031, MACN-bar-ins-

07014, MACN-bar-ins-06983; Copo NP, Santiago del Estero, workers MACN-bar-ins-07538 and MACN-Bar-Ins-ct 07562), and *P. striata* (Calilegua NP, Jujuy).

2.3. Results

2.3.1. Distribution

Though our field collections and the review of museum collections, currently 52 Ponerinae species and 11 genera can be found in Argentina as the result of 10 new records for the country: *Anochetus inermis* (MZSP; Ticucha, Tucumán), *Hypoponera stoica* (MACN, MZSP; La Plata, Buenos Aires), *Hypoponera foeda* (Uritorco, Cordoba), *Leptogenys iheringi* (Iguazú NP, Misiones), *Neoponera curvinodis* (Iguazú NP, Misiones), *Neoponera bactronica (*Iguazú NP, Misiones; but see discussion), *Neoponera billemma* (MACN; Charata, Chaco), *Neoponera verenae* (Iguazú NP, Misiones), *Platythyrea pilosula* (Iguazú NP, Misiones) and *Neoponera aenescens* (Tiraxis, Jujuy). Additionally, four species expanded their distribution in the country: *Neoponera obscuricornis* (Iguazú NP and San Ignacio PR, Misiones), *Odontomachus bauri* (Copo NP, Santiago del Estero), *Pseudoponera stigma* (Iguazú NP, Misiones) and *Rasopone lunaris* (Iguazú NP, Misiones). Finally three morphospecies likely represent undescribed species (*Odontomachus* PEH01, *Neoponera* PEH01 and *Hypoponera* PEH06). Half or more of the species can be found in Misiones (32 species) or in Formosa (26 species) province.

2.3.2. DNA barcoding

We processed a total of 530 individuals from 48 identified species/morphospecies and 11 genera (Ponerinae) for barcode analysis: 413 workers and 117 queens and males (Fig 2.1 and Supplementary Table 2.1). From these, we obtained 423 COI sequences (near 80%), including species from difficult to collect genera (e.g. *Thaumatomyrmex* and *Platythyrea*). After discarding sequences shorter than 500pb (n=6), the complete data set consisted of 417 sequences for 42 of the identified species/morphospecies from 10 genera (divided for analysis in a worker data-set of 311 sequences and a queen/males dataset of 106 sequences). The

mean sequences length was 647bp with 75% of the data set corresponding to full barcode sequences (658bp). In the worker data-set, on average, 7 sequences were analyzed per species (range 1-43). We found a 3-bp deletion in our alignment, present in all individuals of *Dinoponera australis* starting at position 359 which did not result in a frameshift. No stop codons were found, suggesting that no pseudogenes were amplified (Song *et al.* 2008).

Based on 2348 comparisons among 34 species (8 genera) with two or more individuals (303 sequences), the mean intraspecific distance was of 1.6% (range 0% - 6.67%). In contrast, the mean congeneric distance, based on 6926 comparisons among 37 species from 5 genera with two or more species, was 13.4% (range 9.26% - 17.45%), over eight times larger than the mean intraspecific divergence (Fig 2.3).

The average distance to the nearest neighbor (i.e. minimum interspecific distance) was 11.78% (range 0% – 27.9%), only 2.6 times larger than 4.48%, the mean distance to the furthest conspecific (range 0% – 12.8%; Fig 2.4). Four species lacked a barcode gap: *N. bactronica* and *N. curvinodis* (which shared the same DNA barcode), *N. crenata* and *Hypoponera trigona* (Points below the diagonal; Fig 2.4), additionally, *H.* cf*. opacior* was the species with the highest maximum intraspecific divergence (12.8%).

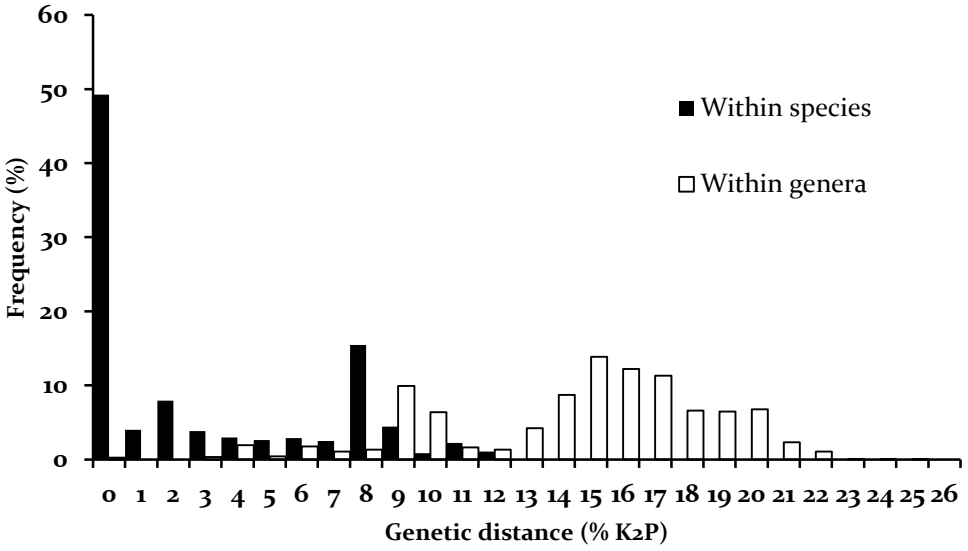


Fig 2.3 Frequency distribution of genetic distances within species (black bars) and among congeneric species (white bars).

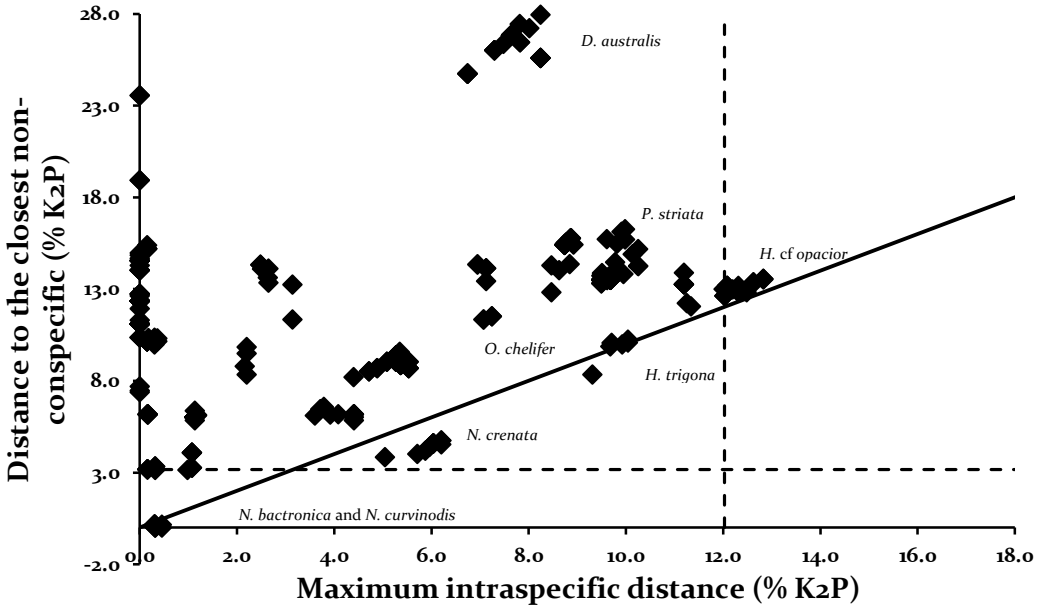


Fig 2.4 Barcode gap analysis for 34 species of ants with two or more individuals. Each individual is represented by a point, and the distance to the furthest conspecific against the minimum distance to the nearest neighbor. The vertical dashed line shows the 95% percentile of all intraspecific distances (12.03%), while the horizontal one corresponds to the lower 5% of congeneric distances (3.16%). Species analyzed in more detail are indicated.

2.3.3. Estimation of MOTUs

From the 42 identified species in the worker data-set, RESL algorithm estimated a 70% increase in the number of hypothetical species (71 MOTUs). Overall, 50% (17) of the species with more than 2 sequences (34) were divided into two or more MOTUs (Fig 2.5). Including males and queens the number of MOTUs, increases to 87. In December 2017, our records were assigned to 92 BINs. The difference is due to three MOTUs that were assigned to three BINs (*Anochetus neglectus* and *Odontomachus haematodus*) or two BINs (*Odontomachus chelifer*). Therefore, with the exception of these three species, MOTUs or BINs are equivalent. Because BINs codes are a more persistent identifier, linked to a web page where information (e.g. photos and comments) can be included, we use the BIN code for the different genetic clusters (Supplementary Table 2.1).

Two of the four species without a barcode gap were split into two or three BINs: *N. crenata* was divided into two BINs (BOLD:ACX7584 and BOLD:ABV2684), both of them found in the three localities were this species was collected (Iguazú, San Ignacio and Oberá; Fig 2.6). In the case of *H. trigona,* specimens were grouped into tree BINs (BOLD:ACZ4059, BOLD:AAU1873, BOLD:ACZ3162), all of them from Iguazú NP. In contrast, *Neoponera bactronica* and *N. curvinodis* shared the same BIN (BOLD:AAW5111), and samples were from Misiones, Corrientes and Santiago del Estero provinces (Fig 2.6). The species that were divided into the highest number of BINs were *P. striata* (6) and D. *australis* (5) (Fig 2.5 and Fig 2.6). A *P. striata* specimen from Minas Gerais (Brazil) clustered with *P. striata* (BOLD:ACO0372) from north of Corrientes and south of Misiones. Two *O. haematodus* specimens from Santa Cruz (Bolivia) were grouped in their own BIN (BOLD:ADI8020) but, if RESL analysis was performed for only our data set, these specimens clustered with the *O. haematodus* MOTU (MOTU-51) from Santiago del Estero, Jujuy and Corrientes. Finally, a *O. chelifer* specimen from Itapua (Brazil) clustered with the *O. chelifer* BIN (BOLD:AAV3356) from Misiones and Corrientes. A

supplementary Neighbor-Joining tree with all the 417 COI sequences, the locality and the BINs code is shown in the supplementary material (Fig S2.1).

2.3.4. Linear morphological analysis

We examine morphological variation between *N. curvinodis* and *N. bactronica* which had identical DNA barcodes in addition to a species from the same group (*N. villosa*). Specimens in this group were identified according Fernandes et al. (2014), being the shape of the anterior border of the petiole in lateral view, an important character to distinguish *N. curvinodis* from *N. bactronica* (Fig. 2.7). The first two principle components in the PCA for the specimens accounted for 92.5% of the total variation (78.7% and 13.8%), and loadings were largely represented by the dorsal and lateral nodal index, and the scape index (Table 2.2). Results were consistent with the DNA barcode: specimens of *N. bactronica* and *N. curvinodis* could not be separated in the multivariate space, in opposition to the other species of the group, *N. villosa* (Fig 2.8).

For *N. crenata* (maximum intraspecific distance: 6.20%), the first two PCs accounted for 99.5% of the total variation (90.5% and 9.0%). The variables that contributed the most to PC1 and PC2 were also the dorsal and lateral nodal Index respectly (Table 2.3). The PCA based on morphology did not separate the two BINs formed by DNA Barcode analysis (Fig 2.9).

The PCA of *Hypoponera* cf. *opacior* (maximum intraspecific distance: 12.83%) revealed that the first PC accounted for 99.4% of the total variation and the dorsal nodal Index was the primary character represented (Table 2.4). Three of the four BINs had a separated morphological space, with some superposition between BINs BOLD:ACM2976 and BOLD:ADJ4097 (Fig 2.10).

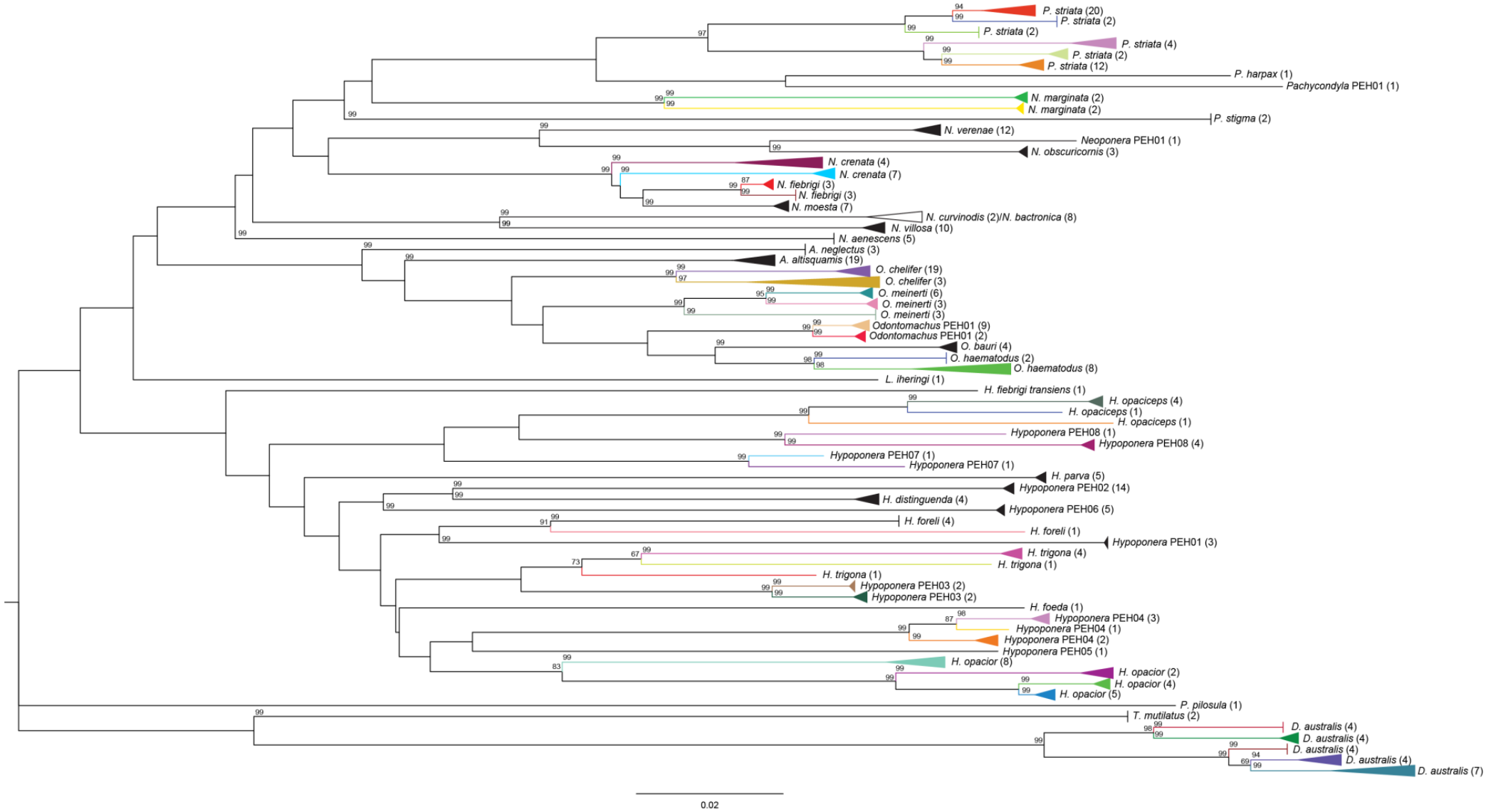


Fig 2.5 Neighbor-Joining (NJ) tree of 311 COI sequences of Ponerinae ants (workers only) computed with a K2P substitution model. The scale bar denotes 0.02 substitutions/site. Numbers at the nodes correspond to NJ bootstrap support values based on 1000 pseudoreplicates. Species are broken down to MOTUs as detail in Supplementary Table S1, groups studied with linear morphology are colored and label accordingly. In brackets, number of specimens is shown.

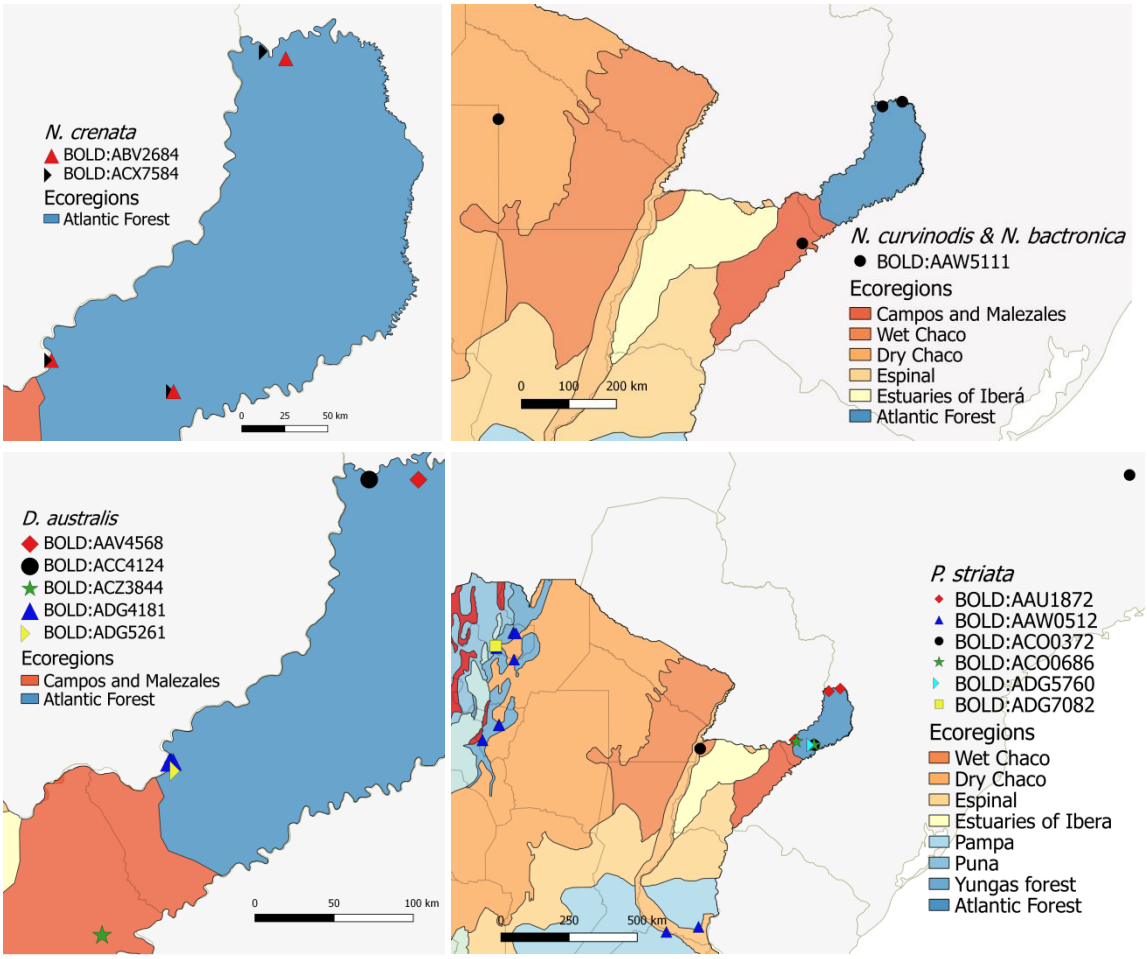


Fig 2.6 BINs distribution of the species: *N. crenata* (Upper left), *N. curvinodis*/*N. bactronica* (Upper right), *D. australis* (Bottom left) and *P. striata* (Bottom right).

Fig 2.7 Shape of the petiole of specimens identified as *N. curvinodis* (left) and *N. bactronica* (right).

Table 2.2 Loadings, eigenvalues, variance and acumulative variance for the first two PCA extracted for *N. villosa*, *N. curvinodis* and *N. bactronica* specimens. Loadings ≥ |0.50| are underlined.

	PC 1	PC 2
Head length	7.20E-05	0.0036335
Head width	0.0095839	-0.01159
Scape length	-0.004067	0.0040598
Weber's length	-0.0041063	-0.024651
Nodal height lateral	-0.0071057	0.013037
Nodal length lateral	-0.0089899	-0.0032553
Nodal width dorsal	0.0081735	-0.0051513
Nodal length lateral	-0.0040983	-0.0084879
Pronotal width	0.0029537	-0.0082923
Scape index	-0.53477	0.62628
Nodal index lateral	-0.21154	-0.7483
Nodal index dorsal	0.81788	0.2161
Eigenv	52.0912	9.15666
% Var	78.701	13.834
%VA	78.701	92.535

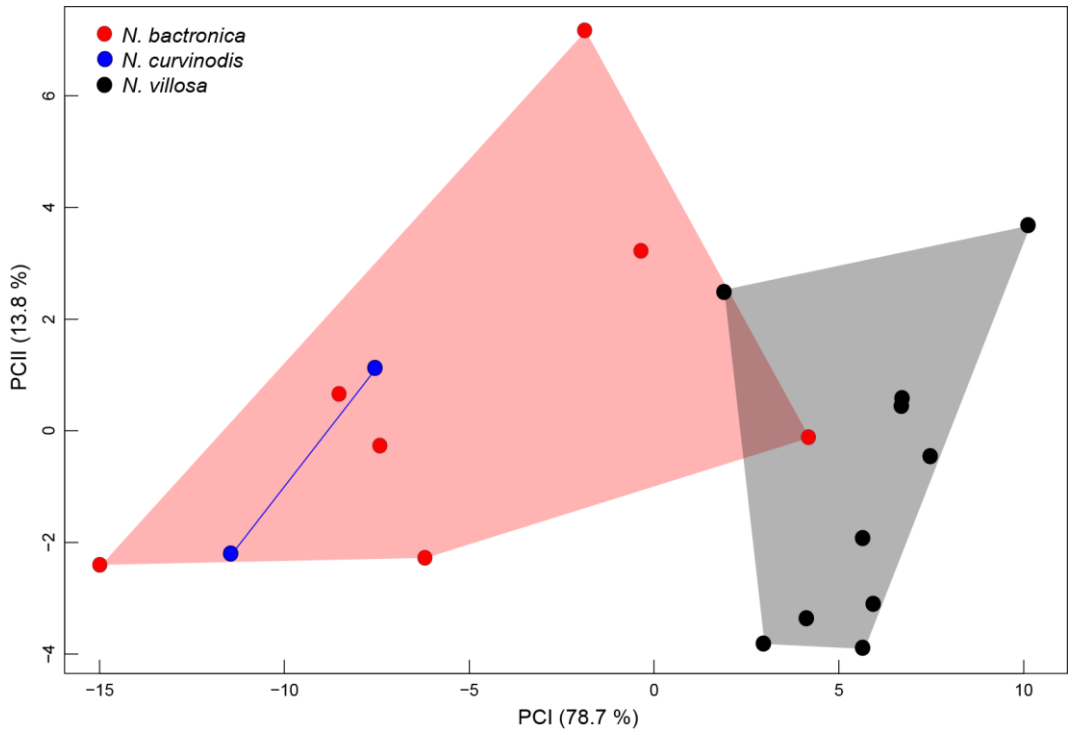


Fig 2.8 Biplot from PCA for worker ants of *N. curvinodis* (n = 2), *N. bactronica* (n = 8) and *N. villosa* (n = 10).

Table 2.3 Loadings, eigenvalues, variance and acumulative variance for the first two PCA extracted for *N. crenata* specimens. Loadings ≥ |0.50| are underlined.

	PC 1	PC 2
Head length	-6.73E-04	0.00063563
Head width	0.00018736	-0.0026884
Scape length	-0.00063713	0.00088841
Weber's length	-0.0015578	0.0020121
Nodal height lateral	-0.0020182	-0.010276
Nodal length lateral	-0.00080168	0.0036127
Nodal width dorsal	0.00062355	-0.0011511
Nodal length lateral	-0.00063796	0.0016514
Pronotal width	-0.00049215	0.0012902
Scape index	-0.067545	0.28556
Nodal index lateral	0.04184	0.95806
Nodal index dorsal	0.99683	-0.020874
Eigenv	422.676	42.0911
% Var	90.496	9.0118
%VA	90.496	99.5078

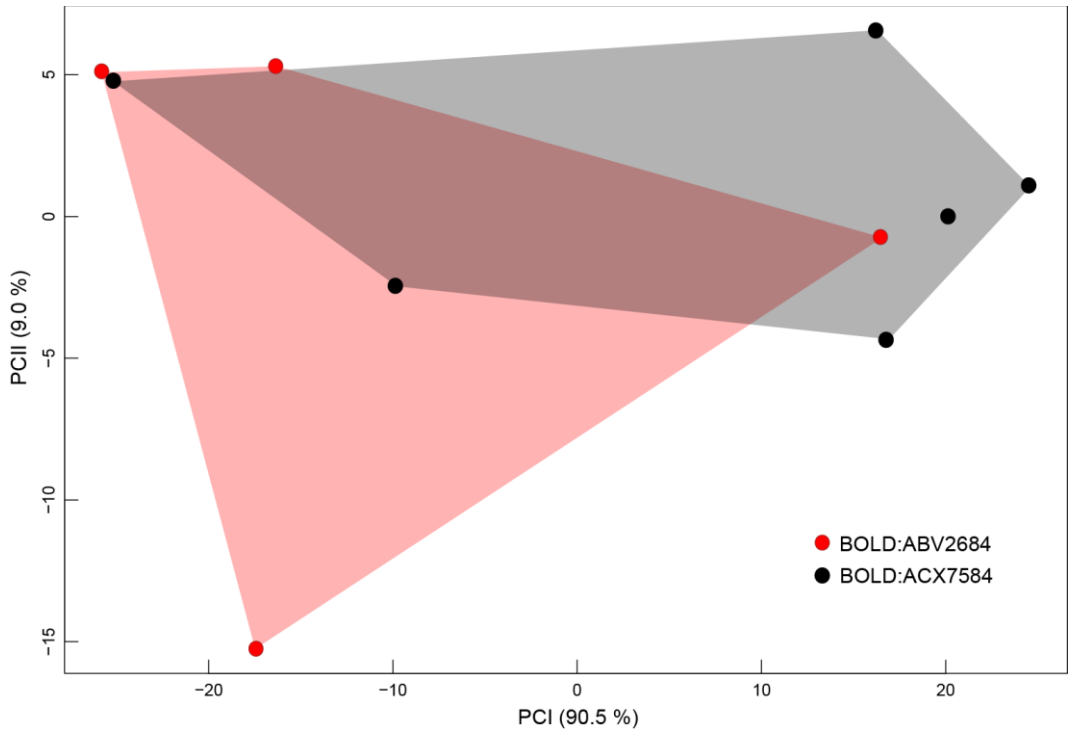


Fig 2.9 Biplot from PCA for worker ants of *N. crenata* (BOLD:ABV2684 (n = 4) and BOLD:ACX7584 (n = 6)).

Table 2.4 Loadings, eigenvalues, variance and acumulative variance for the first two PCA extracted for *H.* cf. *opacior* specimens. Loadings ≥ |0.50| are underlined.

	PC 1	PC 2
Head length	6.76E-05	-0.0068432
Head width	0.0001388	-0.0039163
Scape length	0.00014579	-0.0053871
Weber's length	0.00013697	-0.0085738
Nodal height lateral	-0.00011575	-0.0036922
Nodal length lateral	5.1972E-06	0.0023458
Nodal width dorsal	0.00010029	-0.0050792
Nodal length lateral	-6.8464E-05	-0.0020129
Pronotal width	9.0143E-05	-0.0026938
Scape index	0.0046005	-0.37333
Nodal index lateral	0.012945	0.92752
Nodal index dorsal	0.99991	-0.010287
Eigenv	1126.92	5.26414
% Var	99.379	0.46423
%VA	99.379	99.84323

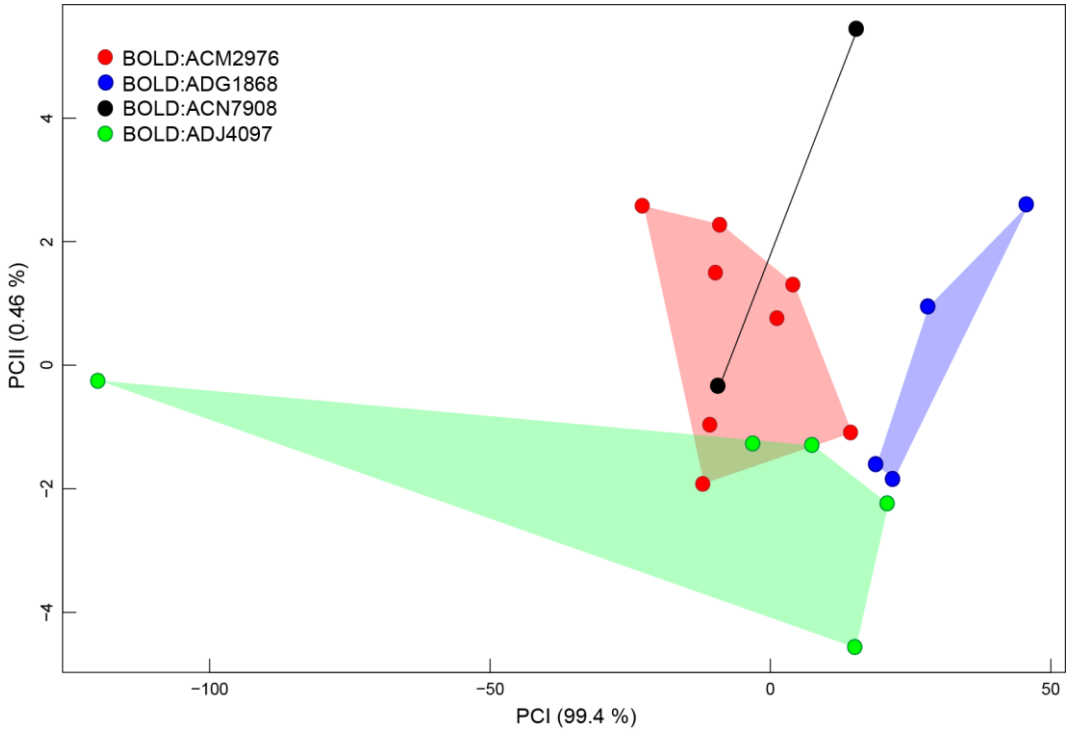


Fig 2.10: Biplot from PCA for worker ants of *H.* cf. *opacior* (BOLD:ADG1868 (n = 4), BOLD:ACN7908 (n = 2), BOLD:ACM2976 (n = 8) and BOLD:ADJ4097 (n = 5)).

In *P. striata* (maximum intraspecific distance: 10.25%), the first two PCs accounted for 97% of the total variation (70.7% and 26.4%). The variables that contributed the most to PC1 and PC2 were dorsal nodal and scape index respectly (Table 2.4). Morphological analysis did not clearly separate the groups formed by DNA barcode analysis (Fig 2.11).

Finally, for *D. australis* (maximum intraspecific distance: 7.82%), the first two PCs accounted for 88.6% of the total variation (52.8% and 35.8%) in the PCA. The variables that contributed the most to PC1 and PC2 were dorsal nodal index and scape index (Table 2.6). Two of the five BINs were separated in morphological space (Fig 2.12).

Table 2.5 Loadings, eigenvalues, variance and acumulative variance for the first two PCA extracted for *P. striata* specimens. Loadings ≥ |0.50| are underlined.

	PC 1	PC 2
Head length	3.60E-03	-0.0035533
Head width	0.0034221	-0.01086
Scape length	0.0048825	0.015753
Weber's length	0.0063015	-0.0068974
Nodal height lateral	0.0044684	-0.0059528
Nodal length lateral	0.001152	-0.0035216
Nodal width dorsal	0.0086898	-0.0040588
Nodal length lateral	-0.0053704	-0.0010965
Pronotal width	0.0029668	-0.0069359
Scape index	0.065109	0.99753
Nodal index lateral	-0.065798	-0.0090336
Nodal index dorsal	0.99559	-0.065734
Eigenv	151.697	56.581
% Var	70.762	26.393
%VA	70.762	97.155

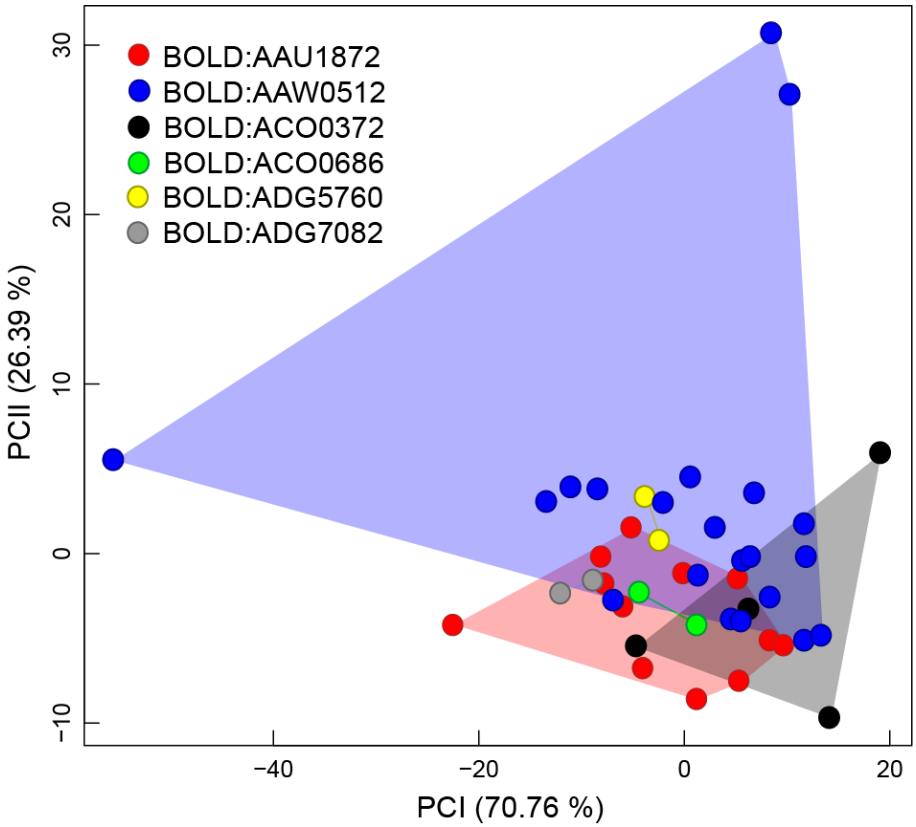


Fig 2.11 Biplot from PCA for worker ants of *P. striata* (BOLD:ADG5760 (n = 2), BOLD:AAU1872 (n = 12), BOLD:AAW0512 (n = 21), BOLD:ADG7082 (n = 2), BOLD:ACO0372 (n = 4) and BOLD:ACO0686 (n = 2)).

Table 2.6 Loadings, eigenvalues, variance and acumulative variance for the first two PCA extracted for *D. australis* specimens. Loadings ≥ |0.50| are underlined.

	PC 1	PC 2
Head length	3.63E-02	0.00076505
Head width	0.057856	-0.027823
Scape length	0.023696	0.012072
Weber's length	0.051776	0.010409
Nodal height lateral	0.024238	-0.016337
Nodal length lateral	0.021641	-0.0010926
Nodal width dorsal	0.028141	0.0038899
Nodal length lateral	0.013678	-0.0077886
Pronotal width	0.027787	-0.014079
Scape index	-0.60518	0.77181
Nodal index lateral	0.16179	0.341
Nodal index dorsal	0.77257	0.53521
Eigenv	16.0887	10.9021
% Var	52.839	35.805
%VA	52.839	88.644

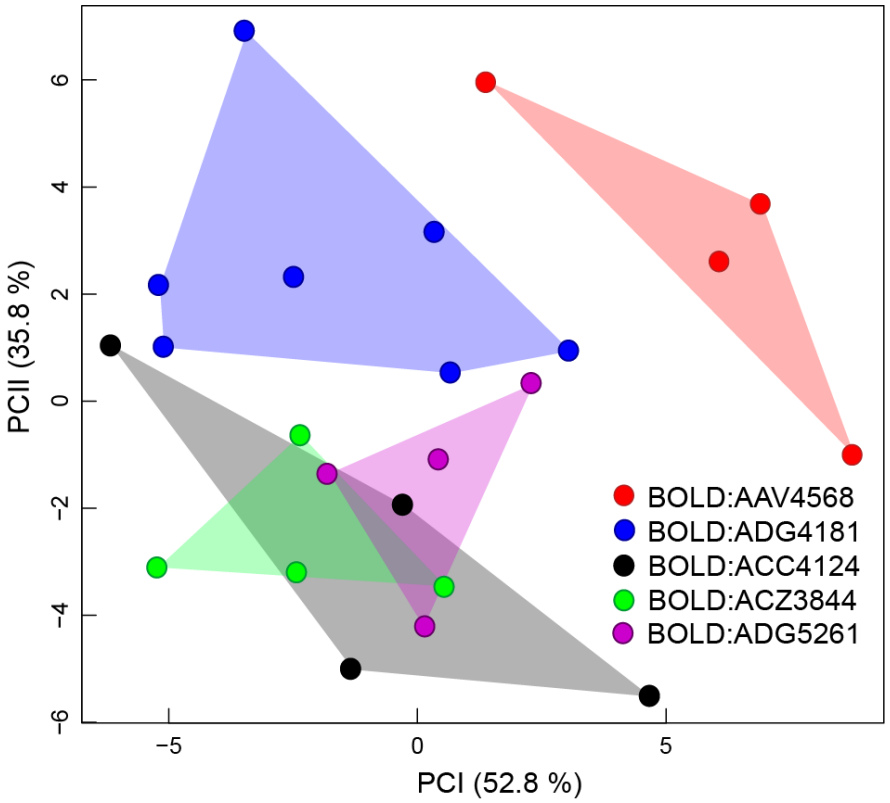


Fig 2.12 Biplot from PCA for worker ants of *D. australis* (BOLD:ADG4181 (n = 7), BOLD:ACC4124 (n = 4), BOLD:AA4568 (n = 4), BOLD:ACZ3844 (n = 4) and BOLD:ADG5261 (n = 4)).

2.3.5. Using DNA Barcode to associate reproductive and worker castes.

When we queried the 106 sequences of males and queens against both our database and the entire DNA barcode library available on BOLD (as of December 2017), a species name was assigned to 62 (58%) specimens based on a 1% divergence threshold (Table 2.7). In all but one specimen, the closest match was a sequence that was part of this study's dataset. Another 33 specimens (94% of the cases with our database) showed a close match at divergence values between 1.1% and 3.85% (Table 2.7). For the remaining 11 sequences, 5 had the closest match with sequences from other projects available on BOLD and 6 to this study, although genetic distances were between 6.9% and 13.1% (Table 2.7) suggesting that the species to which the unknown queries belonged were not yet present in BOLD. In summary, 92% of the unknown sequences (97 out of 106) had a close match provided by the records available in our project and 55% of those (59) resulted in species identification based on 1% divergence threshold

(excluding the case of *N. curvinodis* and *N. bactronica*, but see discussion). For most genera, reproductive individuals were most common during the summer (December to March) (Fig 2.13).

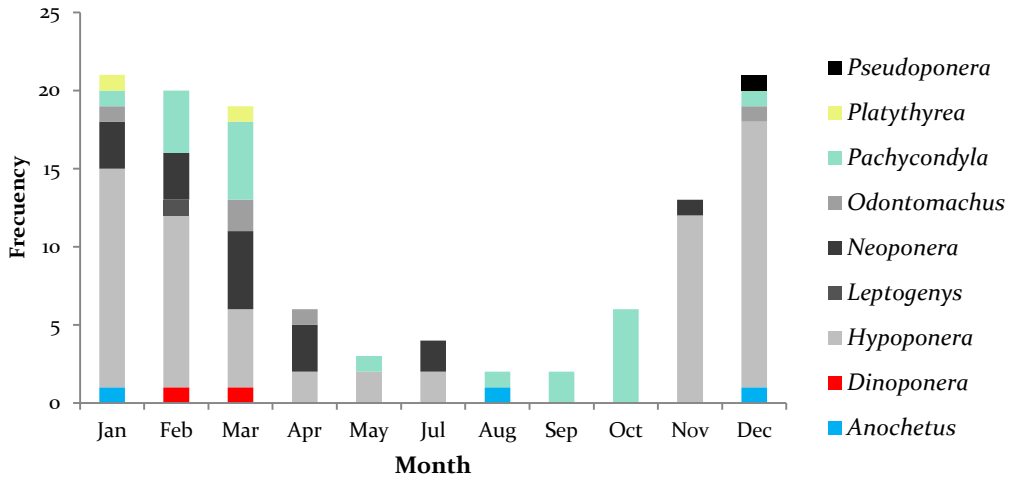


Fig 2.13 Monthly frequency distribution of males and queens for each genus. Half of the samples (55%) belong to two one-year active Malaise trap from Formosa and Misiones province.

Table 2.7 Results of the sequence-based specimen identification of 106 unidentified males and queens using the barcode database reported here and the entire barcode library available on BOLD. The table shows for each query the closest match, their sequence similarity and the database in which that record was found. Matches with 99% or higher similarity constitute solid species identifications according to the BOLD Identification Criterion.

Query				Closest match				
Process id	Sample id	Preliminar ID	Caste	% Similarity	Overlap (bp)	Species ID	Procces ID	Database
ANTPI087-10	T2W52008PNIH03	*Odontomachus*	Queen	100	650	*Odontomachus meinerti*	ANTI126-15	This Study
ANTPI220-13	MACN-Bar-Ins-ct 05059	*Odontomachus*	Queen	100	650	*Odontomachus meinerti*	ANTI126-15	This Study
GMARA1914-14	BIOUG12800-E03	*Pachycondyla*	Male	100	578	*Pachycondyla striata*	ANTI451-16	This Study
GMARB026-14	BIOUG12771-E03	*Odontomachus*	Male	100	650	*Odontomachus* PEH01	ANTI460-16	This Study
GMARD1998-14	BIOUG12908-H10	*Hypoponera*	Male	100	528	*Hypoponera* PEH02	ANTI142-15	This Study
GMARE1190-14	BIOUG12935-A12	*Hypoponera*	Male	100	519	*Hypoponera* PEH02	ANTI142-15	This Study
GMARE1203-14	BIOUG12935-C01	*Hypoponera*	Male	100	528	*Hypoponera* PEH02	ANTI142-15	This Study
GMARN1615-14	BIOUG13556-C01	*Pachycondyla*	Male	100	537	*Pachycondyla harpax*	ANTPI033-10	This Study
GMARO180-14	BIOUG13576-H11	*Pachycondyla*	Male	100	615	*Pachycondyla striata*	ANTI599-16	This Study
GMARP009-14	BIOUG13556-H02	*Pachycondyla*	Male	100	465	*Pachycondyla harpax*	ANTPI033-10	This Study
GMARS492-14	BIOUG13979-A12	*Hypoponera*	Male	100	557	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
GMARS512-14	BIOUG13979-C08	*Hypoponera*	Male	100	557	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
GMART1263-14	BIOUG14027-A03	*Hypoponera*	Male	100	557	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
GMART1322-14	BIOUG14027-F02	*Hypoponera*	Queen	100	557	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
GMAGD107-15	BIOUG22490-E02	*Odontomachus*	Male	100	628	*Odontomachus chelifer*	ANTI120-15	This Study
GMAGB101-15	BIOUG22759-B02	*Pachycondyla*	Queen	100	620	*Neoponera crenata*	ANTI101-15	This Study
GMAGX058-15	BIOUG24734-A09	*Hypoponera*	Male	100	472	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
GMAGV666-15	BIOUG24814-A04	*Hypoponera*	Male	100	489	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
GMAGV717-15	BIOUG24814-E07	*Hypoponera*	Male	100	505	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMAGW384-15	BIOUG24805-B03	*Hypoponera*	Male	100	474	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
GMAGS171-15	BIOUG24953-C06	*Pachycondyla*	Male	100	537	*Pachycondyla harpax*	ANTPI033-10	This Study

ANTPI505-15	MACN-bar-ins-ct 06904	*Hypoponera*	Queen	100	557	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
ANTPI571-16	MACN-bar-ins-ct 06970	*Neoponera*	Male	100	569	*Neoponera verenae*	ANTPI662-16	This Study
ANTI494-16	MACN-Bar-Ins-ct 07364	*Neoponera*	Male	100	580	*Pachycondyla striata*	ANTI813-17	This Study
ANTI501-16	MACN-Bar-Ins-ct 07371	*Neoponera*	Queen	100	650	*Neoponera moesta*	ANTI117-15	This Study
ANTI505-16	MACN-Bar-Ins-ct 07375	*Hypoponera*	Queen	100	521	*Hypoponera parva*	ANTI160-15	This Study
ANTI533-16	MACN-Bar-Ins-ct 07403	*Hypoponera*	Queen	100	527	*Hypoponera* PEH04	ANTI563-16	This Study
ANTI561-16	MACN-Bar-Ins-ct 07431	*Hypoponera*	Queen	100	557	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
ANTI573-16	MACN-bar-ins-07443	*Hypoponera*	Queen	100	537	*Hypoponera* PEH06	ANTI565-16	This Study
ANTI589-16	MACN-bar-ins-07459	*Neoponera*	Queen	100	650	*Neoponera moesta*	ANTI117-15	This Study
ANTI660-16	MACN-bar-ins-07529	*Neoponera*	Queen	100	575	*Neoponera bactronica/ N. curvinodis*	ANTI831-17	This Study
ANTI666-16	MACN-bar-ins-07535	*Neoponera*	Queen	100	575	*Neoponera bactronica/ N. curvinodis*	ANTI831-17	This Study
ANTI688-17	MACN-Bar-Ins-ct 07557	*Hypoponera*	Queen	100	509	*Hypoponera* PEH03	ANTI692-17	This Study
ANTI832-17	MACN-bar-ins-ct 07728	Ponerinae	Male	100	593	*Pachycondyla striata*	ANTPI091-10	This Study
ANTI834-17	MACN-bar-ins-ct 07730	*Neoponera*	Queen	100	617	*Neoponera crenata*	ANTI101-15	This Study
ANTI838-17	MACN-bar-ins-ct 07734	*Hypoponera*	Queen	99.85	628	*Hypoponera* MAS001	ACGAN208-09	BOLD
INSAR375-11	MACN-Bar-Ins-ct 00402	*Anochetus*	Queen	99.85	647	*Anochetus altisquamis*	ANTI816-17	This Study
INSAR738-11	MACN-Bar-Ins-ct 02564	*Neoponera*	Male	99.85	650	*Neoponera crenata*	ANTI525-16	This Study
ANTPI242-13	MACN-Bar-Ins-ct 05121	*Neoponera*	Queen	99.85	615	*Neoponera villosa*	ANTPI247-13	This Study
GMARU775-14	BIOUG14047-C05	*Pachycondyla*	Queen	99.85	569	*Neoponera verenae*	ANTPI662-16	This Study
GMAGA695-15	BIOUG22476-A02	*Hypoponera*	Male	99.85	528	*Hypoponera* PEH02	ANTI142-15	This Study
GMAGZ182-15	BIOUG24430-A08	*Hypoponera*	Male	99.85	528	*Hypoponera* PEH02	ANTI142-15	This Study
GMAGZ189-15	BIOUG24430-B03	*Hypoponera*	Male	99.85	528	*Hypoponera* PEH02	ANTI142-15	This Study
GMARW098-15	BIOUG24425-H02	*Hypoponera*	Male	99.85	528	*Hypoponera* PEH02	ANTI142-15	This Study
ANTI167-15	MACN-bar-ins-ct 06464	*Neoponera*	Queen	99.85	573	*Neoponera bactronica/ N. curvinodis*	ANTI110-15	This Study
ANTPI479-15	MACN-bar-ins-ct 06878	*Hypoponera*	Queen	99.85	521	*Hypoponera trigona*	ANTI133-15	This Study

GMAGC1338-15	BIOUG22488-B12	*Hypoponera*	Male	99.84	521	*Hypoponera* PEH02	ANTI142-15	This Study
GMAGS172-15	BIOUG24953-C07	*Pachycondyla*	Queen	99.84	528	*Pachycondyla striata*	ANTI498-16	This Study
GMARP1219-14	BIOUG13889-A10	*Pachycondyla*	Queen	99.83	497	*Pachycondyla striata*	ANTI813-17	This Study
ANTPI367-14	MACN-Bar-Ins-5621	*Hypoponera*	Queen	99.83	492	*Hypoponera opaciceps*	ANTI663-16	This Study
GMAGY332-15	BIOUG24773-G02	*Hypoponera*	Male	99.8	422	*Hypoponera* PEH02	ANTI142-15	This Study
GMARO026-14	BIOUG13556-G04	*Pachycondyla*	Queen	99.69	650	*Neoponera crenata*	ANTI525-16	This Study
GMARU608-14	BIOUG14044-B03	*Hypoponera*	Male	99.69	563	*Hypoponera* cf. *opacior*	ANTPI249-13	This Study
ANTI484-16	MACN-Bar-Ins-ct 07354	*Platythyrea*	Queen	99.69	578	*Platythyrea pilosula*	ANTI162-15	This Study
ANTI602-16	MACN-bar-ins-07472	*Neoponera*	Queen	99.69	650	*Neoponera fiebrigi*	ANTI104-15	This Study
ANTI612-16	MACN-bar-ins-07482	*Neoponera*	Queen	99.69	650	*Neoponera moesta*	ANTI117-15	This Study
GMAGC1361-15	BIOUG22488-D11	*Hypoponera*	Queen	99.31	494	*Hypoponera* PEH08	ANTI613-16	This Study
GMARA1718-14	BIOUG12779-H09	*Hypoponera*	Queen	99.23	553	*Hypoponera foreli*	ANTPI066-10	This Study
GMARD1948-14	BIOUG12908-D08	*Hypoponera*	Male	99.23	553	*Hypoponera foreli*	ANTPI066-10	This Study
GMARS499-14	BIOUG13979-B07	*Hypoponera*	Male	99.23	553	*Hypoponera foreli*	ANTPI066-10	This Study
GMAGY328-15	BIOUG24773-F10	*Hypoponera*	Male	99.23	553	*Hypoponera foreli*	ANTPI066-10	This Study
ANTPI254-13	MACN-Bar-Ins-ct 05145	*Neoponera*	Queen	99.08	650	*Neoponera moesta*	ANTI117-15	This Study
GMARB126-14	BIOUG12827-D06	*Pachycondyla*	Queen	98.9	630	*Neoponera fiebrigi*	ANTI104-15	This Study
GMAGX086-15	BIOUG24734-D01	*Hypoponera*	Male	98.85	469	*Hypoponera* cf. *opacior*	ANTI559-16	This Study
GMAGQ226-15	BIOUG24992-A09	*Pachycondyla*	Male	98.77	577	*Pachycondyla striata*	ANTI451-16	This Study
ANTPI210-13	MACN-Bar-Ins-ct 05026	*Hypoponera*	Queen	98.61	587	*Hypoponera distinguenda*	ANTI144-15	This Study
GMAFR447-15	BIOUG24612-H08	*Hypoponera*	Male	98.61	572	*Hypoponera* cf. *opacior*	ANTI559-16	This Study
GMAFR448-15	BIOUG24612-H09	*Hypoponera*	Male	98.61	572	*Hypoponera* cf. *opacior*	ANTI559-16	This Study
ANTI694-17	MACN-Bar-Ins-ct 07563	*Pseudoponera*	Queen	98.61	504	*Pseudoponera stigma*	ANTI604-16	This Study
ANTI751-17	MACN-Bar-Ins-ct 07620	*Anochetus*	Queen	98.56	647	*Anochetus neglectus*	GBMIN76932-17	BOLD
GMAFV080-15	BIOUG25336-D02	*Platythyrea*	Male	98.39	551	*Platythyrea pilosula*	ANTI484-16	This Study
GMARA1635-14	BIOUG12779-A10	*Hypoponera*	Male	98.3	532	*Hypoponera foreli*	ANTPI066-10	This Study
MBUIN698-12	MACN-Bar-Ins-ct 01748	Ponerinae	Male	98.18	604	*Anochetus neglectus*	GBMIN76932-17	BOLD

GMAFR450-15	BIOUG24612-H11	*Hypoponera*	Male	98.11	488	*Hypoponera* cf. *opacior*	ANTI567-16	This Study
ANTPI651-16	MACN-bar-ins-ct 07050	*Hypoponera*	Queen	98.06	576	Hypoponera PEH05	ANTPI604-16	This Study
GMAFR915-15	BIOUG24617-H01	*Hypoponera*	Male	98.04	572	*Hypoponera* cf. *opacior*	ANTI567-16	This Study
GMAFY016-15	BIOUG25340-C10	*Odontomachus*	Male	98.01	653	*Odontomachus chelifer*	ANTI802-17	This Study
GMAFN601-15	BIOUG24056-B09	*Hypoponera*	Male	97.88	563	*Hypoponera* cf. *opacior*	ANTI567-16	This Study
GMAFR449-15	BIOUG24612-H10	*Hypoponera*	Male	97.88	563	*Hypoponera* cf. *opacior*	ANTI567-16	This Study
GMARK050-14	BIOUG13160-G04	*Pachycondyla*	Male	97.71	551	*Pachycondyla harpax*	ANTPI033-10	This Study
GMARS490-14	BIOUG13979-A10	*Hypoponera*	Male	97.55	593	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMARS519-14	BIOUG13979-D03	*Hypoponera*	Male	97.55	593	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMART1315-14	BIOUG14027-E07	*Hypoponera*	Male	97.55	593	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMARU621-14	BIOUG14044-C04	*Hypoponera*	Male	97.55	593	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMAGX084-15	BIOUG24734-C11	*Hypoponera*	Male	97.55	593	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMAGV664-15	BIOUG24814-A02	*Hypoponera*	Male	97.55	593	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMAGV706-15	BIOUG24814-D08	*Hypoponera*	Male	97.55	593	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMAGW400-15	BIOUG24805-C07	*Hypoponera*	Male	97.55	593	*Hypoponera* cf. *opacior*	ANTI449-16	This Study
GMARB125-14	BIOUG12827-D05	*Pachycondyla*	Queen	97.09	636	*Neoponera crenata*	ANTPI410-15	This Study
ANTI097-15	MACN-bar-ins-ct 06394	*Dinoponera*	Male	97.03	507	*Dinoponera australis*	ANTI108-15	This Study
ANTI108-15	MACN-bar-ins-ct 06405	*Dinoponera*	Male	97.03	507	*Dinoponera australis*	ANTI097-15	This Study
GMAGB100-15	BIOUG22759-B01	*Pachycondyla*	Queen	96.98	626	*Neoponera crenata*	ANTPI410-15	This Study
ANTI789-17	MACN-bar-ins-ct 07671	*Hypoponera*	Queen	96.69	439	*Hypoponera* PEH04	ANTI805-17	This Study
INSAR745-11	MACN-Bar-Ins-ct 02572	*Neoponera*	Male	96.64	650	*Neoponera crenata*	ANTI101-15	This Study
ANTPI343-14	MACN-Bar-Ins-5597	*Pachycondyla*	Queen	96.15	614	*Pachycondyla striata*	ANTI186-15	This Study
GMAGA706-15	BIOUG22476-B01	Ponerinae	Queen	93.06	497	*Hypoponera* sp.		BOLD
GMAGX096-15	BIOUG24734-D11	Ponerinae	Queen	92.44	495	*Hypoponera* sp.		BOLD
GMAFA491-15	BIOUG23167-F04	Ponerinae	Male	91.28	653	*Pachycondyla* JTL014	ACGAG627-11	BOLD
GMAFF493-15	BIOUG23334-E10	Ponerinae	Male	90.66	530	*Hypoponera opaciceps*	GMRAJ107-14	This Study
GMARJ1825-14	BIOUG13316-F03	Ponerinae	Queen	90.64	561	*Hypoponera opaciceps*	GMRAJ107-14	This Study
ANTI564-16	MACN-Bar-Ins-ct 07434	*Pachycondyla*	Male	89.51	590	*Pachycondyla impressa*		BOLD

ANTI730-17	MACN-Bar-Ins-ct 07599	*Hypoponera*	Queen	89.35	528	*Hypoponera trigona*	ANTPI429-15	This Study
GMAGZ175-15	BIOUG24430-A01	Formicidae	Male	88.78	563	*Hypoponera* EC024		BOLD
GMAFT555-15	BIOUG25250-B01	Ponerinae	Male	88.58	584	*Leptogenys gatu*		BOLD
ANTI681-17	MACN-Bar-Ins-ct 07550	*Hypoponera*	Queen	88.06	581	*Hypoponera trigona*	ANTPI429-15	This Study
ANTI453-16	MACN-Bar-Ins-ct 07323	*Hypoponera*	Queen	86.84	477	*Hypoponera eduardi*	GMAGC1361-15	This Study

2.3.6. Comparisons between reproductive castes

2.3.6.1. Neoponera crenata

One queen (BIOUG13556-G04) and male (MACN-Bar-Ins-ct 02564) matched with one of the two BINs of *N. crenata* (BOLD:ABV2684) while another queen (BIOUG22759-B02) matched with the other BIN (BOLD:ACX7584) of this species (Table 2.7). We compared the queens and found a difference in the middle lobe of the clypeus: Queen BIOUG13556-G04 has a shallow groove without striation, while queen BIOUG22759-B02 has a deeper groove with striation in (Fig 2.14). Additionally, the male, lacked a characteristic subpetiolar proccess of the species (MacKay & Mackay 2010) (Fig 2.15).

Fig 2.14 Clypeo of *N. crenata* queens BIOUG13556-G04 (left) and BIOUG22759-B02 (right).

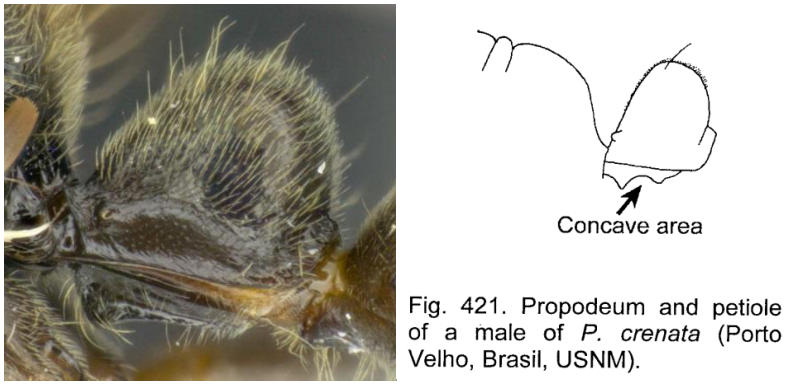


Fig 2.15 Left: Detail of the subpeciolar process of male MACN-Bar-Ins-ct 02564, asociated with BIN BOLD:ABV2684. Right: Drawing of the subpeciolar process of the male of *N. crenata,* extracted from Mackay and Mackay (2010).

2.3.6.2. Neoponera bactronica and *Neoponera curvinodis*

Three queens matched to the cluster of *N. bactronica* and *N. curvinodis* (Table 2.7). The queen for *N. bactronica* is not yet described, but the morphology of these three specimens corresponded to *N. curvinodis* (Fernandes *et al.* 2014*;* Fig 2.16). In the case of the males obtained from a "*N. bactronica"* colony, the individuals have the described morphology of *N. curvinodis* (Fernandes *et al.* 2014; Fig 2.17), for example the subpeciolar process is well developed as in *N. curvinodis* and contrary to *N. bactronica* (Fernandes et al. 2014).

Fig 2.16 Queen MACN-Bar-Ins-7529. (A) head in frontal view; (B) mesosoma in dorsal view; (C) lateral view; (D) petiolar node in lateral view.

Fig 2.17: Male of a colony identified as *N. bactronica* according to worker morphology. (A) Head in frontal view lateral view; (B) mesosoma in dorsal view; (C) lateral view; (D) petiolar node in lateral view.

2.3.6.3. Odontomachus chelifer

With *O. chelifer*, we were interested in comparing the male morphology between the 4.46% divergent BINs BOLD:AAV3356 and BOLD:ADG4860. Both males had a similar morphology, although the males asociated with BIN BOLD:ADG4860 (from Copo NP, Santiago del Estero), had a concave anterior face of the petiolar node, the subpetiolar process had a lump in its posterior side, the general color of the ant was dark brown, and the metasternal process consisted in a very low transverse ridge. In constrast, males asociated with BIN BOLD:AAV3356 (from Oberá, Misiones) had a straight anterior face of the petiolar node, no posterior lump on the subpetiolar process, the general color of the ant was light brown, and

the metasternal process consisted in a conspicuous, bilobed transverse ridge (Fig 2.18 and Fig 2.19).

Fig 2.18 *O. chelifer* male from colony of worker MACN-Bar-Ins-ct 07558 associated with the BIN BOLD:ADG4860. (A) head in frontal view; (B) mesosoma in dorsal view; (C) lateral view; (D) petiolar node in lateral view; (E) detail of the subpeciolar process; (F) metasternal process.

Fig 2.19 *O. chelifer* male BIOUG22490-E02 associated with the BIN BOLD:AAV3356. (A) head in frontal view; (B) mesosoma in dorsal view; (C) lateral view; (D) petiolar node in lateral view; (E) detail of the subpeciolar process; (F) metasternal process.

2.3.6.4. *Odontomachus* PEH01

Workers of *Odontomachus* PEH01 are similar to those of *O. brunneus* and *O. ruginodis,* but they can be differentiated from these species by a bilobed metasternal process, a uniform brown dark coloration, and a petiolar node without conspicuous transversal striation (Brown 1976, Macgown et al. 2014). This morphospecies was found in the Atlantic Forest (Oberá and Osununú PR, Misiones) and in the dry Chaco (Copo NP, Santiago del Estero). The specimens from these two ecoregions were assigned to two BINs with 1.12% divergence (BOLD:ACN0629 and BOLD:ADG7478) and were morphologically similar. Only some differences in the shape of the subpetiolar process were observed between these two populations (Fig 2.20 and 2.21).

Fig 2.20 *Odontomachus* PEH01 worker MACN-bar-ins-07538 asociated with BIN BOLD:ADG7478. (A) head in frontal view; (B) mesosoma in dorsal view; (C) lateral view; (D) petiolar node in lateral view.

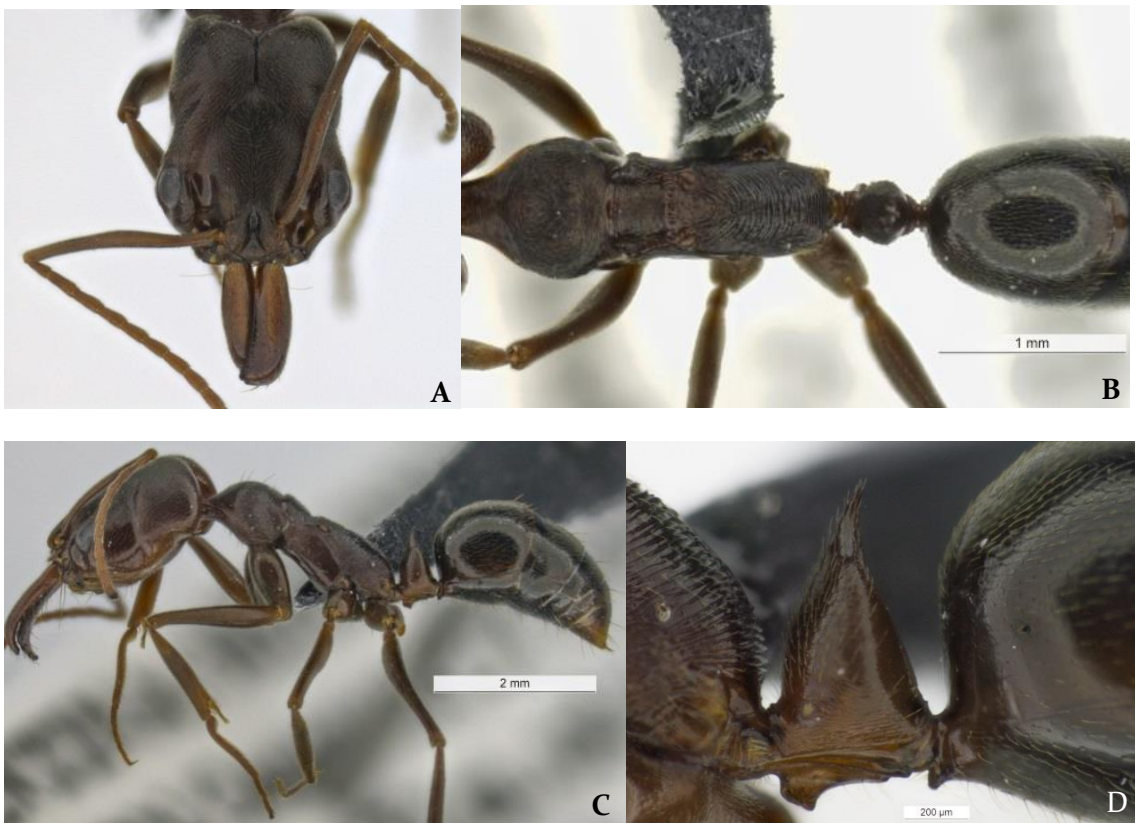


Fig 2.21 *Odontomachus* PEH01 worker MACN-bar-ins-06983 associated with BIN BOLD:ACN0629. (A) head in frontal view; (B) mesosoma in dorsal view; (C) lateral view; (D) petiolar node in lateral view.

We were interested in compare the males of *Odontomachus* PEH01 with those of *O. brunneus* and *O. ruginodis.* Males were obtained from two colonies kept in laboratory conditions from Copo NP and Osununú NR. Males from both colonies were very different from those of *O. brunneus* and *O. ruginodis* including different color (dark brown, lighter in antenna and legs), ocellar structure (the length of each ocellus was shorter than distance between lateral ocellus and the eye margin), and the mesoscutum, mesoscutellum and propodeum sculpture was rugoreticulate. As in *O. ruginodis*, an arcing carina was present in the posterior face of the propodeum (Fig 2.22 and Fig 2.23).

Fig 2.22 *Odontomachus* PEH01 male from Copo NP. (A) head in frontal view; (B) lateral view; (C) mesoscutum; (D) propodeum; (E) petiole in lateral view.

Fig 2.23 *Odontomachus* PEH01 male from Osununú NR. (A) Head in frontal view; (B) lateral view; (C) mesoscutum; (D) propodeum; (E) petiole in lateral view.

2.3.6.5. Pachycondyla striata

Finally, one male of *P. striata* from Misiones (specimen BIOUG13576-H11) and other two males from Jujuy and Entre Ríos showed very diferent subpetiolar process and shape of the petiolar node (Fig 2.24).

Fig 2.24 Petiolar node from (A) *P. striata* male of Obera (Misiones); (B) *P. striata* male of Calilegua NP (Jujuy) and (C) *P. striata* male of Ceibas (Entre Ríos).

2.4. Discussion

2.4.1. Building a comprehensive DNA-barcode reference library for the Ponerinae of Argentina

We assembled a DNA barcode reference library of 311 COI sequences for 42 ant species/morphospecies from the subfamily Ponerinae from Argentina. These include 10 new records for Argentina (but see below the discussion for *N. bactronica*), and represents 56% of the current known Ponerinae diversity. Only one ponerine genus was missing from our survey (*Centromyrmex*). Species we did not sample consisted primarily rare or hard to collect species (like the subterranean ant *Centromyrmes gigas*) or species whose habitats were sampled with less effort (i.e. *Anochetus miserabilis*, a species from the east part of the dry Chaco ecoregion). Rare species we did sample included the second known specimen of *Pachycondyla constricticeps* (MacKay & Mackay 2010), only known to occur in the southeast part of the Atlantic Forest in Argentina (however, this specimen was not successfully sequenced) and *Thaumatomyrmex mutilatus*.

We identified 11 morphospecies that could not be identified with confidence to a current scientific name. Some of these are likely undescribed species (i.e. *Odontomachus* PEH01, *Neoponera* PEH01 and *Hypoponera* PEH06), while others may be described but remain undetermined due to a lack of comprehensive taxonomic keys or revision (*Hypoponera).* Additionally, 11 queens and males did not have a close match (genetic distances between 6.9% and 13.1%) with either our dataset or the BOLD library. It is probable that some of the species whose workers are missing from our dataset, are represented by some of these unidentified males and queens. For example, the male BIOUG25250-B01 is possibly *Leptogenys bohlsi,* a species whose worker we collected, but was not succesfully sequenced. As in many other species, the male is not yet described so we cannot confirm this assumption based on morphological similarity.

2.4.2. Estimating species diversity through Molecular Operational Taxonomic Units

We estimated the number of MOTUs by applying the RESL algorithm to both our dataset and all the DNA-barcode library. Although there were some differences between MOTUs and BINs in trap jaw ants (MOTUs were assigned to two or more BINs in some *Anochetus* and *Odontomachus* species; suplementary Table S2.1), the percentage of matches, split and merges among the 42 species were the same. Specifically, there was a correspondence of 60% (25) of the morphologically defined species with one MOTU/BIN, meanwhile 35% (15) of the morphologically defined species were split into 2 or more MOTU/BIN. Finally two morphologically defined species (5%) were merged into a single MOTU/BIN. If we discard the singletons (8 species represented by one sequence), these percentages change to 50% of matches, 44% of splits and 6% of merges.

Analyzing 8 data sets of different taxonomic groups, Ratnasingham and Hebert (2013) suggest that there is usually good correspondance between BINs and species. In constrast, species split into several BINs can represent cases of unrecognized diversity or cases were the intraspecific divergence is unusually high due to a biological cause (e.g presence of pseudogenes; Song *et al.*, 2008; Smith *et al.*, 2012; Ratnasingham & Hebert, 2013). Similarly, different BINs merged into a single species may represent cases of unrecognized synonymy, difficult to identify species, or biological causes like mitocondrial introgression (Ratnasingham & Hebert 2013). Evidence from other areas (morphology, ecology, behaviour) should aid to determine for each case which explanation is most likely. Additionally, the RESL algorithm is one of several algorithms used to delimit MOTUs. Other common methodologies includes ABGD, GMYC and TCS (Templeton et al. 1992, Pons et al. 2006, Puillandre et al. 2012). In chapter III we will study the influence and behavior of different MOTUs delimitation approaches to the estimation of ant species.

2.4.3. Species studied with linear morphology

For *N. bactronica* and *N. curvinodis*, morphological evidence of workers (Fig 2.8), queens (Fig 2.16) and males (Fig 2.17) suggest that these specimens belong to one species, *N. curvinodis*. Although, number of *N. curvinodis* workers analyzed for PCA analysis was low (n = 2). Additionally, the specimen from BIN BOLD:AAW5111 overlapping the morphospace of *N. villosa* (BOLD:AAZ7290; Fig 2.8) had an unusual morphology; with oblique instead of strait striation in the clypeus, casting doubts on its identification.

In contrast, *N. crenata* specimens that resulted in two different BINs overlapped substantially in morphological space (Fig 2.9). However, two queens identified as *N. crenata* showed a different clypeus morphology (Fig 2.14), and a male associated to one of the BINs lacked a subpeciolar process characteristic of the species (Fig 2.15). Although analysis of more material is needed to resolve taxonomic boundaries, our results corroborate uncertainty about species identity in this group throughout its distribution (Wild 2002). Mackay and Mackay (2010) judge this group as the most difficult complex of the genus, adding that species are separated “on the basis of subtle differences in the workers that are usually supported by more substantial differences in the males”. Similarly, *P. striata* also had specimens with different BINs that overlapped in morphological space (Fig 2.11), and three males from Misiones, Jujuy and Entre Ríos Provinces showed morphological variation in the petiolar node and in the subpetiolar process (Fig 2.24). Together these results suggest that in addition to genetic data, examination of male and queen characters will be integral to identifying species boundaries in taxonomically difficult genera or cryptic species complexes (Boudinot 2013), particularly in *Neoponera* genus.

2.4.4. Morphological differences of males and queens for newly associated species

The DNA barcode library we generated associated more than half of the unknown males and queens to a species name (Table 2.7). We were able to confirm morphologically this association only in the case of *Dinoponera*, due to available taxonomic keys for males. Even with two Malaise trap sampling throughout the year, we collected relative few alates, precluding the comparison across BINs for different castes for most species. Kusnezov (1962) was the only person who studied the flying patterns of the ants in Argentina. Based on his collections in the Yungas forest from 1947 to 1959, he observed that Ponerinae alates fly mainly in the hottest months, especially during December and January. We observed a similar pattern from our samples (Fig 2.13).

Odontomachus is mainly a tropical genus, with little tolerancy to dry conditions. Few *Odontomachus* species (i.e. *Odontomachus clarus*) are known to extend into seasonally dry or semiarid habitats (Brown 1976). Consequently, we were curious about the dry habitat population in Argentina of *O. chelifer*. We also were interested to compare males of *Odontomachus* PEH01 with other similar species (*O. brunneus* and *O. ruginodis).* In the case of *O.chelifer*, males show variation in characters used to distinguish species in Neartic males (Macgown et al. 2014), suggesting the presence of cryptic species. In the case of *Odontomachus* PEH01 the males support our hypothesis that this morphospecies may constitute a new species.

To conclude, the difficulty in obtaining males, and the initial assumption that this caste was taxonomically irrelevant, had prevented their description or inclusion in taxonomic keys. This view is changing and many recent studies include males (Yoshimura & Fisher 2007, Boudinot 2013, Lenhart et al. 2013, Fernandes et al. 2014, Macgown et al. 2014, Wachkoo & Akbar 2016). Our results suggest that DNA barcodes can facilitate the inclusion of the reproductive

individuals. However, it is uncertain which COI distance thresholds or identification criteria are more reliable for species-level classifications in ants. We will address this issue in the next chapter.

Capítulo II en castellano

Las especies crípticas, es decir dos o más especies morfológicamente similares pero incorrectamente bajo un mismo nombre científico, son comunes en el reino animal. Su presencia dificulta los estudios ecológicos y de conservación, pudiendo resultar en recomendaciones inadecuadas de manejo. La incidencia de especies crípticas es probablemente más común en los invertebrados, en particular en grupos como las hormigas, en donde los sentidos químicos y táctiles son más importantes que los visuales. La subfamilia Ponerinae contiene varios grupos de especies crípticas, y en otros su presencia es sospechada.

Una técnica usada para el descubrimiento, identificación o puesta a prueba de especies es el Código de barras genético. Este método se basa en el análisis de una secuencia estandarizada corta (en animales el gen mitocondrial COI). Su utilidad se basa en que la diversidad intraespecífica en este marcador es usualmente mucho más baja que la interespecífica, aún para especies cercanas. Adicionalmente, los códigos de barras genéticos pueden ser usados para delimitar Unidades Taxonómicas Operativas (UTOs) es decir agrupamientos de secuencias basados en su similitud. Los UTOs pueden usarse análogamente a las especies, siendo particularmente útiles en grupos taxonómicamente complejos.

En este capítulo, se generó una biblioteca de referencia de Códigos de barras genéticos para las ponerinas de la Argentina a través de la colecta de nuevo material. Primero investigamos la presencia de especies crípticas estimando el número de UTOs usando RESL como algoritmo. Porque forman parte del sistema numérico indexado del Código de barras genético, se refirió a estos UTOs como BINs (Barcode Index Number System). Adicionalmente, se examinó en más detalle cinco grupos de especies analizando caracteres morfométricos. Finalmente, se comparó los Código de barras genéticos de los alados con la biblioteca de referencia (obreras identificadas) para asociar ambas castas.

Como resultado, a través de nuevas colectas y la revisación de material de colección, se encontraron 10 nuevos registros de especies para la Argentina. Adicionalmente, otras cuatro especies expandieron su distribución dentro del país. De los 530 especímenes procesados para el código de barras genético, se obtuvo secuencias (de más de 500 pb) para 311 obreras y 106 alados. La distancia molecular media intraespecífica fue de 1,6%, ocho veces más chica que la distancia media interespecífica (13,4%). En cambio la mínima distancia interespecífica en promedio fue de 11,78%, sólo 2,6 veces más grande que la máxima distancia intraespecífica promedio (4,48%). Cuatro especies tuvieron una distancia interespecíficas más baja que la distancia intraespecífica: *N. bactronica* y *N. curvinodis* (que compartieron la misma secuencia), *N. crenata* y *Hypoponera trigona*. Adicionalmente *Hypoponera* cf. *opacior* fue la especie con la distancia intraespecífica más alta (12,8%). Finalmente las 311 secuencias pertenecientes a 42 especies, fueron asociadas a 74 BINs.

En referencia al análisis de ordenamiento basado en caracteres morfométricos, fueron separados espacialmente tres y dos BINs de *H*. cf. *opacior* y *D. australis* respectivamente. Por otro lado, el par de especies *N. bactronica* y *N. curvinodis* compartieron el mismo espacio morfométrico. Similarmente, los BINs de *N. crenata* y *P. striata* se agruparon en grupos con un importante solapamiento entre ellos. Finalmente, en los alados asociados a su casta obrera, encontramos diferencias morfológicas consistentes con los resultados obtenidos por los Códigos de Barras Genéticos en el caso de reinas y/o machos de *N. crenata*, *O. chelifer* y *P. striata*. En el caso de *N. bactronica* y *N. curvinodis,* las reinas y machos asociados correspondendieron con *N. curvinodis*, indicando de que posiblemente se trate sólo de esta especie.

Para concluir, la dificultad en obtener alados y la suposición de que los machos son taxonómicamente irrelevantes, ha desalentado su descripción e inclusión en las claves taxonómicas. Esta visión actualmente está cambiando y muchos trabajos recientes incluyen la

descripción y comparación de machos. Nuestros resultados sugieren que la inclusión de los alados efectivamente podría ayudar a resolver muchos casos de especies crípticas, y particularmente, el uso de Códigos de barras genéticos en combinación con estudios morfológicos, puede facilitar la asociación de las distintas castas.

III. Using DNA Barcode to assess ant diversity: the case of the Iguazú NP in the southern extreme of the Atlantic Forest

Abstract

Understanding patterns of species diversity relies on accurate taxonomy which can only be achieved by long-term natural history research and the use of complementary information to identify species boundaries among cryptic taxa. We used DNA barcoding to characterize the ant diversity of Iguazú National Park (INP), a protected area of the Upper Paraná Atlantic Forest ecoregion, located at the southernmost extent of this forest. We assessed ant diversity at INP using both cytochrome c oxidase subunit 1 (COI) sequences and traditional morphological approaches, and compared the results of these two methods. We successfully obtained COI sequences for 312 specimens belonging to 124 species, providing a DNA barcode reference library for near 50% of the known ant fauna of INP. Our results support a clear barcode gap in all but two cases, with a mean intraspecific divergence of 0.72%, and an average congeneric distance of 17.25%. Congruently, the library assembled here was useful for the discrimination of the ants of INP and allowed as to link unidentified males and queens to their worker castes. To detect overlooked diversity, we classified the DNA barcodes into Molecular Operational Taxonomic Units (MOTUs) using three different clustering algorithms, and compared their number and composition to that of reference species identified based on morphology. The MOTU count was always higher than that of reference species regardless of the method, suggesting that the diversity of ants at INP could be between 6% and 10% higher than currently recognized. Lastly, our survey added 36 new records of ant species for the INP, being 23 of them new citations for Argentina.

The results of this chapter have been published in Ecology & Evolution (Hanisch et al. 2017).

3.1. Introduction

Comprehensive species inventories are prerequisites for conservation planning, and for understanding ecological processes such as the role of biodiversity in ecosystem stability and function (Mace 2004, Coleman & Whitman 2005, Bickford et al. 2007). Moreover, a misinterpretation of alpha diversity can have negative impacts on human welfare. For example, misidentification of disease vectors, species subject to human consumption, and agricultural pests can result in substantial harm to economies and human health (Besansky 1999). Nevertheless, the achievement of near complete species inventories requires methodologically diverse sampling and long-term research (Longino et al., 2002; Wild, 2007a). Traditionally, species identification and description rely solely on morphological characters, but with the advent of molecular tools, other approaches have become available. In particular, the use of sequence-based specimen identification, known as DNA barcoding (Hebert et al. 2003a), is increasingly proving to be a useful tool for species identification and diversity assessment (e.g. Delsinne et al., 2012; Ferreira et al., 2010; Hebert et al., 2004; Zenker et al., 2016). This technique is based on the amplification and analysis of a standardized short sequence of mitochondrial DNA near the 5' end of the cytochrome *c* oxidase subunit I (COI) gene (for the majority of the animal kingdom), and relies on the premise that intraspecific diversity is predictably lower than interspecific diversity at this locus, even between closely related (i.e. sister) species (Hebert et al., 2003a; Hebert et al., 2003b).

DNA barcoding can provide a rapid and efficient way to catalog diversity before it disappears as a consequence of human activities (Floyd et al., 2009). This is particularly true for diverse and understudied taxa in threatened habitats, such as insects in tropical forests (Myers et al. 2000). Moreover, when coupled with different clustering algorithms, DNA barcodes can be used to delimit Molecular Operational Taxonomic Units (MOTUs): clusters of sequences grouped together based on similarity (Floyd et al., 2002). These MOTUs can then be used to accelerate specimen identification, unveil cryptic diversity, test species delimitation hypothesis

(e.g. Ramalho et al., 2016a), or to perform fast census of animal diversity that could serve as the basis for subsequent taxonomic work (e.g. Smith et al., 2014).

Ants are an ecologically dominant group of insects in most terrestrial communities, especially in tropical ecosystems where they can exceed vertebrates in biomass (Hölldobler & Wilson 1990). They play a major role in ecosystem functioning as predators, scavengers, mutualists, and ecosystem engineers (Folgarait 1998). As with many arthropod taxa, ants are often difficult to identify to species, with highly diverse and ecologically important ant genera still lacking comprehensive identification tools (e.g. *Solenopsis*, *Pheidole*, *Camponotus*, *Hypoponera*). Moreover, ant morphology varies both among and within castes; species can have polymorphic workers or specialized reproductive forms (as in some *Hypoponera*, *Platythyrea;* Hölldobler & Wilson 1990, Peeters & Ito 2001). The most common ant sampling methods often collect only workers (e.g. pitfall traps) or flying reproductives (e.g. Malaise or light traps) rather than whole colonies where different castes can be associated. Coupled with the limitation that most taxonomic keys to species level are based solely on worker castes, associating queens and males to workers in inventories can be problematic. This undermines the scope of diversity studies and ecological work in general, for example, by impeding the study of the phenology of ant reproduction (e.g. Kaspari *et al.* 2001; Feitosa *et al.* 2016).

DNA barcodes have been used to aid in studies of ant diversity, and to delimit species boundaries in taxonomically difficult groups (e.g. Ferreira et al., 2010; Schlick-Steiner et al., 2006; Smith & Fisher, 2009; Smith et al., 2014). In addition, DNA barcode reference libraries for ants, allow other objectives such as caste associations (e.g. Smith *et al.* 2015). In this study, we generated a DNA barcode reference library for the ants of the Iguazú National Park (INP), a protected area located at the southern extreme of the Atlantic Forest, a biodiversity hotspot in eastern South America (Myers et al. 2000). This reference library included 312 specimens from 182 species, around 50 % of the known ant diversity of the INP (Hanisch et al. 2015). We tested

the efficacy of this DNA library by performing specimen identification simulations, and used the library to identify individuals for which keys were unavailable (mostly males and queens). We also estimated the number of MOTUs using different species delineation algorithms to uncover hidden diversity not detected by morphology. Finally, we compared MOTU counts and their composition across methods and assessed the correspondence between reference species and MOTUs boundaries.

3.2. Materials and Methods

3.2.1. Study site

Iguazú National Park is a 67,000 ha protected area situated in northwestern Misiones, Argentina (S25.68015°, W54.454192°). The climate is humid subtropical with no defined dry season, and mean monthly temperatures ranging from 15°C (June-August) to 26°C (December-February). Annual rainfall ranges between 1,800 and 2,000 mm and humidity is between 70% and 90%.

3.2.2. Ant surveys

We collected ants during different collection events in 1998, 1999, 2003, 2005, 2008, 2009 and 2011 at 21 sites in INP, via light and pitfall traps, litter samples, subterranean and surface baits and hand-collecting (Hanisch et al. 2015). We made additional hand sampling collection during summer of 2015 and 2016 to target other micro habitats and additional areas of INP. Altogether, this study is based on specimens from over 118 litter samples, 78 pitfall traps, 228 surface baits, 57 underground baits, and 348 hand-collecting events. Collected ants were preserved in ethanol 96% and identified using the available literature (Kempf 1962, 1965, Brown 1976, Kugler & Brown 1982, MacKay 1996, Wild 2005, 2007b, Longino & Fernández 2007, Lattke et al. 2007, Jiménez et al. 2008, MacKay & Mackay 2010, Dash 2011, Ortíz Sepúlveda 2012, Boudinot et al. 2013, Lenhart et al. 2013, Fernandes et al. 2014, Ronque et al.

2015). If we were unable to key out specimens reliably to species, they were assigned to a morphospecies.

3.2.3. DNA extraction and amplification

Genomic DNA was obtained from a leg (or more than one in cases of very small specimens) following a glass fiber-based extraction protocol developed by Ivanova et al. (2006). A 658 bp fragment near the 5' end of the COI gene was amplified following standard protocols developed for DNA barcoding (Wilson 2012) and using two sets of primers: LepF1 and LepR1 (Hebert et al. 2004), and the primer cocktails C_LepFolF [LepF1+LCO1490 (Folmer et al. 1994)] and C_LepFolR [(LepR1+HCO2198 (Folmer et al. 1994)]. The cocktails were implemented to increase the amplification success for the oldest samples, for specimens that were not preserved under DNA-friendly conditions (e.g. stored at room temperature), and for cases of poor primer fit. DNA extraction and COI amplification were performed at the Museo Argentino de Ciencias Naturales "Bernardino Rivadavia" (MACN), in Buenos Aires, Argentina, while sequencing was performed bi-directionally at the Canadian Centre for DNA Barcoding (CCDB; University of Guelph, Canada) with the same primers used for amplification. Residual genomic DNA was deposited, together with a tissue sample, at the National Ultrafrozen Tissue Collection at the MACN.

Sequences were edited and aligned using CodonCodeAlligner 4.0.4 (CondonCode Corporation, Dedham, MA) and translated into amino acid sequence to verify the lack of stop codons within the reading frame. Sequences were also examined to assess the presence of indels in the alignment using MEGA 5.0 (Tamura et al. 2011). All sequences obtained in this study together with their corresponding trace files, collection data, taxonomic information, and images are available on BOLD in the public dataset "DS-AOI16ALL" (doi: dx.doi.org/10.5883/DS-AOI16ALL). Sequences are also deposited in GenBank (accession

numbers MF925738– MF926049). All relevant information for each specimen is summarized in the Supplementary Table S3.1.

3.2.4. Sequence analyses

Final dataset: Only sequences belonging to identified individuals, with at least 500 bp and with less than 1% ambiguous calls were included in the genetic analyses described in the next sections. Eight records with contamination were excluded, along with 30 good-quality sequences that were not possible to identify to species with confidence (i.e. minor workers, males, and queens) as required by our analysis. However, we did use these 30 sequences to test the utility of our barcode library for species name assignment.

Genetic distances: We compared intra- and interspecific genetic distances both as uncorrected divergence values (i.e. p-distance) and using the Kimura 2-parameter (K2P) distance model (Kimura 1980). As the results were almost identical between these two methods, and because K2P is the most common model implemented in DNA barcoding and allows a more direct comparison with previous studies, we only report those obtained using K2P. Missing data were handled using the pairwise deletion approach. The mean intraspecific divergence was obtained with the package SPIDER (Brown et al., 2012) in R 3.3.1 (R Core Team, 2016) for all species represented by two or more individuals. As a measure of interspecific distance, we estimated the mean distance among congeneric species for those genera represented by at least two species using the Distance Summary tool available on BOLD. To test for the existence of a barcode gap (i.e. a separation between intra- and interspecific genetic variation; Meier et al., 2008, Meyer & Paulay, 2005), we compared for each specimen the distance to its furthest conspecific and to its closest heterospecific.

Gene trees: We generated a Neighbor-Joining (NJ) tree in BOLD using the Taxon ID tree tool (K2P and pairwise deletion were used). Node support was computed with 1000 bootstrap pseudoreplicates performed in MEGA. Additionally, we estimated a maximum likelihood (ML)

gene tree using RAxML 8.1.22 (Stamatakis 2014). The analysis consisted of 100 independent ML tree searches and 1000 rapid bootstrap pseudoreplicates under the GTRGAMMA model of evolution. Support values were printed on the best tree found among the ML searches. It is worth mentioning that our objective here was not to infer the phylogenetic relationships between the species analyzed but to obtain support values for terminal nodes (i.e. species or morphospecies) and intraspecific genetic clusters that may represent new, cryptic species.

3.2.5. Specimen identification simulations

To assess the utility of our COI barcode library for species name assignment we simulated a sequence-based identification process (Barco et al. 2016). We ran each sequence in our dataset (treated as an unknown specimen for the purpose of the test) against our complete library of identified sequences in order to assign a species name to the "unknown" query. This species name was assigned based on three different criteria: Best Match (BM) and Best Close Match (BCM) as defined by Meier et al. (2006), and the BOLD Identification Criterion (BIC) as implemented in the BOLD ID engine (Ratnasingham & Hebert 2007). In the case of the first two criteria, simulations were carried out using the Species Identifier Tool of Taxon DNA 1.8 (Meier et al. 2006), while for the BIC approach we used SPIDER. Under the BM criterion, a species name is assigned to the query sequence according to the closest match (the one with the lowest genetic distance) available at the library regardless of the divergence. The BCM criterion works like the BM but it incorporates a threshold defined by the user in order to make the identification process more rigorous. Here, a species name is assigned only if the closest match to the query sequence has a sequence divergence below the specified distance threshold. Therefore, if a query sequence has two (or more) equally close matches of different species including at least one conspecific the result would be ambiguous, while if the closest match corresponds to a heterospecific sequence it would be considered an incorrect identification. If the closest match is found outside the threshold, the query remains as unidentified. Lastly, the BIC constitutes an even more strict approach since it looks at all the

sequences within the threshold. When all sequences below the threshold are conspecific to the query the identification is correct, while it is considered ambiguous when both homo- and heterospecific sequences are found within the threshold of the query. An incorrect identification happens when all matches below the threshold correspond to species different to that of the query, while the query remains unidentified when no match is found within the threshold.

For the BCM and the BIC criteria, we implemented four different thresholds: 1- the 95th percentile of all intraspecific distances, where the threshold corresponds to the genetic distance below which 95% of all intraspecific distances are found (Meier et al. 2006), 2- the BOLD ID engine threshold of 1% sequence divergence (Ratnasingham & Hebert 2007), 3- the divergence value that minimizes the false positive and false negative identification errors (i.e. the cumulative error) obtained with the "thresVal" function in SPIDER, and 4- the minimum value in a density plot of all genetic distances which is commonly interpreted as the transition between intra- and interspecific distances, obtained with the function "localMinima" in SPIDER. Singletons were not used as queries but they remained as potential matches for the rest of the sequences. Results were identical using K2P and uncorrected distances, so we report only the former.

In addition to the simulations described above, we queried the 30 sequences that belonged to unidentified males, queens, and minor workers against both our database (using Species Identifier Tool) and BOLD's entire library as of January 2017 (through BOLD's Identification engine) to get a species identification. We registered the closest match for each of both libraries and then compared the outcomes.

3.2.6. Assessment of cryptic diversity through MOTUs delineation

We used three different distance-based clustering methods to delimit MOTUs within our barcode database: Automatic Barcode Gap Discovery (ABGD, Puillandre *et al.* 2012), statistical

parsimony networks (Templeton et al. 1992) as implemented in TCS (Clement et al. 2000), and the Refined Single Linkage algorithm (RESL, Ratnasingham & Hebert 2013). Briefly, these methods partition the sequences into MOTUs based on different similarity cutoffs depending on the clustering algorithm. In the case of ABGD, it is a statistical recursive method that explores the distribution of pairwise distances among all sequences in the dataset looking for the gap between intra- and interspecific distances. To do so, distances are ranked and then a local slope function is computed given a window size to detect significant changes (i.e. increases) in the slope values that correspond to gaps in the initial distribution. Once the barcode gap is found, sequences are divided into groups (MOTUs) amongst which genetic distances are always larger than the gap distance that created the first local maximum slope. This is called the initial or primary partition. This process is then recursively applied to the groups found in the initial partition until no further splitting occurs. These new groups constitute the recursive partition. We used K2P and uncorrected distance matrices generated with MEGA as inputs and tested two relative gap width values (X = 1.0, 0.8). We registered the initial and recursive partitions for a range of prior intraspecific divergence (P) values between 0.001 (0.1%) and 0.1 (10%). Results were almost identical with the two distance metrics, but we observed a tendency to higher MOTU counts in the recursive partitions when X = 0.8. We, therefore, decided to take a more conservative approach and focus on the results obtained with K2P and X = 1.0.

TCS is commonly used to construct statistical parsimony haplotype networks. This method begins by estimating the maximum number of substitutions between two haplotypes as a result of single substitutions (i.e. avoiding homoplasy generated by multiple hits) under a certain probability of parsimony. Haplotypes are then connected to a network until the differences between them exceed the number of substitutions established by the parsimony limit. When the latter happens, the haplotypes end in different unconnected networks. The higher the cut-off value, the lower the number of substitutions allowed between haplotypes

and the greater the count of unconnected networks generated. MOTU counts were recorded for ten different cut-off values (90%-99%) available in the software, but we focused on the MOTUs generated with the 95% cut-off value since this connection limit produced good results for real data in previous analyses (Hart & Sunday 2007). Both for ABGD and TCS, all results can be found in Supplementary Tables S3.3 and S3.4.

Finally, RESL is the algorithm used to group COI barcode sequences uploaded to BOLD into genetic clusters (BINs) which constitute the Barcode Index Number system (Ratnasingham & Hebert 2013). This method first divides the sequence alignment into initial MOTUs based on single linkage clustering with a threshold of 2.2% of maximum intra-cluster divergence. These primary MOTUs are then refined using Markov Clustering and the Silhouette Criterion (Ratnasingham & Hebert 2013). BINs are generated using the information of the entire COI barcode library, so are not comparable with the MOTUs generated with ABGD and TCS. Therefore, we employed the RESL algorithm exclusively to our dataset using the Cluster Sequences analysis tool available on BOLD v4 (http://www.v4.boldsystems.org).

For the three methods described above, and to analyze the correspondence between reference species and MOTUs, each species was assigned to one of three categories: MATCH, SPLIT or MERGE (Ratnasingham & Hebert 2013). When all the specimens from a reference species were found to form a single MOTU, that species was placed in the MATCH category. When representatives of a species were divided into two or more MOTUs, it was assigned to the SPLIT category. Lastly, if members of two or more species were combined into a single MOTU, those species joined the MERGE category.

3.3. Results

3.3.1. Ant diversity

We processed 623 specimens representing 182 species from 50 genera (Table 3.1, Supplementary Table S3.1). Of these, 20% (37) represent new records for INP, and many of them constitute either a new record for Argentina (23) or a range expansion within the country (8) (Supplementary Table S3.1). Among others, new records for the country include the arboreal termite specialist *Cylindromyrmex brasiliensis,* as well as *Megalomyrmex brandaoi, Neoponera curvinodis, Neoponera bactronica (*But see chapter II*), Platythyrea pilosula, Procryptocerus adlerzi* and *Leptogenys iheringi,* the latter collected carrying an isopod in its mandibles. There may be additional new taxa as we also recognized many morphospecies in genera for which the alpha taxonomy is not yet resolved (e.g. *Solenopsi*s, *Hypoponera, Pheidole, Neoponera*). Ant diversity currently includes 257 recognized species or morphospecies from 61 genera. An up-to-date checklist for the ant species of the INP is available on BOLD (CL-INPA).

Table 3.1. The current number of species present at the INP and their representation in this study for ten ant subfamilies.

Subfamily	Species at INP	Specimens /Species processed	Specimen/Species with sequences	Specimens/Species in the final dataset
Amblyoponinae	2	0	0	0
Dolichoderinae	16	32/11	19/8	18/8
Dorylinae	12	36/9	26/8	25/8
Ectatomminae	9	24/7	16/5	13/5
Formicinae	29	116/26	72/21	48/19
Heteroponerinae	4	11/3	7/3	7/3
Myrmicinae	136	283/88	139/56	129/52
Ponerinae	34	103/24	73/24	67/24
Proceratiinae	2	3/1	0	0
Pseudomyrmecinae	13	15/10	5/5	5/5
Total	257	623/182	357/130	312/124

3.3.2. Dataset and genetic distances

The final dataset used for the analyses consisted of 312 sequences from 124 species and 42 genera (Table 3.1, Supplementary Table S3.2, dx.doi.org/10.5883/DS-AOI16PUB). On average, 2.5 sequences were analyzed per species (range 1–15), and the mean sequence length was 656bp with 95% of the dataset corresponding to full barcode sequences (658 bp). We found two 3-bp deletions in our alignment, one present in all individuals of *Dinoponera australis* starting at position 359, and the other in both *Apterostigma* morphospecies (PEH01 and PEH02) starting at position 473. Neither of these events altered the reading frame of the sequences. In fact, no stop codons were found, suggesting that no pseudogenes were amplified (Song *et al.* 2008). Similar cases have been reported for other hymenoptera (Quicke et al. 2012, Hansson et al. 2015). In particular, comparing our results with other available sequences, this deletion is absent in *Dinoponera gigantea,* meanwhile, it appears to be present in all species of *Apterostigma*, with the exception of *A. megacephala* (Sosa-Calvo et al. 2017).

Based on 541 comparisons from 65 species (31 genera) with two or more individuals (253 sequences), the mean intraspecific distance was 0.72% (range 0.00%–7.57%; Figs 3.1 and 3.2). In contrast, and based on 2,502 comparisons among 283 pairs of congeneric species (110 species from 28 genera with two or more species), the mean congeneric distance was 17.25% (range 8.59%–25.22%; Figs 3.1 and 3.2), nearly 24 times larger than the mean intraspecific divergence. The average distance to the nearest neighbor (i.e. minimum interspecific distance) was 15.75% (range 0.00%–25.82%), almost eight times larger than 2.07%, the mean distance to the furthest intraspecific sequence (range 0.00%–18.97%). The lowest distance between two congeners was observed between *Neoponera bactronica* and *N. curvinodis,* which constitute the only case of barcode-sharing (i.e. no sequence divergence) between species in our dataset. The second lowest interspecific distance (3.92%) was found between *Neoponera moesta* and *Neoponera fiebrigi*, while two specimens of *Ectatomma edentatum* showed the highest maximum intraspecific distance (18.97%). The distance to the furthest conspecific was always

lower than the distance to the closest heterospecific for all species with more than one sequence, clearly showing the presence of a barcode gap. The only exceptions were *E. edentatum* and *Neoponera crenata* which fell below (or almost on) the 1:1 relationship line (Fig 3.3). These species were the only ones found to be paraphyletic according to the NJ tree (and the ML tree in the case of *N. crenata;* Fig 3.1). However, the paraphyly of *E. edentatum* was not recovered in the ML gene tree or a Bayesian topology (not shown).

3.3.3. Specimen identification simulations

The application of the BM criterion resulted in nearly 100% correct identifications with only one (0.40%) incorrect assignment (Table 3.2). The BCM criterion with a threshold of 5.75% (95th percentile of intraspecific distances) gave 97.23% of correct and 0.40% of incorrect identifications, and six queries (2.37%) remained unidentified (Table 3.2). The "threshVal" function suggested a threshold between 2.4% and 3.9% (Supplementary Fig S3.1), so we used the mean value (3.15%) for the analyses. With this threshold, the BCM approach delivered 97.23% of correct identifications, 2.77% (seven sequences) of unidentified queries, and no incorrect identifications (Table 3.2). The percentage of true identifications decreased slightly (96.05%, Table 3.2) when the threshold was set to lower divergences like the 1.26% suggested by the "localMinima" function in SPIDER (Supplementary Fig S3.2) and the BOLD's threshold (1%). In those cases, ten sequences (3.95%) did not have a match below the threshold (Table 3.2). The results with the BIC were identical to those obtained with the BCM criterion for the "threshVal", "localMinima" and BOLD's thresholds (Table 3.2). In the case of the 5.75% threshold, the BIC produced 94.86 % of correct identifications, 2.77% ambiguous assignations, and six queries (2.37%) could not be identified (Table 3.2). Finally, it is worth mentioning that since singletons were excluded as queries, we did not include *N. bactronica* and *N. curvinodis*, the species pair that share their barcode sequence. If we had run these sequences against our database, we would have another two incorrect identifications under the BM and BCM criteria and two additional ambiguous assignments based on the BIC approach.

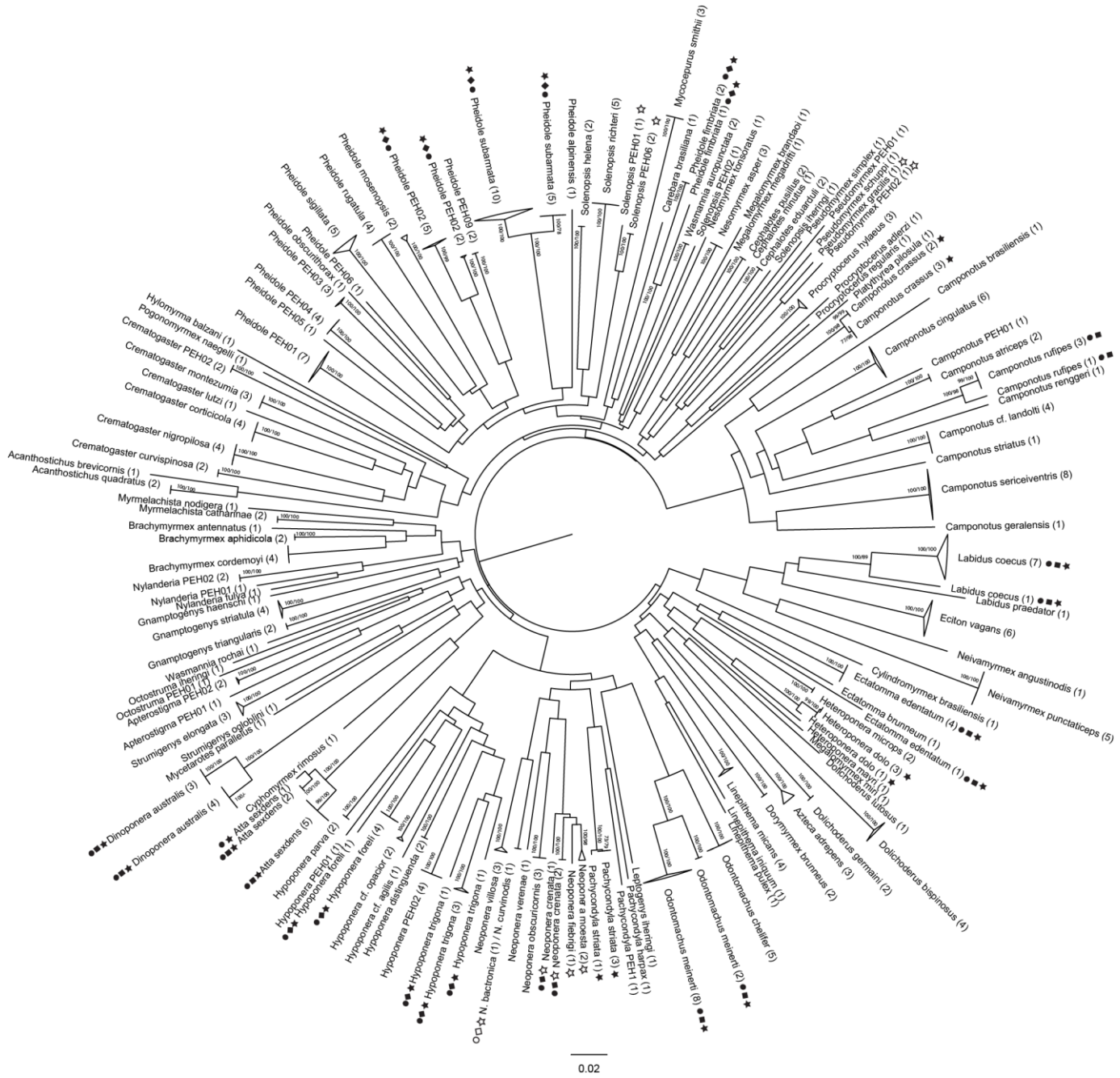


Fig 3.1 Neighbor-Joining (NJ) tree of 312 COI sequences of Iguazú National Park ants computed with a K2P substitution model. Symbols next to the terminals indicate when a species was split (filled) or merged (blank) by RESL (circles), TCS (squares) or ABGD (stars). Numbers above the node correspond to NJ/ML (maximum likelihood) bootstrap support values based on 1000 pseudoreplicates.

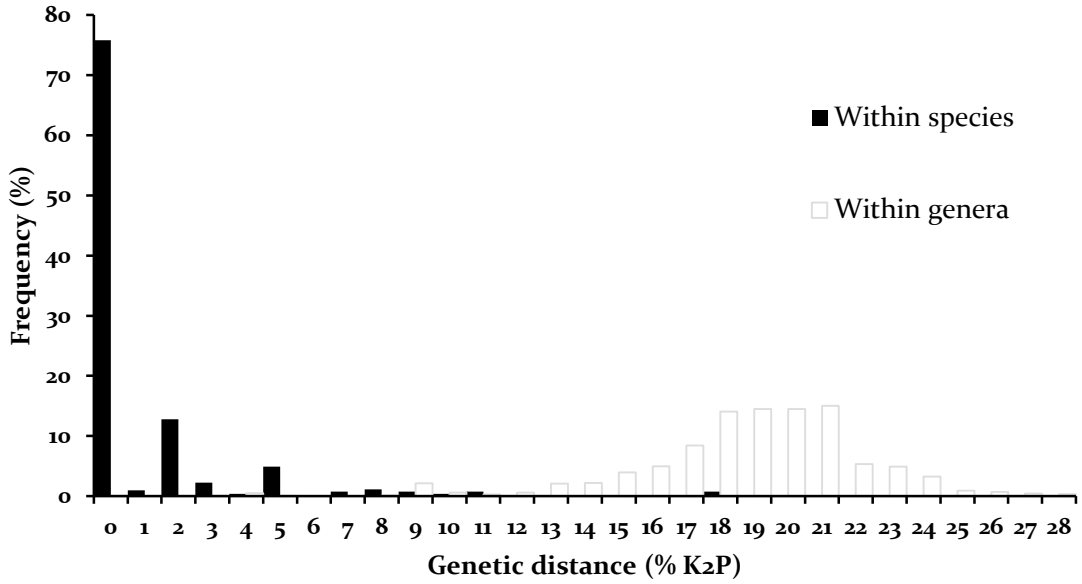


Fig 3.2 Frequency distribution of genetic distances within species and among congeneric species.

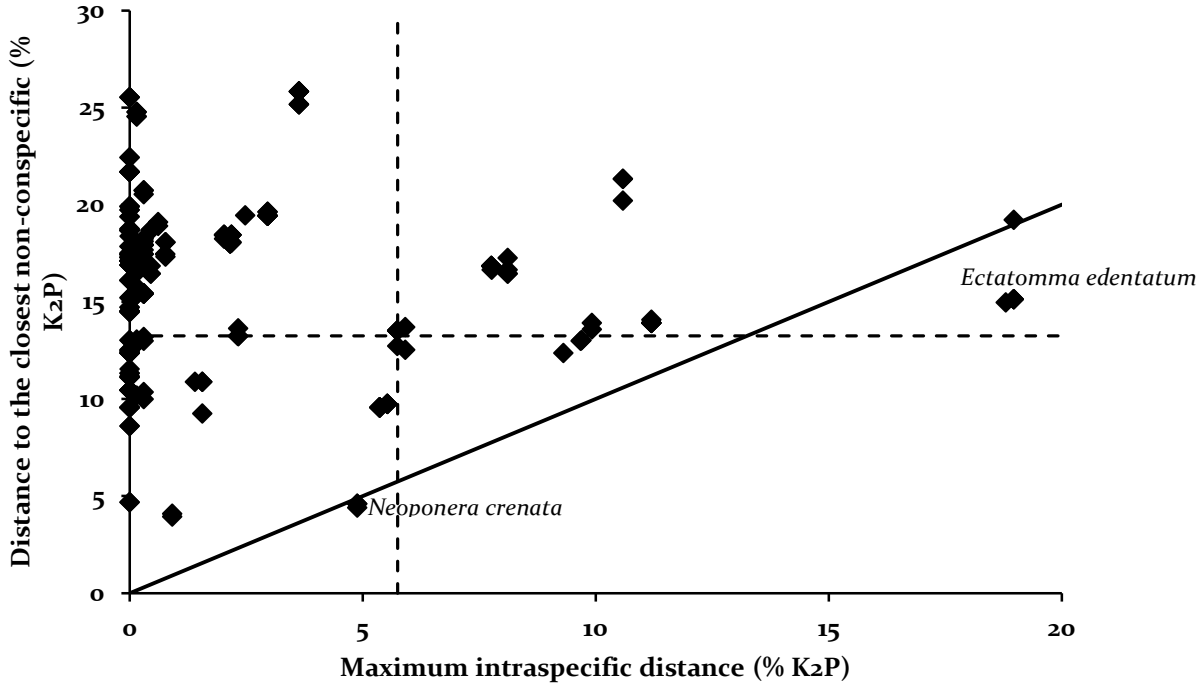


Fig 3.3 Barcode gap analysis for 65 species of ants with two or more individuals. Each individual is represented by a point, and the distance to the furthest heterospecific is plotted against the minimum distance to the nearest neighbor. The vertical dashed line shows the 95th percentile of all intraspecific distances (5.75%), while the horizontal one corresponds to the lower 5% of congeneric distances (13.25%).

When we queried the 30 sequences of males, minor workers, and queens that could not be identified to species based on morphology against both our database and the entire barcode library available on BOLD (as of January 2017), a species name was assigned to 22 (73%) of them based on BOLD's 1% threshold (Table 3.3). In each case, the closest match was a sequence that was part of this study's dataset. Three other cases showed a close match that also belonged to our database at divergence values between 2% and 3.8% (Table 3.3), casting doubt on whether the closest match was from the same species or not. For the remaining 5 sequences, the closest match was delivered by sequences from other projects available on BOLD, although genetic distances were between 6.1% and 14.15% (Table 3.3), suggesting that the species to which the unknown queries belong were not present in BOLD yet. In summary, 86% of the unknown sequences (25 out of 30) had a close match provided by the records available in our project to barcode the ants of INP and 73% of those (22) resulted in species identification.

Table 3.2 Results of the sequence-based identification simulations. Identifications were classified according to three criteria: Best Match (BM), Best Close Match (BCM) and BOLD Identification Criterion (BIC). For BCM and BIC approaches we used four threshold values (5.75%, 3.15%, 1.26% and 1.00%) obtained from different sources (see text). For the 253 queries that were run we inform both the total number of identifications (within each category) and the percentage they represent (values in parenthesis).

		95% percentile of intraspecific distances		"threshVal"		"localMinima"		BOLD's threshold	
Identification/ Criterion	BM	BCM (5.75 %)	BIC (5.75 %)	BCM (3.15%)	BIC (3.15%)	BCM (1.26%)	BIC (1.26%)	BCM (1.00%)	BIC (1.00%)
Correct	252 (99.60%)	246 (97.23%)	240 (94.86)	246 (97.23%)	246 (97.23%)	243 (96.05%)	243 (96.05%)	243 (96.05%)	243 (96.05%)
Incorrect	1 (0.40%)	1 (0.40%)	–	–	–	–	–	–	–
Ambiguous	-	-	7 (2.77%)	–	–	–	–	–	–
No ID	-	6 (2.37%)	6 (2.37%)	7 (2.77%)	7 (2.77%)	10 (3.95%)	10 (3.95%)	10 (3.95%)	10 (3.95%)

Table 3.3 Results of the sequence-based specimen identification of 30 unidentified males, minor workers and queens using the barcode database reported here and the entire barcode library available on BOLD. The table shows for each query the closest match, their sequence similarity and the database in which that record was found. Matches with 99% or higher similarity constitute solid species identifications according to the BOLD Identification Criterion.

Query			Closest match			
Process ID	Sample ID	Preliminary ID	Species ID	Process ID	Similarity (%)	Database
INSAR137-11	MACN-Bar-Ins-ct 00613	*Camponotus*	*Camponotus PEH01*	ANTPI403-15	100.00	This study
INSAR716-11	MACN-Bar-Ins-ct 02539	*Camponotus*	*Camponotus PEH01*	ANTPI403-15	100.00	This study
INSAR729-11	MACN-Bar-Ins-ct 02555	*Ectatomma*	*Ectatomma edentatum*	ANTPI017-10	100.00	This study
INSAR746-11	MACN-Bar-Ins-ct 02573	*Ectatomma*	*Ectatomma edentatum*	ANTPI017-10	100.00	This study
ANTPI185-12	MACN-Bar-Ins-ct 02968	*Camponotus*	*Camponotus rufipes*	ANTI106-15	100.00	This study
ANTPI505-15	MACN-bar-ins-ct 06904	*Hypoponera*	*Hypoponera cf. opacior*	ANTPI249-13	100.00	This study

ANTPI549-15	MACN-bar-ins-ct 06948	*Pheidole*	*Pheidole subarmata*	ANTPI009-10	100.00	This study
INSAR493-11	MACN-Bar-Ins-ct 617	*Camponotus*	*Camponotus cingulatus*	ANTPI197-13	100.00	This study
INSAR497-11	MACN-Bar-Ins-ct 621	*Camponotus*	*Camponotus cf. landolti*	ANTPI037-10	100.00	This study
INSAR498-11	MACN-Bar-Ins-ct 622	*Camponotus*	*Camponotus cf. landolti*	ANTPI037-10	100.00	This study
INSAR499-11	MACN-Bar-Ins-ct 623	*Camponotus*	*Camponotus cf. landolti*	ANTPI037-10	100.00	This study
INSAR500-11	MACN-Bar-Ins-ct 624	*Camponotus*	*Camponotus cf. landolti*	ANTPI037-10	100.00	This study
INSAR501-11	MACN-Bar-Ins-ct 625	*Camponotus*	*Camponotus cingulatus*	ANTPI197-13	100.00	This study
INSAR508-11	MACN-Bar-Ins-ct 632	*Camponotus*	*Camponotus cf. landolti*	ANTPI037-10	100.00	This study
INSAR510-11	MACN-Bar-Ins-ct 635	*Camponotus*	*Camponotus cf. landolti*	ANTPI037-10	100.00	This study
INSAR511-11	MACN-Bar-Ins-ct 636	*Camponotus*	*Camponotus cingulatus*	ANTPI197-13	100.00	This study
ANTPI479-15	MACN-bar-ins-ct 06878	*Hypoponera*	*Hypoponera trigona*	ANTI133-15	99.85	This study
INSAR492-11	MACN-Bar-Ins-ct 616	*Camponotus*	*Camponotus cingulatus*	ANTPI197-13	99.84	This study
INSAR494-11	MACN-Bar-Ins-ct 618	*Camponotus*	*Camponotus cingulatus*	ANTPI197-13	99.84	This study
INSAR507-11	MACN-Bar-Ins-ct 631	*Camponotus*	*Camponotus cingulatus*	ANTPI197-13	99.69	This study
INSAR495-11	MACN-Bar-Ins-ct 619	*Camponotus*	*Camponotus cingulatus*	ANTI166-15	99.53	This study
INSAR738-11	MACN-Bar-Ins-ct 02564	*Neoponera*	*Neoponera crenata*	ANTPI410-15	99.08	This study
INSAR509-11	MACN-Bar-Ins-ct 634	*Camponotus*	*Camponotus PEH01*	ANTPI403-15	97.98	This study
INSAR745-11	MACN-Bar-Ins-ct 02572	*Neoponera*	*Neoponera crenata*	ANTI101-15	96.64	This study
ANTI173-15	MACN-bar-ins-ct 06470	*Neivamyrmex*	*Neivamyrmex angustinodis*	ANTPI409-15	96.18	This study
INSAR751-11	MACN-Bar-Ins-ct 02580	*Dorymyrmex*	*Dorymyrmex sp. CIP01*	NA	93.88	BOLD
INSAR491-11	MACN-Bar-Ins-ct 614	*Camponotus*	*Camponotus EC07*	DRYLO063-15	90.28	BOLD
INSAR512-11	MACN-Bar-Ins-ct 637	*Camponotus*	*Camponotus EC07*	DRYLO063-15	90.28	BOLD
INSAR752-11	MACN-Bar-Ins-ct 02581	Formicinae	*Brachymyrmex cordemoyi*	NA	88.12	BOLD
ANTPI558-15	MACN-bar-ins-ct 06957	Ectatomminae	*Gnamptogenys annulata*	NA	85.85	BOLD

3.3.4. MOTUs delineation analyses

The MOTU counts obtained with the three clustering methods and the setting parameters ranged from 125 to 137 (Table S3.2, Fig 3.4). Therefore, all methods delivered MOTU counts higher than the number of reference species (124; Table S3.2, Fig 3.4).

The RESL algorithm found 137 MOTUs, a 10% increase on the number of reference species in our dataset (Fig 3.4). In terms of MOTU composition, 89% were MATCHES and 10% were SPLITS, while two species (1.61%) were merged into a single MOTU (Supplementary Table S3.2, Fig 3.5). The latter corresponds to *N. bactronica* and *N. curvinodis*, the barcode-sharing species pair that was always merged into one MOTU regardless of the method (Table 3.4). Additionally, twelve species (10%) were divided into two or more genetic clusters by RESL (Table 3.4, Fig 3.1): *Atta sexdens* and *Hypoponera trigona* were the only two species split into three MOTUs, while the remaining 10 species were divided into two (Table 3.4). All of these species showed elevated intraspecific divergences with mean distances always above 1% and average maximum intraspecific distances over 2% (Table 3.4). Six of these species (Table 3.4) showed distances to the furthest conspecific that were higher (or equal) than the 95th percentile of intraspecific distances (5.75%).

The 136 MOTUs delineated by TCS with the 95% cut-off value represents an increase of 10% in the number of reference species (Fig 3.4, Supplementary Table S3.3). The percentages of MATCHES, MERGES and SPLITS were identical to those of RESL (Supplementary Table S3.2, Fig 3.5) and the same twelve species were also split into two genetic clusters, being the only difference was that *Atta sexdens* was split into two MOTUs with TCS, instead of three (Table 3.4, Fig 3.1).

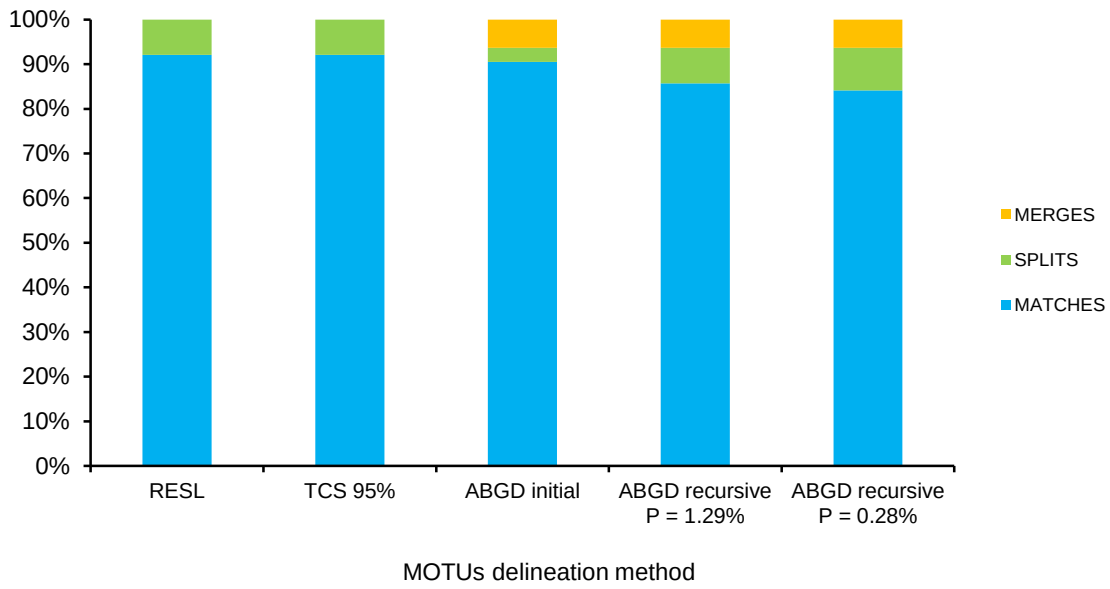


Fig 3.4 Percentages of MATCHES, SPLITS AND MERGES for the different clustering methods discussed in the text based on the correspondence between species and MOTUs boundaries.

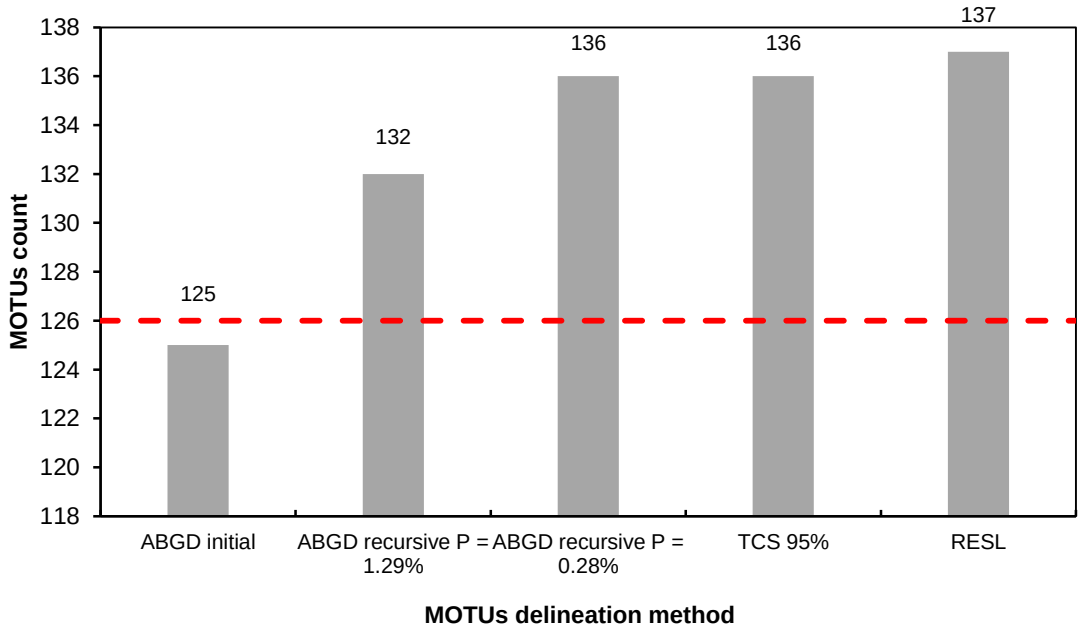


Fig 3.5 MOTU count for each clustering delimitation methods discussed in detailed. Dashed line represents the number of identified species (124).

Table 3.4 Results of the sequence-based specimen identification of 30 unidentified males, minor workers and queens using the barcode database reported here and the entire barcode library available on BOLD. The table shows for each query the closest match, their sequence similarity and the database in which that record was found. Matches with 99% or higher similarity constitute solid species identifications according to the BOLD Identification Criterion.

pecies (22)	N	Mean distance (% K2P)	Max distance (% K2P)	Min distance to NN (% K2P)	RESL (137)	TCS 95% (136)	ABGD initial partition (125)	ABGD recursive P = 1.29% (132)	ABGD recursive P = 0.28% (135)
Atta sexdens	8	1.60	2.97	19.42	SPLIT (3)	SPLIT (2)	MATCH	SPLIT (3)	SPLIT (3)
Camponotus crassus	5	0.46	0.78	17.31	MATCH	MATCH	MATCH	MATCH	SPLIT (2)
Camponotus rufipes	4	1.17	2.33	13.22	SPLIT (2)	SPLIT (2)	MATCH	MATCH	MATCH
Dinoponera australis	7	2.08	3.64	25.16	SPLIT (2)	SPLIT (2)	MATCH	SPLIT (2)	SPLIT (2)
Ectatomma edentatum	5	7.57	18.97	14.95	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)
Heteroponera dolo	4	0.81	1.57	9.23	MATCH	MATCH	MATCH	SPLIT (2)	SPLIT (2)
Hypoponera foreli	5	4.48	11.20	13.90	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)
Hypoponera trigona	5	6.41	9.92	12.35	SPLIT (3)	SPLIT (3)	SPLIT (3)	SPLIT (3)	SPLIT (3)
Labidus coecus	8	2.32	8.12	16.44	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (4)
Neoponera bactronica	1	NA	NA	0.00	MERGE	MERGE	MERGE	MERGE	MERGE
Neoponera crenata	3	3.26	4.88	4.39	SPLIT (2)	SPLIT (2)	MERGE	MERGE	MERGE
Neoponera curvinodis	1	NA	NA	0.00	MERGE	MERGE	MERGE	MERGE	MERGE
Neoponera fiebrigi	1	NA	NA	3.92	MATCH	MATCH	MERGE	MERGE	MERGE
Neoponera moesta	2	0.92	0.92	3.92	MATCH	MATCH	MERGE	MERGE	MERGE
Odontomachus meinerti	10	1.96	5.53	9.55	SPLIT (2)	SPLIT (2)	MATCH	SPLIT (2)	SPLIT (2)
Pheidole fimbriata	3	7.06	10.59	20.19	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)
Pheidole PEH02	7	2.75	5.91	12.52	SPLIT (2)	SPLIT (2)	MATCH	SPLIT (2)	SPLIT (2)
Pheidole subarmata	15	1.09	2.19	17.99	SPLIT (2)	SPLIT (2)	MATCH	SPLIT (2)	SPLIT (2)

Pseudomyrmex gracilis	1	NA	NA	5.84	MATCH	MATCH	MERGE	MERGE	MERGE
Pseudomyrmex PEH02	1	NA	NA	5.84	MATCH	MATCH	MERGE	MERGE	MERGE
Solenopsis PEH01	1	NA	NA	4.67	MATCH	MATCH	MERGE	MERGE	MERGE
Solenopsis PEH06	2	0.00	0.00	4.67	MATCH	MATCH	MERGE	MERGE	MERGE

ABGD produced a single initial partition that consisted of 125 MOTUs (Supplementary Table S3.4, Fig 3.4), the count closest to the number of reference species (124). When we inspected the MOTU composition of this initial partition we observed almost the same percentage (88.71%) of MATCHES as in RESL and TCS, but a higher proportion of MERGES (7.26%) and a lower incidence (4.03%) of SPLITS (Supplementary Table S3.2, Fig 3.5). Five of the twelve species divided by TCS and RESL were also split in ABGD's initial partition (Table 3.4, Fig 3.1). In terms of recursive partitions, extremely low P values (0.1%) produced MOTU counts strikingly higher than the number of reference species due to over-splitting, while extremely high values (10%) lumped all species into a single group (Supplementary Table S3.4). It is worth noting that ABGD was not only the algorithm with the highest incidence of MERGES, but also the only method to merge two or more reference species (other than the barcode sharing species of *Neoponera*) into a single cluster (Table 3.4).

Puillandre et al. (2012), found that a prior value around 1% showed the greatest correspondence between the number of MOTUs and that of reference species for different datasets. In our study, a prior value of 1.29% produced a recursive partitioning scheme that consisted of 132 MOTUs (a 6% increase compared to the number of reference species; Supplementary Table S3.4, Fig 3.4). This MOTU count was also the median number of clusters generated across all prior values (Supplementary Table S3.4), and this prior is very similar to the threshold used for specimen identification by BOLD (1%) and almost identical to that suggested by the "localMinima" function (1.26%), both of which resulted in a high percentage of correct identifications. However, these MOTUs showed a lower correspondence between their boundaries and those of the reference species with 84% of MATCHES, 9% SPLITS and 7% MERGES (Table 3.4, Fig 3.5). In addition, the prior values between 0.17% and 0.46% delivered 135 MOTUs, the closest count to those of the other methods (Table 3.4). These MOTUs represent an increase of 9% compared to the number of reference species (Fig 3.4) and included 83% of MATCHES, 10% of SPLITS and 7% of MERGES (Supplementary Table S3.2, Fig

3.5). These two recursive partitioning schemes split the same twelve species that TCS and RESL, with the exception of *Camponotus rufipes* and *N. crenata* (Table 3.4, Fig 3.1). Additionally, with P = 0.17% - 0.46% (Table 3.4, Fig 3.1), *Labidus coecus* and *Camponotus crassus* were divided into four and two groups respectively. Lastly, *Heteroponera dolo* was recovered as two distinct MOTUs in both recursive partitioning schemes (Table 3.4, Fig 3.1).

To conclude, it is worth mentioning that the MOTUs that were identified within species by the three methodologies employed (i.e. intraspecific splits) showed in most cases high bootstrap support, ranging from 73% to 100% and being over 95% in 80% of the cases (Fig 3.1).

3.4. Discussion

3.4.1. Dataset and genetic distances

We assembled a DNA barcode reference library consisting of 312 COI sequences for 124 species of ants from the southernmost region of the Atlantic Forest. This dataset covers nearly 50% of the ant species known for INP. Despite that over 600 specimens were collected, only 50% of them made it to the final dataset. Our low amplification success may be associated with old samples (up to 10 years, Supplementary Table S3.1) and sample storage conditions that were not DNA-friendly (e.g. ants collected with pitfall traps and litter samples). If these problematic samples are not considered, the amplification success increases to 74%.

Mean interspecific divergence was markedly higher than that registered within species in the ants of INP. More importantly, all species but two (*E. edentatum* and *N. crenata*) had higher distances to their closest heterospecific than to the furthest conspecific, providing evidence of a clear barcode gap for almost all the species represented by at least two sequences. A comparable study of the Ants of Coco Island (but with fewer specimens) showed intra and inter specific mean divergence values similar to those reported here (0.58% and 27% respectively; Smith *et al.* 2013b). It should be noted, however, that our values for intraspecific variation may be underestimated due to the relatively low number of sequences per species.

For instance, the mean intraspecific divergence among species represented by at least five individuals was 1.74%, being markedly higher than that among species with two to four specimens (0.33%). Congruently, we found a positive relationship (p <0.05) between sampling size and mean intraspecific divergence, although the association was weak (Pearson correlation: $R^2 = 0.07$, r = 0.26). However, many of the species that evidenced high intraspecific distances may represent cryptic species (Table 3.4 and see discussion below), so they might not be true representatives of intraspecific variation. Future studies should focus on assessing the real extent of cryptic diversity to achieve a better comprehension of species boundaries before obtaining a new estimate of intraspecific variation for the ants of INP.

3.4.2. Specimen identification

We simulated a sequenced-based identification process to test the utility of our DNA barcode library with three different identification criteria. Most (from 94% to 99%) of the ant species surveyed in this study (represented by at least two sequences) can be identified regardless of the criteria or threshold used (Table 3.3). Singletons were also distinguishable as they all possessed unique (i.e. not shared) DNA barcodes that allowed their discrimination from the closest heterospecific in the gene trees, with the exception of *N. bactronica* and *N. curvinodis* which constitute the only case of barcode-sharing between species in our dataset. In fact, these two species were recorded for the first time in Argentina and are members of a species complex that is difficult to identify (Lucas et al. 2002, Fernandes et al. 2014). This case was discussed with more detail in chapter II.

For species assignments, we explored the use of four different sequence divergence thresholds (5.75%, 3.15%, 1.26% and 1%). Nonetheless, hardly a single distance threshold can be universally applied. For example, a range of 0 - 14% of divergence in COI has been found for the ant species *Crematogaster kelleri* (Blaimer et al. 2013) in Madagascar. The identification success decreased only slightly when using lower thresholds (1% - 1.26%) compared to higher thresholds (3.15 - 5.75%). This reflects the fact that higher

thresholds can aid in the identification of species with high intraspecific variation. However, as stated before, species with deep intraspecifc divergence could represent two or more cryptic taxa. Taking this into consideration, the lower thresholds (1 - 1.26%) could be suitable for ant species discrimination, the identification of intraspecific lineages and the generation of cryptic species hypotheses, an important step in the process of the discovery and description of diversity (Seifert 2009).

Our study was focused on a particular area of the Atlantic Forest, but it would be worth evaluating if a lower threshold compromises the identification success of the ants of Argentina (or Southern South America) as the geographic coverage increases. For example, a study of 1000 species of European Lepidoptera found that large geographic distances had a small impact on genetic intraspecific variation and therefore, on the performance of DNA Barcodes (Huemer et al. 2014). The advantage of using higher vs. lower thresholds will depend on various factors, including the level of intraspecific variation (that in turn depends on the organisms studied and possibly the extent of geographic coverage) and the presence of cryptic species in the group analyzed. This is why we consider that using a range of thresholds and comparing their results as we did here is the best option to assess diversity and also further understand the characteristics of the organisms under study.

We were unable to identify, based on external morphology alone, 30 specimens (mostly males and queens) captured in light traps. Since these specimens were successfully sequenced, we used them to assess whether the database assembled here and the complete DNA barcode library available on BOLD, could assign a species name to them. Twenty-five queries (86%) had a close match that was part of our barcode library, and 73% of them resulted in species identification (less than 1% of divergence between the query and the match). None of the identified males have been formally described, illustrating the difficulty in identifying species based on males alone. This also highlights the great usefulness of DNA barcode libraries in general as an identification tool and in particular for linking reproductive

castes with workers, facilitating their subsequent description, and inclusion in taxonomic keys (e.g. Yoshimura & Fisher, 2007). The fact that all the species name assignments came from our own database reflects the current underrepresentation of ants of the Atlantic Forest in BOLD and emphasize the need for increasing the geographical coverage of the global library in order to fully benefit from the use of DNA barcodes.

3.4.3. MOTU delineation

In terms of composition, all methodologies delivered a high percentage of matches, close to 90% (Fig 3.5). ABGD's initial partition resulted in the MOTU count closest to the number of reference species. This is not surprising since primary partitions are typically stable on a wider range of prior values and are normally close to the number of taxonomic species (Puillandre et al. 2012). At the same time, ABGD was the only algorithm to lump into the same MOTU species that form clearly distinct clades in the NJ and ML trees (Table 3.4, Fig 3.1 and 3.5). This method merged *Neoponera moesta* and *N. fiebrigi* with *N. crenata*, and P*seudomyrmex gracilis* with *Pseudomyrmex PEH02*, and the two morphospecies *Solenopsis PEH01* and *Solenopsis PEH06* (Table 3.4, Fig 3.1). This may be a consequence of the small number of samples for these species; Puillandre et al. (2012) suggested that ABGD works better when there are more than 3 – 5 sequences per species. In our dataset, almost 50% of the sequences correspond to singletons (59) and, 5 of 8 species involved in cases of MERGE are represented by only one sequence (Table 3.4, Fig 3.1). As for TCS and RESL, it is not clear if a high presence of singletons might affect the performance of the clustering algorithms, although, Ratnasingham and Hebert (2013) showed that the performance of RESL does not vary greatly across datasets with varying sampling densities. All three methods split 10 species into two or more MOTUs (Table 3.4, Fig 3.1), while *Camponotus rufipes* was split by RESL and TCS but not ABGD, and *Heteroponera dolo* and *Camponotus crassus* were split into two MOTUs only by ABGD.

3.4.4. Cases of high intraspecific variation and ant diversity

Among species with high intraspecific variation in our dataset, six species had distances higher than the 95th percentile of intraspecific distances (5.75%): *E. edentatum, Hypoponera foreli, P. fimbriata, H. trigona, L. coecus* and *Pheidole* PEH02 with a maximum intraspecific divergence of 18.97%, 11.20%, 10.59%, 9.92%, 8.12% and 5.91% respectively. *Ectatomma edentatum* was split into two MOTUs with one cluster being composed of four individuals with an identical barcode sequence and the other one consisting of only one specimen (MACN-Bar-Ins-ct06433). Additionally, this species was paraphyletic in the NJ tree (Fig 3.1). These two MOTUs can be distinguished morphologically by the interruption of the striate sculpture around the spiracle of the third abdominal segment and the petiolar node shape (Supplementary Fig S3.3); the type material of *E. edentatum* appears to correspond with the morphotype of MACN-Bar-Ins-ct06433 (ANTWEB https://www.antweb.org/), with a taller petiole depressed from the sides (lateral view). This pattern persists even when additional DNA barcoded specimens are included from other localities in Misiones province (Hanisch, unpublished), suggesting that these MOTUs indeed represent different species that are not currently recognized with available taxonomic keys. Additional evidence that *E. edentatum* consist of a complex of species was found by Nettel-Hernanz et al (2015). We also found that *H. foreli, P. fimbriata, L. coecus*, *H. trigona* and *Pheidole* PEH02 were also split into two or more MOTUs but we were unable to find any external morphological traits that support these intraspecific genetic clusters.

Among species with moderate intraspecific variation, three ponerine species stand-out: *Odontomachus meinerti, N. crenata* and *D. australis*, with a maximum intraspecific divergence of 5.53%, 4.48% and 3.64% respectively. Additionally, *N. crenata* was one of the two cases where the barcode gap was absent (Fig 3.3). These values may reflect the variation in reproductive and dispersal strategies (Peeters & Ito 2001). For example, *Dinoponera* lacks a winged queen caste, which is usually associated with low dispersion and subsequently more

marked genetic structure. Moreover, an unknown male identified using our library as *N. crenata* (MACN-Bar-Ins-ct 02564) lacked the characteristic subpetiolar process of the species (Chapter II; Mackay & Mackay 2010), suggesting that both the unknown male and the matching *N. crenata* could actually be other species that currently keys out as *N. crenata*.

The incidence of cryptic species might be high in ants (Seifert 2009), and evidence of cryptic species has been reported recently for genera included in this study. For example, Aguilar-Velasco et al. (2016) using morphology and both nuclear and mitochondrial loci found that *Ectatomma ruidum* is a complex of at least three different species. Similarly, Barth et al. (2015) used morphological and genetic characters to identify cryptic species in Mexican populations of *Labidus praedator*. In our study, deep intraspecific divergence is currently supported in most cases only by COI data. Therefore, alternative explanations need to be considered. For example, high sequence divergence among morphologically similar specimens could arise as a consequence of infection with the maternally transmitted endosymbiont *Wolbachia* (Smith et al. 2012), although its prevalence has been shown to be generally low (Smith et al. 2012). In a similar manner, the co-amplification of pseudogenes could lead to false conclusions (Song et al. 2008), especially in those cases where one of the intraspecific divergent lineages is represented by a single individual. We examined our sequences in search for characteristics that might indicate the presence of pseudogenes, including insertions or deletions that altered the reading frame, biased base compositions, excess of non-synonymous substitutions and the presence of stop codons. Even though our assessment showed no evidence of the co-amplification of pseudogenes, further studies should look into these possibilities in more detail as more specimens become available, given that sometimes pseudogenes can be cryptic and lack insertions, deletions or frame shift mutations (Kerr 2010).

In January 2017, our records (including the 30 unidentified specimens) were assigned to 144 BINs on BOLD, being 78 of them new to the database. This represents a significant addition to the DNA barcode reference library of the ants of South America. At the same time,

our sampling resulted in 37 additions to the species list of INP, with 23 of them representing first records for Argentina. The number of MOTUs estimated with three different clustering algorithms was always higher than the number of species identified based on morphology, suggesting the existence of cryptic diversity. If these cases do reflect new species, the diversity of ants at the INP could be between 6% and 10% higher than currently recognized. Moreover, because nearly half of our sequences are represented by singletons, the extent of cryptic diversity may be underestimated. In conclusion, our study supports the use of clustering algorithms to explore biodiversity and that DNA barcodes can be useful for ant species identification and caste association. We encourage further studies to integrate genetic evidence with morphological and ecological data in order to get a better understanding of ant diversity in southern South America in general and the Atlantic Forest in particular.

Capítulo III en castellano

Los inventarios de especies son fundamentales para un correcto manejo ambiental o el estudio de diversos procesos ecológicos y evolutivos. Sin embargo, realizarlos eficientemente requiere de un continuo muestreo y estudios a largo plazo, especialmente en organismos cuya taxonomía no es completamente conocida. Tradicionalmente, las especies fueron identificadas casi únicamente mediante la observación de caracteres morfológicos, sin embargo, con el advenimiento de las herramientas moleculares, otras técnicas se han desarrollado. Por ejemplo, el uso de identificaciones basadas en secuencias cortas estandarizadas (Código de barras genético).

En este estudio, se usó la morfología tradicional en combinación con el Código de barras genético para estudiar la diversidad de hormigas en el Parque Nacional Iguazú (PNI), un área protegida del Bosque Atlántico. Para ello se procesó 623 especímenes correspondientes a 182 especies, identificadas mediante las claves taxonómicas disponibles. La biblioteca de referencia generada fue puesta a prueba mediante simulaciones de identificación, usando tres criterios (BM, BCM y BIC) y cuatro umbrales de divergencia (5,75%, 3,15%, 1,26% y 1%). Adicionalmente buscamos usar esta biblioteca para asociar 30 especímenes no identificados (mayormente machos y reinas). Finalmente para poner a prueba la diversidad de especies probamos 3 algoritmos distintos de delineamiento de UTOs (Unidades Taxonómicas Operacionales): RESL, TCS y ABGD. En resumen, cada uno de estos tres métodos clasifica las secuencias en UTOs basándose en distintos puntos de corte de similitud según un algoritmo de agrupamiento determinado.

Como resultado obtuvimos 312 secuencias pertenecientes a 124 especies, casi un 50% de la diversidad de hormigas del PNI. La distancia más baja entre dos congéneres se observó en

Neoponera bactronica y *N. curvinodis*, que compartieron la misma secuencia de códigos de barras genéticos. La segunda distancia interespecífica más baja (3,92%) se encontró entre *Neoponera moesta* y *Neoponera fiebrigi*, mientras que dos especímenes de *Ectatomma edentatum* mostraron la distancia intraespecífica más alta (18,97%). Con excepción de *E. edentatum* y *Neoponera crenata,* todas las especies mostraron una distancia máxima intraespecífica menor que la mínima distancia interespecífica. La divergencia media intraespecífica fue de 0,72% y la divergencia media interespecífica 17,25%.

Según las simulaciones realizadas, independientemente del criterio de identificación o del umbral de divergencia usado, más del 94% de las secuencias incógnita fueron identificadas correctamente. Adicionalmente, el 73% de los especímenes no identificados pudieron ser asociados a una especie bajo un umbral de divergencia del 1%. Finalmente, en los 3 métodos, el número de UTOs fue siempre mayor que el número de especies identificadas. Sin embargo el número exacto varió según el método y los ajustes usados. En conclusión, la diversidad del PNI podría ser entre un 6% y un 10% más alta. Aunque si se tiene en cuenta que en el set de datos usado, la mitad de las especies fueron representadas por una sola secuencia, la diversidad podría llegar a ser mayor. Finalmente, en este estudio, encontramos 36 nuevos registros para el PNI, siendo 23 de ellos nuevos registros de especies para la Argentina.

IV. Ponerinae trophic position and diurnal community dynamics

Abstract

Ponerinae is the third largest ant subfamily and the largest outside of the Formicoid clade. While not as dominant as many ants from the Formicoid clade, in Iguazú National Park (INP), the biomass of one ponerine, *Dinoponera australis*, is the highest ever recorded for a single ant species. We examined ant diurnal foraging activities and species interactions in the context of competition for resources in INP. We also estimated the trophic position of ants from the subfamily Ponerinae relative to plants and known predatory and herbivorous insects within these ecosystems using stable isotope analysis at two sites in Misiones Prov. Argentina. We employed surface baiting at three different time periods (morning, midday and afternoon) to examine how foraging activity and species interactions at baits varied with time of day and temperature. The majority of interactions between species at baits were neutral, but a few agonistic interactions were also observed when bait occupancy was highest. Species co-occurrence patterns suggest that this ant community is not heavily influenced by interspecific competition. Two Ponerinae species (*D. australis* and *P. striata*) stood out as the most abundant at baits. Stable isotope analysis revealed that most Ponerinae species occupied high trophic levels (primary and secondary predators), but some species overlapped with known insect herbivores. These low trophic level species were primarily arboreal *Neoponera,* and may rely heavily on nectar or other plant based resources in their diet. In contrast, field observations and isotope analysis suggest that the arboreal *Platythyrea pilosula* is a specialized predator, and has one of the highest δ15N values of any ant at Iguazú National Park. Our results provide insight into ant community structure and the ecology of ants in the subfamily Ponerinae of the Atlantic Forest.

4.1. Introduction

Ant diversity and activity varies spatially and temporally due to a variety of abiotic and biotic factors (Alonso 1998, Yanoviak & Kaspari 2000, Jacquemin et al. 2016). For example, the vertical structure of tropical forests provides extensive variation in temperature, moisture and nest sites, promoting the coexistence of many species. Ecological research often highlights diferent patterns of diversity between the ground and canopy (e.g. Yanoviak & Kaspari 2000, Weiser et al. 2010). However, there is also substantial variation in microhabitats near the surface where species may specialize by foraging or nesting on the ground, in the litter, or in top layers of soil (e.g. Ryder Wilkie et al. 2010, Jacquemin et al. 2016). Similarly, there can be high turnover of ant species on temporal scales (Andersen 1983, Alonso 1998).

Ants are an abundant and ecologically diverse group of insects in most terrestrial communities, particularly in tropical ecosystems where they may exceed the combined mass of all vertebrates (Hölldobler & Wilson 1990). Different methodologies are used to capture ants. Passive sampling methodologies can give information about occurrence and relative abundance and include pitfalls trap (for ground surface-active ants) or Winkler samples (for ants inhabiting leaf litter). In contrast, baiting can be used to study foraging activity and species interactions (Agosti & Alonso 2000). Studies that complement passive sampling (e.g. pitfall trap and litter samples) with baiting can provide insight into how foraging activity and dominance at resources relate to relative abundance across the landscape (Andersen 1992, Cerdá et al. 1997, LeBrun 2005, Adler et al. 2007).

Ants engage in a variety of ecological interactions, including mutualism, competition, parasitism and predation (Rico-Gray & Oliveira 2007, Lach et al. 2010), and play a major role in ecosystem functioning (Folgarait 1998, Del Toro et al. 2012). Interspecific competition is often evoked as a key process in structuring ant community (e.g. Hölldobler & Wilson, 1990; Cerdá *et al.*, 2013). Competition is mainly suggested by the observation of agonistic behavior among individuals or colonies of different or the same ant species. Under the framework of

competition, Wilson (1971) suggested that ant assemblages are structured into dominance hierarchies with regard to speed of resource discovery and fighting ability. However, dominance may not be a major factor in community structure if aggressive interspecific encounters are uncommon (Stuble et al. 2017).

In contrast to competitive interactions, which can be inconspicuous (Davidson 1985), predation is a direct and visible ecological interaction. Ants in the subfamily Ponerinae are typically predators, and include specialized hunters of a particular kind of prey (Brandão et al. 1991, Leal & Oliveira 1995). Nonetheless, several species are known to also collect nectar, seeds and fruits (Evans & Leston 1971, Christianini et al. 2007, Ávila Núñez et al. 2011). Furthermore, Bottcher and Oliveira (2014) found a positive correlation between larva weight and the consumption of lipid-rich seed arils in *Odontomachus chelifer*, suggesting that the ingestion of plant material could be important for nutrition in this species. In addition, many species of ponerines have cryptic habits (e.g. *Hypoponera*) and are difficult to observe, making generalizations about the foraging ecology of this group difficult.

The use of stable isotope analysis facilitates the study of diets in organism that are difficult to observe. It also provides a record of assimilated resources, providing more accurate information of the diet and trophic position of an organism, than possible through observations alone (Deniro & Epstein 1981, Post 2002). In this study, we examined the ant communities of Atlantic Forest in northern Argentina to (1) study temporal variation of ant activity; (2) assess species interactions at surface baits; (3) characterize the trophic position of ants in the subfamily Ponerinae.

4.2. Materials and Methods

4.2.1. Study site

We choose two protected areas of the Atlantic Forest in northwestern Misiones Province, Argentina: Iguazú National Park (INP) (S25.68015°, W54.454192°) and Osununú

Private Reserve (OPR) (S27.279167°, W55.578056°). At both sites, the climate is humid subtropical with no defined dry season. Mean monthly temperatures range from 15-17°C (June-August) to 26-33°C (December-February), annual rainfall between 1,600 and 2,000mm, and humidity between 70% and 90%.

4.2.2. Ant community dynamics

In 2011, at INP we placed a bait station on the surface every 20 m along 200 m transects (10 baits per transect). Bait stations consisted of a plastic box 8 cm in diameter and 5 cm deep with 4 equidistant slots of 2 x 5 cm at the sides. A box was used (instead of a bait card) to prevent the baits from getting stolen and from getting wet during light rains. We also drilled 20-25 2 mm holes on the roof of each box to prevent condensation. In each box, we placed three baits: tuna, honey and cracked corn flakes (Fig 4.1). Baits were distributed along each transect at three different times of day: 8:30, 12:00 and 16:00 hours. After placement, baits were inspected after 15 min, 30 min, and 45 min. At each visit, we recorded which species were present and collected voucher individuals for species identification. We avoided collecting the first individuals that appeared at the bait to allow worker recruitment or subsequent visits for species in case of solitary foragers. To prevent earlier baits from influencing recruitment to baits placed later in the day, we sampled the three different time points on three different days and determined the order of sampling randomly for each transect. We recorded the temperature at each inspection lapse (n = 54 observations [6 transects, 3 day times, 3 observations per bait]). Transects were located at least 50 m away from major trails.

Fig 4.1 Workers of *Camponotus sericeiventris* at surface bait.

Collected ants were placed in 96% ethanol and identified to species when possible using available bibliography (Kempf 1962, 1965, Brown 1976, Kugler & Brown 1982, MacKay 1996, Wild 2005, 2007b, Longino & Fernández 2007, Lattke et al. 2007, Jiménez et al. 2008, MacKay & Mackay 2010, Dash 2011, Ortíz Sepúlveda 2012, Boudinot et al. 2013, Lenhart et al. 2013, Fernandes et al. 2014, Ronque et al. 2015). All individuals collected were deposited in the Museo Nacional de Ciencias Naturales "Bernardino Rivadavia". Images, Cytochrome c oxidase subunit I (COI) sequences, DNA barcode BINs (Barcode Index Numbers) codes and deposit numbers of voucher individuals of this study, in addition to other ant species collected in INP, can be found at dx.doi.org/10.5883/DS-AOI16ALL (Chapter III).

4.2.3. Stable isotopes

Because many metabolic processes discriminate between lighter and heavier isotopes, consumers are enriched in heavy Nitrogen (i.e., they have a higher $^{15}N/^{14}N$ ($\delta^{15}N$)) relative to their prey (Deniro & Epstein 1981). In summer of 2015 (December, February and March) and 2016 (February), we collected Ponerinae species in INP and OPR. We also collected arthropods of known trophic position (e.g., herbivores, predators), plant material and prey items based on field observation and bibliography (Fourcassié & Oliveira 2002). In total, 261 samples were collected in INP and 161 in OPR. All samples were stored in 96 % alcohol and maintain in -20° C until processing (1-7 months after collection). To avoid bias due to undigested food (Tillberg et

al. 2006), for all Ponerinae, only heads, thoraces and legs were used. All samples were dried at 60°C and homogenized in a mortar (with the help of liquid nitrogen if needed). After drying, all samples were weighed to ~ 2.00 µg (invertebrates) or ~ 5.00 µg (plants) on an electronic microbalance (Mettler Toledo XP6, Columbus, OH, USA) and placed in tin capsules. Each sample was replicated twice if enough sample material was present. Analysis of nitrogen and carbon isotopic ratios was performed at the University of Illinois, Department of Plant Biology using an IsoPrime 100 continuous flow IRMS (Cheadle Hulme, UK) interfaced to an Elementar vario MICRO cube elemental analyzer (Hanau, Germany). Stable isotope abundance is expressed using the δ notation with $\delta^{15}N$ (‰= $(R_{sample} - R_{standard})/R_{standard}$ X 1000. R_{sample} and $R_{standard}$ represent the $^{15}N/^{14}N$ ratios of the sample and the international reference standard (air), respectively.

4.2.4. Data analysis

Diurnal community analysis: To examine if species co-occurred at baits more or less than expected by chance, we generated presence/absence matrices (with bait stations as columns and rows as ant species) for each bait observation for the three sampling times (morning, midday and afternoon). We tested for non-random patterns of species co-occurrence using EcoSim (Gotelli & Entsminger 2009) with 5000 randomizations of the original matrix to generate a frequency distribution of co-occurrence indexes. We then compared the observed index to this frequency distribution using the C-Score which measures the average number of “checkerboard units” (CU) between all possible pairs of species (Stone & Roberts 1990). Our null hypothesis is the presence of a given ant species does not influence the occurrence of another species, i.e. there is no evidence for deterministic processes influencing species distribution (Ribas & Schoereder 2002, Gotelli & Entsminger 2009). For the randomizations, we chose fixed rows (species) and equiprobable columns (bait stations) to keep the occurrence of ant species fixed but allowing them to occupy sites with equal probability. This assumption corresponds to a simple model of community assembly in which

species colonize sites independently of one another and has the lowest probability of a type error I (Gotelli & Entsminger 2009). We also retained the degenerate matrices (those that contain missing species or empty sites).

At the last time point for each baiting period, we quantified interactions that occurred between species pairs co-occupying surface baits. We considered an interaction neutral if species ignored/tolerated each other, and aggressive if species engaged in combat or other antagonistic behaviors (Stuble et al. 2017). We characterized species pairs as “neutral” if the ratio of baits with only neutral interactions relative to baits with aggressive interactions (among all co-occupied baits) was equal to or greater than 0.5, and as “aggressive” if the ratio of neutral to aggressive interactions at shared baits was less than 0.5. A bait was considered monopolized at 45 min if a species had multiple individuals present at a bait and also prevented other species from feeding on the resource.

We compared differences in temperature across the three surface baiting periods (8:30 hs, 12:00 hs, 16:00 hs) using a General Linear Model (GLM), with transect as a random factor and observation time as fixed factor. A single surface temperature value was obtained for each bait by averaging the temperature across the three 15 min observation intervals. Normality was graphically inspected by dispersion of residuals. Akaike Information Criterion (AIC) values were calculated to judge the quality of the models and the most parsimonious were chosen. The comparison among dependent variables was performed by least significant difference (LSD) test using Infostat (Di Rienzo et al. 2017).

Finally, to compare the diversity captured in relation to other three ant-sampling methodologies, we compare the ant species composition captured with our surface baits and with other methodologies applied in INP in previous years (Hanisch 2013): Pitfall traps (for ground surface-active ants), litter samples (for ants inhabiting leaf litter), and subterranean baiting (for under-ground foraging ants). Mainly, we were interested in comparing pitfall trap (passive sampling) with the surface baits to relate bait discovery with relative abundance

(Andersen 1992, Cerdá et al. 1997, LeBrun 2005, Adler et al. 2007). These sampling comprises different years during the same period (January 18th – March 04th), when weather conditions were similar (Supplementary Fig 4.1). As a consequence, we consider that any differences in captured species are due to the methodology and not stochastic seasonal variation. The comparison was done using a matrix containing the presence/absence of each species for all sampling methods. We used Non-metric Multi-Dimensional Scaling (NMDS) based on the Jaccard index to evaluate the similarity of ant species composition between the four collecting methods. We performed a non-parametric Analysis of Similarity (ANOSIM) (Clarke 1993) to test if species composition differed between the sampling methodologies. Analysis were performed with PC-ORD v.5 (McCune & Mefford 1999) and PAST v.3.04 (Hammer et al. 2001).

Ponerinae trophic position analysis: Replicated samples with a standard deviation above 0.5 or a coefficient of variance above 1.0 were excluded from the analysis. We defined trophic levels (TL) based on $\delta^{15}N$ data for primary producers (plants, TL = 1), primary consumers (orthopteran and hemipteran herbivores, TL = 2), and secondary consumers (spiders and army ants, TL = 3). We used these specific groups because we were able to determine their diet with confidence using taxonomic information. We then compared $\delta^{15}N$ measurements of ants to these values. We also assumed that trophic levels are separated by an average difference of 3.4 ‰ δ15N due to fractionation (Deniro & Epstein 1981, Cabana & Rasmussen 1994, Post 2002). As a baseline, we used the 25th percentile of the δ15N signature of the plants. After evaluating the homogeneity of variance and the normal distribution of the data, we performed one-way ANOVAs (Infostat ; Di Rienzo *et al.*, 2017) to compare δ15N values of trophic levels and of individual species between localities.

4.3. Results

4.3.1. Activity at surface baits

We captured a total of 41 ant species/morphospecies from 15 genera and 5 subfamilies with the baits. The subfamily Myrmicinae had the greatest number of species (22), followed by Formicinae (10), Dolichoderinae (5) Ponerinae (2) and Ectatomminae (2). We compared species occurrence at surface baits from this study to occurrence in pitfall traps, littler samples or subterranean baiting from previous research (Hanisch 2013). The different methodologies captured a different ant composition (ANOSIM: $R = 0.39$, $p < 0.001$). Pitfall traps and surface baits had a similar species composition (ANOSIM pairwise test: Pitfall traps-Surface baits: $R = 0.06$, $p = 0.07$; Litter samples-Surface baits: $R = 0.72$, $p < 0.001$; Subterranean baits–Surface baits: $R = 0.48$, $p < 0.001$; Fig 4.2), consistent with both methodologies targeting surface foraging ants.

Two of the four most common species at surface baits (across all three time periods) were from the subfamily Ponerinae: *D. australis* (occurring at 45-53% of baits) and *Pachycondyla striata* (40-48% of baits). The other two were from the subfamily Myrmecinae: *Pheidole subarmata* (13-18% of baits) and *Solenopsis PEH04* (10-26% of baits). These four species were also the most common species in pitfall traps (Fig 4.3). A few other species accounted for 10% or more bait discoveries in one or more day times, these include *Pheidole* PEH01 (10-16% of baits), *Linepithema micans* (08-18% of baits), *Crematogaster nigropilosa* (08-16% of baits) and *Camponotus sericeiventris* (05-11% of baits)(Fig 4.3).

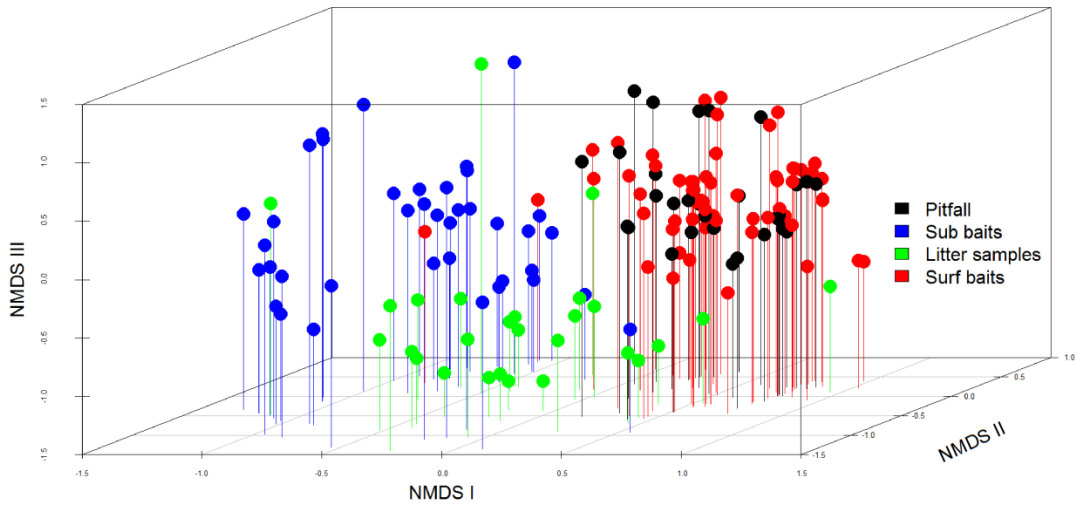


Fig 4.2 Ordination of ant community collected by surface baits (red), pitfall traps (black), litter samples (green), subterranean baits (blue). The ordination was performed by a non-metric multidimensional scaling (NMDS) analysis using the Jaccard similarity index (Stress = 0.20).

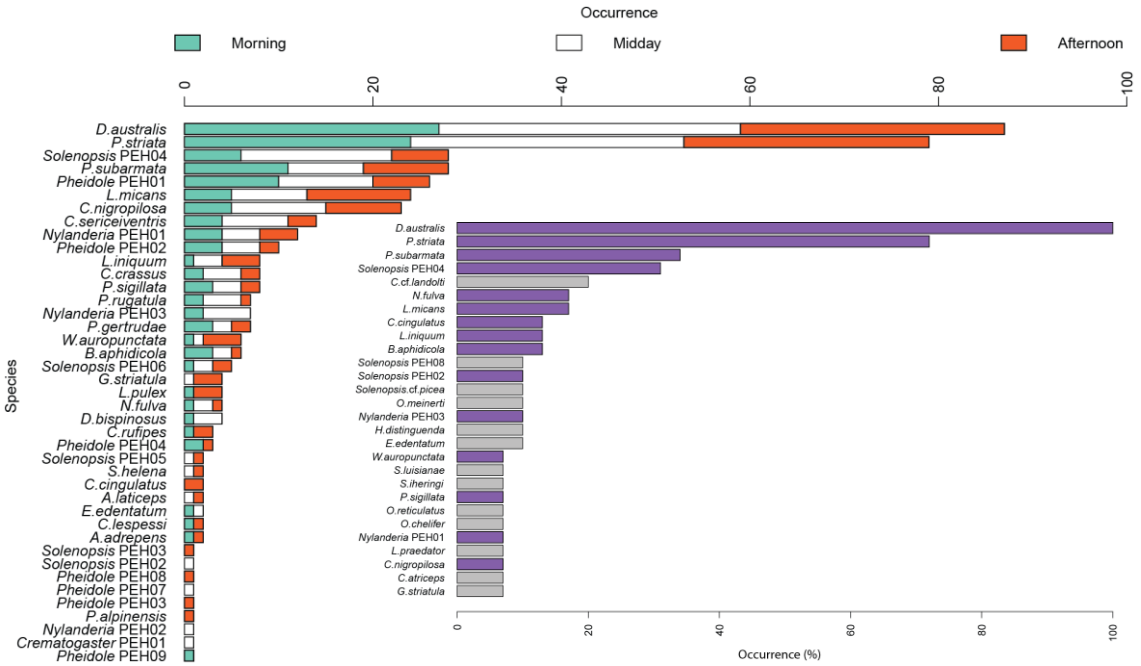


Fig 4.3 Species occurrence of ants at 60 baits placed during the morning (green), midday (white) and afternoon (orange) at the 45 min observation period. The inset figure shows the occurrence (%) for species collected in two or more pitfall traps. Species with purple in the inset were also detected at surface baits.

Ants were discovered between 43 – 61% of the baits during the first observation period (15 min after placement) across all three sample times of the day. By the last observation period (45 min after placement), between 91 – 96% of baits were discovered. There was a tendency for a higher number of species per bait during midday, but this difference was not significant (LMMs; $F = 2.49$, $P = 0.09$). The number of species co-occupying baits increased with observation period (from an average of 0.8 species per bait at 15 min to 1.7 species per bait at 45 min after placement) (LMMs; $F = 32.66$, $P < 0.001$).

Generally, species co-occurrence patterns suggested random co-occurrence of ant species at baits during all times of the day and monitoring events, as most of the observed C-scores did not differ from mean C-scores ($P > 0.05$). However, there were three exceptions. At the last monitoring event (45 min) of the morning and afternoon sample periods, observed co-occurrence indexes ($C\text{-score}_{obs}$) were higher than the mean calculated indexes ($C\text{-score}_{mean}$) (Morning: $C\text{-score}_{obs} = 9.63$, $C\text{-score}_{mean} = 9.08$, $P = 0.022$; Afternoon: $C\text{-score}_{obs} = 9.12$, $C\text{-score}_{mean} = 8.53$, $P = 0.006$). This pattern arose when bait occupancy (91 and 96% morning and afternoon respectively) and co-occurrence at baits (53% and 50% morning and afternoon respectively) were at their highest levels. This pattern was also observed during the second observation period (30 min) at midday, with 95% bait occupancy and 60% had species co-occurring ($C\text{-score}_{obs} = 14.85$, $C\text{-score}_{mean} = 13.98$, $P = 0.0068$).

Variation of temperature among survey periods (LMMs; $F = 88.00$, $P < 0.0001$) (mean ± SD °C, morning: 25.82 ± 1.01, midday: 29.83 ± 1.54, afternoon: 28.61 ± 1.33) and humidity (LMMs; $F = 6.86$, $P = 0.0133$) (mean ± SD %, morning: 92.83 ± 1.72, midday: 76.67 ± 4.31, afternoon: 86.83 ± 2.55) did not appear to influence patterns of co-occurrence as observed C-scores were never below C-scores means. The results for all the observation periods are summarized in table 4.1. Finally, according to the ordination analysis, the ant community composition did not differ across different times of day (NMDS, followed by ANOSIM; $R = -0.0006$, $P = 0.49$) (Supplementary Fig S4.1).

Table 4.1 Observed C-scores at each moment of day (Mo: morning, Mi: midday and Af: afternoon) of each consecutive time (15, 30 and 45 minutes) and C-scores means obtained by 5000 randomizations of the original matrix to generate a frequency distribution of co-occurrence indexes. Significant values of p (observed <= expected) means that abiotic factors may have influenced co-occurrence among species. Meanwhile, significant values of p (observed >= expected) may suggest the influence of biological process on species co-occurrence. Percentage of occupied baits and baits with two or more species for each period are shown in the last columns.

Time	C-scores obs	C-scores mean	p(observed <= expected)	p(observed >= expected)	Occupied baits (%)	Co-occurrence baits (%)
Mo - 15m	5.65	5.51	0.685	0.337	43	15
Mo - 30m	7.51	7.6	0.349	0.656	73	50
Mo - 45m	9.63	9.08	0.978	**0.022**	91	53
Mi - 15m	4.81	5.14	0.051	0.956	55	42
Mi - 30m	14.85	13.98	0.993	**0.007**	95	60
Mi - 45m	12.49	11.96	0.522	0.482	91	58
Af - 15m	6.9	7.27	0.4	0.606	61	41
Af - 30m	10.34	9.8	0.951	0.051	86	48
Af - 45m	9.12	8.53	0.994	**0.006**	96	50

4.3.2. Species interaction at surface baits

A total of thirty-nine species were detected at baits with another species present, and at the last sample period (45 min), between 50 – 58% of the discovered baits were visited by two or more ant species (range: 2 to 6 species). Most species were characterized as neutral – ants exhibited more neutral interactions at co-occupied baits than aggressive interactions (or no aggression at all) (Fig 4.4). In contrast, a few species were often observed interacting antagonistically with others. These species typically had high recruitment rates (*C. sericeiventris*, *Pheidole gertrudae*, *Crematogaster nigropilosa*) and most frequently interacted aggressively with two ponerines (*P. striata* and *D. australis*). The former species visited most of the baits but at low numbers. Most of the aggressive interactions were between *C. sericeiventris-D. australis* and *D. australis-P. striata* (4 observations for each species pair) followed by *P. gertrudae-D. australis*, *L. micans-D. australis* and *P. striata-C. nigropilosa* (3 observations for each species pair) (Fig 4.5). Some interactions left injured individuals. For

example, on one occasion *D. australis* killed a *C. sericeiventris* worker. Only 10% of baits were considered monopolized after 45 mins, and these were occupied by *C. sericeiventris* (5 baits), *L. micans*, *C. nigropilosa* and *P. gertrudae* (4 baits), P. *striata* (1 bait) and *Dolichoderus bispinosus* Olivier (1 bait).

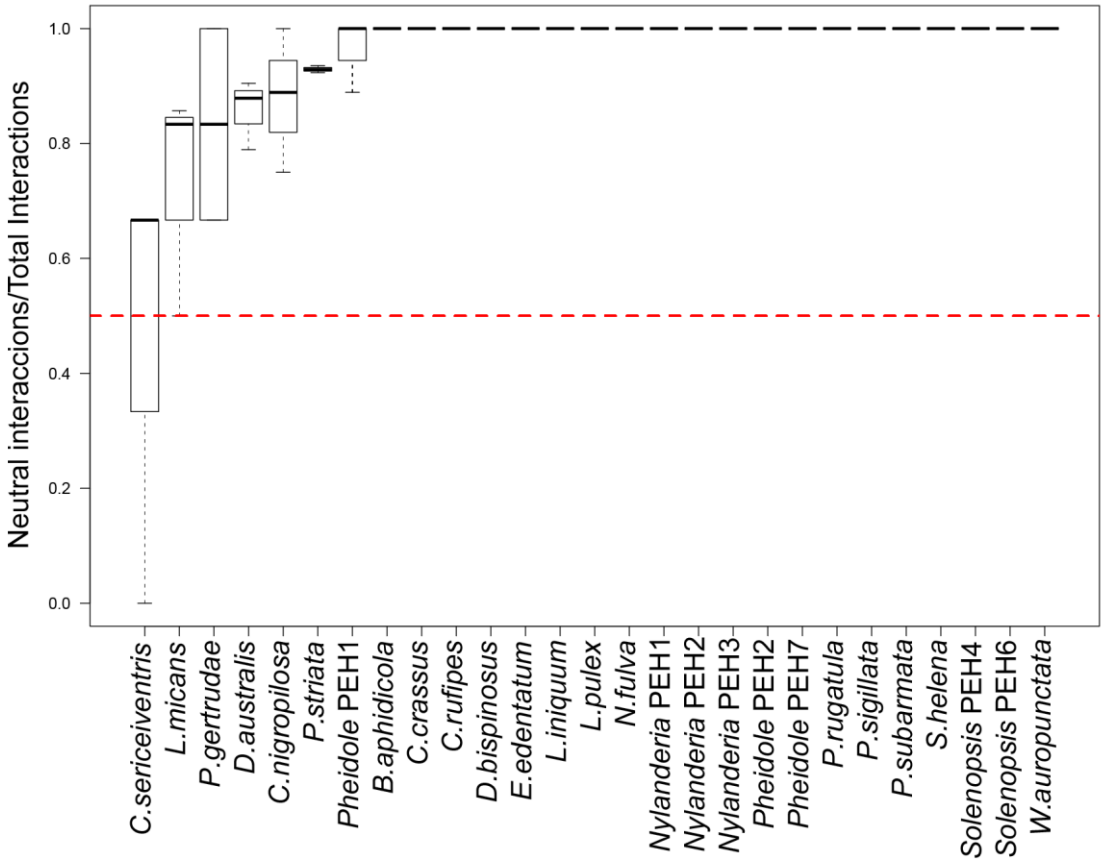


***Fig* 4.4** Proportion of neutral interactions for species present at the 45 min bait observation period (across all three sample times). The Y axis is the proportion of neutral interactions defined as the number of neutral interactions / number of shared baits. Species above dashed line were involved mainly in neutral interactions.

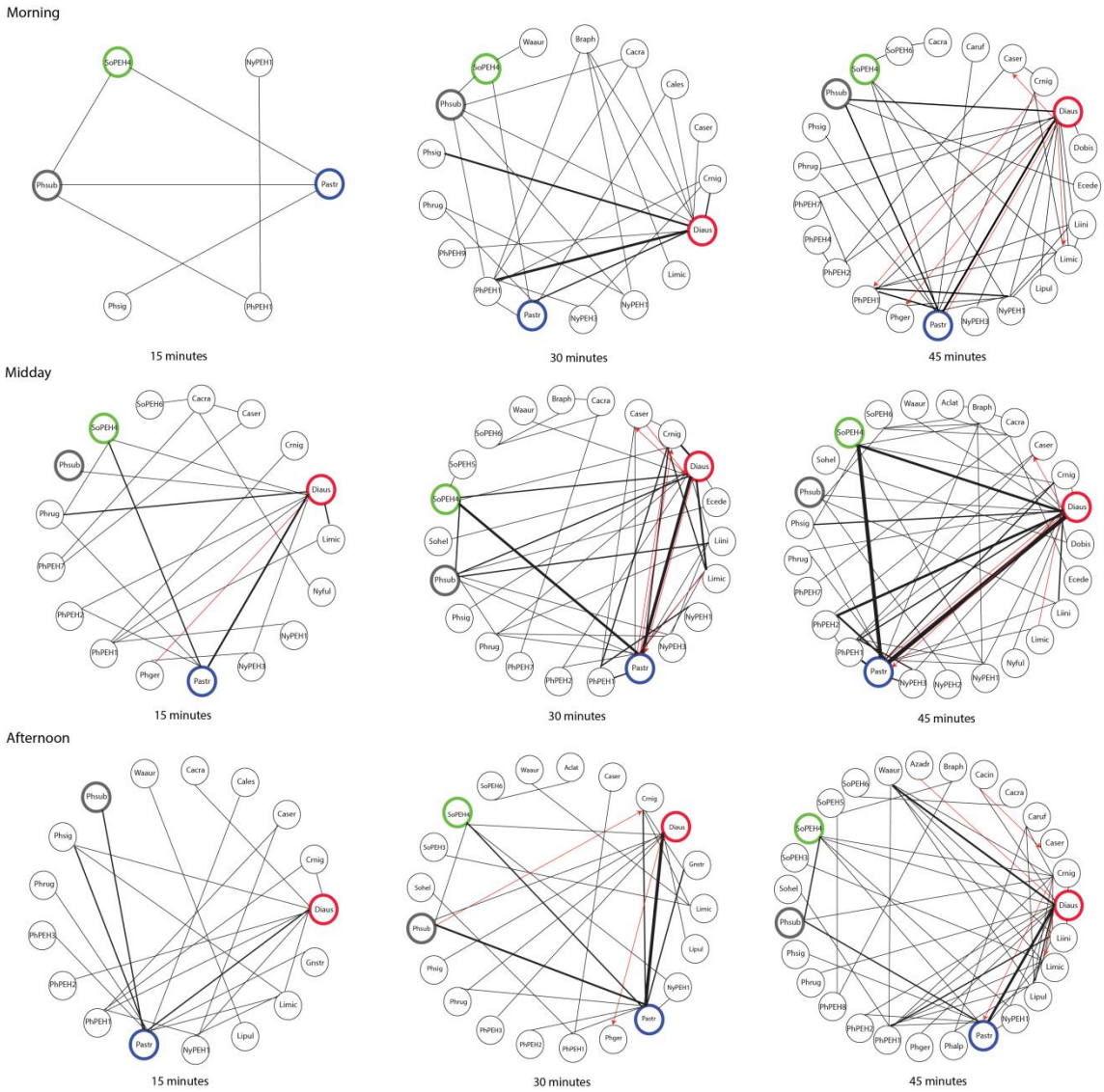


Fig 4.5 Network of species-pair interactions at the 45 min observation period across all three bait sample periods. Neutral interactions are represented by black lines and antagonistic interactions are represented by red lines. If a species was clearly displaced during the interaction, an arrow indicates the "winner". Thicker lines indicate a higher number of interactions among the pair of species. Species name abbreviation shows the first two letters of the genus followed by the three letters of the species name. For clarification, the four most frequent species are highlighted: *D. australis* (red circle), *P. striata* (blue circle), *Solenopsis* PEH04 (green circle) and *P. subarmata* (grey circle).

4.3.3. Ponerinae trophic position

Plant samples (TL1) showed a range of 8.82 δ units in INP and 5.44 δ units in OPR (mean ± SD, range, INP: δ15N = 2.77 ± 1.9 ‰, -2.58 to 6.24 ‰, n = 42; OPR: δ15N = 1.60 ± 1.52 ‰, -0.62 to 4.82 ‰, n = 10). Primary consumers (TL2) were very similar between INP and OPR (mean ± SD, range, INP: δ15N = 4.53 ± 1.83 ‰, 1.53 to 8.21 ‰, n = 19; OPR: δ15N = 4.39 ± 2.18

‰, -0.87 to 7.76 ‰, n = 13), as were the secondary consumers (TL3; mean ± SD, range, INP: δ15N = 9.76 ± 2.36 ‰, 4.19 to 13.25 ‰, n = 20; OPR: δ15N = 9.81 ± 2.49 ‰, 7.62 to 17.25 ‰, n = 15). No difference was found between TL1 between INP and OPR (TL1: ANOVA $F_{(1,50)} = 3.21$, p = 0.07; TL2 ANOVA $F_{(1,30)} = 0.04$, p = 0.84; TL3 ANOVA $F_{(1,33)} = 0.003$, p = 0.95). Assuming a 3.4 ‰ separation per TL, we obtained similar results (TL1 = INP: 1.47-4.87; OPR: 0.53-3.93; TL2= INP: 4.87-8.27; OPR: 3.93-7.33; TL3 = INP: 8.27-11.67; OPR: 7.33-10.73; Fig 4.6 and Fig 4.7). Taxonomic information of all samples is listed in Supplementary material Table S4.1.

δ15N signatures of species from the subfamily Ponerinae ranged from 5.8-15.9 (INP) and 5.1-14.2 (OPR), forming a gradient of near 10 δ units or roughly 3 trophic positions. Most species were located at trophic level 3 and 4 (primary and secondary predators), and a few species appeared more reliant on plant-based resources for their diet. The arboreal *Neoponera* had the lowest N enrichment: *N. fiebrigi* had the lowest value (INP: δ15N average 6.50 ± o.o7 ‰; OPR: δ15N 5.61 ‰), followed by *N. villosa* (INP δ15N average 7.90 ± 1.23 ‰; ONP δ15N average 8.39 ± 0.4 ‰). Additionally, in OPR *H. agils* (δ15N 6.89 ‰), *N. verenae* (δ15N average 7.22 ± 1.28 ‰) and *N. moesta* (δ15N average 7.31 ± 1.80 ‰) have similar values. The rest of the species were recorded up to TL3 (Fig 4.6 and Fig 4.7). The top Ponerinae predators were *H. parva* and *Platythyrea pilosula* in INP and *N. marginata* in OPR. Some species had a high variation (*Neoponera crenata* in INP: δ15N average 10.30 ± 3.58 ‰ and *P. harpax* in OPR: δ15N average 10.81 ± 3.04 ‰; Fig 4.6 and Fig 4.7). Five species present at both localities with more than 3 samples were tested to look for differences between localities (*D. australis*, *P. striata*, *O. meinerti*, *N. villosa* and *Hypoponera* PEH02). In OPR the δ15N signal for *D. australis* and *P. striata* were lower (*D. australis* ANOVA $F_{(1,9)} = 18.76$, p = 0.001; *P. striata* ANOVA $F_{(1,12)} = 13.95$, p = 0.002; Fig 4.8).

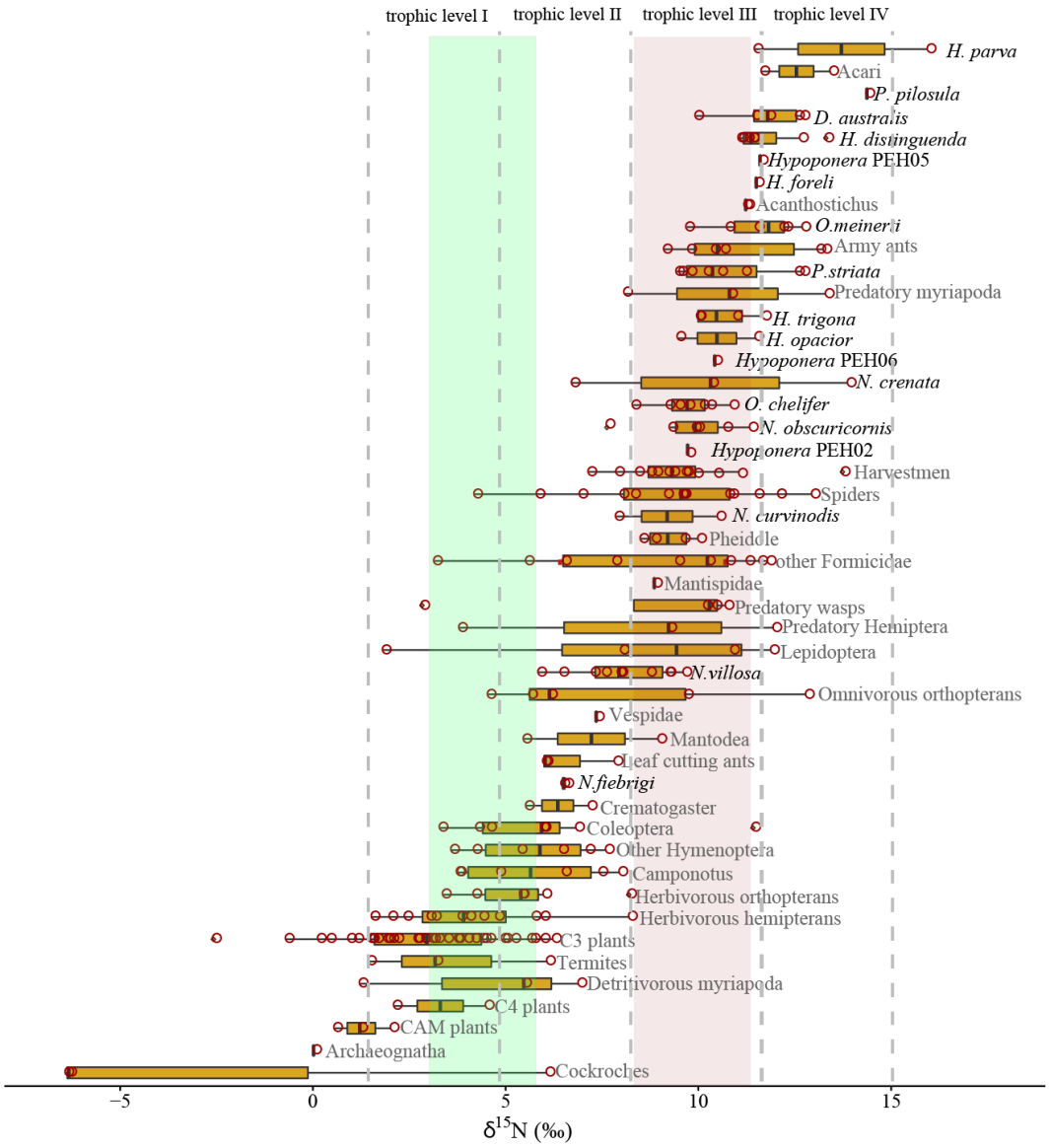


Fig 4.6 Isotopic composition (δ15N) of Ponerinae (in black) and plants and other arthopods (in grey) for Iguazú National Park. Green and red represent the 25th and 75th percentile for trophic levels 2 and 3 respectively measured from known herbivores and predators. Red circles represent individual sample values.

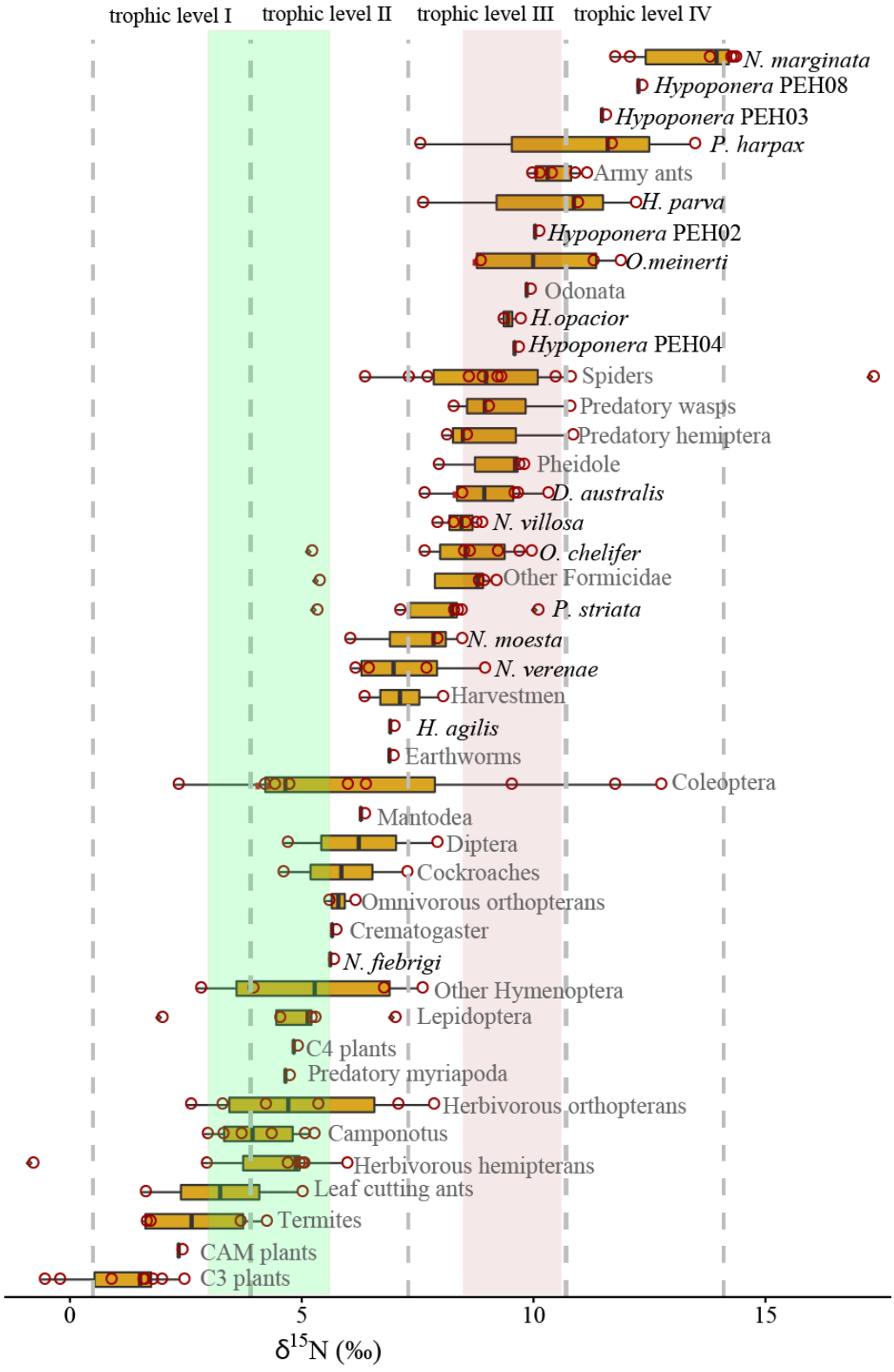


Fig 4.7 Isotopic composition (δ15N) of Ponerinae (in black) and plants and other arthopods (in grey) for Osununú Private Reserve. Green and red represent the 25th and 75th percentile for trophic levels 2 and 3 respectively measured from known herbivores and predators. Red circles represent individual sample values.

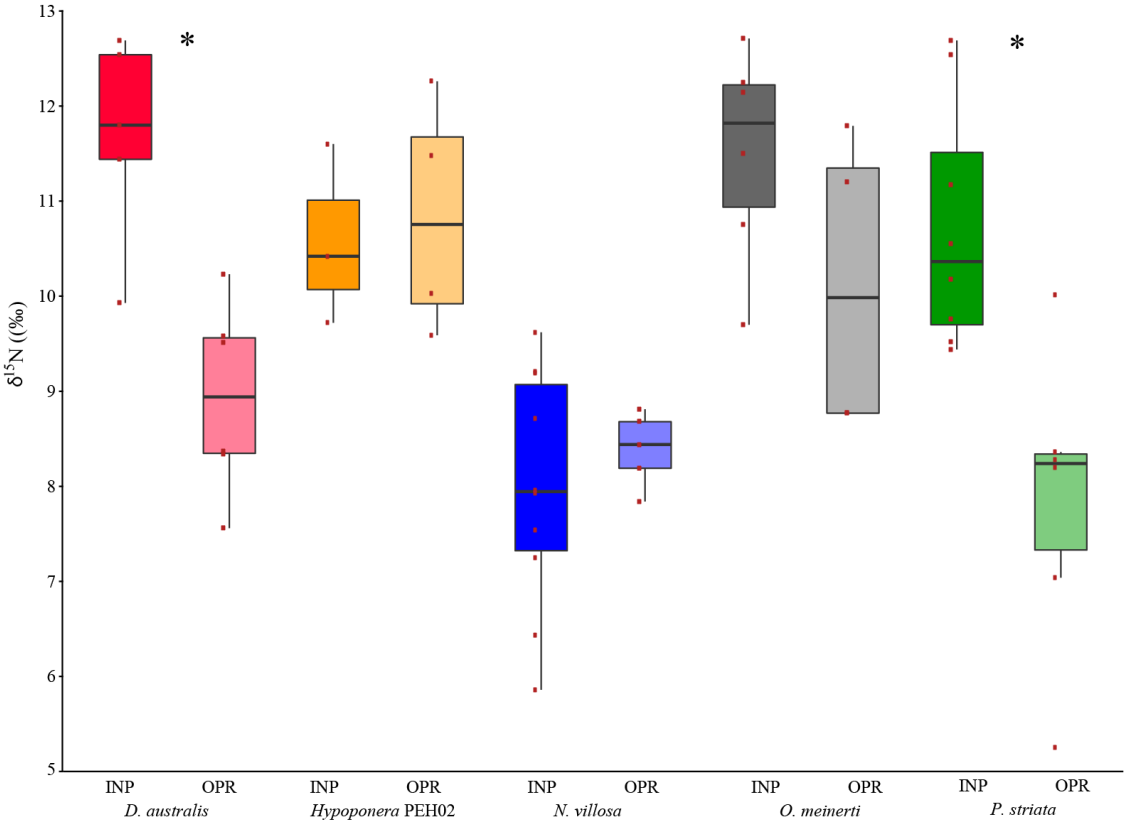


Fig 4.8 Differences in isotopic composition (δ15N) of five Ponerinae species between the two localities. Different species are marked with a different color. (*) Significant differences.

4.4. Discussion

Four ant species that were the most common in pitfall traps (occurring in more than 25% of the traps; Hanisch, 2013) were also common visitors at our surface baits (*D. australis*, *P. striata*, *P. subarmata* and *Solenopsis* PEH04), indicating that their prevalence at baits may be explained by their relative abundance in the study site. The two ponerines (*D. australis* and *P. striata*), with an occurrence at surface baits between 40-53% (across all three time periods), stand out from the rest of the ant community. Unlike other "dominant" ants, which usually live in large colonies (Hölldobler & Wilson 1990, Tsutsui & Suarez 2003), these species have relative small colony sizes. However, they occur in relatively high colony densities. In INP, *D. australis* have an average of 44 workers per nest (range 18–86), with a density of ~ 180 nests / ha (Tillberg et al. 2014). *Pachycondyla striata* nests have an average of 36.7 workers (range 7-

80) (Rodrigues et al. 2010), but unfortunately there is no record of nest density for this species at INP.

Both *P. striata* and *D. australis* are solitary foragers and do not typically recruit nestmates to help retrieve or defend resources. *Pachycondyla striata* will occasionally recruit a few nest mates using tandem running (Giannotti & Machado 1992) and *D. australis* appears to use tandem running only in the context of colony fission (Fowler 1985). This foraging behavior typically corresponds with the collection of small, fairly common resources that are distributed unpredictably in space, and that are not depleted by colony foraging effort (Lanan 2014). The large size of these species allows them to quickly grab resources and run away, avoiding confrontations with other species. However, they have also been seen stealing prey or resources from smaller ants (Raimundo *et al.*, 2009). In contrast, their large size may prevent them from exploiting smaller resources or foraging effectively within the leaf-litter (Agosti & Alonso 2000, Farji-Brener et al. 2004), reducing competition among species (Brown & Davidson 1977).

Our observed species interactions at surface baits revealed a prevalence of neutral interactions and random species co-occurrence, patterns consistent with other research in tropical areas (e.g. Baccaro et al., 2012; Stuble et al., 2013, 2017). However, with increasing time post bait placement (30 min at midday and 45 min at morning and afternoon), patterns of co-occurrence were less than expected by chance (Table 4.1). These were the times when the few agonistic interactions were most often observed (Fig 4.5) and bait occupancy was highest (Table 4.1). Aggressive interactions were recorded for 6 of the 41 species that visit the baits (*C. sericeiventris, L. micans*, *Ph. gertrudae*, *D. australis*, *C. nigropilosa* and *P. striata*). With the exception of *D. australis* and *P. striata*, these species usually recruit a high number of individuals and behaved like “extirpators” (Wilson 1971) by occasionally preventing other species from feeding on the bait. Additionally, *C. sericeiventris, L. micans* and *P. gertrudae*

were the species with the lesser proportion of neutral interactions (Fig 4.4). Notably, northern Argentina includes the native range of many introduced ant species elsewhere that have been suggested to be highly competitive and ecologically dominant where they occur (LeBrun et al. 2007, Calcaterra et al. 2008, Foucaud et al. 2009). Four of these species have been recorded at INP: *Linepithema humile*, *Solenopsis invicta*, *Nylanderia fulva* and *Wasmannia auropunctata* (Hanisch et al. 2015). However, only *W. auropunctata* was collected in this study and at a relatively low abundance; it did not monopolize or dominate any of the baits. Although competition might be an important factor in structuring some ant communities, other biological processes or stochastic events can explain positive or negative patterns of species co-occurrence (Ribas & Schoereder 2002, Cerdá et al. 2013, Ellwood et al. 2016). Additionally, competitive interactions can be diffuse (Davidson 1985) and the simple observation of agonistic behavior (or its absence) does not necessarily imply the presence or absence of interspecific competition.

Thermal tolerance can influence ant foraging biology and measures of dominance and competition including the discovery and monopolization of resources (Cerdá et al. 1997, Farji-Brener et al. 2004, Godoy & Camargos 2013). The ability to forage at extreme temperatures may allow species to break trade-offs between resource discovery and dominance by providing foraging periods where dominant species are absent (Cerdá et al. 1997). The relatively narrow range of temperatures (25-30°C) across our three baiting periods at INP may not have included thermal conditions that prevented many ants from foraging. Only *Solenopsis* PEH04 appeared to benefit from higher temperatures. Nocturnal baiting would likely show greater variation in community structure and species interactions related to temperature as night time summer temperatures can decrease to 18°C. In addition, there is an entire guild of common crepuscular and nocturnal foraging species at INP including *Camponotus sericeiventris* (Yamamoto & Del-Claro 2008) and *Odontomachus chelifer* (Raimundo et al. 2009). It would be worth documenting if these species show similar patterns of bait occupancy and species interaction

as our most common diurnal foragers *D. australis* and *P. striata.* The lack of influence of temperature on community structure in this study is similar to the results of Dáttilo and Izzo (2012) who sampled contrasting environments (tree fall gaps vs dense forest) within the Amazonian rain forest at five different hours of the day. Finally, a different pattern could arise in a higher temporal scale (across different seasons).

We estimated the trophic levels of ants and other insects using the literature and a trophic level separation of 3.4 ‰ (Post 2002). Differences among the two methods in TL 1 and 2 are probably due to the large variation of δ15N in our reference plant samples (8.82 and 5.4 δ units in INP and OPR respectively; Fig 4.6 and Fig 4.7). This variability is common as δ15N in plants can be affected by several factors like precipitation, nitrogen fixation, mycorrhizae or microbial processes (Handley & Raven 1992, Austin & Vitousek 1998, Evans 2001). We did not find differences in δ15N values for estimated trophic levels between the two studied localities. Furthermore, all species present at both localities had similar δ15N values with the exception of *D. australis* and *P. striata*, the two most abundant ponerines. Both species had lower δ15N values in OPR (Fig 4.8). However, this difference was not sufficient to imply a change in trophic level between sites (Fig 4.6 and 4.7). Since these species are generalist predators, this variation likely reflects differences in prey availability between sites during sample periods.

Eighteen Ponerinae species were included in the trophic position analysis. The majority of these species were predatory (recorded at TL3 or TL4) in the two Atlantic Forest localities. The δ15N values for *N. marginata*, *P. pilosula*, *H. parva* and two morphotypes of *Hypoponera* (PEH03 and PEH08) placed them among the top predators of the insect food webs at these sites (Fig 4.6 and Fig 4.7). Some of these species may be represented by specialist predators. For example, *N. marginata* are specialists feeding only on the termite *Neocapritermes opacus* (Leal & Oliveira 1995). DNA barcoded prey captured from *N. marginata* specimens in Copo National Park support this diet (data not shown). In OPR the termites have a δ15N value of 2.7

± 1.3 ‰, too low to be the prey of *N. marginata*. However, termites can have higher δ15N values depending on their diet and habitus (Tayasu et al. 1997) and *Neocapritermes opacus* is known to be a wood eating termite (Gontijo & Domingos 1991). In the case of *P. pilosula*, termites and other food items were offered to workers in an attempt to localize the colony; none of the food items were accepted, and captured individuals died shortly, suggesting that this species might also have a specialized diet (Jacquemin et al. 2014).

In contrast, some arboreal *Neoponera*, like *N. fiebrigi*, tended to have lower δ15N values (Fig 4.6 and Fig 4.7), suggesting they incorporate more plant-based resources in their diet (possibly nectar or honey dew). Additionally, greater variation in δ15N values in *N. crenata* and *P. harpax* (6-7 δ units; Fig 4.6 and 4.7) suggest a highly variable diet in these species and that individual colonies may specialize in specific resources based on availability or colony demography (Tillberg & Breed 2004). However, as an alternative explanation, diet differences may due to ecological variation between morphologically similar, yet different species. In the case of *N. crenata,* two samples of this species were used both for stable isotope and DNA barcode analysis (chapter II). Specimen MACN-bar-ins-ct 06416 was associated with BIN BOLD:ACX7584 and with a δ15N value of 6.72, meanwhile specimen MACN-bar-ins-ct 07761 was associated with BIN BOLD:ABV2684 and with a δ15N value of 13.88.

Taken together, our results show that the more frequent species at baits were also the most abundant at INP, indicating that the frequency of bait discovery was driven by the natural abundance of the species and not by the species ability to find the bait. Despite the observation of some aggressive interactions, the majority of species tolerate and coexisted with each other. In addition, with a few exceptions, the co-occurrence patterns of species at baits were random. Finally, we show that the most noticeable species within the ant community were two ponerine primary predators: *D. australis* and *P. striata*. In the next chapter, we will study the foraging behavior of the former.

Capítulo IV en castellano

Las hormigas son un grupo abundante y ecológicamente diverso en la mayoría de los ecosistemas terrestres, particularmente en los trópicos, donde su biomasa puede exceder la de los vertebrados. Adicionalmente, la diversidad de las hormigas puede variar tanto espacial, como temporalmente. Distintos métodos se usan para capturar hormigas: los más comunes son los métodos pasivos que nos pueden dar información acerca de la ocurrencia y la abundancia relativa de las especies (por ejemplo trampas de caída y extractores Winklers), mientras que otros métodos como el cebado puede ser usado para estudiar la actividad, dieta e interacciones entre las especies.

Las hormigas participan en una variedad de interacciones ecológicas, incluidas el mutualismo, la competencia, el parasitismo y la depredación. Siendo la competencia interespecífica usualmente sugerida como un proceso clave en la estructuración de las comunidades de hormigas. Sin embargo, la competencia podría ser un fenómeno poco frecuente si las interacciones agresivas entre especies son poco comunes. Caso contrario a la competencia, la depredación es una interacción directa y relativamente fácil de demostrar. En particular, las ponerinas son clasificadas usualmente como predadoras, pero la dieta es desconocida para una gran mayoría de especies. Adicionalmente muchas especies son conocidas por consumir materia vegetal (frutos, semillas, néctar).

En este capítulo se propuso en el Parque Nacional Iguazú (PNI) (1) estudiar la variación temporal de la activad de las hormigas mediante cebos puestos en tres momentos del día; (2) estudiar las interacciones entre las especies en los cebos; (3) caracterizar la posición trófica de las ponerinas mediante análisis de isótopos estables. Adicionalmente, este último objetivo se realizó también en otra área protegida del Bosque Atlántico: la Reserva Privada Osununú (RPO).

Como resultado, de las 41 especies capturadas mediante cebos superficiales, sólo 8 estuvieron presentes en el 10% de los cebos en algún momento del día (mañana, mediodía o tarde). Entre las especies que más visitaron los cebos, dos ponerinas se destacaron como las más frecuentes (40%-53% de los cebos, dependiendo del momento del día), estas especies fueron *D. australis* y *P. striata* seguidas por otras dos especies de mirmicinas. Un patrón similar de ocurrencia fue también encontrado en trampas de caída colocadas en un muestreo previo, es decir que es probable que el número mayor de visitas a los cebos de estas especies, se deba a su abundancia relativa en el PNI. La mayoría de las interacciones entre las especies en los cebos fueron neutrales, es decir que la mayoría de las especies se ignoraron o toleraron. Respecto a la actividad diurna de las hormigas, no encontramos un recambio de especies entre los distintos momentos del día y los análisis de co-ocurrencia sugirieron que la comunidad no está fuertemente estructurada por algún proceso biológico (por ejemplo por competencia).

El análisis de isótopos estables reveló que no hubo diferencias entre los niveles tróficos de PNI y RPO. La mayoría de las especies de ponerinas ocuparon niveles tróficos altos, correspondiente con depredadoras primarias y secundarias. En cambio, la señal δ15N en algunas especies (del género *Neoponera*) fue similar a la de los herbívoros en el ecosistema, indicando que estas especies tienen una dieta con una alta proporción de materia vegetal. En contraste, las observaciones de campo y el análisis de isótopos sugieren que la especie *Platythyrea pilosula* es un depredador especializado, teniendo uno de los valores de δ15N más alto para cualquier hormiga del PNI. Finalmente encontramos que las especies *D. australis* y *P. striata* tuvieron una señal de δ15N más baja en RPO (sin que esto signifique un cambio de nivel trófico), indicando una variación en su dieta en esta localidad.

V. Ecology and foraging behavior of *Dinoponera australis*

5.1. Abstract

Social organisms benefit from group foraging behavior. However, if individuals overlap widely in the areas they search for food these benefits may not be proportional to the number of individuals that take part in searching for food. We examined foraging behavior and route fidelity in colonies of *Dinoponera australis* (hormiga Tigre) in Iguazú National Park, Argentina. Their large worker size, lack of nestmate recruitment while foraging, and relatively small colonies with few active foragers makes *D. australis* a useful model to study individual and colony foraging strategies. At six colonies, we marked individual forgers and mapped their foraging routes to test the hypotheses that each ant specialized in a particular area around the nest, and that nestmates exhibited little overlap in foraging area. Additionally, we recorded the direction and duration of each foraging trip, foraging success, maximal distance from the nest, and total foraging area of the colony. We mapped 120 complete foraging routes from 42 different foragers. The total area used by each colony averaged 52m^2, individual worker foraging times average 45 mins (range 0 - 298 mins), and 31% of forgers returned with food. Colonies ranged in size from 45 to 100 workers and ants involved in foraging activities accounted for 11% (range7% - 17%) of the total individuals in the nest. Over 50% of the foragers exhibited a high degree of route fidelity. Nest-mate pairs foraging areas overlapped less than 10% for the majority of the foragers in 4 of the 6 colonies. Our results suggest that *D. australis* workers exhibit strong route fidelity which increases foraging efficiency and search area which may be particularly important for a species with relatively few foragers. The lower route fidelity and increased overlap in foraging area of workers seen in two colonies suggest that this species may adjust foraging behavior depending on food availability. Future work that experimentally varies food distribution around the nest will reveal how biotic and abiotic factors interact to shape individual and colony foraging behavior in this species.

5.2. Introduction

The localization and exploitation of resources are essential for survival, reproduction and growth. Resource distribution can favor cooperative behaviors in some environments and social organisms benefit from group foraging through a variety of mechanisms (Clark & Mangel 1986, Sutton et al. 2015). These benefits often increase with the number of individuals taking part in foraging and include covering a larger area, increasing encounter rates with prey, and for species with recruitment, being able to handle larger prey than would be possible by an individual. However, if group members do not use information from previous foraging trips, or overlap widely in their search routes, many of these benefits will not be proportional to the number of individuals taking part in foraging (Valone 1989).

In eusocial insects like ants, food is acquired to meet current needs of the colony, growth (the production of new workers) and reproduction (the production of new queens and males). Obtaining resources for growth is particularly important for small colonies as larger colonies often suffer lower mortality rates from competitors or from environmental stochasticity (Ryti & Case 1986, Thurber et al. 1993, Adams & Tschinkel 1995, Gordon & Kulig 1998, Gordon 2010). Social insects exhibit a variety of solitary and group foraging behaviors (Traniello 1989, Richter 2000, Dornhaus & Powell 2010).

Principal factors in the structuring of the search pattern and foraging behavior in ant species include how food is distributed, and intra- and inter-specific interactions (Bernstein 1975, Nonacs & Dill 1988, Traniello 1989, Guénard & Mcglynn 2013). For example, solitary foraging seems to be correlated with food randomly distributed in space and time (Pie 2004, Lanan 2014). Additionally, abiotic conditions like temperature and humidity can affect foraging, creating diurnal and seasonal variation in behavior (Porter & Tschinkel 1987, Raimundo et al. 2009, Gordon 2013). Also, nutritional state and requirements of the colony will influence decisions and diet preference of the foragers. Finally, individual variation,

experience and age of the foragers will also influence an individual's decision-making (Gordon 2010).

Route fidelity, or regional specialization of foragers, has been observed in several ant species, particularly in the subfamily Ponerinae (Fresneau 1985, Traniello 1989, Fewell 1990, Fourcassié et al. 1999, Pie 2004, Azevedo et al. 2014). This behavior may provide a mechanism to reduce the possibility of solitary foragers getting lost in species that do not use chemical trials for orientation (Fourcassié et al. 1999). In addition, route fidelity can increase colony efficiency by reducing the overlap in search area among foragers: a disproportionate number of workers exploring the same area, coupled with randomly distributed resources, will decrease the total area explored of the colony and reduce colony food intake (Pie 2004).

In this study, we quantified the foraging behavior of individual *Dinoponera australis* workers. Specifically, we were interested in how a species with small colonies (average 44.6 ± 21.4 adults per nest; Tillberg et al. 2014) with a small proportion of foragers (average 26% of the colony; Smith et al. 2011), can be among the most successful species (in terms of biomass) of the ant community in Iguazú (Tillberg et al. 2014). The high biomass in Iguazú of *D. australis* (2.5 kg / ha; Tillberg et al. 2014) may be explained, in part, by an efficient foraging behavior (Tillberg et al. 2014). By measuring the initial direction of foragers in *D. australis*, Tillberg and colleagues (2014) observed a direction fidelity of individuals, suggesting that route fidelity might be a mechanism to increase colony foraging efficiency in this species. But only observations of complete foraging trips could prove this assumption. Our hypothesis is that *D. australis* workers forage in a particular area around the nest, with different ants foraging in different sections in order to increase the explored territory of the colony, maximizing foraging colony effort.

5.3. Materials and Methods

5.3.1. Study area

The study was performed during summer of 2016 and 2017 in Iguazú National Park (INP), a 67,000 ha protected area in northwestern Misiones, Argentina (S25.68015°, W54.454192°). The climate is humid subtropical with no defined dry season. Mean monthly temperatures range from 15°C (June-August) to 26°C (December-February), annual rainfall between 1,800 and 2,000 mm, and humidity between 70% and 90%. Data were collected in disturbed / secondary forest.

5.3.2. Study organism

The genus *Dinoponera* is restricted to South America and currently comprises 8 recognized species with a body size ranging from 3 to 4 cm (Lenhart et al. 2013), making them among the largest species of ants in the world. Dietary studies of *Dinoponera* reveal they are largely predatory but will also scavenge for dead insects, seeds, and fruit (Fourcassié & Oliviera 2002, Araujo & Rodriguez 2006, Tillberg *et al.* 2014). They lack morphologically specialized queens and reproduction is carried out by a single mated worker (Paiva & Brandão 1995), known as gamergate. In *D. australis*, nutritional state is correlated with the division of labor; the probability of foraging and foraging effort are associated with decreased fat storage (Smith et al. 2011). In *D. australis* and *D. gigantea*, foragers leave the nest in a preferred initial direction and forage solitary in the search of food (Fourcassié and Oliviera 2002, Tillberg *et al.* 2014). If an encounter with a non-nestmate occurs, the ants will engage in a ritualized antagonistic behavior, fight or avoid confrontation (Fourcassié & Oliviera 2002, Tillberg *et al.* 2014). If food is found, foragers do not recruit nestmates to help with food transportation (Fowler 1985, Fourcassié & Oliveira 2002) and foraging routes do not seem to be based on any chemical substance laid down during previous trips (Fourcassié et al. 1999).

5.3.3. Foraging behavior

To investigate the spatial pattern of foraging routes, six *D. australis* colonies were observed during March 2017. First, we made maps of the terrain surrounding each colony by creating an x-y coordinate system with rope. Using measurement tape, we added fixed reference points (i.e. a particular tree at X = -2 m, Y= 1.5 m) to the map. Additionally, we used a compass and measurement tape to register angles and distances between landmarks to test the accuracy of the maps. At each colony, foragers were individually marked as they exited the nest. Initially, two different marking types were used: enamel painting (Testers Co., Rockford, Illinois) and gluing color/number tags designed for queen bees (EH Thorne (Beehives) Ltd, UK). The tags were more persistent and required less handling time, so we choose this method (Fig 5.1). Occasionally, ants lost their marks and needed to be remarked.

Between 1-2 days after marking, tagged ants were followed and their foraging route was drawn on the map. We took note of the departure/exit time, and whether the forager returned to the colony with food (successful trip). If successful, we marked the location where food was collected. To help maintain an accurate position of where the ants were foraging, if necessary, small color flags were placed into the soil to mark the location of where an ant had been for latter measurement. *D. australis* workers rarely climb onto vegetation, but when they did we noted the climbing event. Each colony was observed the necessary time needed to obtain at least 3 foraging trips for the majority of the marked ants. The required observation time varied among the colonies and depended on weather conditions, ant activity levels and number of foraging ants. Colonies were observed between 3 - 9 days for 6 hr / day (range 1 – 10 hr) between 09:00 and 19:00. After data collection was complete, we excavated three of the colonies.

Foraging routes were digitalized by scanning the maps. For each trip, we calculated the maximum distance from the nest, the initial and mean direction, and the total foraging area. A

few trips (7 trips from 5 ants in colony 5, and 2 foraging trips from 2 ants in colony 6) did not have a clear foraging direction (i.e. ants looked for food in a circular area around the nest) so a mean direction was not calculated for these cases. For each pair of nestmates with at least three foraging trips, we calculated the overlapping foraging area of all the trips between the two ants, relative to the total foraging area of one of the ants (randomly determined). At the level of the colony, we calculated the total foraging area as the enclosed area by all the overlapping foraging routes. We use the North (0°) as a reference to measure all the angles. The areas were calculated with the software Octave (Eaton et al. 2016) an a function which estimated the area traveled by the ants using the $1m^2$ reference of each map (Appendix 5.1). The error associated to the estimation of the position of an object (e.g. ant) in the different maps was 0.28 m.

We used Spearman's correlation test (Rs) to verify the occurrence of a relationship between the time spent outside the nest and the maximum distance to the nest. We also look for a relationship between the total foraging area and the colony size. To investigate nonrandom distribution patterns of foraging trips and food, we performed a Rayleigh (Z) test. For analysis at the individual level (route fidelity), only complete trips were analyzed, but for food distribution and colony activity, we used all observed data (including incomplete trips). Non parametric tests Kruskal–Wallis were calculated to look for differences between successful and non-successful trips regarding the maximum traveled distance or the total area covered. We used SPSS (version 15.0) and Oriana (version 4.02, Kovach Computing Services) software programs to perform these analyses. Finally, the size of the non-excavated colonies was estimated using the average proportion of foragers for excavated colonies.

Fig 5.1 Marked *D. australis* ants used for the study.

5.4. Results

We observed 120 complete foraging trips by 42 different workers, resulting in more than 91 hours of direct worker observation (colony 1 = 16 hrs, colony 2 = 6 hrs, colony 3 = 22 hrs, colony 4 = 18 hrs, colony 5 = 22 hrs and colony 6 = 8 hrs). The more time that workers spent outside the nest, the further they traveled from it ($R_s = 0.70$, $p < 0.0001$, $N = 120$; Fig 5.2). The median time spent outside the nest for all foragers was 45 min (range 0 min – 298 min). The median distance traveled per ant was 4 m (range 0.4 m - 11.3 m). Each foraging trip covered an average area of 5.5 m^2 but varied greatly between individuals (range 0.06 m^2 - 22.12 m^2). The total area covered by the colony averaged 52 m^2 (range 34.4 m^2 – 89.9 m^2) and no relationship between size of the colony and foraging area covered was found ($R_s = 0.55$, $p = 0.2$, $N = 6$; Table 5.1).

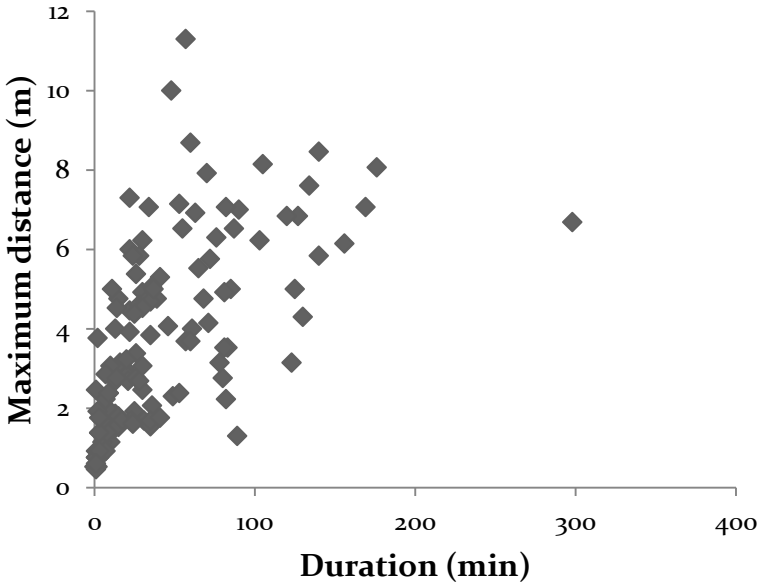


Fig 5.2 The relationship between foraging trip duration and maximum distance traveled by *Dinoponera australis* workers during foraging behavior.

Table 5.1 Summary for the observed colonies. (*) Means estimated values of colony size based on the number of foragers.

Colony	Foraging ants	Colony size	Complete observed trips	Successful trips (%)	Total nest foraging area (m^2)	Average foraging area per ant (m^2)	Average foragin time (min)	Average maximum distance per ant (m)
1	8	52	19	53	69.0	5.2	48	4.4
2	4	52	12	42	38.9	5.3	29	4.6
3	7	84	18	50	89.9	9.4	75	6.2
4	7	64*	20	15	35.5	3.7	53	3.4
5	11	100*	34	26	44.7	4.6	38	2.9
6	5	45*	17	0	34.4	5.0	27	3.0

Workers returned with food in 31% of the trips (range: colony 6 = 0/17 successful trips/total trips, colony 1 = 10/19 successful trips/total trips; Table 5.1). Food was found more frequently on foraging trips with a greater maximum distance from the nest (Kruskal-Wallis test: H = 12.39, P = 0.0004) or with a larger covered area (Kruskal-Wallis test H = 7.36, P = 0.0067). Ants returned to the nest with a range of food items including small frogs,

lepidopterans, hemipterans, caterpillars, “Pindo” seeds, “Yacaratiá” fruits, and other ants (i.e. *Camponotus sericeiventris* and *Atta* sp.). They scavenged for dead animals but they also actively hunt different preys (Fig 5.3), and sometimes robbed food from other ant species. We also observed them extracting nectar from fallen flowers of *Luehea divaricata*, a flower known to have two big nectar-rich nectaries (Lattar et al. 2018).

Fig 5.3 Left: *D. australis* hunting a beetle. Photo credit: PEH. Right: *D. australis* taking a *Syagrus romanzoffiana* (Pindo) seed to the nest. Photo credit: Carolina I. Paris.

Foraging activity peaked between 09:00 – 11:00, and was lowest between 16:00 – 18:00 (Fig 5.4). During heavy rains foraging stopped and ants from one colony without dense canopy were observed moving leaves on top of the colony entrance to prevent water entering the nest (Fig 5.5). Outside of the observation times (between 20:00 and 09:00), there was little activity (Hanisch personal observation), although some ants were observed leaving the nest at sunset. Ants from 2 nests (L from colony 4 and F from colony 3) were observed climbing trees, occasionally returning with caterpillars.

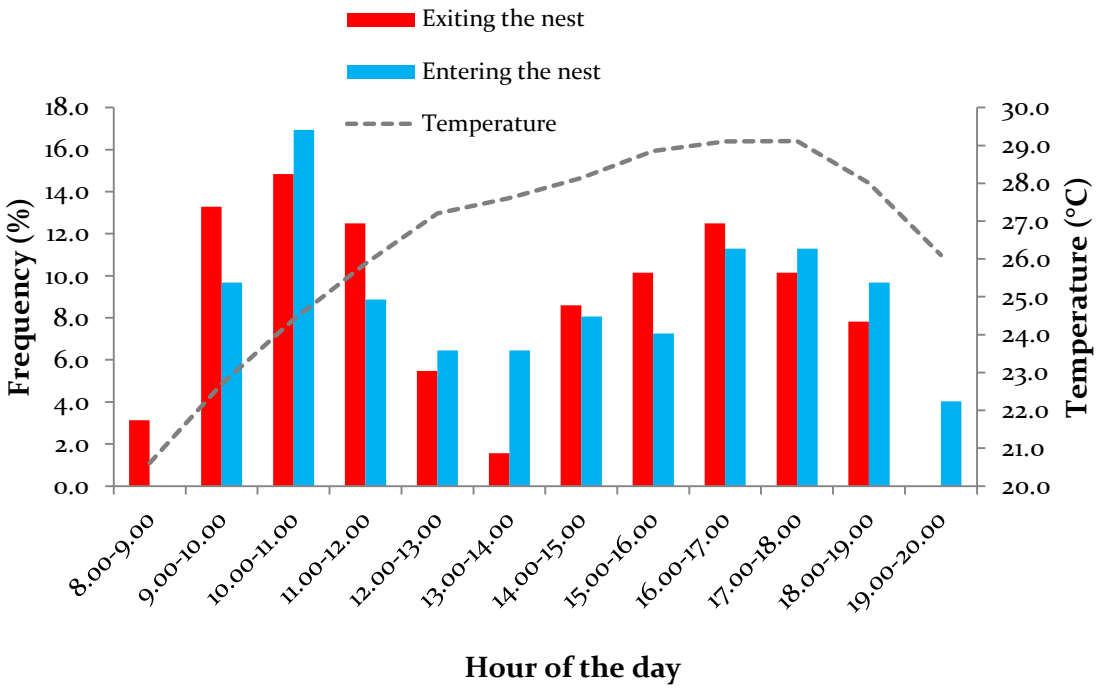


Fig 5.4 Frequency of ants leaving the nest (blue bars, N = 128 observations) and entering the nest (red bars, N = 124 observations) for the 6 observed colonies. Average temperature for each hour range during all the observed days is shown in a grey line (Source Servicio Meteorológico Nacional).

Fig 5.5 Left: *D. australis* nest with visible entrance. Right: Same nest with entrance covered with leaves during a heavy rain, previously, workers were observed positioning the leaves. Arrow is pointing the entrance. Photo credit: Elián Hanisch.

General foraging patterns varied among the six colonies (Fig 5.6 - Fig 5.8). Across all colonies, half of the foragers that had 3 or more foraging trips mapped had a preferred foraging area (Colony 1 = 100% of foragers, Colony 2 = 25%, Colony 3 = 75%, Colony 4 = 66%, Colony 5 = 25%, Colony 6 = 25%; Fig 5.9 and Table 5.2). Foraging areas of nestmates overlapped by less than 10% in colonies 1-4, but overlapped up to 65% in colonies 5 and 6 (Fig 5.10). The average foraging direction for colonies was random (Fig 5.11) as was the distribution of the food items relative to the nest, with the exception of colony 1 (Fig 5.12). Three excavated colonies (colonies 1-3) had between 52 and 84 total workers revealing that foraging workers accounted for an average of 11% of the total number of ants in the colony (range 7-17%). If we used the average proportion of foragers to estimate the size of remaining colonies, colonies 4, 5 and 6 had 64, 100 and 45 workers (Table 5.1). Pupae and larvae were present only at colony 3. All excavated colonies had a maximum depth near 90 cm. Detailed information of the structure of nest and organisms found living within it can be found in Appendix 5.2.

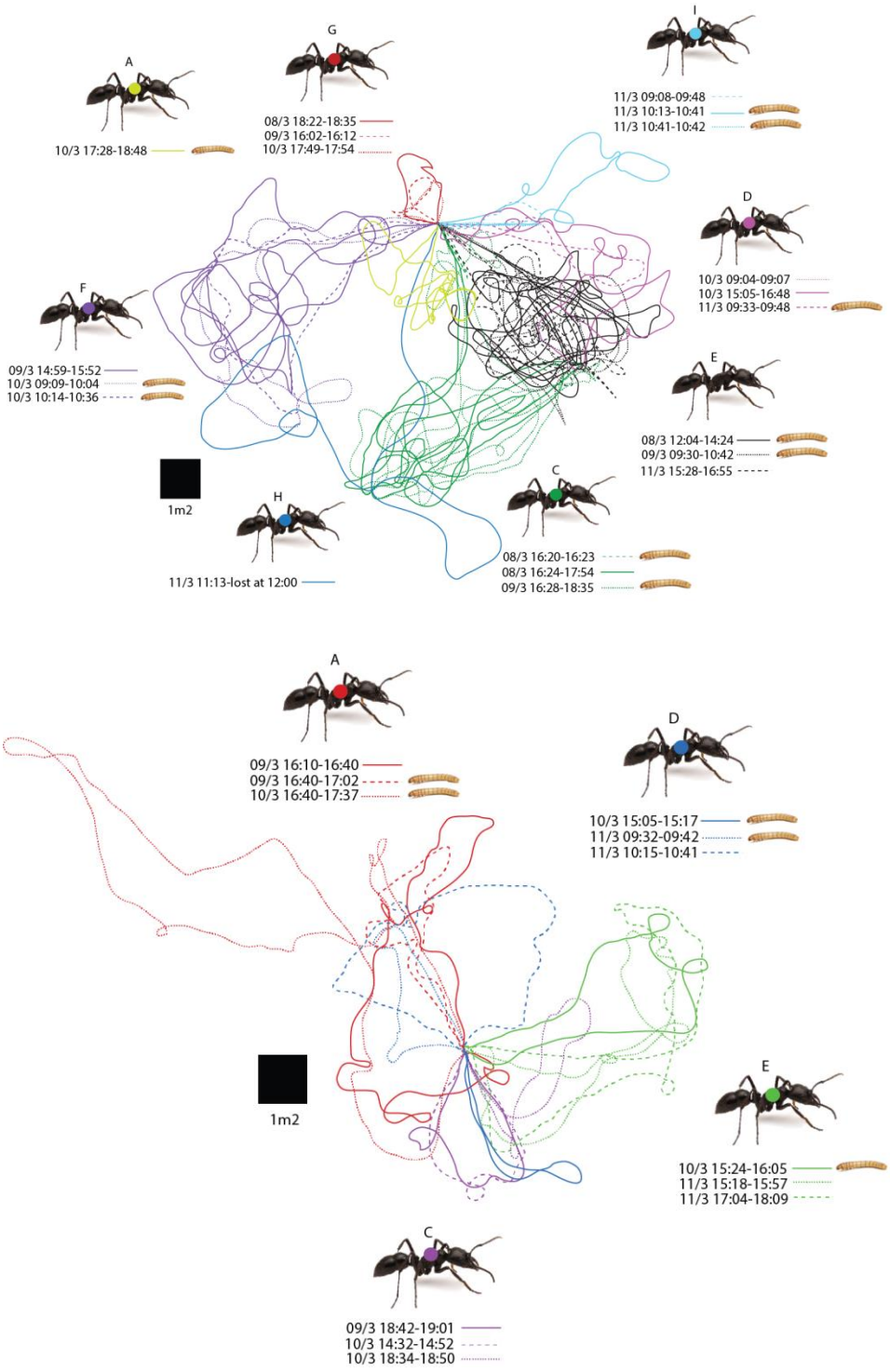


Fig 5.6 Foraging routes for workers from Colony 1 (above) and Colony 2 (bottom). Different foragers are marked with different colors. Each line type represents a different foraging trip. Day and hour of nest exit and entry are provided. A mealworm indicates that the ant brought food back to the nest.

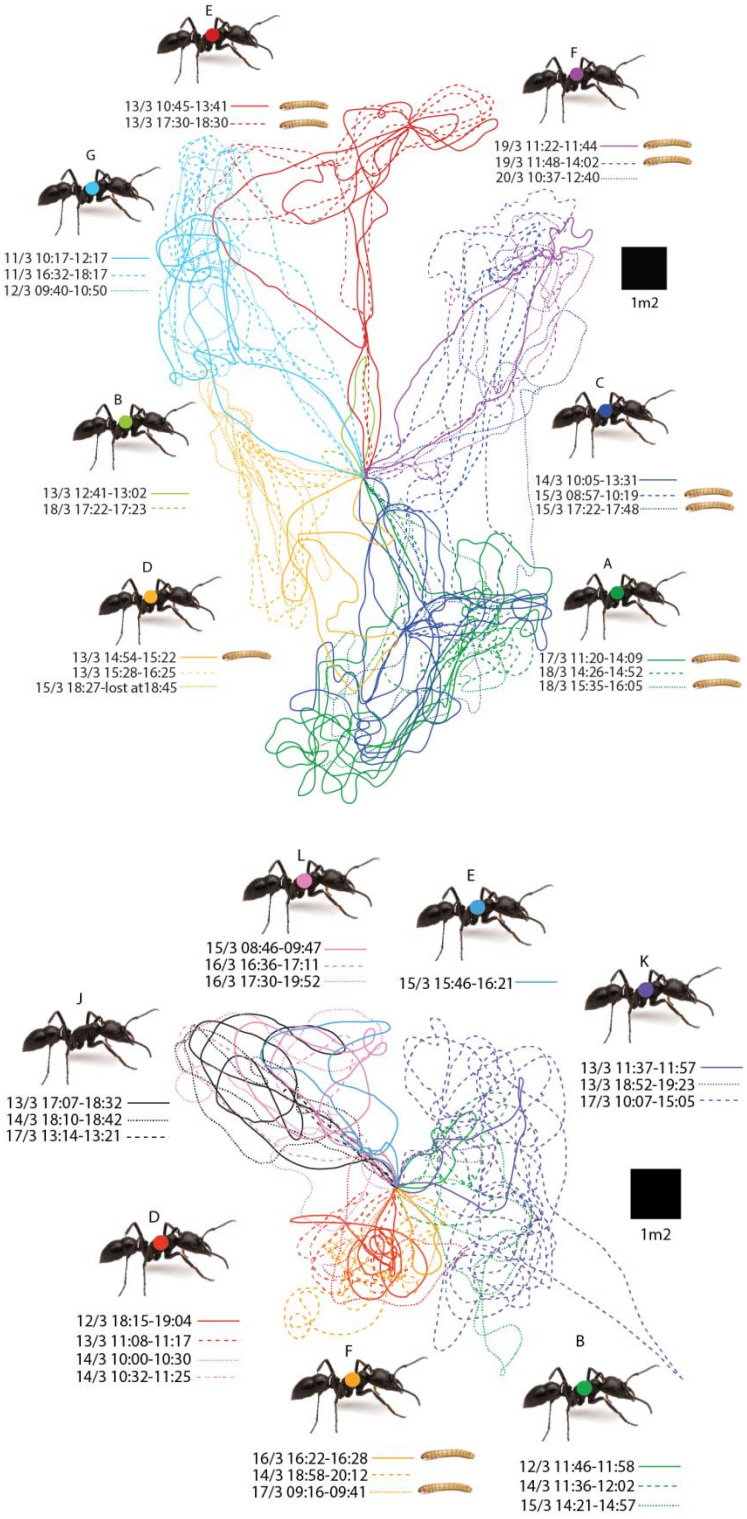


Fig 5.7 Foraging routes for workers from Colony 3 (above) and Colony 4 (bottom). Different foragers are marked with different colors. Each line type represents a different foraging trip. Day and hour of nest exit and entry are provided. A mealworm indicates that the ant brought food back to the nest.

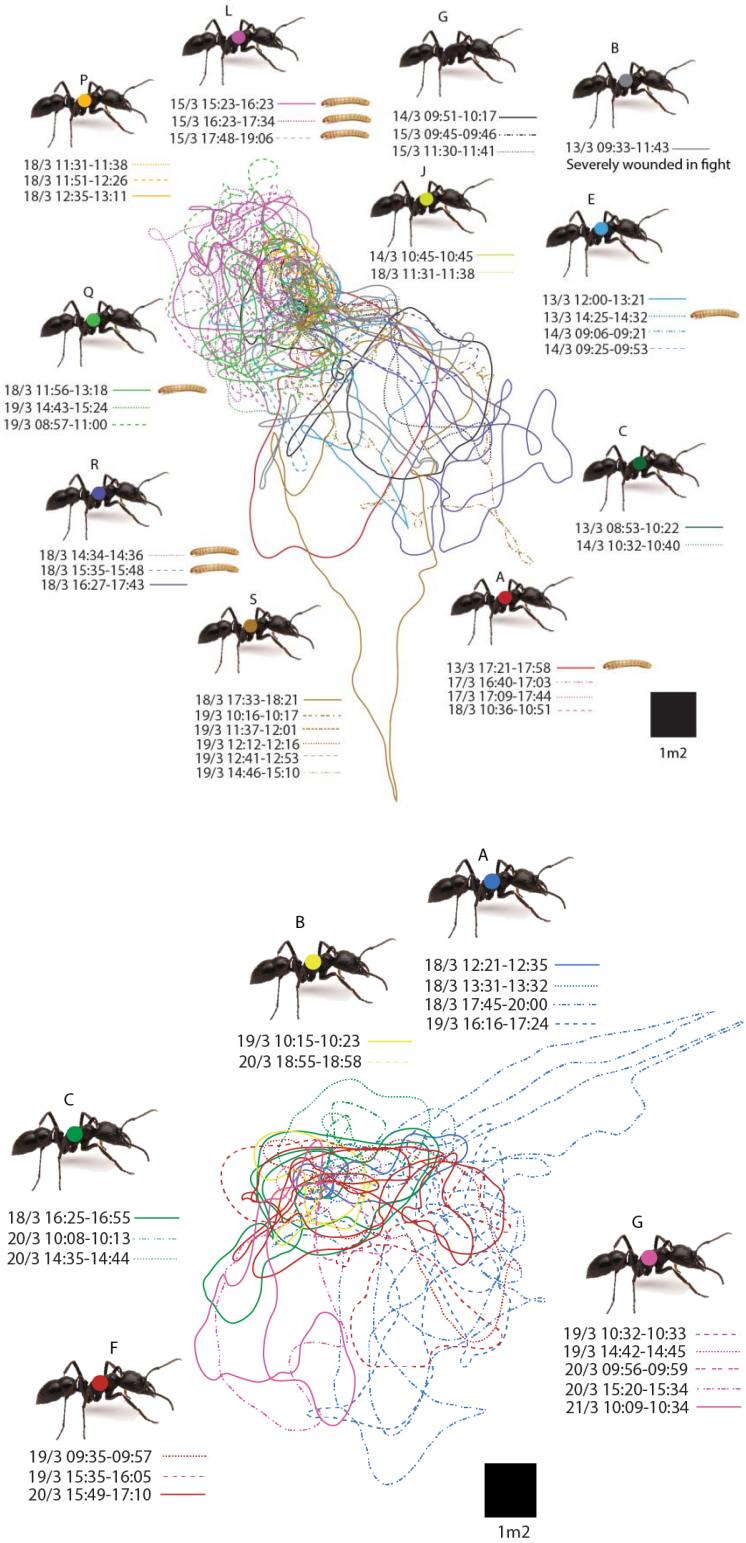


Fig 5.8 Foraging routes for workers from Colony 5 (above) and Colony 6 (bottom). Different foragers are marked with different colors. Each line type represents a different foraging trip. Day and hour of nest exit and entry are provided. A mealworm indicates that the ant brought food back to the nest.

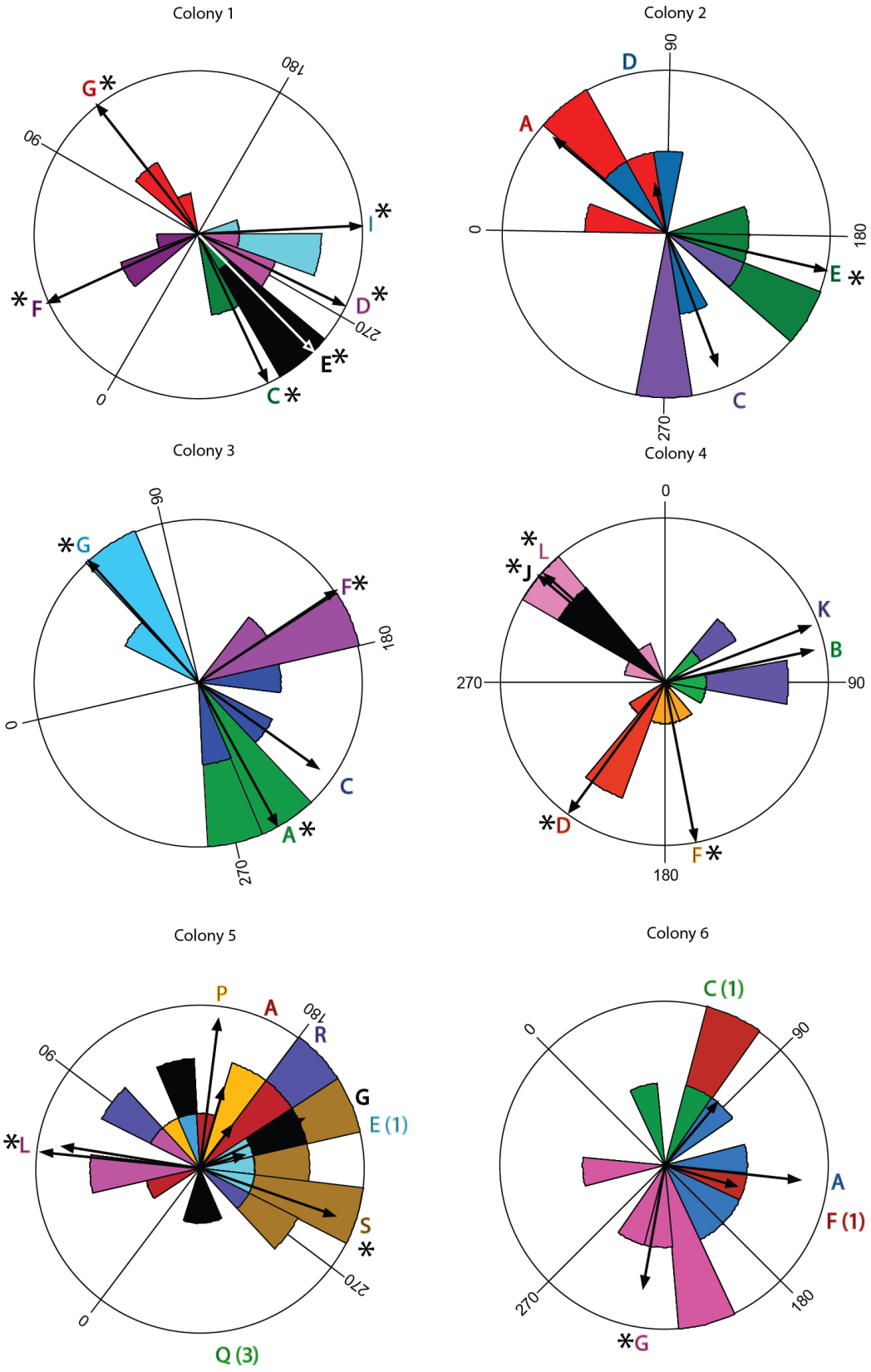


Fig 5.9 Raylech test results for all foragers with 3 or more complete foraging trips. Significance is shown with a * next to the forager letter. Numbers in brackets means number of trips without a preferred direction.

Table 5.2 Summary of Raylech test for all the foragers with three or more trips. In **bold**, p values equal or lower than 0.05. Numbers in brackets represent number of trips without a preferred direction.

Colony	Forager	N	Z	p
1	C	3	2.922	**0.038**
1	D	3	2.86	**0.042**
1	E	3	2.995	**0.034**
1	F	3	2.974	**0.035**
1	G	3	2.963	**0.036**
1	I	3	2.921	**0.038**
2	C	3	2.191	0.108
2	D	3	0.271	0.793
2	E	3	2.908	**0.039**
2	A	3	2.397	0.082
3	C	3	2.364	0.086
3	F	3	2.969	**0.035**
3	G	3	2.946	**0.036**
3	A	3	2.917	**0.038**
4	D	4	3.788	**0.011**
4	B	3	2.477	0.074
4	F	3	2.832	**0.044**
4	J	3	2.982	**0.034**
4	K	3	2.654	0.057
4	L	3	2.843	**0.043**
5	L	3	2.755	**0.049**
5	A	4	1.001	0.394
5	E	3 (1)	1.049	0.385
5	G	3	0.228	0.823
5	P	3	2.462	0.075
5	Q	(3)	-	-
5	R	3	0.311	0.766
5	S	6	4.431	**0.006**
6	A	4	2.659	0.061
6	G	5	2.837	**0.05**
6	C	2 (1)	1.707	0.199
6	F	2 (1)	0.913	0.464

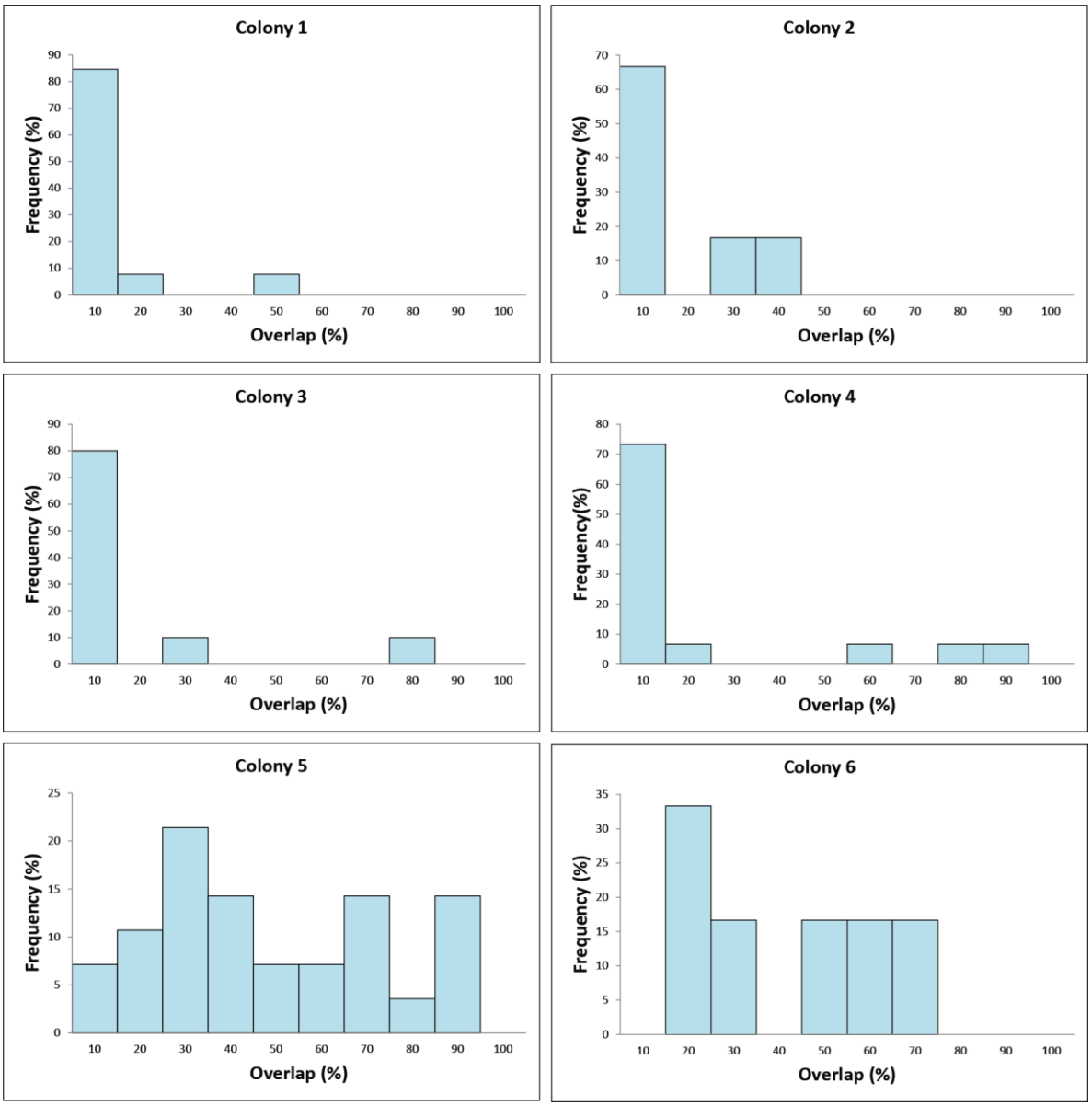


Fig 5.10 Frequency distribution of overlapping foraging areas, relative to the total foraging area across all nestmates pairs for the six *D. australis* colonies.

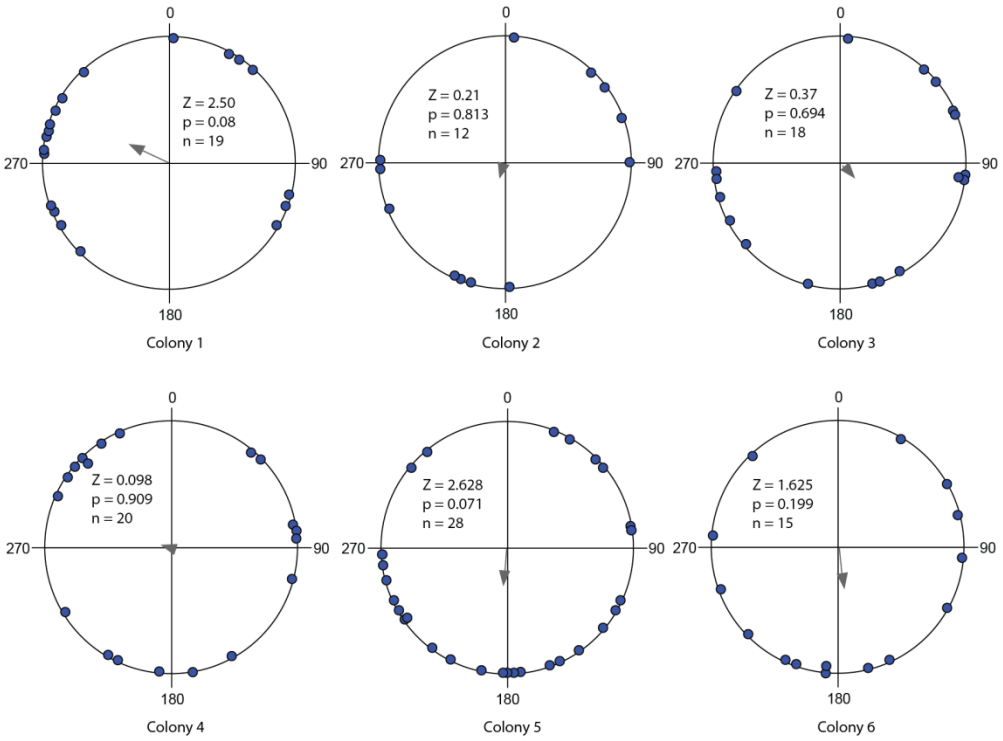


Fig 5.11 Average foraging direction for the six *D. australis* colonies. Inside the circles, results for Raylech test are shown. Grey arrow represents the mean vector.

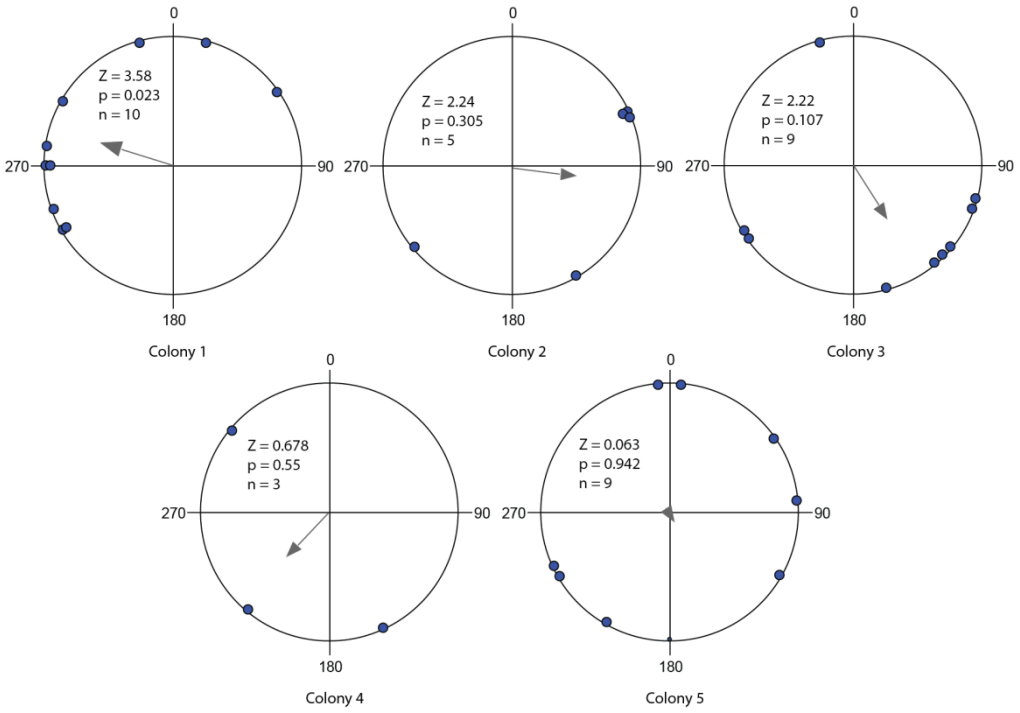


Fig 5.12 Distribution of the collected food for the five *D. australis* colonies that returned with food during the observation period. Inside the circles, results for Raylech test are shown. Grey arrow represents the mean vector.

5.5. Discussion

We observed the foraging behavior of *D. australis* workers from 6 colonies at Iguazú National Park. By mapping and observing 120 complete foraging routes, we found that half of the foragers exhibited route fidelity having a preferred foraging area. Additionally, in four colonies, overlap in foraging area among nestmates was less than 10%. Three of these colonies had foraging success rates of nearly 50%. In contrast, in two colonies (5 and 6) workers were less likely to exhibit route fidelity, had greater overlap in foraging area between nestmates, and foraging success was under 26%. In these colonies we also found foragers with trips without a preferred direction (Table 5.2).

Although additional research is still needed, our results suggest food availability may influence foraging patterns. As observed in other species (Fourcassié & Oliveira 2002, Araújo & Rodrigues 2006, Azevedo et al. 2014), we observed foragers returning with food quickly return to the same place where they have previously found food (for example, foragers I and C of Colony 1, forager F of Colony 3, and forager L of Colony 5; Fig 5.6 – 5.8). Additionally, Azevedo et al. (2014) found that a previous successful trip increased the percentage of success on the next trip in *D. quadriceps*. Using a computer model based on quantitative data of *Catagliphis bicolor* foraging behavior, Harkness and Maroudas (1985) found that a simple spatial reinforcement (i.e. returning to the location were food was found) can lead to spatial fidelity and, when food is randomly distributed, a partitioning of foraging area at the colony level. However, we also observed ants that did not find food in any of the observed foraging trips still showed a preference for a specific foraging area (for example: forager G of Colony 1, forager G of Colony 3, foragers L, J and D of Colony 4, forager S of Colony, and forager G of Colony 6; Fig 5.6 - 5.8 and Fig 5.11). This suggests the ants may develop a preference for a particular area regardless of previus foraging success (Fourcassie et al. 1999). In contrast, low food availability around the colony could lead to an absence of route fidelity (as seen in Colony

6). Other factors like the encounter with foes (i.e. a forager from a neighboring colony) could also influence colony foraging patterns (Nonacs & Dill 1988).

Foraging was performed by 7-17% of the workers in the colony (determined after nest excavations). As found by Tillberg and colleagues (2014), colonies in INP were much bigger (52-84 individuals) than previously reported for Brazil populations (12-25 individuals; Fowler 1985; Monnin *et al.* 2003). The percentage of foragers during our observations was lower than observed by Smith et al. (2011) (average 26% of the colony), this is likely due to seasonal differences in when we conducted field work. In contrast to Smith et al. (2011), our observations were during the end of the breeding season and only 1 of the 3 colonies had larvae present (Appendix 5.2). The seasonal pattern of brood reproduction may also influence our results as higher foraging activity may occur when larvae are present (September to April). Future research should include examining seasonal variation in foraging behavior.

Average duration of the foraging trips we observed (45 min; range 0 min - 298 min) were similar to other species of *Dinoponera* (*D. quadriceps*: 36 min, range 10-175 (Araújo & Rodrigues 2006, Azevedo et al. 2014); *D. gigantea*: 30-60 min (Fourcassié & Oliveira 2002)). In contrast, foraging success (31%) and maximum distance traveled (range: 0.4 - 11.3 meters) was lower than for *D. quadriceps* (foraging success: 76%, range distance: 1.52 – 172.56 m; Azevedo *et al.* 2014). Foragers that make more distant foraging routes tend to find food more frequently, as found in *Neoponera apicalis* (Fresneau 1985). Congruently, the two colonies with the greatest foraging area (more than 50 m^2), were more successful in finding food (more than 50% of successful trips). Fowler (1985) observed foragers of *D. australis* walk away from the nest for more than 40 m, a distance 4 times higher than our maximum observed distance. This difference might be related to the higher density of colonies in INP, leading to a more intensive intra-specific territoriality interactions (Tillberg et al. 2014) and a division of foraging territories among different colonies. Nest distributions of *D. australis* at Iguazú are over-

dispersed (Tillberg et al. 2014) suggesting strong territorial competition among colonies as in other ants (Ryti & Case 1986, Thurber et al. 1993). Notably, we observed two marked workers from different colonies fighting each other several times, during different foraging trips, until finally one of them was severely injured. However, we did not see the "ritualized" interactions between non-nestmates described in other studies of *D. australis* (Fourcassié & Oliviera 2002, Tillberg *et al.* 2014).

The colony with the largest foraging area (3) was also the biggest excavated colony (84 individuals), although we estimated a size of 100 workers for colony 5 and this colony did not have a larger foraging area. More colonies need to be surveyed before we can determine the relationship between colony size and foraging area. However, it is likely that larger colonies will have more foragers which cover a larger area in search of resources. In contrast with *D. gigantea*, who forage exclusively on the ground, some foragers of *D. australis* were observed looking for food in vegetation including, on one occasion (colony 4), foraging up to 5 meters high in a tree. We also found a tendency for foraging activities to peak between 09:00 – 11:00 and 16:00 – 18:00 hours, a similar bimodal pattern was found in *D. gigantea* (Fourcassié & Oliveira 2002) were foraging activity is negative correlated with temperature, although in our study, the hottest hours were recorded during 16 - 18 hours of the afternoon.

In conclusion, our research supports the hypothesis that workers of *D. australis* exhibit route fidelity when foraging. This preference for foraging in a particular area, coupled with low overlap in foraging area among nestmates, may increase foraging efficiency and search area. Variation in the degree to which individual foragers and whole colonies exhibit this behavior suggests that environmental factors (such as food distribution) and past experience (foraging success) may be important in determining foraging behavior. Future work observing additional colonies that vary in size, as well as experiments that manipulate food abundance and

distribution, are needed to determine how individual and colony level foraging behaviors are shaped in this species.

Capítulo V en castellano

Los organismos sociales se benefician del comportamiento de alimentación grupal. Sin embargo, si los individuos se superponen ampliamente en las áreas de forrajeo, estos beneficios pueden no ser proporcionales a la cantidad de individuos que participan en la búsqueda de alimento. La fidelidad de ruta o especialización en un sector particular del nido, ha sido observada en varias especies de hormigas, incluyendo en Ponerinae. Este comportamiento puede reducir la probabilidad de perderse en hormigas que no usan marcación química para orientarse. Adicionalmente, la fidelidad de ruta puede llegar a incrementar la eficiencia de la colonia al reducir el solapamiento de rutas entre forrajeras del mismo nido si distintas obreras exploran distintos sectores.

En este capítulo, se examinó el comportamiento de forrajeo y la fidelidad de ruta en 6 colonias de *Dinoponera australis* en el Parque Nacional Iguazú. Su gran tamaño, el no reclutar a otras compañeras de nido a fuentes de comida, y las colonias con pocos individuos (44,6 ± 21,4 hormigas por nido) hacen de *D. australis* un buen modelo para estudiar las estrategias de forrajeo en hormigas. Adicionalmente es llamativa la alta biomasa que alcanza esta especie en el lugar de estudio (2.5 kg / ha). La hipótesis de este trabajo es que las forrajeras de *D. australis* se especializan en un área particular del nido, con diferentes forrajeras especializándose en distintas áreas para aumentar el territorio explorado de la colonia.

Se marcó individualmente a todas las forrajeas (42 individuos en total) y se mapeó 120 rutas de búsqueda de alimento completas. Adicionalmente, se registró otras variables como dirección, duración, encuentro de comida y distancia máxima al nido. Asimismo para cada colonia se calculó el área total de forrajeo (superposición de todas las rutas), distribución de la comida y distribución de las direcciones de forrajeo.

Como resultado, el tiempo medio de forrajeo fue de 45 min (rango 0 – 298 min). Por hormiga, la distancia media recorrida fue de 4 m (rango 0,4 – 11,3 m) y el área total media fue de 5,5 m^2 (rango 0,06 – 22,12 m^2). En cambio, el territorio de forrajeo de cada colonia en promedio fue de 52m^2 (rango 34,4 – 89,9 m^2). En el 31% de los viajes, las hormigas encontraron alimento. Siendo la distribución del alimento en casi todas las colonias aleatorio.

Se encontró que más del 50% de las forrajeras mostraron fidelidad de ruta. Con excepción de las colonias 5 y 6, la mayoría de los viajes se superpusieron en menos de un 10% con las áreas de forrajeo de otras compañeras de nido. Los resultados indican que las forrajeras de *D. australis* exhiben una fuerte fidelidad de ruta. Variación en el grado de este comportamiento a nivel individual y de la colonia puede deberse a factores ambientales (por ejemplo la distribución y disponibilidad de la comida) o biológicos (por ejemplo edad y experiencia de las hormigas). Futuros experimentos que varíen la disponibilidad y distribución de comida alrededor del nido podrían revelar cómo los factores bióticos y abióticos afectan el comportamiento de forrajeo en esta especie.

VI. General conclusions

This thesis describes patterns of diversity in the ant subfamily Ponerinae in Argentina, provides insights into the ecology and behavior of ponerines living in the Atlantic Forest, and generates novel genetic and taxonomic resources for future research. Altogether, We (1) provide evidence (molecular and/or morphological) illuminating species boundaries in six species (*D. australis*, *P. striata*, *O. chelifer*, *N. crenata, N. curvinodis* and *Hypoponera* cf. *opacior*), (2) provide quantitative evidence of the relative trophic positions of 18 species, (3) quantify the dominance of *D. australis* in an Atlantic Forest ant community and describe how foragers use route fidelity as a strategy to efficiently locate food and, (4) discuss the use of different algorithms, identification criteria and divergence thresholds in the application of DNA barcode in ants.

6.1. How many species?

By studying 408 new species of mammals discovered during 1993-2008 Ceballos and Ehrlich (2009) point out that even for charismatic and "well studied taxa", species diversity is poorly underestimated. In support of the authors' argument, a number of new mammal species have recently been discovered (Helgen et al. 2013, Hrbek et al. 2014, D'Elía et al. 2016, Fennessy et al. 2016, Nater et al. 2017). These new species are not all small animals from remotes places, but include a giraffe and river dolphin (Hrbek et al. 2014, Fennessy et al. 2016). If vertebrate diversity is not as well-known as we thought, how many species of insects remain to be found and described? A recent evaluation suggests that up to 80% of insects (of the nearly one million described) remain to be discovered (Stork 2018).

Because taxonomy provides the foundation for many other biological disciplines, mistaken taxonomy can lead to a variety of conceptual and methodological errors. For example, morphologically similar species and the resulting difficulty in identifying them can lead to undetected species invasions (Geller 1999), environmental management errors (Kittelson &

Boyd 1997, Van Bortel et al. 2001), and inaccurate measurements of the impact of processes like climate change (Knowlton 1993).

The discovery of cryptic species is hardly random: Cryptic species are usually first noted by ecological, behavioral or genetic variation (Wolf & Adis 1992, Hebert et al. 2004, Smith et al. 2006, Ferreira et al. 2010). For example, the strikingly polyphagia of many tachinid parasitoids lead to the discovery that 16 species of "generalist" were actually 73 distinct evolutionary lineages (as indicated by DNA barcoding), including many lineages specialized to attack different hosts (Smith et al. 2006). Similarly, *Neoponera apicalis* was suggested to be a species complex based on morphological variation in the group (Ferreira et al. 2010) according to petiole shape (Wild 2005) and subsequently cyto-genetic and ecological differences in sympatry, as well as differences in male morphology (Delabie et al. 2008).

We analyzed ant specimens using morphology and DNA barcoding in chapters II and III, and suggest six cryptic species candidates: *N. crenata*, *O. chelifer*, *D. australis*, *H.* cf *opacior, P. striata* and *E. edentatum*. Some of these taxa are conspicuous and relatively common, and are included in many ecological, behavioral and physiological studies (Medeiros et al. 1992, Pizo & Oliveira 1998, Orivel & Dejean 2001, Morgan et al. 2003, Passos & Oliveira 2004, Spagna et al. 2008, Medeiros & Oliveira 2009, Orivel et al. 2009, Raimundo et al. 2009, Rodrigues et al. 2010, Ávila Núñez et al. 2011, Bottcher et al. 2014, Nettel-Hernanz et al. 2015, Oliveira et al. 2016, Rosumek 2017). In the case of *E. edentatum* and *N. crenata,* the presence of cryptic species was already suggested in previous studies (Wild 2002, Nettel-Hernanz et al. 2015). Moreover, stable isotope analysis (chapter IV) revealed different diet compositions between populations for two of these species. In the case of *D. australis,* the average δ15N value was of 11.7 ‰ in Iguazú NP and 8.9 ‰ in Osununú PR. Similarly, the average δ15N value of *P. striata* was 10.7 ‰ in Iguazú NP and 7.8 ‰ in Osununú PR. Additionally, samples of *N. crenata* from Iguazú NP varied considerably in their estimated diet with N isotope values corresponding to

three trophic levels. Is this variation due to local adaptation in dietary specialization or spatial variation in food availability, or are dietary preferences an evidence for the presence of ecological variation between morphologically similar, yet different species? Similar variation in genetics and ecology can be seen in other ant groups; for example the ant *Tapinoma sessile* has a high COI intraspecific divergence in addition to a great variability of ecological traits (Menke et al. 2010). As in *T. sessile*, the taxonomic status of *N. crenata*, *O. chelifer*, *D. australis*, *H.* cf *opacior, P. striata* and *E. edentatum* warrants further investigation.

6.2. Species boundaries

Inferring species boundaries is not straightforward. Ambiguous boundaries are particularly common in cryptic or hybridizing species (Delabie et al. 2008, Ross et al. 2010), as illustrated in this thesis by *N. curvinodis*/*N. bactronica* (chapter II). An integrative taxonomic approach can be essential to ensuring that accurate species boundaries are obtained (Ross et al. 2010, Ramalho et al. 2016a, 2016b). For example, to distinguish cryptic species, acoustic signals are used in diverse taxa (Henry 1994, Ferreira et al. 2010). All species of *Ectatomma*, *Dinoponera*, *Hypoponera*, *Neoponera* and many *Odontomachus* communicate via acoustic signals (Schmidt & Shattuck 2014, Golden & Hill 2016). These signals are produced by raising and lowering the abdominal cuticle causing a series of ridges on the medial dorsal area of the abdomen to rub against a stridulatory file on the border of the preceding segment (Spangler 1967). These signals are generally barely audible without amplification, but acoustic signals of medium and large ants like *N. villosa* and *D. australis* are audible to the human ear.

Additionally, the petiolar node shape (represented by the height and the width at dorsal or lateral view) was the character that most contributed to PCA analysis (chapter II) in all analyzed species. This is consistent with previous taxonomic work that uses the morphology of the petiole as an important character for species delimitation in the subfamily Ponerinae (Brown 1976, Lucas et al. 2002, Wild 2005, Fernández 2007, Delabie et al. 2008, Jiménez et al.

2008, MacKay & Mackay 2010, Fernandes et al. 2014). Petiole shape likely influences the gaster's flexibility: it provides a flexible junction between the mesosoma and gaster. This allows an ant to bring the sting forward towards the front of its body; a movement that may be used to sting prey or for defense. Additionally, in ponerines this movement it is also used in competitive behaviors among females for reproduction or in territorial contest (Monnin & Peeters 1999, Fourcassié & Oliveira 2002). The presence of other structures on the petiole, like spines, may also provide defense against predators (Ito et al. 2017). However, the biological or environmental factors that may influence the morphological change in the petiole within or across species is still unknown. A modern technique to analyze shape is geometric morphometrics. Integration the results of this thesis with the study of acoustic signals and variation in the shape of the petiolar node (using geometric morphometrics) would likely help to resolve species boundaries in this group.

6.3. DNA barcode as a tool for species identification

In chapters II and III, we constructed a barcode library for nearly half of the known Argentine diversity of ants in the subfamily Ponerinae and for ants of Iguazú National Park. Together, these libraries include 563 sequences from 142 identified species. This dataset allow us to asociate 81 individual to a species name (e.g. males) and reveal inconsistencies between molecular variation and current taxonomy in 26 species (merge and split cases based on RESL algorithm in chapters II and III). Although more information is needed to resolve these cases, molecular tools like DNA Barcodes, in combination with other types of data, can help to accelerate the species discovery process in times of biodiversity crisis. Additionally, other applications, like early detection of invasive species can benefit from the generated global biodiversity databases (Dejean et al. 2012). As of January 2018, 70% of the ant records in BOLD are from North America, Africa and Central America. As a consequence, the DNA barcode library generated in this thesis represents an important addition to the reference library of the ants of the region.

6.4. Influence of ponerines in their ecosystems

Knowledge of species diversity and taxonomy constitutes the groundwork for ecological research. However, this information is best combined with careful study of the basic biology, including diet and activity, of organisms. Chapters IV and V of this thesis attempted to fill the natural history gap for many of the ponerine species living in the Atlantic Forest. We found that the majority of 18 analyzed species were primary or secondary predators. These species may regulate the invertebrate and plant community via "top-down" effects in which predators limit herbivore abundance thereby preventing them from overexploiting the vegetation (Hairston et al. 1960, Terborgh et al. 2006). As a consequence, perturbation in one trophic level can propagate trough lower levels (Ripple et al. 2016). By removing predacious ants, different studies reported changes in different trophic levels, including herbivores, spiders and seed plant production (Schmitz et al. 2000, Moya-Laraño & Wise 2007, Philpott et al. 2008, Sanders & Van Veen 2011).

Ants in general are considered a dominant and abundant component of ecosystems; however, within ants, most ecological studies report ants from the Formicoid clade as dominant (Fellers 1987, Perfecto & Vandermeer 2013, Stuble et al. 2013, Ronque et al. 2018). For example, in his article "Which are the most prevalent ant genera", Wilson (1976) ranked several genera based on their species diversity, extent of geographic range, diversity of adaptations, and local abundance. The "winners" were *Camponotus*, *Pheidole* and *Crematogaster*, two myrmicines and one formicine.

However, in Iguazú NP, two ponerines species were the most captured species: *D. australis* and *P. striata* (using pitfall trap and surface baits). Moreover, *D. australis* has a biomass of 2.5 kg / ha at Iguazú NP (Tillberg et al. 2014). Contrary to *D. australis*, the inconspicuous colonies of *P. striata* make the calculation of nest density and biomass difficult. However, capture frequency in pitfall traps and surface baits suggest a high colony density as well. As a

consequence, in terms of biomass and abundance, *P. striata* and *D. australis* can be characterized as dominant in Iguazú NP. It is worth noting that the high abundance of *D. australis* may be unique to Iguazú, been a less common species in other localities of Misiones. For example, in Osununú PR, 50 pitfall traps were placed as part of our diversity survey and *D. australis* was captured in only 12% of the traps (in contrast with the near 100% of frequency capture in Iguazú NP).

Lacking a queen caste, the fertility of egg-laying by gamergates in *Dinoponera* is low (Peeters 1991a). Indeed, from observations in the lab, gamergates lay less than one egg per day (data not shown) during the reproductive season. Additionally, larva development can take several months. However, their high density at Iguazú may be explained by the life span of individual workers and colony fission (a group of ants will migrate from the mother colony to establish a new nest) (Fowler 1985). Moreover, other factors like their large size and foraging strategy (chapter V) can give them advantage in foraging efficiency, overcoming prey, and competition with other ants. Nonetheless we do not know why their high biomass occurs only in our studied areas in Iguazú, and not in other similar locations.

Within colonies of *D. australis*, another ant (*Pheidole dinophila)* can be commonly found. Samples of these *Pheidole* were included in the stable isotope analysis. The δN signal (9.50 ± 0.49) was very similar to that of *D. australis*. It is possible that this ant feeds on prey and refuse generated by *D. australis*. Also, *P. dinophila* was not seen foraging outside the nest. Other fauna associated with *D. australis* include a spider, terrestrial snail, a number of beetles, cockroaches, moths, millipedes and fly larva. Many of these are found in the underground refuse depositories of their nests. Moreover, the snail and spider seem to constitute new species (Sergio Michel and Alexandre Bonaldo personal communication). As a result, the colony density, high biomass, trophic position, and organisms associated with colonies of *D. australis*, suggest that this species is a key component of the invertebrate community in Iguazú

NP. Future studies should assess their impact on the invertebrate community (for example with exclusion experiments).

Capítulo VI en castellano

En esta tesis se describieron los patrones de diversidad en la subfamilia de hormigas Ponerinae en Argentina, proporcionando información sobre la ecología y el comportamiento de las especies que habitan en el Bosque Atlántico. Adicionalmente se generó recursos genéticos y taxonómicos para futuras investigaciones. En general, (1) se proporcionó evidencias (moleculares y / o morfológicas) que cuestionan los límites de las especies en seis ponerinas (*D. australis*, *P. striata*, *O. chelifer*, *N. crenata*, *N. curvinodis*, *Hypoponera* cf. *opacior*), (2) se generó evidencia cuantitativa sobre la posición trófica de 18 especies, (3) se estudió la dominancia de *D. australis* en una comunidad de hormigas del Bosque Atlántico y se describió cómo las forrajeras usan la fidelidad de ruta como estrategia para encontrar alimento y finalmente (4) se discutió el uso de diferentes algoritmos, criterios de identificación y umbrales de divergencia en la aplicación de los códigos de barras genéticos en hormigas.

Durante los últimos años, nuevas especies de mamíferos se han descubierto, muchas de ellas a raíz de nuevas herramientas moleculares y taxonómicas. Por ejemplo, recientemente se ha descubierto que la jirafa consiste en no una, sino cuatro especies distintas. Si la diversidad en un grupo carismático y relativamente bien estudiado, como lo son los vertebrados, no es tan conocida como se pensaba, ¿qué es lo que se sabe sobre la diversidad de grupos como los insectos? Una nueva estimación sobre la diversidad global de insectos indica que alrededor del 80% (sobre el casi millón de especies ya descriptas) faltan por describir.

Debido a que la taxonomía proporciona la base para muchas otras disciplinas biológicas, errores en la identificación de especies puede conducir a una diversidad de errores conceptuales y metodológicos. Adicionalmente, el descubrimiento de especies crípticas es difícilmente aleatorio: Diferencias comportamentales, fisiológicas, genéticas o ecológicas

suelen ser frecuentemente el origen de muchos descubrimientos de especies crípticas (por ejemplo, *Neoponera apicalis*). En esta tesis, se analizó la morfología y los códigos de barras genéticos de las ponerinas de Argentina (capítulos II y III), encontrando evidencias que cuestionan el estado de especies únicas de *N. crenata*, *O. chelifer*, *D. australis*, *H.* cf *opacior*, *P. striata* y *E. edentatum*. Adicionalmente, análisis de isótopos estables (capítulo IV) revelaron diferentes composiciones de dieta entre poblaciones para dos de estas especies: En el caso de *D. australis*, el valor promedio de δ15N fue de 11.7 ‰ en el PN Iguazú y de 8.9 ‰ en RP Osununú. De manera similar, el valor promedio δ15N de *P. striata* fue 10.7 ‰ en el PN Iguazú y 7.8 ‰ en RP Osununú. Por otra parte, las muestras de *N. crenata* del PN Iguazú variaron considerablemente, correspondientes a tres niveles tróficos. ¿Estas diferencias se deben a adaptaciones locales o variaciones en la disponibilidad de alimentos? o ¿son preferencias de especies morfológicamente similares pero diferentes? Sólo con los datos proporcionados en esta tesis no se puede llegar a una conclusión, pero herramientas, hoy en día poco usadas en la mirmecología, como la morfometría geométrica o los análisis acústicos podrán posiblemente ayudar a resolver estas preguntas.

El conocimiento de la diversidad de especies y la taxonomía constituye la base de la ecología. Sin embargo, a su vez, esta información es mejor comprendida en el contexto de la biología o la historia natural de la especie. En esta tesis, los capítulos IV y V estuvieron enfocados en entender la historia natural, ecología y comportamiento de las ponerinas del Bosque Atlántico. Como resultado, se encontró que de las 18 especies analizadas mediante isótopos estables, la mayoría de las especies son depredadoras (primarias o secundarias). Esto resalta la función de las ponerinas en los ecosistemas como reguladoras de la comunidad de invertebrados y plantas a través de efectos "hacia-abajo" en la cadena trófica. Adicionalmente, en el PN Iguazú se encontró que dos ponerinas, *P. striata* y *D. australis,* en términos de biomasa y abundancia son dominantes en la comunidad de hormigas.

La fecundidad y tasa de puesta de huevos en *D. australis* es relativamente baja. Adicionalmente las larvas pueden tardar varios meses en desarrollarse. Es probable que la alta densidad de esta especie en Iguazú se pueda explicar por la larga vida de las obreras y la división de las colonias como método reproducción. Además, otros factores, como su gran tamaño y su estrategia de búsqueda de alimento (capítulo V), pueden darles ventaja en la eficiencia de la búsqueda de alimento, la captura de presas y la competencia con otras hormigas. No obstante, se desconoce por qué su alta biomasa ocurre solo en Iguazú, y no en otras ubicaciones similares.

Dentro de las colonias de *D. australis*, se puede encontrar comúnmente otra especie de hormiga (*Pheidole dinophila*). Muestras de esta especie fueron incluidas en los análisis de isótopos estables, siendo la señal de δN (9.50 ± 0.49) muy similar a la de *D. australis*. Como resultado, es posible que esta hormiga se aproveche de las presas capturadas por *D. australis*. Adicionalmente otra fauna asociada a *D. australis* incluye una araña, un caracol terrestre, varios escarabajos, cucarachas, milpies y larvas de moscas y polillas. Muchos de ellos, asociados a su vez con los depósitos de desechos subterráneos de los nidos. Como resultado, la densidad de esta especie, alta biomasa, posición trófica y los organismos asociados a *D. australis* sugieren que esta especie es un componente clave de la comunidad de invertebrados en el PN Iguazú. Estudios futuros podrán evaluar su impacto en la comunidad de invertebrados (por ejemplo, con experimentos de exclusión).

Bibliography

ADAMS, E. S. & TSCHINKEL, W. R. 1995. Density-Dependent competition in Fire Ants: Effects on colony survivorship and size variation. *The Journal of Animal Ecology* 64:315.

ADLER, F. R., LEBRUN, E. G. & FEENER JR., D. H. 2007. Maintaining diversity in an ant community: Modeling, extending, and testing the Dominance-Discovery trade-off. *The American Naturalist* 169:323–333.

AGOSTI, D. & ALONSO, L. 2000. The ALL Protocol. *Ants: standard methods for measuring and monitoring biodiversity*. Smithsonian Institution Press, Washington, DC. 204-206 pp.

AGUILAR-VELASCO, R. G., POTEAUX, C., MEZA-LÁZARO, R., LACHAUD, J.-P. P., DUBOVIKOFF, D. & ZALDÍVAR-RIVERÓN, A. 2016. Uncovering species boundaries in the Neotropical ant complex *Ectatomma ruidum* (Ectatomminae) under the presence of nuclear mitochondrial paralogues. *Zoological Journal of the Linnean Society* 178:226–240.

ALONSO, L. E. 1998. Spatial and temporal variation in the ant occupants of a facultative ant-plant. *Biotropica* 30:201–213.

ANDERSEN, A. N. 1983. Species diversity and temporal distribution of ants in the semi-arid mallee region of northwestern Victoria. *Austral Ecology* 8:127–137.

ANDERSEN, A. N. 1992. Regulation of 'Momentary' diversity by dominant species in exceptionally rich ant communities of the australian seasonal tropics. *The American naturalist* 140:401–420.

ARAÚJO, A. & RODRIGUES, Z. 2006. Foraging behavior of the queenless ant *Dinoponera quadriceps* Santschi (Hymenoptera: Formicidae). *Neotropical entomology* 35:159–164.

ARIA, C., PERRICHOT, V. & NEL, A. 2011. Fossil Ponerinae (Hymenoptera: Formicidae) in Early Eocene amber of France. *Zootaxa* 2870:53–62.

AUSTIN, A. T. & VITOUSEK, P. M. 1998. Nutrient dynamics on a precipitation gradient in Hawai'i. *Oecologia* 113:519–529.

ÁVILA NÚÑEZ, J. L., NAYA, M., CALCAGNO-PISSARELLI, M. P. & OTERO, L. D. 2011. Behaviour of *Odontomachus chelifer* (Latreille) (Formicidae: Ponerinae) Feeding on Sugary Liquids. *Journal of Insect Behavior* 24:220–229.

AZEVEDO, D. L. O., MEDEIROS, J. C. & ARAÚJO, A. 2014. Adjustments in the time, distance and direction of foraging in *Dinoponera quadriceps* workers. *Journal of Insect Behavior* 27:177–191.

BACCARO, F. B., DE SOUZA, J. L. P., FRANKLIN, E., LANDEIRO, V. L. & MAGNUSSON, W. E. 2012. Limited effects of dominant ants on assemblage species richness in three Amazon forests. *Ecological Entomology* 37:1–12.

BADANO, E. I., REGIDOR, H. A., NUNEZ, H. A., ACOSTA, R. & GIANOLI, E. 2005. Species richness and structure of ant communities in a dynamic archipelago: Effects of island area and age. *Journal of Biogeography* 32:221–227.

BARCELLOS, M. S., MARTINS, L. C. B., COSSOLIN, J. F. S., SERRÃO, J. E., DELABIE, J. H. C. & LINO-NETO, J. 2015. Testes and spermatozoa as characters for distinguishing two ant species of the genus *Neoponera* (Hymenoptera: Formicidae). *Florida Entomologist* 98:1254–1256.

BARCO, A., RAUPACH, M. J., LAAKMANN, S., NEUMANN, H. & KNEBELSBERGER, T. 2016. Identification of North Sea molluscs with DNA barcoding. *Molecular Ecology Resources* 16:288–297.

BARTH, M. B., MORITZ, R. F. A. A. & KRAUS, F. B. 2015. Genetic differentiation at species level in the Neotropical army ant *Labidus praedator*. *Insectes Sociaux* 62:299–306.

BERNSTEIN, R. A. 1975. Foraging strategies of ants in response to variable food density. *Ecology* 56:213–219.

BESANSKY, N. J. 1999. Complexities in the analysis of cryptic taxa within the genus *Anopheles*. *Parassitologia* 41:97–100.

BESTELMEYER, B. T. & WIENS, J. A. 1996. The effects of land use on the structure of ground-foraging ant communities in the Argentine Chaco. *Ecological Applications* 6:1225–1240.

BICKFORD, D., LOHMAN, D. J., SODHI, N. S., NG, P. K. L., MEIER, R., WINKER, K., INGRAM, K. K. & DAS, I. 2007. Cryptic species as a window on diversity and conservation. *Trends in Ecology & Evolution* 22:148–155.

BLAIMER, B. B., FISHER, B. L., FELDHAAR, H., MACKAY, D. & NEI, M. 2013. How much variation can one ant species hold? Species delimitation in the *Crematogaster kelleri*-Group in Madagascar. *PLoS ONE* 8:e68082.

BOLTON, B. 2003. Synopsis and classification of Formicidae. Memoirs of the American Entomological Institute. 370 pp.

BOLTON, B. & FISHER, B. L. 2011. Taxonomy of Afrotropical and West Palaearctic ants of the ponerine genus *Hypoponera* Santschi (Hymenoptera: Formicidae). *Zootaxa* 2843:1–118.

BORGMEIER, T. 1948. Einige Ameisen aus Argentinien (Hym. Formicidae). *Revista de Entomologia (Rio de Janeiro)* 19:459–471.

VAN BORTEL, W., HARBACH, R. E., TRUNG, H. D., ROELANTS, P., BACKELJAU, T. & COOSEMANS, M. 2001. Confirmation of *Anopheles varuna* in vietnam, previously misidentified and mistargeted as the malaria vector *Anopheles minimus*. *The American Journal of Tropical Medicine and Hygiene* 65:729–732.

BOTTCHER, C., OLIVEIRA, P. S. 2014. Consumption of lipid-rich seed arils improves larval development in a Neotropical primarily carnivorous ant, *Odontomachus chelifer* (Ponerinae). *Journal of Tropical Ecology* 30:621–624.

BOUDINOT, B. 2013. The male genitalia of ants: musculature, homology, and functional morphology (Hymenoptera, Aculeata, Formicidae). *Journal of Hymenoptera Research* 30:29–49.

BOUDINOT, B. E., SUMNICHT, T. P. & ADAMS, R. M. 2013. Central American ants of the genus *Megalomyrmex* Forel (Hymenoptera: Formicidae): six new species and keys to workers and males. *Zootaxa* 3732:1–82.

BRANDÃO, C. R. F., DINIZ, J. L. M. & TOMOTAKE, E. M. 1991. *Thaumatomyrmex* strips millipedes for prey: a novel predatory behaviour in ants, and the first case of sympatry in the genus (Hymenoptera: Formicidae). *Insectes Sociaux* 38:335–344.

BROWN, J. H. & DAVIDSON, D. W. 1977. Competition between Seed-Eating rodens and ants in

desert ecosystems. *Science* 196:880–882.

BROWN, S. D. J., COLLINS, R. A., BOYER, S., LEFORT, M.-C., MALUMBRES-OLARTE, J., VINK, C. J. & CRUICKSHANK, R. H. 2012. Spider: An R package for the analysis of species identity and evolution, with particular reference to DNA barcoding. *Molecular Ecology Resources* 12:562–565.

BROWN, W. L. 1976. Contributions toward a reclassification of the Formicidae. Part VI. Ponerinae, Tribe Ponerini, Subtribe Odontomachiti. Section B. Genus *Anochetus* and bibliography. *Studia Entomologica* 19:549–638.

BRUCH, C. 1914. Catálogo sistemático de los formícidos argentinos. *Revista del Museo de La Plata* 19:211–234.

BRUCH, C. 1915. Suplemento al catálogo de los formícidos argentinos. I. (Addenda et corrigenda). *Revista del Museo de La Plata* 19:527–537.

CABANA, G. & RASMUSSEN, J. 1994. Modelling food chain structure and contaminant bioaccumulation using stable nitrogen isotopes. *Nature* 372:255–257.

CALCATERRA, L. A., CUEZZO, F., CABRERA, S. M. & BRIANO, J. A. 2010. Ground Ant Diversity (Hymenoptera: Formicidae) in the Iberá Nature Reserve, the largest wetland of Argentina. *Annals of the Entomological Society of America* 103:71–83.

CALCATERRA, L. A., LIVORE, J. P., DELGADO, A. & BRIANO, J. A. 2008. Ecological dominance of the red imported fire ant, *Solenopsis invicta*, in its native range. *Oecologia* 156:411–421.

CEBALLOS, G. & EHRLICH, P. R. 2009. Discoveries of new mammal species and their implications for conservation and ecosystem services. *Proceedings of the National Academy of Sciences of the United States of America* 106:3841–6.

CERDÁ, X., ARNAN, X. & RETANA, J. 2013. Is competition a significant hallmark of ant (Hymenoptera: Formicidae) ecology? *Myrmecological News* 18:131–147.

CERDÁ, X., RETANA, J. & CROS, S. 1997. Thermal disruption of transitive hierarchies in Mediterranean ant communities. *Journal of Animal Ecology* 66:363–374.

CHRISTIANINI, A. V., MAYHÉ-NUNES, A. J. & OLIVEIRA, P. S. 2007. The role of ants in the removal of non-myrmecochorous diaspores and seed germination in a neotropical savanna. *Journal of Tropical Ecology* 23:343–351.

CHRISTIANINI, A. V. & OLIVEIRA, P. S. 2010. Birds and ants provide complementary seed dispersal in a neotropical savanna. *Journal of Ecology* 98:573–582.

CLARK, C. W. & MANGEL, M. 1986. The evolutionary advantages of group foraging. *Theoretical Population Biology* 30:45–75.

CLARKE, K. R. 1993. Non-parametric multivariate analyses of changes in community structure. *Austral Ecology* 18:117–143.

CLEMENT, M., POSADA, D. C. K. A. & CRANDALL, K. A. 2000. TCS: a computer program to estimate gene genealogies. *Molecular Ecology* 9:1657–1659.

COLEMAN, D. C. & WHITMAN, W. B. 2005. Linking species richness, biodiversity and ecosystem function in soil systems. *Pedobiologia* 49:479–497.

CUEZZO, F. 1998. Formicidae. Pp. 452–462in Morrone, J. J. & Coscarón, S. (eds.).*Diversidad de Artrópodos Argentinos. Una perspectiva biotaxonómica.* (Ediciones). La Plata, Buenos Aires.

D'ELÍA, G., HURTADO, N. & D'ANATRO, A. 2016. Alpha taxonomy of *Dromiciops* (Microbiotheriidae) with the description of 2 new species of monito del monte. *Journal of Mammalogy* 97:1136–1152.

DASH, S. T. 2011. A taxonomic revision of the new world Hypoponera Santschi, 1938 (Hymenoptera: Formicidae). University of Texas, El Paso. 1-294 pp.

DÁTTILO, W. & IZZO, T. J. 2012. Temperature Influence on Species Co-Occurrence Patterns in Treefall Gap and Dense Forest Ant Communities in a Terra- Firme Forest of Central Amazon, Brazil. *Sociobiology* 59:351–367.

DAVIDSON, D. W. 1985. An Experimental Study of Diffuse Competition in Harvester Ants. *The American Naturalist* 125:500–506.

DEJEAN, A. & SUZZONI, J. P. 1997. Surface Tension Strengths in the Service of a Ponerine Ant: a New Kind of Nectar Transport. *Naturwissenschaften* 84:76–79.

DEJEAN, T., VALENTINI, A., MIQUEL, C., TABERLET, P., BELLEMAIN, E. & MIAUD, C. 2012. Improved detection of an alien invasive species through environmental DNA barcoding: the example of the American bullfrog *Lithobates catesbeianus*. *Journal of Applied Ecology* 49:953–959.

DELABIE, J. H. C., FRESNEAU, D. & PEZON, A. 2000. Notes on the ecology of *Thaumatomyrmex* spp. (Hymenoptera: Formicidae: Ponerinae) in Southest Bahia, Brazil. *Sociobiology* 36:571–584.

DELABIE, J. H. C., MARIANO, C. S. F., MENDES, L. F., POMPOLO, S. G. & FRESNEAU, D. 2008. Problemas apontados por estudos morfológicos, ecológicos e citogenéticos no gênero *Pachycondyla* na região neotropical: o caso do complexo *apicalis*. Pp. 197–222 in Vilela, E., Santos, I., Schoereder, J. H., Serrao, J., LAO, C. & Neto, L. (eds.).*Insetos Sociais: da Biologia à Aplicação*. UFV.

DELSINNE, T., SONET, G., NAGY, Z. T., WAUTERS, N., JACQUEMIN, J. & LEPONCE M. 2012. High species turnover of the ant genus *Solenopsis* (Hymenoptera:Formicidae) along an altitudinal gradient in the Ecuadorian Andes, indicated by a combined DNA sequencing and morphological approach. *Invertebrate Systematics* 26:457–469.

DENIRO, M. J. & EPSTEIN, S. 1981. Influence of diet on the distribution of nitrogen isotopes in animals. *Geochimica et cosmochimica acta*, 45: 341-351.

DEVRIES, P. J. 1991. Mutualism between *Thisbe irenea* butterflies and ants, and the role of ant ecology in the evolution of larval-ant associations. *Biological Journal of the Linnean Society* 43:179–195.

DIETEMANN, V. & PEETERS, C. 2000. Queen influence on the shift from trophic to reproductive eggs laid by workers of the ponerine ant *Pachycondyla apicalis*. *Insectes Sociaux* 47:223–228.

DORNHAUS, A. & POWELL, S. 2010. Foraging and defence strategies. Pp. 210–230 in *Ant ecology*.

EATON, J. W., BATEMAN, D., HAUBERG, S. & WEHBRING, R. 2016. GNU Octave.

ELLWOOD, M. D. D. F. F., BLÜTHGEN, N., FAYLE, T. M., FOSTER, W. A., MENZEL, F., BLUTHGEN, N., FAYLE, T. M., FOSTER, W. A. & MENZEL, F. 2016. Competition can lead to unexpected patterns in tropical ant communities. *Acta Oecologica* 75:24–34.

EMERY, C. 1888. Alcune formiche della Repubblica Argentina raccolte dal Dott. C. Spegazzini. *Annali del Museo Civico di Storia Naturale* 6:690–694.

EMERY, C. 1894. Viaggio del dottor Alfredo Borelli nella Repubblica Argentina e nel Paraguay. VIII. Formiche. *Bollettino dei Musei di Zoologia ed Anatomia Comparata della Reale Università di Torino* 9:1–4.

EMERY, C. 1901. Notes sur les sous-familles des Dorylines et Ponérines (Famille des Formicides). *Annales de la Société Entomologique de Belgique* 45:32–54.

EMERY, C. 1906. Studi sulle formiche della fauna neotropica. XXVI. *Bullettino della Società Entomologica Italiana* 37:107–194.

EVANS, H. C. & LESTON, D. 1971. A Ponerine ant (Hym., Formicidae) associated with Homoptera on cocoa in Ghana. *Bulletin of Entomological Research* 61:357.

EVANS, R. D. 2001. Physiological mechanisms influencing plant nitrogen isotope composition. *Trends in Plant Science* 6:121–126.

FARJI-BRENER, A. G., BARRANTES, G. & RUGGIERO, A. 2004. Environmental rugosity, body size and access to food: a test of the size-grain hypothesis in tropical litter ants. *Oikos* 104:165–171.

FEITOSA, R. M., SILVA, R. R. DA, AGUIAR, A. P., FEITOSA, R. M., SILVA, R. R. DA & AGUIAR, A. P. 2016. Diurnal flight periodicity of a Neotropical ant assemblage (Hymenoptera, Formicidae) in the Atlantic Forest. *Revista Brasileira de Entomologia* 60:241–247.

FELLERS, J. H. 1987. Interference and Exploitation in a Guild of Woodland Ants. *Ecology* 68:1466–1478.

FENNESSY, J., BIDON, T., REUSS, F., KUMAR, V., ELKAN, P., NILSSON, M. A., VAMBERGER, M., FRITZ, U. & JANKE, A. 2016. Multi-locus analyses reveal four giraffe species instead of one. *Current Biology* 26:2543–2549.

FERNANDES, I. O., DE OLIVEIRA, M. L. & DELABIE, H. C. 2014. Description of two new species in the Neotropical *Pachycondyla foetida* complex (Hymenoptera : Formicidae : Ponerinae) and taxonomic notes on the genus. *Myrmecological News* 19:133–163.

FERNÁNDEZ, F. 2007. Two new South American species of *Monomorium* Mayr with taxonomic notes on the genus. *Memoirs of the American Entomological Institute* 80:128–145.

FERREIRA, R. S., POTEAUX, C., DELABIE, J. H. C., FRESNEAU, D. & RYBAK, F. 2010. Stridulations reveal cryptic speciation in neotropical sympatric ants. *PLoS ONE* 5:e15363.

FEWELL, J. H. 1990. Directional fidelity as a foraging constraint in the western harvester ant, *Pogonomyrmex occidentalis*. *Oecologia* 82:45–51.

FLOYD, R., ABEBE, E., PAPERT, A. & BLAXTER, M. 2002. Molecular barcodes for soil nematode identification. *Molecular Ecology* 11:839–850.

FLOYD, R., WILSON, J. J. & HEBERT, P. D. 2009. DNA barcodes and insect biodiversity. Pp. 417–431 in *Insect Biodiversity: Science and Society.*

FOLGARAIT, P. J. 1998. Ant biodiversity and its relationship to ecosystem functioning: a review. *Biodiversity & Conservation* 7:1221–1244.

FOLMER, O., HOEH, W. R., BLACK, M. B. & VRIJENHOEK, R. C. 1994. Conserved primers for PCR amplification of mitochondrial DNA from different invertebrate phyla. *Molecular Marine Biology and Biotechnology* 3:294–299.

FOREL, A. 1909. Ameisen aus Guatemala usw., Paraguay und Argentinien (Hym.). *Deutsche Entomologische Zeitschrift*:239–263.

FOREL, A. 1913. Fourmis d'Argentine, du Brésil, du Guatémala & de Cuba reçues de M. M. Bruch, Prof. v. Ihering, Mlle Baez, M. Peper et M. Rovereto. *Bulletin de la Société Vaudoise des Sciences Naturelles* 49:203–250.

FOUCAUD, J., ORIVEL, J., FOURNIER, D., DELABIE, J. H. C., LOISEAU, A., LE BRETON, J., CERDAN, P. & ESTOUP, A. 2009. Reproductive system, social organization, human disturbance and ecological dominance in native populations of the little fire ant, *Wasmannia auropunctata*. *Molecular Ecology* 18:5059–5073.

FOURCASSIÉ, V., HENRIQUES, A. & FONTELLA, C. 1999. Route fidelity and spatial orientation in the ant *Dinoponera gigantea* (Hymenoptera: Formicidae) in a primary forest: a preliminar study. *Sociobiology* 34:505–524.

FOURCASSIÉ, V. & OLIVEIRA, P. S. 2002. Foraging ecology of the giant Amazonian ant *Dinoponera gigantea* (Hymenoptera, Formicidae, Ponerinae): Activity schedule, diet and spatial foraging patterns. *Journal of Natural History* 36:2211–2227.

FOWLER, H. G. 1985. Populations, foraging and territoriality in *Dinoponera australis* (Hymenoptera, Formicidae). *Revista Brasileira de Entomologia* 29:443–447.

FRESNEAU, D. 1985. Individual foraging and path fidelity in a ponerine ant. *Insectes Sociaux* 32:109–116..

GALLARDO, A. 1918. Las hormigas de la República Argentina. Subfamilia Ponerinas. *Anales del Museo Nacional de Historia Natural de Buenos Aires* 30:1–112.

GELLER, J. B. (1999), Decline of a native mussel masked by sibling species invasion. *Conservation Biology*, 13: 661-664

GIANNOTTI, E. & MACHADO, V. L. L. 1992. Notes on the foraging of two species of Ponerinae ants: food resources and daily hunting activities (Hymenoptera, Formicidae). *Bioikos* 6:7–17.

GODOY, B. S. & CAMARGOS, L. M. DE. 2013. Does body size of neotropical ant species influence their recruitment speed? *Biota Neotropica* 13:91–96.

GOLDEN, T. M. J. & HILL, P. S. M. 2016. The evolution of stridulatory communication in ants, revisited. *Insectes Sociaux* 63:309–319.

GONTIJO, T. A. & DOMINGOS, D. J. 1991. Guild distribution of some termites from cerrado vegetation in south-east Brazil. *Journal of Tropical Ecology* 7:523–529.

GONZÁLEZ-CAMPERO, M. C. & ELIZALDE, L. 2008. A new species of *Anochetus* (Hymenoptera:

Formicidae: Ponerini) from Argentina and Paraguay, associated with a leaf cutter ants. *Entomotropica* 23:97–102.

GORDON, D. M. 2010. Ant encounters: interaction networks and colony beaviour. Princeton University Press. 182 pp.

GORDON, D. M. 2013. The rewards of restraint in the collective regulation of foraging by harvester ant colonies. *Nature* 498:91–93.

GORDON, D. M. & KULIG, A. 1998. The effect of neighbours on the mortality of harvester ant colonies. *Journal of Animal Ecology* 67:141–148.

GOTELLI, N. J. & ENTSMINGER, G. L. 2009. EcoSim: Null models software for ecology. Acquired Intelligence Inc. & Kesey-Bear.

GUÉNARD, B. & MCGLYNN, T. P. 2013. Intraspecific thievery in the ant *Ectatomma ruidum* is mediated by food availability. *Biotropica* 45:497–502.

HAIRSTON, N. G., SMITH, F. E. & SLOBODKIN, L. B. 1960. Community structure, population control, and competition. *The American Naturalist* 94:421–425.

HAMMER, Q., HARPER, D. & RYAN, P. 2001. PAST: Paleontological statistics software package for education and data analysis. *Palaeontologia Electronica* 1:9.

HANDLEY, L. L. & RAVEN, J. A. 1992. The use of natural abundance of nitrogen isotopes in plant physiology and ecology. *Plant, Cell and Environment* 15:965–985.

HANISCH, P. E. 2013. Biodiversidad de hormigas epígeas e hipógeas del Parque Nacional Iguazú. Universidad de Buenos Aires. 55 pp.

HANISCH, P. E., CALCATERRA, L. A., LEPONCE, M., ACHURY, R., SUAREZ, A. V, SILVA, R. R. R. & PARIS, C. 2015. Check list of ground-dwelling ant diversity (Hymenoptera: Formicidae) of the Iguazú National Park with a comparison at a regional scale. *Sociobiology* 62:213–227.

HANSSON, C., SMITH, M. A., JANZEN, D. H. & HALLWACHS, W. 2015. Integrative taxonomy of New World *Euplectrus* Westwood (Hymenoptera, Eulophidae), with focus on 55 new species from Area de Conservación Guanacaste, northwestern Costa Rica. *ZooKeys*:1–236.

HARKNESS, R. D. & MAROUDAS, N. G. 1985. Central place foraging by an ant (*Cataglyphis bicolor* Fab.): a model of searching. *Animal Behaviour* 33:916–928.

HART, M. W. & SUNDAY, J. 2007. Things fall apart: biological species form unconnected parsimony networks. *Biology Letters* 3(5): 509-512.

HEBERT, P. D. N., CYWINSKA, A., BALL, S. L. & DEWAARD, J. R. 2003a. Biological identifications through DNA barcodes. *Proceedings. Biological sciences / The Royal Society* 270:313–321.

HEBERT, P. D. N., PENTON, E. H., BURNS, J. M., JANZEN, D. H. & HALLWACHS, W. 2004. Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*. *Proceedings of the National Academy of Sciences of the United States of America* 101:14812–14817.

HEBERT, P. D. N., RATNASINGHAM, S. & DEWAARD, J. R. 2003b. Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proceedings. Biological sciences / The Royal Society* 270 Suppl:S96–S99.

HELGEN, K. M., PINTO, C. M., KAYS, R., HELGEN, L. E., TSUCHIYA, M. T. N., QUINN, A., WILSON, D. E. & MALDONADO, J. E. 2013. Taxonomic revision of the olingos (Bassaricyon), with description of a new species, the Olinguito. *ZooKeys*:1–83.

HENRY, C. S. 1994. Singing and cryptic speciation insects. *Trends in Ecology & Evolution* 9:388–392.

HIGASHI, S., ITO, F., SUGIURA, N. & OHKAWARA, K. 1994. Worker's age regulates the linear dominance hierarchy in the queenless ponerine ant, *Pachycondyla sublaevis* (Hymenoptera: Formicidae). *Animal Behaviour* 47:179–184.

HOLLDOBLER, B. 1985. Liquid food transmission and antennation signals in ponerine ants. *Israel Journal of Entomology* XIX:89–99.

HÖLLDOBLER, B. & WILSON, E. O. 1990. The Ants. Harvard University Press. 732 pp.

HRBEK, T., DA SILVA, V. M. F., DUTRA, N., GRAVENA, W., MARTIN, A. R. & FARIAS, I. P. 2014. A New species of river dolphin from Brazil or: How little do we know our biodiversity. *PLoS ONE* 9:e83623.

HUEMER, P., MUTANEN, M., SEFC, K. M., HEBERT, P. D. N., FRIC, Z. & ZHANG, Z. 2014. Testing DNA barcode performance in 1000 species of European lepidoptera: Large geographic distances have small genetic impacts. *PLoS ONE* 9:e115774.

ITO, F., TANIGUCHI, K. & BILLEN, J. 2017. Defensive function of petiole spines in queens and workers of the formicine ant *Polyrhachis lamellidens* (Hymenoptera: Formicidae) against an ant predator, the japanese tree frog *Hyla japonica*. *Asian Myrmecology* 8:81–86.

IVANOVA, N. V., DEWAARD, J. R. & HEBERT, P. D. N. 2006. An inexpensive, automation-friendly protocol for recovering high-quality DNA. *Molecular Ecology Notes* 6:998–1002.

JACQUEMIN, J., DELSINNE, T., MARAUN, M. & LEPONCE, M. 2014. Trophic ecology of the armadillo ant, *Tatuidris tatusia*, assessed by stable isotopes and behavioral observations. *Journal of Insect Science* 14:1–12.

JACQUEMIN, J., ROISIN, Y. & LEPONCE, M. 2016. Spatio-temporal variation in ant (Hymenoptera: Formicidae) communities in leaf-litter and soil layers in a premontane tropical forest. *Myrmecological News* 22:129–139.

JIMÉNEZ, E., FERNÁNDEZ, F., ARIAS, T. M. & LOZANO-ZAMBRANO, F. H. 2008. Sistemática, biogeografía y conservación de las hormigas cazadoras de Colombia. Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Bogotá, Colombia. 609 pp.

KASPARI, M., PICKERING, J. & WINDSOR, D. 2001. The reproductive flight phenology of a neotropical ant assemblage. *Ecological Entomology* 26:245–257.

KEMPF, W. W. 1960. Miscellaneus studies on Neotropical ants (Hymenoptera, Formicidae). *Studia Entomologica* 3:417–466.

KEMPF, W. W. 1962. Retoques à classificação das formigas neotropicais do gênero *Heteroponera* Mayr (Hym., Formicidae). *Pap. Avulsos Zool. (São Paulo)* 15:29–47.

KEMPF, W. W. 1965. A Revision of the Neotropical Fungus-growing Ants of the genus *Cyphomyrmex* Mayr. Part II: Group of rimosus (Spinola) (Hym. Formicidae). *Studia Entomologica* 8:161–200.

KEMPF, W. W. 1972. Catálogo abreviado das formigas da região Neotropical. *Studia Entomologica* 15:3–344.

KERR, K. C. R. 2010. A cryptic, intergeneric cytochrome c oxidase I pseudogene in tyrant (family: Tyrannidae). *Genome* 53:1103–1109.

KIMURA, M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16:111–120.

KITTELSON, P. M. & BOYD, M. J. 1997. Mechanisms of expansion for an introduced species of cordgrass, *Spartina densiflora*, in Humboldt Bay, California. *Estuaries* 20:770.

KNOWLTON, N. 1993. Sibling species in the sea. *Annual Review of Ecology and Systematics* 24:189–216.

KUGLER, C. & BROWN, W. L. J. 1982. Revisionary and other studies on the ant genus *Ectatomma*, including the descriptions of two new species. *Search agriculture - New York State Agricultural Experiment Station, Ithaca* 24:8.

KUSNESOV, N. 1953. La fauna mirmecológica de Bolivia. *Folia Universitaria. Cochabamba* 6:211–229.

KUSNESOV, N. 1956. Claves para la identificación de las hormigas de la fauna argentina. *Idia*, 56pp.

KUSNESOV, N. 1957. Die Solenopsidinen-Gattungen von Südamerika (Hymenoptera, Formicidae). *Zoologischer Anzeiger* 158:266–280.

KUSNESOV, N. 1962. El vuelo nupcial de las hormigas. *Acta Zoologica Lilloana* 18:385–422.

KUSNESOV, N. 1969. Nuevas especies de hormigas. *Acta Zoologica Lilloana* 24:33–38.

KUSNESOV, N. 1978. Hormigas Argentinas, clave para su identificación. Miscelanea Fundacion Miguel Lillo. 147 pp.

LACH, L., PARR, C. L. & ABOTT, K. L. 2010. Ant Ecology. Oxford University Press. 383 pp.

LANAN, M. 2014. Spatiotemporal resource distribution and foraging strategies of ants (Hymenoptera: Formicidae). *Myrmecological News* 20:53–70.

LARABEE, F. J., FISHER, B. L., SCHMIDT, C. A., MATOS-MARAVÍ, P., JANDA, M. & SUAREZ, A. V. 2016. Molecular phylogenetics and diversification of trap-jaw ants in the genera *Anochetus* and *Odontomachus* (Hymenoptera: Formicidae). *Molecular Phylogenetics and Evolution* 103:143–154.

LATTAR, E. C., GALATI, B. G., CARRERA, C. S., FERRUCCI, M. S. (2018) Floral nectaries of *Heliocarpus popayanensis* and *Luehea divaricata* (Malvaceae-Grewioideae): structure and ultrastructure. *Australian Journal of Botany* 66, 59-73

LATTKE, J. E. 2011. Revision of the new world species of the genus *Leptogenys* Roger (Insecta: Hymenoptera: Formicidae: Ponerinae). *Arthropod Systematics and Phylogeny* 69:127–264.

LATTKE, J. E., FERNÁNDEZ, F. & PALACIO, E. E. 2007. Identification of the species of *Gnamptogenys* Roger in the Americas. Pp. 254–270 in *Advances In Ant Systematics*

(Hymenoptera: Formicidae): Homage To E. O. Wilson – 50 Years Of Contributions. Memoirs of the American Entomological Institute, Gainesville, USA.

LEAL, I. R. & OLIVEIRA, P. S. 1995. Behavioral ecology of the neotropical termite-hunting ant *Pachycondyla* (= *Termitopone*) *marginata*: colony founding, group-raiding and migratory patterns. *Behavioral Ecology and Sociobiology* 37:373–383.

LEBRUN, E. G. 2005. Who is the top dog in ant communities? Resources, parasitoids, and multiple competitive hierarchies. *Oecologia* 142:643–652.

LEBRUN, E. G., TILLBERG, C. V., SUAREZ, A. V., FOLGARAIT, P. J., SMITH, C. R. & HOLWAY, D. A. 2007. An experimental study of competition between Fire Ants and Argentine Ants in their native range. *Ecology* 88:63–75.

LENHART, P., DASH, S. T. & MACKAY, W. P. 2013. A revision of the giant Amazonian ants of the genus *Dinoponera* (Hymenoptera, Formicidae). *Journal of Hymenoptera Research* 31:119–164.

LEPONCE, M., THEUNIS, L., DELABIE, J. H. C. & ROISIN, Y. 2004. Scale dependence of diversity measures in a leaf-litter ant assemblage. *Ecography* 27:253–267.

LIEBIG, J., PEETERS, C. & HOLLDOBLER, B. 1999. Worker policing limits the number of reproductives in a ponerine ant. *Proceedings of the Royal Society B: Biological Sciences* 266:1865–1870.

LONGINO, J. T., CODDINGTON, J. & COLWELL, R. K. 2002. The ant fauna of a tropical rain forest: Estimating species richness three different ways. *Ecology* 83:689–702.

LONGINO, J. T. & FERNÁNDEZ, F. 2007. A taxonomic review of the genus *Wasmannia*. Pp. 271–289 in *Advances in ant systematics (Hymenoptera: Formicidae): Homage to E. O. Wilson – 50 years of contributions.* American Entomological Institute, Gainesville, USA.

LUCAS, C., FRESNEAU, D., KOLMER, K., HEINZE, J., DELABIE, J. H. C. & PHO, D. B. 2002. A multidisciplinary approach to discriminating different taxa in the species complex *Pachycondyla villosa* (Formicidae). *Biological Journal of the Linnean Society* 75:249–259.

MACE, G. M. 2004. The role of taxonomy in species conservation. *Philosophical transactions of the Royal Society of London. Series B, Biological Sciences* 359:711–9.

MACGOWN, J. A., BOUDINOT, B. E., DEYRUP, M. & SORGER, D. M. 2014. A review of the Nearctic *Odontomachus* (Hymenoptera: Formicidae: Ponerinae) with a treatment of the males. *Zootaxa* 3802:515–552.

MACKAY, W. P. 1996. A revision of the ant genus *Acanthostichus*. *Sociobiology* 27:129–179.

MACKAY, W. P. & MACKAY, E. 2010. Systematics and biology of the New World ants of the genus *Pachycondyla* (Hymenoptera: Formicidae). Edwin Mellen Press, Lewiston, New York. 664 pp.

MAYR, E. 1970. Populations, species and evolution: An a bridgment of animal species and evolution. Harvard University Press, Belknap. 453 pp.

McCUNE, B. & MEFFORD, M. J. 1999. PC-ORD: multivariate analysis of ecological data. MjM Software Design, Gleneden Beach, Oregon, U.S.A.

MEDEIROS, F. N. S., LOPES, L. E., MOUTINHO, P. R. S., OLIVEIRA, P. S. & HOLLDOBLER, B. 1992.

Functional polygyny, agonistic interactions and reproductive dominance in the Neotropical ant *Odontomachus chelifer* (Hymenoptera, Formicidae, Ponerinae). *Ethology* 91:134–146.

MEDEIROS, F. N. S. & OLIVEIRA, P. S. 2009. Season-Dependent foraging patterns: Case study of a neotropical forest-dwelling ant (*Pachycondyla striata*; Ponerinae). Pp. 81–95 in *Food Exploitation by Social Insects: Ecological, Behavioral and Theoretical Approaches*. Taylor & Francis Group, Boca Raton, USA.

MEIER, R., SHIYANG, K., VAIDYA, G., NG, P. & HEDIN, M. 2006. DNA Barcoding and taxonomy in Diptera: A tale of high intraspecific variability and low identification success. *Systematic Biology* 55:715–728.

MEIER, R., ZHANG, G., ALI, F. & ZAMUDIO, K. 2008. The use of mean instead of smallest interspecific distances exaggerates the size of the 'Barcoding Gap' and leads to misidentification. *Systematic Biology* 57:809–813.

MENKE, S. B., BOOTH, W., DUNN, R. R., SCHAL, C., VARGO, E. L. & SILVERMAN, J. 2010. Is it easy to be urban? Convergent success in urban habitats among lineages of a widespread native ant. *PLoS ONE* 5:e9194.

MEYER, C. P. & PAULAY, G. 2005. DNA Barcoding: Error rates based on comprehensive sampling. *PLoS Biology* 3:2229–2238.

MONNIN, T. & PEETERS, C. 1999. Dominance hierarchy and reproductive conflicts among subordinates in a monogynous queenless ant. *Behavioral Ecology* 10:323–332.

MONNIN, T., RATNIEKS, F. L. W. & BRANDÃO, C. R. F. 2003. Reproductive conflict in animal societies: Hierarchy length increases with colony size in queenless ponerine ants. *Behavioral Ecology and Sociobiology* 54:71–79.

MORGAN, E. D., JUNGNICKEL, H., KEEGANS, S. J., DO NASCIMENTO, R. R., BILLEN, J., GOBIN, B. & ITO, F. 2003. Comparative survey of abdominal gland secretions of the ant subfamily ponerinae. *Journal of Chemical Ecology* 29:95–114.

MOYA-LARAÑO, J. & WISE, D. H. 2007. Direct and indirect effects of ants on a forest-floor food web. *Ecology* 88:1454–1465.

MYERS, N., MITTERMEIER, R. A., MITTERMEIER, C. G., DA FONSECA, G. A. B. & KENT, J. 2000. Biodiversity hotspots for conservation priorities. *Nature* 403:853–858.

NATER, A., MATTLE-GREMINGER, M. P., NURCAHYO, A., NOWAK, M. G., DE MANUEL, M., DESAI, T., GROVES, C., PYBUS, M., SONAY, T. B., ROOS, C., LAMEIRA, A. R., WICH, S. A., ASKEW, J., DAVILA-ROSS, M., FREDRIKSSON, G., DE VALLES, G., CASALS, F., PRADO-MARTINEZ, J., GOOSSENS, B., VERSCHOOR, E. J., WARREN, K. S., SINGLETON, I., MARQUES, D. A., PAMUNGKAS, J., PERWITASARI-FARAJALLAH, D., RIANTI, P., TUUGA, A., GUT, I. G., GUT, M., OROZCO-TERWENGEL, P., VAN SCHAIK, C. P., BERTRANPETIT, J., ANISIMOVA, M., SCALLY, A., MARQUES-BONET, T., MEIJAARD, E. & KRÜTZEN, M. 2017. Morphometric, behavioral, and genomic evidence for a new Orangutan species. *Current Biology* 27:3487–3498.e10.

NETTEL-HERNANZ, A., LACHAUD, J.-P., FRESNEAU, D., LÓPEZ-MUÑOZ, R. A. & POTEAUX, C. 2015. Biogeography, cryptic diversity, and queen dimorphism evolution of the Neotropical ant genus *Ectatomma* Smith, 1958 (Formicidae, Ectatomminae). *Organisms Diversity & Evolution* 15:543–553.

NONACS, P. & DILL, L. M. 1988. Foraging response of the ant *Lasius pallitarsis* to food sources with associated mortality risk. *Insectes Sociaux* 35:293–303.

OLIVEIRA, P. S., CAMARGO, R. X. & FOURCASSIÉ, V. 2011. Nesting patterns, ecological correlates of polygyny and social organization in the neotropical arboreal ant *Odontomachus hastatus* (Formicidae, Ponerinae). *Insectes Sociaux* 58:207–217.

OLIVEIRA, P. S. & FREITAS, A. V. L. 2004. Ant-plant-herbivore interactions in the neotropical cerrado savanna. *Naturwissenschaften* 91:557–570.

OLIVEIRA, T. B. DE, FERRO, M., BACCI, M., SOUZA, D. J. DE, FONTANA, R., DELABIE, J. H. C. & SILVA, A. 2016. Bacterial communities in the midgut of Ponerine ants (Hymenoptera: Formicidae: Ponerinae). *Sociobiology* 63:637.

ORIVEL, J. & DEJEAN, A. 2001. Comparative effect of the venoms of ants of the genus *Pachycondyla* (Hymenoptera: Ponerinae). *Toxicon* 39:195–201.

ORIVEL, J., MALHERBE, M. C. & DEJEAN, A. 2009. Relationships between pretarsus morphology and arboreal life in Ponerine ants of the genus *Pachycondyla* (Formicidae: Ponerinae). *Annals of the Entomological Society of America* 94:449-456.

ORTÍZ SEPÚLVEDA, C. M. 2012. Revisión taxonómica de las hormigas del género *Brachymyrmex* Mayr (Hymenoptera: Formicidae: Formicinae). Universidad Nacional de Colombia. 146 pp.

PAIVA, R. V. S. & BRANDÃO, C. R. F. 1995. Nests, worker population, and reproductive status of workers, in the giant queenless ponerine ant *Dinoponera* Roger (Hymenoptera Formicidae). *Ethology Ecology & Evolution* 7:297–312.

PASSOS, L. & OLIVEIRA, P. S. 2002. Ants affect the distribution and performance of seedlings of *Clusia criuva* , a primarily bird-dispersed rain forest tree. *Journal of Ecology* 90:517–528.

PASSOS, L. & OLIVEIRA, P. S. 2004. Interaction between ants and fruits of *Guapira opposita* (Nyctaginaceae) in a Brazilian sandy plain rainforest: ant effects on seeds and seedlings. *Oecologia* 139:376–382.

PEETERS, C. 1991a. The occurrence of sexual reproduction among ant workers. *Biological Journal of the Linnean Society* 44:141–152.

PEETERS, C. P. 1991b. Ergatoid queens and intercastes in ants: Two distinct adult forms which look morphologically intermediate between workers and winged queens. *Insectes Sociaux* 38:1–15.

PEETERS, C. & HIGASHI, S. 1989. Reproductive dominance controlled by mutilation in the queenless ant *Diacamma australe*. *Naturwissenschaften* 76:177–180.

PEETERS, C. & ITO, F. 2001. Colony dispersal and the evolution of queen morphology in social Hymenoptera. *Annual Review of Entomology* 46:601–630.

PERFECTO, I. & VANDERMEER, J. 2013. Ant assemblage on a coffee farm: Spatial mosaic versus shifting patchwork. *Environmental Entomology* 42:38–48.

PHILPOTT, S. M., PERFECTO, I. & VANDERMEER, J. 2008. Effects of predatory ants on lower trophic levels across a gradient of coffee management complexity. *Journal of Animal Ecology* 77:505–511.

PONS, J., BARRACLOUGH, T., GOMEZ-ZURITA, J., CARDOSO, A., DURAN, P., HAZELL, S., KAMOUN, S., SUMLIN, W., VOGLER, A. 2006. Sequence-based species delimitation for the DNA taxonomy of undescribed insects, *Systematic Biology*, 55: 595–609.

PIE, M. R. 2004. Foraging ecology and behaviour of the ponerine ant *Ectatomma opaciventre* Roger in a Brazilian savannah. *Journal of Natural History* 38:717–729.

PIGNALBERI, C. T. 1961. Contribución al conocimiento de los formícidos de la provincia de Santa Fé. P. 276 in *Actas y trabajos del primer Congreso Sudamericano de Zoología*. Librart, Buenos Aires.

PIZO, M. A. & OLIVEIRA, P. S. 1998. Interaction between ants and seeds of a nonmyrmecochorous neotropical tree, *Cabralea canjerana* (Meliaceae), in the Atlantic forest of southeast Brazil. *American Journal of Botany* 85:669–674.

PORTER, S. D. & TSCHINKEL, W. R. 1987. Foraging in *Solenopsis invicta* (Hymenoptera: Formicidae): Effects of weather and season. *Environmental Entomology* 16:802–808.

POST, D. M. 2002. Using stable isotopes to estimate trophic position: Models, methods, and assumptions. *Ecology* 83:703–718.

PUILLANDRE, N., LAMBERT, A., BROUILLET, S. & ACHAZ, G. 2012. ABGD, Automatic barcode gap discovery for primary species delimitation. *Molecular Ecology* 21:1864–1877.

QUICKE, D. L. J., SMITH, M. A., JANSEN, D. H., HALLWACHS, W., FERNANDEZ-TRIANA, J., LAURENNE, N. M., ZALDIVAR-RIVERON, A., SHAW, M. R., BROAD, G. R., KLOPFSTEIN, S., SHAW, S. R., HRCEK, J., HEBERT, P. D. ., MILLER, S. E., RODRIGUEZ, J. J., WHITFIELD, J. B., SHARKEY, M. J., SHARANOWSKI, B. J., JUSSILA, R., GAULD, I. D., CHESTERS, D. & VOGLER, A. P. 2012. Utility of the DNA barcoding gene fragment for parasitic wasp phylogeny (Hymenoptera: Ichneumonoidea): data release and new measure of taxonomic congruence. *Molecular Ecology Resources* 12:676–685.

R CORE TEAM. 2016. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

RAIMUNDO, R. L. G., FREITAS, A. V. L. & OLIVEIRA, P. S. 2009. Seasonal patterns in activity rhythm and foraging ecology in the Neotropical forest-dwelling ant, *Odontomachus chelifer* (Formicidae: Ponerinae). *Annals of the Entomological Society of America* 102:1151–1157.

RAMALHO, M. O. F., SANTOS, R. M., FERNANDES, T. T., MORINI, M. S. C. & BUENO, O. C. 2016a. 'Cytochrome c oxidase I DNA sequence of *Camponotus* ants with different nesting strategies is a tool for distinguishing between morphologically similar species'. *Genetica* 144:375–383.

RAMALHO, M. O., MARTINS, C., SILVA, L. M. R., MARTINS, V. G. & BUENO, O. C. 2016b. Molecular profile of the Brazilian weaver ant *Camponotus textor* Forel (Hymenoptera, Formicidae). *Neotropical Entomology* 45:463–470.

RATNASINGHAM, S. & HEBERT, P. D. . 2007. BOLD: The Barcode of Life Data System (http://www.barcodinglife.org). *Molecular Ecology Notes* 7:355–364.

RATNASINGHAM, S. & HEBERT, P. D. N. 2013. A DNA-based registry for all animal species: The Barcode Index Number (BIN) System. *PLoS ONE* 8:e66213.

RIBAS, C. R. & SCHOEREDER, J. H. 2002. Are all ant mosaics caused by competition? *Oecologia* 131:606–611.

RICHTER, M. R. 2000. Social wasp (Hymenoptera: Vespidae) foraging behavior. *Annual Review of Entomology* 45:121–150.

RICO-GRAY, V. & OLIVEIRA, P. S. 2007. The ecology and evolution of ant-plant interactions. University of Chicago Press. 320 pp.

DI RIENZO, J. A., CASANOVES, F., BALZARINI, M. G., L., G., TABLADA, M. & ROBLEDO, C. W. 2017. InfoStat. Grupo InfoStat, FCA, Universidad Nacional de Córdoba, Argentina.

RIPPLE, W. J., ESTES, J. A., SCHMITZ, O. J., CONSTANT, V., KAYLOR, M. J., LENZ, A., MOTLEY, J. L., SELF, K. E., TAYLOR, D. S. & WOLF, C. 2016. What is a Trophic Cascade? *Trends in Ecology & Evolution* 31:842–849.

RODRIGUES, M., VILELA, E., AZEVEDO, D. & HORA, R. 2010. Multiple queens in founding colonies of the neotropical ant *Pachycondyla striata* Smith (Formicidae: Ponerinae). *Neotropical Entomology* 40:293–299.

RONQUE, M. U. V., AZEVEDO-SILVA, M., MORI, G. M., SOUZA, A. P. & OLIVEIRA, P. S. 2015. Three ways to distinguish species: using behavioural, ecological, and molecular data to tell apart two closely related ants, *Camponotus renggeri* and *Camponotus rufipes* (Hymenoptera: Formicidae). *Zoological Journal of the Linnean Society* 176(1):170-181.

RONQUE, M. U. V., FOURCASSIÉ, V. & OLIVEIRA, P. S. 2018. Ecology and field biology of two dominant *Camponotus* ants (Hymenoptera: Formicidae) in the Brazilian savannah. *Journal of Natural History* 52:237–252.

ROSS, K. G., GOTZEK, D., ASCUNCE, M. S. & SHOEMAKER, D. D. 2010. Species delimitation: A case study in a problematic ant taxon. *Systematic Biology* 59:162–184.

ROSUMEK, F. B. 2017. Natural history of ants: What we (do not) know about trophic and temporal niches of Neotropical species. *Sociobiology* 64:244.

RYDER WILKIE, K. T., MERTL, A. L. & TRANIELLO, J. F. A. 2010. Species diversity and distribution patterns of the ants of Amazonian Ecuador. *PloS one* 5:1–12.

RYTI, R. T. & CASE, T. J. 1986. Overdispersion of ant colonies: a test of hypotheses. *Oecologia* 69:446–453.

SAITOH, T., SUGITA, N., SOMEYA, S., IWAMI, Y., KOBAYASHI, S., KAMIGAICHI, H., HIGUCHI, A., ASAI, S., YAMAMOTO, Y. & NISHIUMI, I. 2015. DNA barcoding reveals 24 distinct lineages as cryptic bird species candidates in and around the Japanese Archipelago. *Molecular Ecology Resources* 15:177–186.

SANDERS, D. & VAN VEEN, F. J. F. 2011. Ecosystem engineering and predation: the multi-trophic impact of two ant species. *Journal of Animal Ecology* 80:569–576.

SANTANA, F. D., CAZETTA, E. & DELABIE, J. H. C. 2013. Interactions between ants and non-myrmecochorous diaspores in a tropical wet forest in southern Bahia, Brazil. *Journal of Tropical Ecology* 29:71–80.

SANTSCHI, F. 1916. Formicides sudaméricains nouveaux ou peu connus. *Physis (Buenos Aires)* 2:365–399.

SANTSCHI, F. 1919. Nouveaux formicides de la République Argentine. *Anales de la Sociedad Cientifica Argentina* 87:37–57.

SANTSCHI, F. 1921. Ponerinae, Dorylinae et quelques autres formicides néotropiques. *Bulletin de la Société Vaudoise des Sciences Naturelles* 54:81–103.

SANTSCHI, F. 1922. Description de nouvelles fourmis de l'Argentine et pays limitrophes. *Anales de la Sociedad Cientifica Argentina* 94:241–262.

SANTSCHI, F. 1925. Fourmis des provinces argentines de Santa Fe, Catamarca, Santa Cruz, Córdoba et Los Andes. *Comunicaciones del Museo Nacional de Historia Natural 'Bernardino Rivadavia'* 2:149–168.

SANTSCHI, F. 1929. Nouvelles fourmis de la République Argentine et du Brésil. *Anales de la Sociedad Cientifica Argentina* 107:273–316.

SANTSCHI, F. 1933. Fourmis de la République Argentine en particulier du territoire de Misiones. *Anales de la Sociedad Cientifica Argentina* 116:105–124.

SCHLICK-STEINER, B. C., STEINER, F. M., MODER, K., SEIFERT, B., SANETRA, M., DYRESON, E., STAUFFER, C. & CHRISTIAN, E. 2006. A multidisciplinary approach reveals cryptic diversity in Western Palearctic *Tetramorium* ants (Hymenoptera: Formicidae). *Molecular Phylogenetics and Evolution* 40:259–273.

SCHMIDT, C. A. & SHATTUCK, S. O. 2014. The higher classification of the ant subfamily Ponerinae (Hymenoptera: Formicidae), with a review of Ponerine ecology and behavior. *Zootaxa* 3817(1):1-242.

SCHMITZ, O. J., HAMBÄCK, P. A. & BECKERMAN, A. P. 2000. Trophic cascades in terrestrial systems: A review of the effects of carnivore removals on plants. *The American naturalist* 155:141–153.

SEIFERT, B. 2009. Cryptic species in ants (Hymenoptera: Formicidae) revisited: we need a change in the alpha-taxonomic approach. *Myrmecological News* 12:149–166.

SMITH, A. A., MILLAR, J. G., HANKS, L. M. & SUAREZ, A. V. 2013a. A conserved fertility signal despite population variation in the cuticular chemical profile of the trap-jaw ant *Odontomachus brunneus*. *The Journal of experimental biology* 216:3917–24.

SMITH, C. R., SUAREZ, A. V, TSUTSUI, N. D., WITTMAN, S. E., EDMONDS, B., FREAUFF, A. & TILLBERG, C. V. 2011. Nutritional asymmetries are related to division of labor in a queenless ant. *PloS one* 6:e24011.

SMITH, M. A., BERTRAND, C., CROSBY, K., EVELEIGH, E. S., FERNANDEZ-TRIANA, J., FISHER, B. L., GIBBS, J., HAJIBABAEI, M., HALLWACHS, W., HIND, K., HRCEK, J., HUANG, D.-W., JANDA, M., JANZEN, D. H., LI, Y., MILLER, S. E., PACKER, L., QUICKE, D., RATNASINGHAM, S., RODRIGUEZ, J., ROUGERIE, R., SHAW, M. R., SHEFFIELD, C., STAHLHUT, J. K., STEINKE, D., WHITFIELD, J., WOOD, M. & ZHOU, X. 2012. Wolbachia and DNA barcoding insects: patterns, potential, and problems. *PloS one* 7:e36514.

SMITH, M. A. & FISHER, B. L. 2009. Invasions, DNA barcodes, and rapid biodiversity assessment using ants of Mauritius. *Frontiers in zoology* 6:31.

SMITH, M. A., HALLWACHS, W., JANZEN, D. H. & LONGINO, J. T. 2014. Diversity and phylogenetic community structure of ants along a Costa Rican elevational gradient.

Ecography 37:720–731.

SMITH, M. A., HALLWACHS, W., JANZEN, D. H. & SEGURA, R. B. 2013b. Dna barcoding a collection of ants (Hymenoptera: Formicidae) from Isla Del Coco, Costa Rica. *Florida Entomologist* 96:1500–1507.

SMITH, M. A., JANZEN, D. H., HALLWACHS, W. & LONGINO, J. T. 2015. Observations of *Adelomyrmex* (Hymenoptera: Formicidae) reproductive biology facilitated by digital field microscopy and DNA barcoding. *The Canadian Entomologist* 6:1–6.

SMITH, M. A., WOODLEY, N. E., JANZEN, D. H., HALLWACHS, W. & HEBERT, P. D. N. 2006. DNA barcodes reveal cryptic host-specificity within the presumed polyphagous members of a genus of parasitoid flies (Diptera: Tachinidae). *Proceedings of the National Academy of Sciences of the United States of America* 103:3657–3662.

SONG, H., BUHAY, J. E., WHITING, M. F. & CRANDALL, K. A. 2008. Many species in one: DNA barcoding overestimates the number of species when nuclear mitochondrial pseudogenes are coamplified. *Proceedings of the National Academy of Sciences of the United States of America* 105:13486–91.

SOSA-CALVO, J., JEŠOVNIK, A., LOPES, C. T., RODRIGUES, A., RABELING, C., BACCI, M., VASCONCELOS, H. L. & SCHULTZ, T. R. 2017. Biology of the relict fungus-farming ant *Apterostigma megacephala* Lattke, including descriptions of the male, gyne, and larva. *Insectes Sociaux* 64:329–346.

SPAGNA, J. C., VAKIS, A. I., SCHMIDT, C. A, PATEK, S. N., ZHANG, X., TSUTSUI, N. D. & SUAREZ, A. V. 2008. Phylogeny, scaling, and the generation of extreme forces in trap-jaw ants. *The Journal of experimental biology* 211:2358–2368.

SPANGLER, H. G. 1967. Ant stridulations and their synchronization with abdominal movement. *Science* 155:1687–9.

STAMATAKIS, A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large philogenies. Bioinformatics.

STONE, L. & ROBERTS, A. 1990. The checkerboard score and species distributions. *Oecologia* 85:74–79.

STORK, N. E. 2018. How many species of insects and other terrestrial arthropods are there on Earth? *Annual Review of Entomology* 63:31–45.

STUBLE, K. L., JURIC, I., CERDA, X. & SANDERS, N. J. 2017. Dominance hierarchies are a dominant paradigm in ant ecology (Hymenoptera: Formicidae), but should they be? and what is a dominance hierarchy anyways? *Myrmecological News* 24:71–81.

STUBLE, K. L., RODRIGUEZ-CABAL, M. A., MCCORMICK, G. L., JURIĆ, I., DUNN, R. R. & SANDERS, N. J. 2013. Tradeoffs, competition, and coexistence in eastern deciduous forest ant communities. *Oecologia* 171:981–992.

SUTTON, G. J., HOSKINS, A. J. & ARNOULD, J. P. Y. 2015. Benefits of group foraging depend on prey type in a small marine predator, the little Penguin. *PLOS ONE* 10:e0144297.

TAMURA, K., PETERSON, D., PETERSON, N., STECHER, G., NEI, M. & KUMAR, S. 2011. MEGA5: Molecular evolutionary genetics analysis using Maximum Likelihood, evolutionary distance, and Maximum Parsimony methods. *Molecular Biology and Evolution* 28:2731–

2739.

TAYASU, I., ABE, T., EGGLETON, P. & BIGNELL, D. E. 1997. Nitrogen and carbon isotope ratios in termites: an indicator of trophic habit along the gradient from wood-feeding to soil-feeding. *Ecological Entomology* 22:343–351.

TEMPLETON, A. R., CRANDALL, K. A. & SING, C. F. 1992. A cladistic analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping and DNA sequence data. *Genetics* 132:619–633.

TERBORGH, J., FEELEY, K., SILMAN, M., NUNEZ, P. & BALUKJIAN, B. 2006. Vegetation dynamics of predator-free land-bridge islands. *Journal of Ecology* 94:253–263.

THEUNIS, L., GILBERT, M., ROISIN, Y. & LEPONCE, M. 2005. Spatial structure of litter-dwelling ant distribution in a subtropical dry forest. *Insectes Sociaux* 52:366–377.

THURBER, D. K., BELK, M. C., BLACK, H. L., JORGENSEN, C. D., HUBBELL, S. P. & FOSTER, R. B. 1993. Dispersion and mortality of colonies of the tropical ant *Paraponera clavata*. *Biotropica* 25:215.

TILLBERG, C. V., EDMONDS, B., FREAUFF, A., HANISCH, P. E., PARIS, C., SMITH, C. R., TSUTSUI, N. D., WILLS, B. D., WITTMAN, S. E. & SUAREZ, A. V. 2014. Foraging ecology of the tropical giant hunting ant *Dinoponera australis* (Hymenoptera: Formicidae) - evaluating mechanisms for high abundance. *Biotropica* 46:229–237.

TILLBERG, C. V., MCCARTHY, D. P., DOLEZAL, A. G. & SUAREZ, A. V. 2006. Measuring the trophic ecology of ants using stable isotopes. *Insectes Sociaux* 53:65–69.

TILLBERG, C. V & BREED, M. D. 2004. Placing an omnivore in a complex food web: Dietary contributions to adult biomass of an ant. *Biotropica* 36:266–271.

DEL TORO, I., RIBBONS, R. R. & PELINI, S. L. 2012. The little things that run the world revisited: A review of ant-mediated ecosystem services and disservices (Hymenoptera: Formicidae). *Myrmecological News* 17:133–146.

TRANIELLO, J. F. A. 1989. Foraging strategies of ants. *Annual Review of Entomology* 34:191–210.

TSUTSUI, N. D. & SUAREZ, A. V. 2003. The colony structure and population biology of Invasive Ants. *Conservation Biology* 17:48–58.

VALONE, T. J. 1989. Group Foraging, Public Information, and Patch Estimation. *Oikos* 56:357.

VITTAR, F. 2008. Hormigas (Hymenoptera: Formicidae) de la Mesopotamia Argentina. Pp. 447–466*Temas de la biodiversidad del litoral fluvial argentino III*. INSUGEO Miscelanea, Tucumán.

WACHKOO, A. & AKBAR, S. 2016. First description of the sexuals of *Camponotus opaciventris* Mayr, 1879 (Hymenoptera, Formicidae), with notes on distribution in Western Himalaya. *Biodiversity Data Journal* 4:e10464.

WARD, P. S. 2007. Phylogeny, classification, and species-level taxonomy of ants (Hymenoptera: Formicidae). *Zootaxa* 1668:549–563.

WEISER, M. D., SANDERS, N. J., AGOSTI, D., ANDERSEN, A. N., ELLISON, A. M., FISHER, B. L., GIBB, H., GOTELLI, N. J., GOVE, A. D., GROSS, K., GUÉNARD, B., JANDA, M., KASPARI, M.,

LESSARD, J.-P., LONGINO, J. T., MAJER, J. D., MENKE, S. B., MCGLYNN, T. P., PARR, C. L., PHILPOTT, S. M., RETANA, J., SUAREZ, A. V, VASCONCELOS, H. L., YANOVIAK, S. P. & DUNN, R. R. 2010. Canopy and litter ant assemblages share similar climate-species density relationships. *Biology letters* 6:769–72.

WILD, A. L. 2002. The genus *Pachycondyla* (Hymenoptera: Formicidae) in Paraguay. *Boletin Museo de Historia Natural Paraguay* 14:1–18.

WILD, A. L. 2005. Taxonomic revision of the *Pachycondyla apicalis* species complex (Hymenoptera: Formicidae). *Zootaxa* 834:1.

WILD, A. L. 2007a. A catalogue of the ants of Paraguay (Hymenoptera: Formicidae). *Zootaxa* 55:1–55.

WILD, A. L. 2007b. Revision of the Ant Genus *Linepithema* (Hymenoptera : Formicidae). *University of California Press*. University of California Press, Berkeley and Los Angeles, California. 150 pp.

WILSON, E. O. 1971. The insects societies. Harvard University Press, Cambridge. 548 pp.

WILSON, E. O. 1976. Which are the most prevalent ant genera? *Studia Entomologica* 19:187-.

WILSON, J. J. 2012. DNA barcodes for insects. Pp. 17–46 in *DNA barcodes: Methods and protocols*. Springer, United States.

WITTE, V. & MASCHWITZ, U. 2000. Raiding and emigration dynamics in the ponerine army ant *Leptogenys distinguenda* (Hymenoptera, Formicidae). *Insectes Sociaux* 47:76–83.

WOLF, H. G. & ADIS, J. 1992. Genetic differentiation between populations of *Neomachilellus scandens* (Meinertellidae, Archaeognatha, Insecta) inhabiting neighbouring forests in Central Amazonia. *Verhandlungen des Naturwissenschaftlichen Vereins in Hamburg* 33:5–13.

YAMAMOTO, M. & DEL-CLARO, K. 2008. Natural history and foraging behavior of the carpenter ant *Camponotus sericeiventris* Guérin, 1838 (Formicinae, Campotonini) in the Brazilian tropical savanna. *Acta ethologica* 11:55–65.

YANOVIAK, S. P. & KASPARI, M. 2000. Community estruture and the habitat templet: ants in the tropical forest canopy and litter. *Oikos* 89:259–266.

YOSHIMURA, M. & FISHER, B. L. 2007. A revision of male ants of the Malagasy region (Hymenoptera: Formicidae): Key to subfamilies and treatment of the genera of Ponerinae. *Zootaxa* 1654:21–40.

ZENKER, M. M., ROUGERIE, R., TESTON, J. A., LAGUERRE, M., PIE, M. R., FREITAS, A. V. L., CARVALHO, C. DE, CASARI, S. & CONSTANTINO, R. 2016. Fast census of moth diversity in the Neotropics: A comparison of field-assigned morphospecies and DNA Barcoding in Tiger moths. *PLOS ONE* 11:e0148423.

Appendix Chapter II

2.1 List of examined material for each species. Abbreviations of entomological collections used in this study: Museu de Zoologia da Universidade de São Paulo (MZSP), the Natural History Museum (BMNH), the Royal Belgian Institute of Natural Sciences (RBINS), the Museo de Ciencias Naturales "Bernardino Rivadavia" (MACN) and the Instituto y Museo de Ciencias Naturales Miguel Lillo (IMML).

Anochetus altisquamis

Argentina: Catamarca: Monte Potrero, (W65.6675°, S28.1737°), Alvaro Galbán, 14/Dec/2016, 1 worker (MACN-bar-ins-ct 07664); 1 worker (MACN-bar-ins-ct 07665); 1 worker (MACN-bar-ins-ct 07722). Jujuy: Calilegua NP, Alisal, (W65.4667°, S24.15°, 1508m), M. Andia, 12/Aug/2010, 1 ♀ (MACN-Bar-Ins-ct 00402); Tiraxis, (W65.3531°, S24.008°), Alvaro Galbán, 01/Mar/2017, 1 worker (MACN-bar-ins-ct 07632); 01/Mar/2018, 1 worker (MACN-bar-ins-ct 07661); Nest under log, 01/Mar/2019, 1 worker (MACN-bar-ins-ct 07702); 01/Mar/2020, 1 worker (MACN-bar-ins-ct 07710); 01/Mar/2021, 1 worker (MACN-bar-ins-ct 07719). Salta: 1 worker (MACN_En21404), 1 worker (MACN_En21405), 1 worker (MACN_En21406); 1 worker (MACN_En21407); 1 worker (MACN_En21408). Tucumán: Between Villa Padre Monti and Nio river, (W65.0025°, S26.4743°), Alvaro Galbán, 24/Nov/2015, 1 worker (MACN-bar-ins-ct 07658); 1 worker (MACN-bar-ins-ct 07680); 1 worker (MACN-bar-ins-ct 07700); Campo de los Alisos NP, Los chorizos, Nest at the base of the tree, Hand, (W65.892°, S27.26°, 1132m), Priscila E. Hanisch, 16/Apr/2016, 1 worker (MACN-bar-ins-07496); 1 worker (MACN-bar-ins-07513); Trail "La Selva Misteriosa", in tree, (W65.874°, S27.28°, 1050m), 19/Apr/2016, 1 worker (MACN-bar-ins-07493); Cerro San Javier, Heading to Taficillo, Alvaro Galbán, 17/Feb/2015, 1 worker (MACN-bar-ins-ct 07675); 1 worker (MACN-bar-ins-ct 07695); 1 worker (MACN-bar-ins-ct 07713); Heading to Cajon, RP310, (W64.9185°, S26.432°), 1 worker (MACN-bar-ins-ct 07641); 1 worker (MACN-bar-ins-ct 07643); 1 worker (MACN-bar-ins-ct 07687); San Miguel de Tucumán, Cerro San Javier, (W65.3297°, S26.7831°), Marta Ayup, 15/Aug/2010, 1 worker (MACN-Bar-Ins-ct 07078); (W65.3797°, S26.8547°), 1 worker (MACN-Bar-Ins-ct 07087); (W65.379°, S26.8391°), 15/Oct/2011, 1 worker (MACN-Bar-Ins-ct 07098); 15/Dec/2010, 1 worker (MACN-Bar-Ins-ct 07106); (W65.3269°, S26.7711°), 15/Dec/2011, 1 worker (MACN-Bar-Ins-ct 07110); (W65.3797°, S26.8547°), 15/Oct/2011, 1 worker (MACN-Bar-Ins-ct 07123); 15/Dec/2010, 1 worker (MACN-Bar-Ins-ct 07132); (W65.3797°, S26.8547°), 15/Aug/2010, 1 worker (MACN-Bar-Ins-ct 07137); 1 worker (MACN_En21410).

Anochetus diegensis

Brazil: Gallego-Ropero M.C. & Oliveira D.E., 1 worker (MZSP).

Anochetus emarginatus

Bolivia: 2 workers (MACN_En21433); 2 workers (MACN_En21434).

Anochetus inermis

Argentina: Tucumán: Ticucha, 06/Nov/1965, 2 workerss (EHB525-MZSP).

Anochetus miserabilis

Argentina: Tucumán: Siambon, Bosq, C. Bruch, 01/Jul/1933, 1 worker (MACN_En21435).

Anochetus neglectus

Argentina: Córdoba: Alta Gracia, La granja, Sierras de Córdoba, C. Bruch, Jan/1911, 2 workers (MACN_En21421); 01/Feb/1922, 3 workerss (MACN_En21422); Dec/1926, 2 ♀ 1 worker (MACN_En21423); 2 ♀ (MACN_En21424); San Javier, La Paz, 1-20/Jan/1929, 1 worker (MACN_En21411); 2 workers (MACN_En21412); 15-31/Dec/1928, 2 workers (MACN_En21413); 1-20/Jan/1929, 2 workers (MACN_En21414). Salta: 1 worker (MACN_En21428); 1 worker (MACN_En21429); 1 worker (MACN_En21430); 1 worker (MACN_En21431); 1 worker (MACN_En21432). Santa Fe: Fives Lille, Weiser, 1 worker (3814-MZSP); 3 workerss (MACN_En21415); 3 workerss (MACN_En21416); 30/Oct/1923, 1 ♀ 2 workers (MACN_En21417); 3 workerss (MACN_En21418); 3 workerss (MACN_En21419); 3 workerss (MACN_En21420); Saladillo, Rosario, J. Hubrick, 2/Apr/1922, 2 workers (MACN_En21425); 2 workers (MACN_En21426). Santiago del Estero: Pampa de los Guanacos, Copo NP, Centro Operativo, under log, Hand, (W61.958°, S25.9725°, 170m), Priscila E. Hanisch, 08/Dec/2016, 1 ♀ (MACN-Bar-Ins-ct 07620); Secc Aibal, ground, (W61.716°, S25.9206°, 157m), 11/Dec/2016, 1 worker (MACN-Bar-Ins-ct 07547); 1 worker (MACN-Bar-Ins-ct 07626); Litter sample, 1 worker (MACN-bar-ins-ct 07735). Tucumán: Tafi Viejo, 1 worker (MACN_En21427).

Centromyrmex gigas

Argentina: Misiones: Loreto, in termite nest, 1 worker (IMML); Dr. A. A. Oglobin, In *Syntermes grandis* Rhamb, 1 worker (MACN_En21459); In *Syntermes grandis* Rhamb, 1 worker (MACN_En21460); In *Syntermes grandis* Rhamb, 1 worker (MACN_En21461). **Brazil:** Sao Paulo: Cidade, 1 worker (MACN_En21458).

Dinoponera australis

Argentina: Corrientes: Santo Tome, Estancia Lirocay, (W55.964°, S28.265°, 126m), Ezequiel Nunez Bustos, 06/Jan/2015, 1 worker (MACN-bar-ins-ct 06462); ground, Hand, Priscila E. Hanisch, 24/May/2015, 1 worker (MACN-bar-ins-07490); 1 worker (MACN-bar-ins-07528); 1 worker (MACN-bar-ins-ct 07787). Misiones: Bompland, F & M Edwards, 13-14/Jan/1927, 1 worker (BM1927-63); Jörgensen,

1 worker (MACN_En21462); 1 worker (MACN_En21463); Iguazú, Alb To Breyer, 1 worker (MACN_En21465); 1 worker (MACN_En21467); Iguazú NP, CIES, (W54.446°, S25.6801°), Priscila E. Hanisch, 19/Mar/2017, 1 worker (MACN-bar-ins-ct 07724); 21/Mar/2017, 1 worker (MACN-bar-ins-ct 07752); 17/Mat/2017, 1 worker (MACN-bar-ins-ct 07773); Secc Apepú, (W54.2957°, S25.5635°, 216m), Nunez Bustos, E: Tubaro, P. L., 22/Sep/2012, 1 worker (MACN-Bar-Ins-ct 05752); Secc Timbo, (W54.17°, S25.68°, 240m), E. Nunez Bustos, C. Kopuchian, P.L. Tubaro, A. Fortino, 11/Apr/2011, 1 worker (MACN-Bar-Ins-ct 02520); Secc Yacui, E. Nunez Bustos, A. Fortino, P. Tubaro y D. Lijtmaer, 18/Dec/2010, 1 worker (MACN-Bar-Ins-ct 00615); E. Nunez Bustos, C. Kopuchian, P.L. Tubaro, A. Fortino, 11/Apr/2011, 1 worker (MACN-Bar-Ins-ct 02519); 1 worker (MACN-Bar-Ins-ct 02521); 140m, C & M Vardy, 8-11/Apr/1974, 7 worker (BM1974-204); P.E. Hanisch, 15/Feb/2011, 1 worker (MACN-Bar-Ins-ct 02973); Hand, (W54.45°, S25.679°), Priscila E. Hanisch, 28/Feb/2015, 1 ♂ (MACN-bar-ins-ct 06394); (W54.456°, S25.673°, 195.524m), 03/Mar/2015, 1 ♂ (MACN-bar-ins-ct 06405); Pitfall trap, Carolina Paris, 20/Jan/2008, 1 worker (MACN-Bar-Ins-ct 3109); Loreto, Dr. A. A. Oglobin, 27/Jul/1928, 1 ♂ (MACN_En21469); ground, Hand, Priscila E. Hanisch, 24/May/2015, 1 worker (MACN-bar-ins-07477); 1 worker (MACN-bar-ins-ct 07681); 1 worker (MACN-bar-ins-ct 07777); 1 worker (MACN-bar-ins-ct 07780); San Ignacio, Bosque de Canela, in tree, (W55.5848°, S27.2862°, 199m), 21/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07405); Osununú PR, (W55.5722°, S27.2808°, 178m), 12/Jan/2015, 1 worker (MACN-bar-ins-ct 06480); (W55.5782°, S27.2802°), 17/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07441); Pitfall, (W55.5805°, S27.2853°, 203.924m), PE Hanisch, CI Paris, A Sanchez, 21/Jan/2015, 1 worker (MACN-bar-ins-ct 07788); (W55.5742°, S27.2826°, 232m), 15/Jan/2015, 1 worker (MACN-bar-ins-ct 07789); (W55.5805°, S27.285°, 205.606m), 21/Jan/2015, 1 worker (MACN-bar-ins-ct 07790); Pastizal de Urunday, ground, Hand, (W55.5609°, S27.2813°, 140m), Priscila E. Hanisch, 21/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07351); C & M Vardy, 4-5/Apr/1974, 1 worker (BM1974-204); Bemberg Hoyward, 17/May/1905, 2 workers (BMNH); C. Bruch, 1 worker (MACN_En21464); Molfino, 1 worker (MACN_En21466); F. Barreto, 1 worker (MACN_En21471). **Bolivia:** 1 worker (MACN_En21468); 1 worker (MACN_En21470).

Hypoponera agilis

Argentina: Misiones: Iguazú NP, Macuco Trail, nest in soil, (W54.4482°, S25.6751°, 173m), Andrew Suarez, 13/Dec/2005, 1 worker (MACN-bar-ins-ct 06929).

Hypoponera argentina

Argentina: Santa Fe: Fives Lille, Weiser, 3 workers (MZSP).

Hypoponera cf. *opacior*

Argentina: Córdoba: Alta Gracia, Jan/1921, 3 workers (MACN_En21367); 2 workers (MACN_En21368); Uritorco, Sombra del Toro, Andres Porta, 28/Mar/2016, 1 worker (MACN-bar-ins-ct

07673); 1 worker (MACN-bar-ins-ct 07694); 1 worker (MACN-bar-ins-ct 07705); 1 worker (MACN-bar-ins-ct 07711); 1 worker (MACN-bar-ins-ct 07714). Jujuy: Calilegua NP, Secc Aguas Negras, Sendero El Pedemontano, Litter sample, (W64.854°, S23.76°, 736m), Priscila E. Hanisch, 13/Apr/2016, 1 worker (MACN-bar-ins-07492); Secc Mesada de las Colmenas, Trail El Negrito, in log, Hand, (W64.8502°, S23.7571°), 1 worker (MACN-bar-ins-07486); (W64.85°, S23.76°), 1 worker (MACN-bar-ins-07527). Misiones: Iguazú NP, along Highway 101, (W54.4546°, S25.6832°), Andrew Suarez, 11/Dec/2005, 1 worker (MACN-bar-ins-ct 06901); AVS2888, Litter sample, (W54.4482°, S25.6751°, 173m), Andrew V. Suarez, 10/Dec/2005, 1 worker (MACN-bar-ins-ct 06996); Macuco Trail, (W54.4498°, S25.678°), Andrew Suarez, 04/Dec/2003, 1 worker (MACN-bar-ins-ct 06888); (W54.4482°, S25.6751°), 27/Jan/2008, 1 worker (MACN-bar-ins-ct 06895); (W54.4493°, S25.6785°), Priscila Hanisch, 18/Jul/2011, 1 worker (MACN-Bar-Ins-ct 05140); Oberá, CIAR, (W54.94°, S27.4447°, 233m), 07/Feb/2013, 1 worker (MACN-Bar-Ins-5607); Litter, Hand, (W54.94°, S27.445°), Priscila E. Hanisch, 05/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07319); San Ignacio, Bosque de Canela, (W55.5846°, S27.2862°, 187m), 21/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07369); Soil and litter sample, (W55.5847°, S27.2862°, 213m), 1 worker (MACN-Bar-Ins-ct 07429); 1 worker (MACN-Bar-Ins-ct 07437); Osununú PR, Soil sample, (W55.5787°, S27.2797°, 177m), 15/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07393); (W55.5795°, S27.2797°, 169m), 14/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07399); 1 worker (MACN-Bar-Ins-ct 07409); (W55.5787°, S27.2797°, 177m), 15/Jan/2015, 1 ♀ (MACN-Bar-Ins-ct 07431). Tucumán: Estancia Los Pinos, Litter sample, (W65.843°, S27.3°, 771m), 16/Apr/2016, 1 worker (MACN-bar-ins-07489).

Hypoponera clavatula

Argentina: Córdoba: Tanti Viejo, 1 worker (MZSP); C. Bruch, 1 worker (3870-MZSP). Tucumán: San Miguel de Tucumán, Cerro San Javier, (W65.3297°, S26.7831°), Marta Ayup, 15/Dec/2010, 1 worker (MACN-Bar-Ins-ct 07089); (W65.3269°, S26.7711°), 15/Aug/2010, 1 worker (MACN-Bar-Ins-ct 07099); (W65.3297°, S26.7831°), 15/Nov/2010, 1 worker (MACN-Bar-Ins-ct 07140).

Hypoponera distinguenda

Argentina: Córdoba: Alta Gracia, La granja, Sierras de Córdoba, 4 workers (MACN_En21325); San Javier, La Paz, C. Bruch, 1-20/Jan/1929, 2 workers (MACN_En21327); 15-31/Dec/1928, 2 workers (MACN_En21328); 1 worker (MACN_En21329). Misiones: Iguazú NP, Secc Apepú, Litter sample, Priscila E. Hanisch, 23/Feb/2016, 1 worker (MACN-bar-ins-ct 07765); rotten log, Hand, 05/Mar/2015, 1 worker (MACN-bar-ins-07454); 03/Mar/2015, 1 worker (MACN-bar-ins-07524); log, (W54.4486°, S25.6736°), Carolina Paris, 14/Dec/2011, 1 ♀ (MACN-Bar-Ins-ct 05026); Under log, Hand, (W54.449°, S25.678°, 190.489m), Priscila E. Hanisch, 02/Mar/2015, 1 worker (MACN-bar-ins-ct 06441); Litter sample, (W54.433°, S25.718°), Leponce, Roisin & Theunis, 23/Sep/1999, 1 worker (MACN-Bar-Ins-ct 06844); Winkler sample, Carolina Paris, 20/Jan/2008, 1 worker (MACN-Bar-Ins-ct 3116); 1 worker (MACN_En21333); log, Hand, 1 worker (MACN-Bar-Ins-ct 05028). **Brazil:** Sao Paulo: Salto Grande, 2

workers (MACN_En21332). **Argentina:** Santa Fe: Fives Lille, Weiser, 1 worker (MACN_En21330); 2 workers (MACN_En21331).

Hypoponera fiebrigi

Argentina: Misiones: Iguazú NP, Litter sample, Priscila E. Hanisch, 22/Dec/2015, 1 worker (MACN-bar-ins-07533).

Hypoponera fiebrigi transiens

Argentina: Córdoba: Alta Gracia, La granja, Sierras de Córdoba, C. Bruch, 1 worker (MACN_En21386); 4 workers (MACN_En21387); Jan/1921, 3 workers (MACN_En21369); C. Bruch, 1-8/Apr/1920, 1 worker (MACN_En21372); 04/Feb/1927, 1 worker (MACN_En21373).

Hypoponera foeda

Argentina: Córdoba: Uritorco, Andres Porta, 28/Mar/2016, 1 worker (MACN-bar-ins-ct 07676).

Hypoponera foreli

Argentina: Misiones: Iguazú NP, Secc Apepú, (W54.295°, S25.567°, 219m), Priscila E. Hanisch, 23/Feb/2016, 1 worker (MACN-bar-ins-ct 06981); (W54.2953°, S25.5672°, 219m), 1 worker (MACN-bar-ins-ct 07053); Hand, (W54.454°, S25.662°, 195.767m), 02/Mar/2015, 1 worker (MACN-bar-ins-ct 06453); Soil and litter sample, (W54.45°, S25.666°, 184.121m), 01/Mar/2015, 1 worker (MACN-bar-ins-ct 06456); Litter sample, (W54.392°, S25.719°), Leponce & Roisin, 22/Sep/1998, 1 worker (MACN-Bar-Ins-ct 06819); Ground, (W54.4546°, S25.6832°), Priscila E. Hanisch, 18/Jul/2011, 1 worker (MACN-bar-ins-ct 06941); Winkler sample, Carolina Paris, 20/Jan/2008, 1 worker (MACN-Bar-Ins-ct 3134).

Hypoponera opaciceps

Argentina: Buenos Aires: C. Bruch, 29/Jun/1925, 3 workers (MACN_En21344); 3 workers (MACN_En21345); 26/Jul/1917, 3 workers (MACN_En21363); 3 workers (MACN_En21364). Córdoba: 1 ♀ (MACN_En21337); 1 ♀ (MACN_En21338); 1 ♀ (MACN_En21339). Jujuy: Calilegua NP, Secc Aguas Negras, Sendero El Pedemontano, Litter sample, (W64.854°, S23.76°, 736m), Priscila E. Hanisch, 13/Apr/2016, 1 worker (MACN-bar-ins-07515). Misiones: Iguazú, 1 worker (IMML); Iguazú NP, Macuco Trail, Litter sample, (W54.4498°, S25.678°), Andrew Suarez, 04/Dec/2003, 1 worker (MACN-bar-ins-ct 06923). Salta: C. Bruch, 2 workers (MACN_En21342); 1 worker (MACN_En21343). Santa Fe: Rosario, Predio Municipal, Hand, Priscila E. Hanisch, 08/Jan/2015, 1 worker (MACN-bar-ins-07508); 1 worker (MACN-bar-ins-07518); C. Bruch, 2 ♀ (MACN_En21340); 2 ♀ (MACN_En21347). Tucumán: Estancia Los Pinos, Light tramp, (W65.845°, S27.3°, 802m), Priscila E. Hanisch, 15/Apr/2016, 1 worker (MACN-bar-ins-07500); nest inside pinecone, Hand, (W65.843°, S27.3°, 771m), 16/Apr/2016, 1 worker (MACN-bar-ins-07505); under stone, 15/Apr/2016, 1 worker (MACN-bar-ins-07532); San Miguel de Tucumán, Cerro San

Javier, (W65.3717°, S26.825°), Marta Ayup, 15/Aug/2010, 1 worker (MACN-Bar-Ins-ct 07071); (W65.3334°, S26.7864°), 1 worker (MACN-Bar-Ins-ct 07094); 1 worker (MACN-Bar-Ins-ct 07112); C. Bruch, 1 worker (MACN_En21335); 1 worker (MACN_En21336).

Hypoponera opaciceps pampana

Argentina: Buenos Aires: Monte hermoso, 1 worker (MACN_En21358); 1 worker (MACN_En21359); Tandil, 1 worker (MACN_En21355); 1 worker (MACN_En21356); Tandil viejo, 2 workers (MACN_En21360); C. Bruch, 14/Sep/1919, 3 workers (MACN_En21361). Catamarca: Cerro Colorado, Weiser, 3 ♀ 1 worker (MACN_En21353). Córdoba: Alta Gracia, La granja, Sierras de Córdoba, C. Bruch, Dec/1921, 2 workers (MACN_En21326); 4 workers (MACN_En21350); 3 workers (MACN_En21352); 1-8/Apr/1920, 2 ♀ 1 worker (MACN_En21357); 2 workers (3778-MZSP). Misiones: Loreto, 2 workers (MACN_En21354). Santa Fe: Fives Lille, Weiser, 3 workers (MACN_En21351).

Hypoponera opacior

Argentina: Buenos Aires: C. Bruch, 10-Feb/1893, 1 ♀ (MACN_En21348); 10-Jan/1893, 1 ♀ (MACN_En21349). Misiones: Iguazú, 1 worker (IMML). Tucumán: San Miguel de Tucumán, Cerro San Javier, (W65.3333°, S26.7986°), Marta Ayup, 15/Nov/2010, 1 worker (MACN-Bar-Ins-ct 07074); (W65.3334°, S26.7864°), 1 worker (MACN-Bar-Ins-ct 07081). **Panamá**: Panamá oeste: Cerro Campana, (950 m), Anderson R, 05/Jul/1995, Compared with type material by W Mackay, 2 workers (MACN).

Hypoponera parva

Argentina: Misiones: Iguazú NP, Macuco Trail, Litter sample, (W54.4482°, S25.6751°, 173m), Andrew Suarez, 10/Dec/2005, 1 worker (MACN-bar-ins-ct 06935); 1 worker (MACN-bar-ins-ct 06944); (W54.4498°, S25.678°, 173m), Andrew V. Suarez, 04/Dec/2003, 1 worker (MACN-bar-ins-ct 06975); (W54.449°, S25.6776°, 213m), Priscila E. Hanisch, 08/Mar/2015, 1 worker (MACN-bar-ins-07450); 1 worker (MACN-bar-ins-07471); Hand, (W54.457°, S25.671°, 191.391m), 03/Mar/2015, 1 worker (MACN-bar-ins-ct 06457); Under log, (W54.449°, S25.678°, 190.489m), 02/Mar/2015, 1 worker (MACN-bar-ins-ct 06481); Litter sample, (W54.355°, S25.704°), Leponce & Roisin, 24/Sep/1999, 1 worker (MACN-Bar-Ins-ct 06823); (W54.433°, S25.718°), Leponce, Roisin & Theunis, 23/Sep/1999, 1 worker (MACN-Bar-Ins-ct 06850); (W54.355°, S25.704°), Leponce & Roisin, 24/Sep/1999, 1 worker (MACN-Bar-Ins-ct 06859); San Ignacio, Bosque de Canela, Hand, (W55.5846°, S27.2862°, 187m), Priscila E. Hanisch, 21/Jan/2015, 1 ♀ (MACN-Bar-Ins-ct 07375); Osununú PR, Under stone, (W55.5702°, S27.2797°, 92m), 19/Jan/2015, 1 worker (MACN-bar-ins-07442).

Hypoponera PEH01

Argentina: Misiones: Iguazú NP, log, Hand, (W54.4495°, S25.6776°, 190.49m), Priscila E. Hanisch, 02/Mar/2015, 1 worker (MACN-bar-ins-07466); 1 worker (MACN-bar-ins-07467); dead tree,

20/Dec/2015, 1 worker (MACN-bar-ins-07512); (W54.481°, S25.69°, 242.392m), 05/Mar/2015, 1 worker (MACN-bar-ins-ct 06450).

Hypoponera PEH02

Argentina: Misiones: Iguazú NP,log, Hand, (W54.4495°, S25.6776°, 190.49m), Priscila E. Hanisch, 02/Mar/2015, 1 worker (MACN-bar-ins-07461); Soil and litter sample, (W54.4478°, S25.6708°, 175.74m), 28/Feb/2015, 1 worker (MACN-bar-ins-07475); Under log, Hand, (W54.449°, S25.678°, 190.489m), 02/Mar/2015, 1 worker (MACN-bar-ins-ct 06434); Litter sample, (W54.449°, S25.678°, 213m), 08/Mar/2015, 1 worker (MACN-bar-ins-ct 06439); Hand, (W54.456°, S25.675°, 171.13m), 03/Mar/2015, 1 worker (MACN-bar-ins-ct 06444); Soil and litter sample, (W54.448°, S25.671°, 175.74m), 28/Feb/2015, 1 worker (MACN-bar-ins-ct 06447); Litter sample, (W54.433°, S25.718°), Leponce, Roisin & Theunis, 23/Sep/1999, 1 worker (MACN-Bar-Ins-ct 06870); Oberá, CIAR, (W54.94°, S27.4447°, 231m), 15/Feb/2013, 1 worker (MACN-Bar-Ins-5605); San Ignacio, Osununú PR, Litter, Hand, (W55.5805°, S27.2871°, 206m), Carolina I. Paris, 19/Jan/2015, 1 worker (MACN-bar-ins-07445); Log, Priscila E. Hanisch, 15/Jan/2015, 1 worker (MACN-bar-ins-07452); soil, (W55.5757°, S27.2803°, 191m), 19/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07374); ground, (W55.5702°, S27.2797°, 92m), 1 worker (MACN-Bar-Ins-ct 07420); Yaboti, (W53.8795°, S26.3956°), Alvaro Galbán, 09/Apr/2016, 1 worker (MACN-bar-ins-ct 07652); 1 worker (MACN-bar-ins-ct 07655); 1 worker (MACN-bar-ins-ct 07685).

Hypoponera PEH03

Argentina: Santiago del Estero: Pampa de los Guanacos, Copo NP, Secc Aibal, Litter sample, (W61.716°, S25.9206°, 157m), Priscila E. Hanisch, 11/Dec/2016, 1 worker (MACN-Bar-Ins-ct 07554); 1 ♀ (MACN-Bar-Ins-ct 07557); 1 worker (MACN-Bar-Ins-ct 07559); 1 worker (MACN-Bar-Ins-ct 07561); 1 worker (MACN-Bar-Ins-ct 07591).

Hypoponera PEH04

Argentina: Córdoba: Uritorco, Andres Porta, 28/Mar/2016, 1 worker (MACN-bar-ins-ct 07635); 1 worker (MACN-bar-ins-ct 07692). Misiones: Iguazú NP, Macuco Trail, Litter sample, (W54.4482°, S25.6751°, 173m), Andrew Suarez, 10/Dec/2005, 1 worker (MACN-bar-ins-ct 06897); San Ignacio, Osununú PR, Hand, (W55.5782°, S27.2787°, 170m), Priscila E. Hanisch, 18/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07366); (W55.5805°, S27.2871°, 206m), Carolina I. Paris, 19/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07381); at the base of palm tree, Hand, (W55.581°, S27.2835°, 205m), Priscila E. Hanisch, 16/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07433).

Hypoponera PEH05

Argentina: Formosa: Herradura, Litter sample, (W58.29°, S26.498°, 59m), Andrew V. Suarez, 27/Nov/2003, 1 worker (MACN-bar-ins-ct 07003).

Hypoponera PEH06

Argentina: Misiones: San Ignacio, Bosque de Canela, Soil sample, (W55.5848°, S27.2862°, 199m), Priscila E. Hanisch, 21/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07397); 1 worker (MACN-Bar-Ins-ct 07414); Osununú PR, Under rock, Hand, (W55.5702°, S27.2797°, 92m), 19/Jan/2015, 1 ♀ (MACN-bar-ins-07443); (W55.5784°, S27.279°), 1 worker (MACN-Bar-Ins-ct 07361); Litter, (W55.5776°, S27.2797°), 16/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07427); Under rock, (W55.5784°, S27.279°), 19/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07435).

Hypoponera PEH07

Argentina: Buenos Aires: Tandil, Sierra del tigre, Andres Porta, 24/Oct/2014, 1 worker (MACN-bar-ins-ct 07649). Tucumán: Campo de los Alisos NP, Trail "La Selva Misteriosa", Hand, (W65.874°, S27.28°, 1050m), Priscila E. Hanisch, 19/Apr/2016, 1 worker (MACN-bar-ins-07502).

Hypoponera PEH08

Argentina: Buenos Aires: Costanera Sur, ground, Hand, Priscila E. Hanisch, 28/Feb/2017, 1 worker (MACN-bar-ins-ct 07763); 1 worker (MACN-bar-ins-ct 07776); 1 worker (MACN-bar-ins-ct 07778); 1 worker (MACN-bar-ins-ct 07782). Jujuy: Calilegua, under stone, Hand, (W64.7726°, S23.7761°, 473m), 12/Apr/2016, 1 worker (MACN-bar-ins-07483).

Hypoponera schmalzi

Argentina: Misiones: Iguazú NP, Macuco Trail, Litter sample, (W54.4482°, S25.6751°, 173m), Andrew Suarez, 10/Dec/2005, 1 worker (MACN-bar-ins-ct 06883); (W54.4498°, S25.678°), 04/Dec/2003, 1 worker (MACN-bar-ins-ct 06885).

Hypoponera stoica

Argentina: Buenos Aires: La Plata, bosque, 22/Feb/1920, 2 workers (1256-MZSP); C. Bruch, 22/Jan/1920, 1 ♀ 1 worker (MACN_En21376).

Hypoponera trigona

Argentina: Buenos Aires: La Plata, 1 worker (17234-MZSP); C. Bruch, 2 workers (MACN_En21366). Formosa: Formosa NR, Secc Rio Teuco, (W61.7941°, S24.3167°, 190m), M. Izquierdo, C. Kopuchian, L. Calderon, 27/Jun/2010, 1 worker (MACN-Bar-Ins-5447). Misiones: Iguazú NP, Macuco Trail, Litter sample, (W54.4498°, S25.678°), Andrew Suarez, 04/Dec/2003, 1 worker (MACN-bar-ins-ct 06938); 1 worker (MACN-bar-ins-ct 06951); Winkler sample, Carolina Paris, 20/Jan/2008, 1 worker (MACN-Bar-Ins 03160); litter, (W54.4502°, S25.6659°, 177.84m), Priscila E. Hanisch, 01/Mar/2015, 1 worker (MACN-bar-ins-07448); Soil and litter sample, (W54.458°, S25.656°, 193m), 1 worker (MACN-bar-ins-ct 06428); Log,

Hand, 1 worker (MACN-bar-ins-ct 06430); Litter sample, (W54.449°, S25.678°, 213m), 08/Mar/2015, 1 worker (MACN-bar-ins-ct 06432); (W54.433°, S25.718°), Leponce, Roisin & Theunis, 23/Sep/1999, 1 worker (MACN-Bar-Ins-ct 06828); Winkler sample, Carolina Paris, 20/Jan/2008, 1 worker (MACN-Bar-Ins-ct 3086); 1 worker (MACN-Bar-Ins-ct 3088); Loreto, 1 worker (IMML); A. Ogloblin, 1 worker (MACN_En21388); 1 worker (MACN_En21389); 1 worker (MACN_En21390). Tucumán: Famaillá, 2 workers (MACN_En21365). **Brazil:** Santa Catarina: G. Mayr, Syntype, 1 worker ((E)1015615).

Leptogenys arcuata

Bolivia: 1 worker (MACN_En21402); 1 worker (MACN_En21403).

Leptogenys australis

Argentina: Buenos Aires: C. Bruch, 1 worker (MACN_En21391); 1 worker (MACN_En21392); 1 worker (MACN_En21393). Santa Fe: Rosario, Saladillo, J. Hubrick, 14/Apr/1922, 1 worker (1171-MZSP); Hubrich, 1 worker (MACN_En21395); C. Bruch, 1 worker (MACN_En21394).

Leptogenys bohlsi

Argentina: Formosa: Formosa NR, Secc Río Teuco, (W61.47°, S24.19°, 178m), M. Izquierdo, C. Kopuchian, L. Calderon, 27/Jun/2010, 1 worker (MACN-Bar-Ins-ct 00359). Santa Fe: Fives Lille, Weiser, 1 worker (3871-MZSP); 3 workers (MACN_En21396); 2 workers (MACN_En21397); 3 workers (MACN_En21398); 2 workers (MACN_En21399); 1 worker (MACN_En21400); 1 worker (MACN_En21401); 1 worker (MZSP).

Leptogenys iheringi

Argentina: Misiones: Iguazú NP, Secc Apepú, Hand, (W54.296°, S25.563°, 192m), Priscila E. Hanisch, 24/Feb/2016, with isopode prey, 1 worker (MACN-bar-ins-ct 07007).

Neoponera aenescens

Argentina: Jujuy: Tiraxis, (W65.3531°, S24.008°), Alvaro Galbán, 01/Mar/2017, 1 worker (MACN-bar-ins-ct 07672); 1 worker (MACN-bar-ins-ct 07686); 1 worker (MACN-bar-ins-ct 07689); 1 worker (MACN-bar-ins-ct 07715); 1 worker (MACN-bar-ins-ct 07791).

Neoponera bactronica

Argentina: Corrientes: Santo Tome, Estancia Lirocay, (W55.964°, S28.265°, 126m), Ezequiel Nunez Bustos, 06/Jan/2015, 1 ♀ (MACN-bar-ins-ct 06464); 1 worker (MACN-bar-ins-ct 06471). Formosa: Pilcomayo NP, [25°4'6''S, 58°5'36''W], Leponce, Roisin & Theunis, 8/Oct/1999, 1 worker (RBINS-4355). Misiones: Comandante Andresito, Yacutinga, under stone, (W54.0742°, S25.5912°, 260m), Ezequiel N.

Bustos, 06/Nov/2015, 1 worker (MACN-bar-ins-ct 07029); Hand, Ezequiel Nunez Bustos, 15/Nov/2010, 1 worker (MACN-Bar-Ins-ct 07149); Iguazú NP, CIES, (W54.449°, S25.679°, 197.098m), Priscila E. Hanisch, 28/Feb/2015, 1 worker (MACN-bar-ins-ct 06396); Secc Apepú, in tree, Hand, 24/Feb/2016, 1 worker (MACN-bar-ins-ct 07697); 05/Mar/2015, 1 worker (MACN-bar-ins-07514). Santiago del Estero: Pampa de los Guanacos, Copo NP, Secc Aibal, in tree, (W61.716°, S25.9206°, 157m), 11/Dec/2016, 1 worker (MACN-Bar-Ins-ct 07536); 1 worker (MACN-bar-ins-ct 07540). **Brazil:** Bahia: Ilhéus, CEPEC Genética, PI24 bis Phenotype 2, D. Fresneau, Nov/1998, Holotype, 1 worker (MZSP).

Neoponera billemma

Argentina: Chaco: Charata, 1 worker (MACN_En21481). **Brazil:** Pará: Benevides, Morelandia, Bittencourt, 16/Jun/1988, Holotype, 1 worker (MZSP).

Neoponera commutata

Brazil. Manaos: Amazon, 1 worker (MACN_En21473); 1 ♀ (MACN_En21475).

Neoponera crenata

Argentina: Misiones: Iguazú, 1 worker (IMML); Iguazú NP, CIES, Hand, (W54.446°, S25.6801°), Priscila E. Hanisch, 10/Mar/2017, 1 worker (MACN-bar-ins-ct 07638); Macuco Trail, on bamboo, (W54.4482°, S25.6751°), Andrew Suarez, 13/Dec/2005, 1 worker (MACN-bar-ins-ct 06891); (W54.4482°, S25.6751°, 173m), 1 worker (MACN-bar-ins-ct 06943); Hand, (W54.456°, S25.673°, 195.524m), Priscila E. Hanisch, 03/Mar/2015, 1 worker (MACN-bar-ins-ct 06398); shrub, (W54.45°, S25.666°, 185.436m), 01/Mar/2015, 1 worker (MACN-bar-ins-ct 06416); Litter sample, (W54.433°, S25.718°), Leponce, Roisin & Theunis, 23/Sep/1999, 1 worker (MACN-Bar-Ins-ct 06779); (W54.355°, S25.704°), Leponce & Roisin, 24/Sep/1999, 1 worker (MACN-Bar-Ins-ct 06809); in tree, Hand, Priscila E. Hanisch, 21/Dec/2015, 1 worker (MACN-bar-ins-ct 07761); Oberá, CIAR, (W54.94°, S27.4447°, 174m), 13/Feb/2013, 1 worker (MACN-Bar-Ins-5548); (W54.94°, S27.4447°, 185m), 15/Feb/2013, 1 worker (MACN-Bar-Ins-5559); Hand, (W54.94°, S27.445°), Priscila E. Hanisch, 14/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07343); San Ignacio, Osununú PR, (W55.5753°, S27.2808°, 151m), 12/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07387); (W55.5779°, S27.281°, 200m), 1 worker (MACN-Bar-Ins-ct 07395); (W55.5753°, S27.2808°, 151m), 1 worker (MACN-Bar-Ins-ct 07424).

Neoponera curvinodis

Argentina: Misiones: Iguazú NP, Hand, (W54.449°, S25.679°, 201.272m), Priscila E. Hanisch, 02/Mar/2015, 1 worker (MACN-bar-ins-ct 06407); Puerto Iguazú, ground, 23/May/2015, 1 worker (MACN-bar-ins-07509).

Neoponera fauveli

Argentina: Jujuy: 1 worker (MACN_En21323).

Neoponera fiebrigi

Argentina: Misiones: Iguazú NP, CIES, Hand, (W54.446°, S25.6801°), Priscila E. Hanisch, 10/Mar/2017, 1 worker (MACN-bar-ins-ct 07733); 15/Mar/2017, 1 worker (MACN-bar-ins-ct 07766); Log, (W54.4502°, S25.666°, 184.12m), 01/Mar/2015, 1 worker (MACN-bar-ins-07476); shrub, (W54.456°, S25.675°, 171.13m), 03/Mar/2015, 1 worker (MACN-bar-ins-ct 06401); San Ignacio, Osununú PR, (W55.577°, S27.28°, 135m), 15/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07365); shrub, (W55.5784°, S27.2792°, 191m), 16/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07439).

Neoponera insignis

Peru: Madre de Dios: Río Alto Madre de Dios, Pantiacolla Lodge, Malaise trap, [12°39.34'''S, 71°13.91'''W, 400m], G. Martín, M. Barclay, H. Mendel, Nov/2011, 1 ♀ (BMNH(E) 2011-216).

Neoponera inversa

Ecuador: Napo: Lectotype, 1 worker (BMNH(E)1015556).

Neoponera marginata

Argentina: Chaco: Chavata, 1 worker (MACN_En21316). Jujuy: 1 worker (MACN_En21317); 1 ♀ (MACN_En21318); 2 workers (MACN_En21319). Misiones: Bompland, Jörgensen, 1 worker (MACN_En21311); 1 worker (MACN_En21312); 1 worker (MACN_En21315); Loreto, 1 worker (IMML); Oberá, CIAR, (W54.94°, S27.4447°, 207m), 05/Feb/2013, 1 worker (MACN-Bar-Ins-5581); (W54.94°, S27.4447°, 212m), 12/Feb/2013, 1 worker (MACN-Bar-Ins-5586); ground, Hand, (W54.94°, S27.445°), Priscila E. Hanisch, 05/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07316); San Ignacio, Osununú PR, (W55.5702°, S27.2797°, 92m), 19/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07360); (W55.5702°, S27.2783°, 107m), 1 worker (MACN-Bar-Ins-ct 07413); Teyú Cuare NP, (W55.594°, S27.284°, 140.818m), 20/Jan/2015, 1 worker (MACN-bar-ins-ct 06486); 1 worker (IMML); 1 worker (MACN_En21310); 1 worker (MACN_En21313); 1 worker (MACN_En21314). Santiago del Estero: Copo NP, Sec Aibal - Sendero, ground, Hand , (W61.716°, S25.9206°, 157m), Priscila E. Hanisch, 11/Dec/2016, 1 worker (MACN-bar-ins-ct 07726); 1 worker (MACN-bar-ins-ct 07729); Pampa de los Guanacos, Copo NP, Secc Aibal, Hand, 1 worker (MACN-Bar-Ins-ct 07567); 1 worker (MACN-bar-ins-ct 07743). **Brazil:** Sao Paulo: Franca, 2 workers (MACN_En21321); 2 workers (MACN_En21322). **Paraguay:** 2 workers (MACN_En21320).

Neoponera moesta

Argentina: Formosa: Reserva El Bagual, Malaise Trap, (W58.815°, S26.303°, 57m), Pablo Tubaro, 06/Dec/2013, 1 worker (BIOUG24141-A02). Misiones: Bompland, 1 worker (MACN_En21324); Iguazú NP, Hand, (W54.4563°, S25.674°), Priscila Hanisch, 21/Jul/2011, 1 ♀ (MACN-Bar-Ins-ct 05145); (W54.481°, S25.689°, 208.27m), Priscila E. Hanisch, 05/Mar/2015, 1 worker (MACN-bar-ins-ct 06414); San Ignacio, Osununú PR, nest in tree, (W55.579°, S27.279°, 96m), 03/Dec/2015, 1 worker (MACN-bar-ins-ct 06989); Litter sample, (W55.579°, S27.279°), 30/Nov/2015, 1 worker (MACN-bar-ins-ct 07023); Hand, (W55.5753°, S27.2808°, 151m), 12/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07406); ground, (W55.5784°, S27.2791°), 1 worker (MACN-Bar-Ins-ct 07430); Teyú Cuare NP, in tree, (W55.5785°, S27.2791°), 21/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07355).

Neoponera obscuricornis

Argentina: Misiones: Iguazú NP, CIES, Hand, (W54.449°, S25.679°, 197.098m), Priscila E. Hanisch, 16/Feb/2016, 1 worker (MACN-bar-ins-ct 07054); Log, (W54.449°, S25.678°, 190.489m), 02/Mar/2015, 1 ♀ (MACN-bar-ins-ct 06435); ground, (W54.449°, S25.678°, 213m), 06/Mar/2015, 1 worker (MACN-bar-ins-ct 06440); dead tree, (W54.45°, S25.679°, 173m), 20/Dec/2015, 1 worker (MACN-bar-ins-ct 07017); 1 worker (MACN-bar-ins-ct 07038).

Neoponera PEH01

Argentina: Misiones: Iguazú NP,Log, Hand, (W54.4495°, S25.6776°, 190.49m), Priscila E. Hanisch, 02/Mar/2015, 1 worker (MACN-bar-ins-07447).

Neoponera verenae

Argentina: Formosa: Pilcomayo NP, [25°4'6''S, 58°5'36''W], Leponce, Roisin & Theunis, 8/Oct/1999, 1 worker (RBINS-06516); 1 worker (RBINS-06565); 1 worker (RBINS-07902); 1 worker (RBINS-07918). Misiones: Iguazú NP, Trail Yacaratia, Ground, (W54.4547°, S25.6772°), Priscila E. Hanisch, 18/Jul/2011, 1 worker (MACN-bar-ins-ct 07061); Oberá, CIAR, Malaise Trap, (W54.9403°, S27.4447°, 147m), Pablo Tubaro, 21/Mar/2013, 1 worker (BIOUG12771-E04); (W54.94°, S27.4447°, 218m), 05/Feb/2013, 1 worker (MACN-Bar-Ins-5592); Hand, (W54.94°, S27.4447°, 164m), Priscila E. Hanisch, 13/Feb/2013, 1 worker (MACN-bar-ins-ct 07051); (W54.94°, S27.445°), 05/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07315); 14/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07345); San Ignacio, Osununú PR, ground, (W55.578°, S27.279°), 21/Jan/2015, 1 worker (MACN-bar-ins-ct 06487); nest in log, (W55.579°, S27.279°, 77m), 30/Nov/2015, 1 worker (MACN-bar-ins-ct 06997); (W55.579°, S27.279°), 1 worker (MACN-bar-ins-ct 07004); Teyú Cuare NP, ground, (W55.5923°, S27.2839°, 95m), 20/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07353); 1 worker (MACN-Bar-Ins-ct 07400); (W55.5939°, S27.284°, 141m), 1 worker (MACN-Bar-Ins-ct 07440).

Neoponera villosa

Argentina: Formosa: Rio Pilcomayo, 1 worker (MACN_En21478); 1 worker (MACN_En21480); 1 worker (MACN_En21476). Misiones: Comandante Andresito, Yacutinga, (W54.0742°, S25.5912°, 260m), Ezequiel N. Bustos, 06/Nov/2015, 1 worker (MACN-bar-ins-ct 06976); 06/Nov/2016, 1 worker (MACN-bar-ins-ct 07010); 06/Nov/2017, 1 worker (MACN-bar-ins-ct 07047); Iguazú, 1 worker (IMML); Iguazú NP, In Linea regularis tree, Hand, (W54.4491°, S25.6788°, 201.27m), Priscila E. Hanisch, 01/Mar/2015, 1 worker (MACN-bar-ins-07446); shrub, (W54.4807°, S25.69°, 242m), 05/Mar/2015, 1 worker (MACN-bar-ins-07451); in liana, (W54.4478°, S25.6708°, 175.74m), 28/Feb/2015, 1 worker (MACN-bar-ins-07460); (W54.4536°, S25.6789°), Priscila Hanisch, 18/Jul/2011, 1 ♀ (MACN-Bar-Ins-ct 05121); (W54.4563°, S25.674°), 1 worker (MACN-Bar-Ins-ct 05138); Hand, (W54.456°, S25.675°, 192.044m), Priscila E. Hanisch, 08/Mar/2015, 1 worker (MACN-bar-ins-ct 06404); San Ignacio, Osununú PR, (W55.5739°, S27.2824°, 222m), 13/Jan/2015, Tandem walking, 1 worker (MACN-Bar-Ins-ct 07350); Teyú Cuare NP, ground, (W55.5785°, S27.2791°), 21/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07386). **Paraguay:** Sa. Trinidad: 01/May/1915, 1 worker (MACN_En21479). **Brazil:** Santa Caterina: Hammonia, 2 workers (MACN_En21477).

Odonomachus affinis

Brazil. Sao Paulo: Cidade, 1 worker (MACN_En21442); 1 worker (MACN_En21445); 1 worker (MACN_En21446); S. Sebast., 1 worker (MACN_En21440); 1 worker (MACN_En21441).

Odontomachus bauri

Argentina: Santiago del Estero: Copo NP, Sec Aibal - Sendero, ground, Hand, (W61.716°, S25.9206°, 157m), Priscila E. Hanisch, 10/Dec/2016, 1 worker (MACN-bar-ins-ct 07764); Pampa de los Guanacos, Copo NP, Centro Operativo, in log, (W61.958°, S25.9725°, 170m), 08/Dec/2016, 1 worker (MACN-Bar-Ins-ct 07570); 09/Dec/2016, 1 worker (MACN-Bar-Ins-ct 07573); Heading to Sec Aibal, ground, (W61.711°, S26.1119°, 156m), 1 worker (MACN-Bar-Ins-ct 07565).

Odontomachus chelifer

Argentina: Corrientes: Ebco, Ivan L. F. Magalhaes, 14/Sep/2016, 1 worker (MACN-Bar-Ins-ct 07421); 1 worker (MACN-Bar-Ins-ct 07425); Santo Tome, Ruta 14, ground, Hand, (W56.0774°, S28.5486°, 62m), Priscila E. Hanisch, 24/May/2015, 1 worker (MACN-bar-ins-ct 06972); (W56.0774°, S28.5486°), 1 worker (MACN-bar-ins-ct 07046). Formosa: Reserva El Bagual, Malaise Trap, (W58.815°, S26.3028°, 57m), Pablo Tubaro, 12/Apr/2014, 1 ♂ (BIOUG25340-C10). Misiones: Bompland, Jörgensen, 1 worker (MACN_En21436); 1 ♀ (MACN_En21437); Comandante Andresito, Yacutinga, (W54.0742°, S25.5912°, 260m), Ezequiel N. Bustos, 06/Nov/2015, 1 worker (MACN-bar-ins-ct 07002); 1 worker (MACN-bar-ins-ct 07030); Iguazú, 1 worker (IMML); Iguazú NP, ground, Hand, (W54.4536°, S25.6789°), Priscila Hanisch,

18/Jul/2011, 1 worker (MACN-Bar-Ins-ct 05137); (W54.4518°, S25.6638°), 1 worker (MACN-Bar-Ins-ct 05141); (W54.454°, S25.662°, 195.767m), Priscila E. Hanisch, 02/Mar/2015, 1 worker (MACN-bar-ins-ct 06399); ground, (W54.45°, S25.666°, 184.121m), 01/Mar/2015, 1 worker (MACN-bar-ins-ct 06417); Pitfall trap, Carolina Paris, 20/Jan/2008, 1 worker (MACN-Bar-Ins-ct 3114); Oberá, CIAR, Malaise Trap, (W54.9403°, S27.4447°, 147m), Pablo Tubaro, 28/Mar/2013, 1 ♂ (BIOUG22490-E02); Hand, (W54.94°, S27.445°), Priscila E. Hanisch, 05/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07314); San Ignacio, Osununú PR, 01/Dec/2015, 1 worker (MACN-bar-ins-07473); (W55.5753°, S27.2803°), 12/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07352); ground, Nigh hand collection, (W55.5784°, S27.2792°, 191m), 11/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07362); Hand, (W55.5747°, S27.2792°), 17/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07396); (W55.5807°, S27.2847°, 202m), 14/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07423); Yaboti, (W53.8795°, S26.3956°), Alvaro Galbán, 09/Apr/2016, 1 worker (MACN-bar-ins-ct 07651); 1 worker (MACN-bar-ins-ct 07688); 1 worker (MACN_En21438). Salta: Rosario de la frontera, Los Baños, (W64.9296°, S25.8355°), Alvaro Galbán, 09/Feb/2004, 1 worker (MACN-bar-ins-ct 07631); 1 worker (MACN-bar-ins-ct 07639); 1 worker (MACN-bar-ins-ct 07656); 1 worker (MACN-bar-ins-ct 07660); 1 worker (MACN-bar-ins-ct 07674). Santiago del Estero: Pampa de los Guanacos, Copo NP, Secc Aibal, ground, Hand, (W61.716°, S25.9206°, 157m), Priscila E. Hanisch, 11/Dec/2016, 1 worker (MACN-Bar-Ins-ct 07552); 1 worker (MACN-Bar-Ins-ct 07558); C. Bruch, 1 ♀ (MACN_En21439). Tucumán: Cruz Alta, La Soledad, Cañete, H.E. Bucher, 09/Sep/1965, 1 worker (EHB340-MZSP); 1 worker (EHB390-MZSP). **Brazil:** Itapua: Viamao, (W51.0325°, S30.3398°, 27m), 05/Jan/2017, 1 worker (MACN-bar-ins-ct 07647).

Odontomachus haematodus

Argentina: Corrientes: Ebco, (E0°, N0°), Ivan L. F. Magalhaes, 14/Sep/2016, 1 worker (MACN-Bar-Ins-ct 07367); 1 worker (MACN-Bar-Ins-ct 07373); ground, Hand, Priscila E. Hanisch, 24/May/2015, 1 worker (MACN-bar-ins-07470); 1 worker (MACN-bar-ins-07479). Formosa: Laishi, Zurflüh, 1 worker (MACN_En21447); 1 worker (MACN_En21448). Jujuy: Libertador General San Martin, Hand, Ezequiel N. Bustos, 01/Apr/2015, 1 worker (MACN-bar-ins-07520); 1 worker (MACN_En21449); B. Barreto, 2 workers (MACN_En21453); 2 workers (MACN_En21454). Misiones: Puerto Iguazú, ground, Hand, (W54.5709°, S25.5939°), Priscila E. Hanisch, 23/May/2015, 1 worker (MACN-bar-ins-ct 07040); (W54.5911°, S25.6056°), 1 worker (MACN-Bar-Ins-ct 07139). Santa Fe: Fives Lille, Weiser, 2 workers (MACN_En21450); 2 workers (MACN_En21451); 2 workers (MACN_En21452). **Guyana:** Onderneeming: GE Bodkin, 20/Apr/1915, Holotype, 1 worker (BMNH(E)1013976). **Bolivia:** Santa Cruz: Chiquitos, Yabare, Univ. A. Gabriel R. Moreno, Pitfall, (W62.1725°, S16.4417°, 260m), C. Grismado, S. Avila & M. Perez, 20/Oct/2010, 1 worker (MACN-bar-ins-ct 07738); 1 worker (MACN-bar-ins-ct 07779). **Brazil:** Santarem: Syntype, 1 worker (BMNH(E)1013975). **Argentina:** Santiago del Estero: Bañado en ruta 34, ground, Hand, (W62.235°, S29.5694°, 110m), Priscila E. Hanisch, 12/Dec/2016, 1 worker (MACN-Bar-Ins-ct 07604). Tucumán: Raco, N. Kusnezov, spines not visible, 2 workers (MZSP). **Bolivia:** 1 worker (MACN_En21455).

Odontomachus hastatus

Brazil: Sao Paulo: Cidade, 1 worker (MACN_En21443); 1 worker (MACN_En21444).

Odontomachus insularis

Brazil. Sao Paulo: Franca, 2 workers (MACN_En21456).

Odontomachus meinerti

Argentina: Misiones: Iguazú NP, Secc Apepú, Nest at the base of the tree, Hand, (W54.2955°, S25.5647°), Priscila E. Hanisch, 24/Feb/2016, 1 worker (MACN-bar-ins-ct 07018); 27/Feb/2016, 1 worker (MACN-bar-ins-ct 07060); Winkler sample, Carolina Paris, 20/Jan/2008, 1 ♀ (MACN-Bar-Ins 03155); at base of Anchico colorado, Hand, Priscila E. Hanisch, 42067, 1 worker (MACN-bar-ins-07506); log, (W54.4536°, S25.6789°), Carolina Paris, 15/Dec/2011, 1 ♀ (MACN-Bar-Ins-ct 05059); Priscila Hanisch, 15/Dec/2011, 1 worker (MACN-Bar-Ins-ct 05061); Subterranean bait, (W54.4298°, S25.7037°), Priscila Hanish y Carolina Paris, 03/Mar/2009, 1 worker (MACN-Bar-Ins-ct 05065); Pitfall, (W54.4563°, S25.674°), Carolina Paris, 24/Jan/2008, 1 worker (MACN-Bar-Ins-ct 05067); Hand, (W54.456°, S25.675°, 192.044m), Priscila E. Hanisch, 08/Mar/2015, 1 worker (MACN-bar-ins-ct 06402); ground, (W54.456°, S25.675°, 230.835m), 1 worker (MACN-bar-ins-ct 06418); Log, (W54.45°, S25.666°, 185.436m), 01/Mar/2015, 1 worker (MACN-bar-ins-ct 06421); Litter sample, (W54.449°, S25.678°, 213m), 08/Mar/2015, 1 worker (MACN-bar-ins-ct 06423); San Ignacio, Bosque de Canela, Soil and litter sample, (W55.5847°, S27.2862°, 213m), 21/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07370); Osununú PR, ground, Hand, (W55.579°, S27.279°), 29/Nov/2015, 1 worker (MACN-bar-ins-ct 06999); Bait, (W55.5784°, S27.279°), 19/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07410); Litter sample, 1 worker (MACN-Bar-Ins-ct 05071).

Odontomachus PEH01

Argentina: Misiones: Oberá, CIAR, (W54.94°, S27.4447°, 183m), 14/Feb/2013, 1 worker (MACN-Bar-Ins-5557); (W54.94°, S27.4447°, 190m), 06/Feb/2013, 1 worker (MACN-Bar-Ins-5564); (W54.94°, S27.4447°, 196m), 13/Feb/2013, 1 worker (MACN-Bar-Ins-5570); (W54.94°, S27.4447°, 250m), 06/Feb/2013, 1 worker (MACN-Bar-Ins-5624); Hand, (W54.94°, S27.445°), Priscila E. Hanisch, 05/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07320); 1 worker (MACN-Bar-Ins-ct 07325); 06/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07330); San Ignacio, Osununú PR, (W55.579°, S27.28°, 172m), 15/Jan/2015, 1 worker (MACN-bar-ins-ct 06983); ground, (W55.575°, S27.279°, 77m), 02/Dec/2015, 1 worker (MACN-bar-ins-ct 07014); 1 worker (MACN-bar-ins-ct 07031). Santiago del Estero: Pampa de los Guanacos, Copo NP, Secc Aibal, (W61.716°, S25.9206°, 157m), 11/Dec/2016, 1 worker (MACN-Bar-Ins-ct 07538); 1 worker (MACN-Bar-Ins-ct 07562).

Pachycondyla constricticeps

Argentina: Misiones: 20km E Wanda, Picada Tirica, loose on ground, W&E Mackay, 2/Jan/2008, Holotype, 1 worker (IMML); Iguazú NP, Pitfall, (W54.457°, S25.675°), Carolina Paris, 24/Jan/2008, 1 worker (MACN-bar-ins-ct 06409).

Pachycondyla harpax

Argentina: Misiones: Iguazú NP, Subterranean bait, Priscila Hanisch y Carolina Paris, 07/Mar/2009, 1 worker (MACN-Bar-Ins-ct 3101).

Pachycondyla PEH01

Argentina: Misiones: Iguazú NP, Hand, (W54.456°, S25.675°, 171.13m), Priscila E. Hanisch, 03/Mar/2015, 1 worker (MACN-bar-ins-ct 06411).

Pachycondyla striata

Argentina: Buenos Aires: Vuelta de obligado, (W59.809°, S33.599°, 11m), Ezequiel Nunez Bustos, 04/Apr/2015, 1 worker (MACN-bar-ins-ct 06426). Corrientes: Ebco, Ivan L. F. Magalhaes, 14/Sep/2016, 1 worker (MACN-Bar-Ins-ct 07368). Entre Ríos: Ceibas, (W58.75°, S33.433°), Ignacio Agudelo, 28/Sep/2013, 1 worker (MACN-bar-ins-ct 06395); 1 worker (MACN-bar-ins-ct 06460). Jujuy: Calilegua NP, Picada herradura, Hand, (W64.85°, S23.76°, 471m), Priscila E. Hanisch, 12/Apr/2016, 1 worker (MACN-bar-ins-07501); Secc Aguas Negras, Sendero El Pedemontano, (W65.4167°, S24.25°, 726m), M. Andia, 12/Aug/2010, 1 worker (MACN-Bar-Ins-ct 00397); 1 worker (MACN-Bar-Ins-ct 00398); 1 worker (MACN-Bar-Ins-ct 00399); (W65.4167°, S24.25°, 723m), 06/Aug/2010, 1 worker (MACN-Bar-Ins-ct 00400); Secc Mesada de las Colmenas, Trail El Negrito, (W65.4333°, S24.1833°, 1135m), 11/Aug/2010, 1 worker (MACN-Bar-Ins-ct 00401); Hand, (W64.8508°, S23.7338°, 844m), Priscila E. Hanisch, 13/Apr/2016, 1 worker (MACN-bar-ins-07481); Ezequiel N. Bustos, 01/Apr/2015, 1 worker (MACN-bar-ins-07531); (W64.77°, S23.773°), Ezequiel Nunez Bustos, 05/Nov/2014, 1 worker (MACN-bar-ins-ct 06474). Misiones: Comandante Andresito, Yacutinga, (W54.0742°, S25.5912°, 260m), Ezequiel N. Bustos, 06/Nov/2015, 1 worker (MACN-bar-ins-ct 06994); 1 worker (MACN-bar-ins-ct 07016); Iguazú, Willink, 1945, 1 worker (IMML); A. Martínez, Oct/1964, 1 ♀ (MZSP); Iguazú NP, Secc Apepú, (W54.2957°, S25.5635°, 218m), Nunes Bustos, E., 21/Feb/2014, 1 ♀ (MACN-Bar-Ins-ct 05729); (W54.2957°, S25.5635°, 224m), 1 ♀ (MACN-Bar-Ins-ct 05735); Pitfall trap, Carolina Paris, 20/Jan/2008, 1 worker (MACN-Bar-Ins 03159); C. I Paris, 02/Jan/2008, 1 worker (MACN-Bar-Ins-ct 02937); Pitfall, (W54.4563°, S25.674°), Carolina Paris, 24/Jan/2008, 1 worker (MACN-Bar-Ins-ct 05051); ground, Hand , Priscila E. Hanisch, 06/Mar/2015, 1 worker (MACN-bar-ins-ct 07732); Hand, 28/Feb/2015, 1 worker (MACN-bar-ins-ct 07739); nest in log, (W54.449°, S25.6776°, 213m), 06/Mar/2015, 1 worker (MACN-bar-ins-ct 07755); under stone, (W54.4366°, S25.7036°, 185.449m), 07/Mar/2015, 1 worker (MACN-bar-ins-ct

07772); Pitfall trap, Carolina Paris, 20/Jan/2008, 1 worker (MACN-Bar-Ins-ct 3118); Loreto, ground, Hand, Priscila E. Hanisch, 24/May/2015, 1 worker (MACN-bar-ins-07469); Oberá, CIAR, Malaise Trap, (W54.9403°, S27.4447°, 147m), Pablo Tubaro, 21/Feb/2013, 1 ♂ (BIOUG12800-E03); (W54.94°, S27.4447°, 204m), 14/Feb/2013, 1 worker (MACN-Bar-Ins-5578); (W54.94°, S27.4447°, 223m), 10/Feb/2013, 1 ♀ (MACN-Bar-Ins-5597); (W54.94°, S27.4447°, 235m), 06/Feb/2013, 1 worker (MACN-Bar-Ins-5609); ground, Hand, (W54.94°, S27.445°), Priscila E. Hanisch, 06/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07321); Pitfall, 12/Feb/2013, 1 worker (MACN-Bar-Ins-ct 07338); San Ignacio, Bosque de Canela, Hand, (W55.5846°, S27.2862°, 187m), 21/Jan/2015, 1 worker (MACN-Bar-Ins-ct 07359); Osununú PR, (W55.579°, S27.28°, 177m), 15/Jan/2015, 1 worker (MACN-bar-ins-ct 06483); (W55.5722°, S27.2808°, 156m), Carolina Paris, 15/Jan/2015, 1 worker (MACN-bar-ins-ct 06484); Yaboti, (W53.8795°, S26.3956°), Alvaro Galbán, 09/Apr/2016, 1 worker (MACN-bar-ins-ct 07637); 1 worker (MACN-bar-ins-ct 07654); 1 worker (MACN-bar-ins-ct 07704). Salta: El rey NP, (W64.833°, S24.633°), Carolina Paris, 25/Jan/2011, 1 worker (MACN-bar-ins-ct 06393). Tucumán: Between Villa Padre Monti and Nio river, (W65.0025°, S26.4743°), Alvaro Galbán, 24/Nov/2015, 1 worker (MACN-bar-ins-ct 07693); 1 worker (MACN-bar-ins-ct 07709); Campo de los Alisos NP, Trail "La Selva Misteriosa", Hand, (W65.874°, S27.28°, 1050m), Priscila E. Hanisch, 19/Apr/2016, 1 worker (MACN-bar-ins-07497); (W65.872°, S27.29°, 957m), 1 worker (MACN-bar-ins-07503); Heading to Cajon, RP310, (W64.9185°, S26.432°), Alvaro Galbán, 25/Nov/2015, 1 worker (MACN-bar-ins-ct 07633); 1 worker (MACN-bar-ins-ct 07648); 1 worker (MACN-bar-ins-ct 07662); La ramadita ±65Km, L.R. Fontes, 1/dec/1981, 1 worker (MZSP); San Miguel de Tucumán, Cerro San Javier, (W65.3297°, S26.7831°), Marta Ayup, 15/Nov/2010, 1 worker (MACN-Bar-Ins-ct 07066); 1 worker (MACN-Bar-Ins-ct 07069); (W65.3335°, S26.7878°), 1 worker (MACN-Bar-Ins-ct 07079); (W65.3333°, S26.7986°), 15/Oct/2011, 1 worker (MACN-Bar-Ins-ct 07085); (W65.3269°, S26.7711°), 15/Aug/2010, 1 worker (MACN-Bar-Ins-ct 07113); 1 worker (MACN-Bar-Ins-ct 07129); (W65.3335°, S26.7878°), 15/Nov/2010, 1 worker (MACN-Bar-Ins-ct 07135). **Brazil:** Minas Gerais: 1 worker (MACN-bar-ins-ct 07745).

Platythyrea pilosula

Argentina: Formosa: Reserva El Bagual, Malaise Trap, (W58.815°, S26.3028°, 57m), Pablo Tubaro, 01/Mar/2014, 1 ♀ (BIOUG25336-D02). Misiones: Iguazú NP, in tree, Hand, (W54.479°, S25.69°, 194.397m), Priscila E. Hanisch, 05/Mar/2015, 1 worker (MACN-bar-ins-ct 06459); San Ignacio, Osununú PR, (W55.5784°, S27.2792°, 191m), 16/Jan/2015, 1 ♀ (MACN-Bar-Ins-ct 07354).

Platythyrea sinuata

Bolivia: 1 worker (MACN_En21380).

Pseudoponera stigma

Argentina: Formosa: Ingeniero Juarez, N. Kusnezov, 01/Jul/1958, 1 worker (10479-MZSP). Misiones: Iguazú NP, dead tree, Hand, Priscila E. Hanisch, 20/Dec/2015, 1 worker (MACN-bar-ins-07474); Litter sample, 1 worker (MACN-bar-ins-07480). Santiago del Estero: Pampa de los Guanacos, (W61.7122°, S26.2827°, 150m), 10/Dec/2016, 1 ♀ (MACN-Bar-Ins-ct 07563). **Indonesia:** Maffin Bay: ES Ross, 20/Jun/1958, Paratype, 1 worker (BMNH(E)1015551).

Rasopone lunaris

Argentina: Misiones: Iguazú NP, Litter sample, (W54.4478°, S25.6708°, 185m), Carolina I. Paris, 22/Jan/2008, 1 worker (MACN-bar-ins-ct 05032).

Thaumatomyrmex mutilatus

Argentina: Misiones: San Ignacio, Osununú PR, Litter sample, (W55.5804°, S27.285°, 203.4m), C.I. Paris, P.E. Hanisch, A.F. Sanchez, 21/Jan/2015, 1 worker (MACN-bar-ins-07516); (W55.5742°, S27.2826°, 232m), Carolina I. Paris, 13/Jan/2015, 1 worker (MACN-bar-ins-ct 06984); 1 worker (MACN-bar-ins-ct 07049).

Supplementary material

Table S2.1 Summary of 530 specimens proceeded for this study. We provide the Sample and Process IDs for all the individuals along with the caste and locality collection. For those individuals that were successfully amplified we provide information on the length of the COI sequence together with the BIN information.

Identification	Sample ID	Process ID	MOTU	BIN	Sequence lenght (bp)	Locality	Caste
Anochetus altisquamis	MACN-Bar-Ins-ct 07078	ANTI208-16			0	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-Bar-Ins-ct 07087	ANTI217-16			0	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-Bar-Ins-ct 07098	ANTI228-16			0	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-Bar-Ins-ct 07106	ANTI236-16			0	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-Bar-Ins-ct 07123	ANTI253-16			0	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-Bar-Ins-ct 07132	ANTI262-16			0	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-Bar-Ins-ct 07137	ANTI267-16			0	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07643	ANTI771-17			0	Cajon, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07632	ANTI763-17			231[2n]	Tiraxis, Jujuy	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07700	ANTI811-17	MOTU-8	BOLD:AAW0352	551[0n]	Villa Padre Monti, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07658	ANTI782-17	MOTU-8	BOLD:AAW0352	580[0n]	Villa Padre Monti, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07680	ANTI797-17	MOTU-8	BOLD:AAW0352	621[0n]	Villa Padre Monti, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07665	ANTI787-17	MOTU-8	BOLD:AAW0352	625[0n]	Monte Potrero, Catamarca	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07713	ANTI818-17	MOTU-8	BOLD:AAW0352	638[0n]	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07661	ANTI784-17	MOTU-8	BOLD:AAW0352	644[0n]	Tiraxis, Jujuy	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07719	ANTI822-17	MOTU-8	BOLD:AAW0352	644[0n]	Tiraxis, Jujuy	Worker
Anochetus altisquamis	MACN-bar-ins-07493	ANTI623-16	MOTU-8	BOLD:AAW0352	658[0n]	Campo de los Alisos NP, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-07496	ANTI626-16	MOTU-8	BOLD:AAW0352	658[0n]	Campo de los Alisos NP, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-07513	ANTI644-16	MOTU-8	BOLD:AAW0352	658[0n]	Campo de los Alisos NP, Tucumán	Worker
Anochetus altisquamis	MACN-Bar-Ins-ct 07110	ANTI240-16	MOTU-8	BOLD:AAW0352	658[0n]	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07641	ANTI770-17	MOTU-8	BOLD:AAW0352	658[0n]	Cajon, Tucumán	Worker

Anochetus altisquamis	MACN-bar-ins-ct 07664	ANTI786-17	MOTU-8	BOLD:AAW0352	658[0n]	Monte Potrero, Catamarca	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07675	ANTI793-17	MOTU-8	BOLD:AAW0352	658[0n]	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07687	ANTI801-17	MOTU-8	BOLD:AAW0352	658[0n]	Cajon, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07695	ANTI808-17	MOTU-8	BOLD:AAW0352	658[0n]	Cerro San Javier, Tucumán	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07702	ANTI812-17	MOTU-8	BOLD:AAW0352	658[0n]	Tiraxis, Jujuy	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07710	ANTI816-17	MOTU-8	BOLD:AAW0352	658[0n]	Tiraxis, Jujuy	Worker
Anochetus altisquamis	MACN-bar-ins-ct 07722	ANTI825-17	MOTU-8	BOLD:AAW0352	658[0n]	Monte Potrero, Catamarca	Worker
Anochetus altisquamis	MACN-Bar-Ins-ct 00402	INSAR375-11	MOTU-8	BOLD:AAW0352	664[0n]	Calilegua NP, Jujuy	Dealated queen
Anochetus neglectus	MACN-Bar-Ins-ct 07547	ANTI678-17	MOTU-11	BOLD:ADH3105	658[0n]	Copo NP, Santiago del Estero	Worker
Anochetus neglectus	MACN-Bar-Ins-ct 07620	ANTI751-17	MOTU-11	BOLD:ADH3106	658[0n]	Copo NP, Santiago del Estero	Dealated queen
Anochetus neglectus	MACN-Bar-Ins-ct 07626	ANTI757-17	MOTU-11	BOLD:ADH3105	658[0n]	Copo NP, Santiago del Estero	Worker
Anochetus neglectus	MACN-bar-ins-ct 07735	ANTI839-17	MOTU-11	BOLD:ADH3105	658[0n]	Copo NP, Santiago del Estero	Worker
Dinoponera australis	MACN-Bar-Ins-ct 05752	INSAR1416-15			0	Iguazú NP, Misiones	Female
Dinoponera australis	T6P22008PNID05	ANTPI041-10			0	Iguazú NP, Misiones	Female
Dinoponera australis	MACN-bar-ins-ct 07788	ANTI889-17	MOTU-81	BOLD:ADG4181	585[0n]	Osununú PR, Misiones	Worker
Dinoponera australis	MACN-bar-ins-ct 07787	ANTI888-17	MOTU-82	BOLD:ACZ3844	627[0n]	Corrientes	Worker
Dinoponera australis	MACN-bar-ins-ct 07789	ANTI890-17	MOTU-81	BOLD:ADG4181	627[0n]	Osununú PR, Misiones	Worker
Dinoponera australis	MACN-bar-ins-07477	ANTI607-16	MOTU-87	BOLD:ADG5261	655[0n]	Loreto, Misiones	Female
Dinoponera australis	MACN-bar-ins-07490	ANTI620-16	MOTU-82	BOLD:ACZ3844	655[0n]	Corrientes	Female
Dinoponera australis	MACN-bar-ins-07528	ANTI659-16	MOTU-82	BOLD:ACZ3844	655[0n]	Corrientes	Female
Dinoponera australis	MACN-bar-ins-ct 07681	ANTI798-17	MOTU-87	BOLD:ADG5261	655[0n]	Loreto, Misiones	Worker
Dinoponera australis	MACN-bar-ins-ct 07724	ANTI827-17	MOTU-12	BOLD:ACC4124	655[0n]	Iguazú NP, Misiones	Worker
Dinoponera australis	MACN-bar-ins-ct 07752	ANTI855-17	MOTU-12	BOLD:ACC4124	655[0n]	Iguazú NP, Misiones	Worker
Dinoponera australis	MACN-bar-ins-ct 07773	ANTI874-17	MOTU-12	BOLD:ACC4124	655[0n]	Iguazú NP, Misiones	Worker
Dinoponera australis	MACN-bar-ins-ct 07777	ANTI878-17	MOTU-87	BOLD:ADG5261	655[0n]	Iguazú NP, Misiones	Worker
Dinoponera australis	MACN-bar-ins-ct 07780	ANTI881-17	MOTU-87	BOLD:ADG5261	655[0n]	Loreto, Misiones	Worker

Dinoponera australis	MACN-bar-ins-ct 07790	ANTI891-17	MOTU-81	BOLD:ADG4181	655[0n]	Osununú PR, Misiones	Worker
Dinoponera australis	MACN-Bar-Ins-ct 00615	INSAR138-11	MOTU-7	BOLD:AAV4568	658[0n]	Iguazú NP, Misiones	Female
Dinoponera australis	MACN-Bar-Ins-ct 02519	INSAR660-11	MOTU-7	BOLD:AAV4568	658[0n]	Iguazú NP, Misiones	Female
Dinoponera australis	MACN-Bar-Ins-ct 02520	INSAR661-11	MOTU-7	BOLD:AAV4568	658[0n]	Iguazú NP, Misiones	Female
Dinoponera australis	MACN-Bar-Ins-ct 02521	INSAR662-11	MOTU-7	BOLD:AAV4568	658[0n]	Iguazú NP, Misiones	Female
Dinoponera australis	MACN-Bar-Ins-ct 02973	ANTPI190-12	MOTU-12	BOLD:ACC4124	658[0n]	Iguazú NP, Misiones	Female
Dinoponera australis	MACN-bar-ins-ct 06394	ANTI097-15	MOTU-12	BOLD:ACC4124	658[0n]	Iguazú NP, Misiones	Male
Dinoponera australis	MACN-bar-ins-ct 06405	ANTI108-15	MOTU-12	BOLD:ACC4124	658[0n]	Iguazú NP, Misiones	Male
Dinoponera australis	MACN-bar-ins-ct 06462	ANTI165-15	MOTU-82	BOLD:ACZ3844	658[0n]	Santo Tome, Corrientes	Female
Dinoponera australis	MACN-bar-ins-ct 06480	ANTI183-15	MOTU-81	BOLD:ADG4181	658[0n]	Osununú PR, Misiones	Female
Dinoponera australis	MACN-Bar-Ins-ct 07351	ANTI481-16	MOTU-81	BOLD:ADG4181	658[0n]	San Ignacio, Misiones	Female
Dinoponera australis	MACN-Bar-Ins-ct 07405	ANTI535-16	MOTU-81	BOLD:ADG4181	658[0n]	San Ignacio, Misiones	Female
Dinoponera australis	MACN-Bar-Ins-ct 07441	ANTI571-16	MOTU-81	BOLD:ADG4181	658[0n]	Osununú PR, Misiones	Female
Hypoponera	MACN-bar-ins-ct 07011	ANTPI612-16			0	CABA, Buenos Aires	Dealated queen
Hypoponera	MACN-bar-ins-07453	ANTI583-16			0	Osununú PR, Misiones	Worker
Hypoponera	MACN-Bar-Ins-5446	ANTI004-14			0	Loreto, Misiones	Worker
Hypoponera	MACN-bar-ins-ct 07026	ANTPI627-16			0	Corrientes	Worker
Hypoponera	MACN-Bar-Ins-ct 07302	ANTI432-16			0	CABA, Buenos Aires	Worker
Hypoponera	MACN-Bar-Ins-ct 07306	ANTI436-16			0	CABA, Buenos Aires	Worker
Hypoponera	MACN-Bar-Ins-ct 07310	ANTI440-16			0	CABA, Buenos Aires	Worker
Hypoponera	MACN-Bar-Ins-ct 07312	ANTI442-16			0	CABA, Buenos Aires	Worker
Hypoponera	MACN-Bar-Ins-ct 07317	ANTI447-16			0	CABA, Buenos Aires	Worker
Hypoponera	MACN-Bar-Ins-ct 07324	ANTI454-16			0	CIAR, Misiones	Worker
Hypoponera	MACN-Bar-Ins-ct 07326	ANTI456-16			0	CIAR, Misiones	Worker
Hypoponera	MACN-Bar-Ins-ct 07327	ANTI457-16			0	CIAR, Misiones	Worker
Hypoponera	MACN-Bar-Ins-ct 07331	ANTI461-16			0	CIAR, Misiones	Worker
Hypoponera	MACN-Bar-Ins-ct 07384	ANTI514-16			0	San Ignacio, Misiones	Worker

Hypoponera	MACN-Bar-Ins-ct 07422	ANTI552-16			0	San Ignacio, Misiones	Worker
Hypoponera	MACN-bar-ins-ct 07640	ANTI769-17			0	Uritorco, Córdoba	Worker
Hypoponera	MACN-bar-ins-ct 07645	ANTI772-17			0	Uritorco, Córdoba	Worker
Hypoponera	MACN-bar-ins-ct 07657	ANTI781-17			0	Uritorco, Córdoba	Worker
Hypoponera	MACN-bar-ins-ct 07666	ANTI788-17			0	Uritorco, Córdoba	Worker
Hypoponera	MACN-bar-ins-ct 07690	ANTI804-17			0	Yaboti, Misiones	Worker
Hypoponera	MACN-bar-ins-ct 07699	ANTI810-17			0	Uritorco, Córdoba	Worker
Hypoponera	MACN-bar-ins-ct 07717	ANTI821-17			0	Uritorco, Córdoba	Worker
Hypoponera	MACN-bar-ins-ct 07749	ANTI852-17			0	Rio Pilcomayo NP, Formosa	Worker
Hypoponera	MACN-bar-ins-ct 07771	ANTI872-17			0	Rio Pilcomayo NP, Formosa	Worker
Hypoponera	MACN-Bar-Ins-5565	ANTPI311-14			0	CIAR, Misiones	Alated queen
Hypoponera	MACN-Bar-Ins-ct 07334	ANTI464-16			0	CIAR, Misiones	Alated queen
Hypoponera	MACN-Bar-Ins-ct 07337	ANTI467-16			0	CIAR, Misiones	Alated queen
Hypoponera	MACN-Bar-Ins-ct 07341	ANTI471-16			0	CIAR, Misiones	Alated queen
Hypoponera	MACN-bar-ins-ct 07022	ANTPI623-16			0	Herradura, Formosa	Dealated queen
Hypoponera	MACN-bar-ins-07495	ANTI625-16			230[0n]	Iguazú NP, Misiones	Worker
Hypoponera	BIOUG24773-G02	GMAGY332-15	MOTU-20	BOLD:ACN1914	510[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24734-D01	GMAGX086-15	MOTU-15		528[0n]	CIAR, Misiones	Male
Hypoponera	MACN-bar-ins-ct 07671	ANTI789-17	MOTU-69	BOLD:ADJ3843	529[1n]	Uritorco, Córdoba	Dealated queen
Hypoponera	BIOUG24734-A09	GMAGX058-15	MOTU-15	BOLD:ACM2976	546[1n]	CIAR, Misiones	Male
Hypoponera	BIOUG24805-B03	GMAGW384-15	MOTU-15	BOLD:ACM2976	555[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24612-H11	GMAFR450-15	MOTU-15	BOLD:ACM2976	564[0n]	El Bagual, Formosa	Male
Hypoponera	BIOUG22488-D11	GMAGC1361-15	MOTU-29	BOLD:ADG2585	576[0n]	CIAR, Misiones	Alated queen
Hypoponera	BIOUG24814-A04	GMAGV666-15	MOTU-15	BOLD:ACM2976	576[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24814-E07	GMAGV717-15	MOTU-26	BOLD:ACN7908	591[0n]	CIAR, Misiones	Male
Hypoponera	MACN-Bar-Ins-5621	ANTPI367-14	MOTU-31	BOLD:ADG0841	595[0n]	CIAR, Misiones	Alated queen

Hypoponera	MACN-Bar-Ins-ct 07323	ANTI453-16	MOTU-53	BOLD:ADG5297	625[0n]	CIAR, Misiones	Alated queen
Hypoponera	BIOUG12935-A12	GMARE1190-14	MOTU-20	BOLD:ACN1914	636[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG22488-B12	GMAGC1338-15	MOTU-20	BOLD:ACN1914	637[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG12779-H09	GMARA1718-14	MOTU-5	BOLD:AAU1875	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG12908-D08	GMARD1948-14	MOTU-5	BOLD:AAU1875	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG12908-H10	GMARD1998-14	MOTU-20	BOLD:ACN1914	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG12935-C01	GMARE1203-14	MOTU-20	BOLD:ACN1914	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG13979-A10	GMARS490-14	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG13979-A12	GMARS492-14	MOTU-15	BOLD:ACM2976	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG13979-B07	GMARS499-14	MOTU-5	BOLD:AAU1875	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG13979-C08	GMARS512-14	MOTU-15	BOLD:ACM2976	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG13979-D03	GMARS519-14	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG14027-A03	GMART1263-14	MOTU-15	BOLD:ACM2976	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG14027-E07	GMART1315-14	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG14027-F02	GMART1322-14	MOTU-15	BOLD:ACM2976	658[0n]	CIAR, Misiones	Alated queen
Hypoponera	BIOUG14044-B03	GMARU608-14	MOTU-15	BOLD:ACM2976	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG14044-C04	GMARU621-14	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG22476-A02	GMAGA695-15	MOTU-20	BOLD:ACN1914	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24056-B09	GMAFN601-15	MOTU-15	BOLD:ACM2976	658[0n]	El Bagual, Formosa	Male
Hypoponera	BIOUG24425-H02	GMARW098-15	MOTU-20	BOLD:ACN1914	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24430-A08	GMAGZ182-15	MOTU-20	BOLD:ACN1914	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24430-B03	GMAGZ189-15	MOTU-20	BOLD:ACN1914	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24612-H08	GMAFR447-15	MOTU-15	BOLD:ACM2976	658[0n]	El Bagual, Formosa	Male
Hypoponera	BIOUG24612-H09	GMAFR448-15	MOTU-15	BOLD:ACM2976	658[0n]	El Bagual, Formosa	Male
Hypoponera	BIOUG24612-H10	GMAFR449-15	MOTU-15	BOLD:ACM2976	658[0n]	El Bagual, Formosa	Male
Hypoponera	BIOUG24617-H01	GMAFR915-15	MOTU-15	BOLD:ACM2976	658[0n]	El Bagual, Formosa	Male
Hypoponera	BIOUG24734-C11	GMAGX084-15	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24773-F10	GMAGY328-15	MOTU-5	BOLD:AAU1875	658[0n]	CIAR, Misiones	Male

Hypoponera	BIOUG24805-C07	GMAGW400-15	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24814-A02	GMAGV664-15	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Male
Hypoponera	BIOUG24814-D08	GMAGV706-15	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Male
Hypoponera	MACN-bar-ins-ct 06878	ANTPI479-15	MOTU-1	BOLD:AAU1873	658[0n]	Iguazú NP, Misiones	Dealated queen
Hypoponera	MACN-bar-ins-ct 06904	ANTPI505-15	MOTU-15	BOLD:ACM2976	658[0n]	Iguazú NP, Misiones	Dealated queen
Hypoponera	MACN-bar-ins-ct 07050	ANTPI651-16	MOTU-43	BOLD:ADE0472	658[0n]	Herradura, Formosa	Dealated queen
Hypoponera	MACN-Bar-Ins-ct 07403	ANTI533-16	MOTU-77	BOLD:ADJ3037	658[0n]	Osununú PR, Misiones	Dealated queen
Hypoponera	MACN-Bar-Ins-ct 07550	ANTI681-17	MOTU-62	BOLD:ADG6514	658[0n]	Copo NP, Santiago del Estero	Alated queen
Hypoponera	MACN-Bar-Ins-ct 07599	ANTI730-17	MOTU-68	BOLD:ADG5296	658[0n]	Copo NP, Santiago del Estero	Dealated queen
Hypoponera	MACN-bar-ins-ct 07734	ANTI838-17	MOTU-65	BOLD:AAK3085	658[0n]	Iguazú NP, Misiones	Alated queen
Hypoponera	BIOUG12779-A10	GMARA1635-14	MOTU-5	BOLD:AAU1875	658[1n]	CIAR, Misiones	Male
Hypoponera agilis	MACN-bar-ins-ct 06929	ANTPI530-15			0	Iguazú NP, Misiones	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-ct 06888	ANTPI489-15			0	Iguazú NP, Misiones	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-ct 06901	ANTPI502-15			0	Iguazú NP, Misiones	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-ct 06996	ANTPI597-16			0	Iguazú NP, Misiones	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07074	ANTI204-16			0	Cerro San Javier, Tucumán	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07081	ANTI211-16			0	Cerro San Javier, Tucumán	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-5607	ANTPI353-14	MOTU-26	BOLD:ACN7908	547[0n]	CIAR, Misiones	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-ct 07705	ANTI814-17	MOTU-79	BOLD:ADJ4097	577[0n]	Uritorco, Córdoba	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-ct 07694	ANTI807-17	MOTU-79	BOLD:ADJ4097	579[0n]	Uritorco, Córdoba	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07393	ANTI523-16	MOTU-15	BOLD:ACM2976	611[0n]	Osununú PR, Misiones	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07437	ANTI567-16	MOTU-15	BOLD:ACM2976	621[0n]	San Ignacio, Misiones	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-07486	ANTI616-16	MOTU-80	BOLD:ADG1868	658[0n]	Calilegua NP, Jujuy	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-07489	ANTI619-16	MOTU-80	BOLD:ADG1868	658[0n]	Alpachiri, Tucumán	Worker

Hypoponera cf. *opacior*	MACN-bar-ins-07492	ANTI622-16	MOTU-80	BOLD:ADG1868	658[0n]	Calilegua NP, Jujuy	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-07527	ANTI658-16	MOTU-80	BOLD:ADG1868	658[0n]	Calilegua NP, Jujuy	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 05140	ANTPI249-13	MOTU-15	BOLD:ACM2976	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-ct 06895	ANTPI496-15	MOTU-15	BOLD:ACM2976	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07319	ANTI449-16	MOTU-26	BOLD:ACN7908	658[0n]	CIAR, Misiones	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07369	ANTI499-16	MOTU-15	BOLD:ACM2976	658[0n]	San Ignacio, Misiones	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07399	ANTI529-16	MOTU-15	BOLD:ACM2976	658[0n]	Osununú PR, Misiones	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07409	ANTI539-16	MOTU-15	BOLD:ACM2976	658[0n]	Osununú PR, Misiones	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07429	ANTI559-16	MOTU-15	BOLD:ACM2976	658[0n]	San Ignacio, Misiones	Worker
Hypoponera cf. *opacior*	MACN-Bar-Ins-ct 07431	ANTI561-16	MOTU-15	BOLD:ACM2976	658[0n]	Osununú PR, Misiones	Dealated queen
Hypoponera cf. *opacior*	MACN-bar-ins-ct 07673	ANTI791-17	MOTU-79	BOLD:ADJ4097	658[0n]	Uritorco, Córdoba	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-ct 07711	ANTI817-17	MOTU-79	BOLD:ADJ4097	658[0n]	Uritorco, Córdoba	Worker
Hypoponera cf. *opacior*	MACN-bar-ins-ct 07714	ANTI819-17	MOTU-79	BOLD:ADJ4097	658[0n]	Uritorco, Córdoba	Worker
Hypoponera clavatula	MACN-Bar-Ins-ct 07089	ANTI219-16			0	Cerro San Javier, Tucumán	Worker
Hypoponera clavatula	MACN-Bar-Ins-ct 07099	ANTI229-16			0	Cerro San Javier, Tucumán	Worker
Hypoponera clavatula	MACN-Bar-Ins-ct 07140	ANTI270-16			0	Cerro San Javier, Tucumán	Worker
Hypoponera distinguenda	MACN-Bar-Ins-ct 05028	ANTPI280-13			0	Misiones	Worker
Hypoponera distinguenda	MACN-Bar-Ins-ct 06844	ANTPI445-15			0	Iguazú NP, Misiones	Worker
Hypoponera distinguenda	T1W32008PNID12	ANTPI048-10			0	Iguazú NP, Misiones	Worker
Hypoponera distinguenda	MACN-bar-ins-ct 07765	ANTI867-17	MOTU-13	BOLD:ACM2219	632[0n]	Iguazú NP, Misiones	Worker
Hypoponera distinguenda	MACN-bar-ins-07454	ANTI584-16	MOTU-13	BOLD:ACM2219	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera distinguenda	MACN-bar-ins-07524	ANTI655-16	MOTU-13	BOLD:ACM2219	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera distinguenda	MACN-Bar-Ins-ct 05026	ANTPI210-13	MOTU-13	BOLD:ACM2219	658[0n]	Iguazú NP, Misiones	Alated queen
Hypoponera distinguenda	MACN-bar-ins-ct 06441	ANTI144-15	MOTU-13	BOLD:ACM2219	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera fiebrigi	MACN-bar-ins-07533	ANTI664-16	MOTU-61	BOLD:ADG1591	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera foeda	MACN-bar-ins-ct 07676	ANTI794-17	MOTU-64	BOLD:ADJ3541	658[0n]	Uritorco, Córdoba	Worker
Hypoponera foreli	MACN-Bar-Ins-ct 06819	ANTPI420-15			0	Iguazú NP, Misiones	Worker

Hypoponera foreli	MACN-bar-ins-ct 06981	ANTPI582-16			0	Iguazú NP, Misiones	Worker
Hypoponera foreli	MACN-bar-ins-ct 06453	ANTI156-15	MOTU-42	BOLD:ACZ3327	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera foreli	MACN-bar-ins-ct 06456	ANTI159-15	MOTU-42	BOLD:ACZ3327	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera foreli	MACN-bar-ins-ct 06941	ANTPI542-15	MOTU-42	BOLD:ACZ3327	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera foreli	MACN-bar-ins-ct 07053	ANTPI654-16	MOTU-42	BOLD:ACZ3327	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera foreli	T6W32008PNIF06	ANTPI066-10	MOTU-5	BOLD:AAU1875	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera opaciceps	MACN-bar-ins-ct 06923	ANTPI524-15			0	Iguazú NP, Misiones	Worker
Hypoponera opaciceps	MACN-Bar-Ins-ct 07071	ANTI201-16			0	Cerro San Javier, Tucumán	Worker
Hypoponera opaciceps	MACN-Bar-Ins-ct 07094	ANTI224-16			0	Cerro San Javier, Tucumán	Worker
Hypoponera opaciceps	MACN-Bar-Ins-ct 07112	ANTI242-16			0	Cerro San Javier, Tucumán	Worker
Hypoponera opaciceps	MACN-bar-ins-07500	ANTI630-16	MOTU-31	BOLD:ADG0841	658[0n]	Alpachiri, Tucumán	Worker
Hypoponera opaciceps	MACN-bar-ins-07505	ANTI635-16	MOTU-59	BOLD:ADG1592	658[0n]	Alpachiri, Tucumán	Worker
Hypoponera opaciceps	MACN-bar-ins-07508	ANTI638-16	MOTU-31	BOLD:ADG0841	658[0n]	Rosario, Santa Fe	Worker
Hypoponera opaciceps	MACN-bar-ins-07515	ANTI646-16	MOTU-60	BOLD:ADF8923	658[0n]	Calilegua NP, Jujuy	Worker
Hypoponera opaciceps	MACN-bar-ins-07518	ANTI649-16	MOTU-31	BOLD:ADG0841	658[0n]	Rosario, Santa Fe	Worker
Hypoponera opaciceps	MACN-bar-ins-07532	ANTI663-16	MOTU-31	BOLD:ADG0841	658[0n]	Alpachiri, Tucumán	Worker
Hypoponera parva	MACN-Bar-Ins-ct 06823	ANTPI424-15			0	Iguazú NP, Misiones	Worker
Hypoponera parva	MACN-Bar-Ins-ct 06850	ANTPI451-15			0	Iguazú NP, Misiones	Worker
Hypoponera parva	MACN-Bar-Ins-ct 06859	ANTPI460-15			0	Iguazú NP, Misiones	Worker
Hypoponera parva	MACN-bar-ins-ct 06935	ANTPI536-15			0	Iguazú NP, Misiones	Worker
Hypoponera parva	MACN-bar-ins-ct 06944	ANTPI545-15			0	Iguazú NP, Misiones	Worker
Hypoponera parva	MACN-bar-ins-ct 06975	ANTPI576-16			0	Iguazú NP, Misiones	Worker
Hypoponera parva	MACN-Bar-Ins-ct 07375	ANTI505-16	MOTU-40	BOLD:ACZ4236	632[0n]	San Ignacio, Misiones	Dealated queen
Hypoponera parva	MACN-bar-ins-07442	ANTI572-16	MOTU-40	BOLD:ACZ4236	658[0n]	Osununú PR, Misiones	Worker
Hypoponera parva	MACN-bar-ins-07450	ANTI580-16	MOTU-40	BOLD:ACZ4236	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera parva	MACN-bar-ins-07471	ANTI601-16	MOTU-40	BOLD:ACZ4236	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera parva	MACN-bar-ins-ct 06457	ANTI160-15	MOTU-40	BOLD:ACZ4236	658[0n]	Iguazú NP, Misiones	Worker

Hypoponera parva	MACN-bar-ins-ct 06481	ANTI184-15	MOTU-40	BOLD:ACZ4236	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH01	MACN-bar-ins-07467	ANTI597-16			0	Iguazú NP, Misiones	Worker
Hypoponera PEH01	MACN-bar-ins-ct 06450	ANTI153-15	MOTU-41	BOLD:ACZ4369	624[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH01	MACN-bar-ins-07466	ANTI596-16	MOTU-41	BOLD:ACZ4369	636[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH01	MACN-bar-ins-07512	ANTI642-16	MOTU-41	BOLD:ACZ4369	637[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH02	MACN-Bar-Ins-ct 06870	ANTPI471-15			0	Iguazú NP, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-ct 07655	ANTI779-17	MOTU-20	BOLD:ACN1914	596[0n]	Yaboti, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-07445	ANTI575-16	MOTU-20	BOLD:ACN1914	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-07452	ANTI582-16	MOTU-20	BOLD:ACN1914	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-07461	ANTI591-16	MOTU-20	BOLD:ACN1914	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-07475	ANTI605-16	MOTU-20	BOLD:ACN1914	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH02	MACN-Bar-Ins-5605	ANTPI351-14	MOTU-20	BOLD:ACN1914	658[0n]	CIAR, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-ct 06434	ANTI137-15	MOTU-20	BOLD:ACN1914	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-ct 06439	ANTI142-15	MOTU-20	BOLD:ACN1914	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-ct 06444	ANTI147-15	MOTU-20	BOLD:ACN1914	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-ct 06447	ANTI150-15	MOTU-20	BOLD:ACN1914	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera PEH02	MACN-Bar-Ins-ct 07374	ANTI504-16	MOTU-20	BOLD:ACN1914	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH02	MACN-Bar-Ins-ct 07420	ANTI550-16	MOTU-20	BOLD:ACN1914	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-ct 07652	ANTI777-17	MOTU-20	BOLD:ACN1914	658[0n]	Yaboti, Misiones	Worker
Hypoponera PEH02	MACN-bar-ins-ct 07685	ANTI799-17	MOTU-20	BOLD:ACN1914	658[0n]	Yaboti, Misiones	Worker
Hypoponera PEH03	MACN-Bar-Ins-ct 07559	ANTI690-17	MOTU-75	BOLD:ADG7188	600[0n]	Copo NP, Santiago del Estero	Worker
Hypoponera PEH03	MACN-Bar-Ins-ct 07557	ANTI688-17	MOTU-76	BOLD:ADG7187	601[0n]	Copo NP, Santiago del Estero	Dealated queen
Hypoponera PEH03	MACN-Bar-Ins-ct 07554	ANTI685-17	MOTU-76	BOLD:ADG7187	635[0n]	Copo NP, Santiago del Estero	Worker
Hypoponera PEH03	MACN-Bar-Ins-ct 07561	ANTI692-17	MOTU-76	BOLD:ADG7187	658[0n]	Copo NP, Santiago del Estero	Worker
Hypoponera PEH03	MACN-Bar-Ins-ct 07591	ANTI722-17	MOTU-75	BOLD:ADG7188	658[0n]	Copo NP, Santiago del Estero	Worker
Hypoponera PEH04	MACN-bar-ins-ct 07635	ANTI765-17	MOTU-69	BOLD:ADJ3843	582[0n]	Uritorco, Córdoba	Worker
Hypoponera PEH04	MACN-bar-ins-ct 06897	ANTPI498-15	MOTU-78	BOLD:ACZ2699	651[0n]	Iguazú NP, Misiones	Worker

Hypoponera PEH04	MACN-Bar-Ins-ct 07366	ANTI496-16	MOTU-77	BOLD:ADJ3037	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH04	MACN-Bar-Ins-ct 07381	ANTI511-16	MOTU-77	BOLD:ADJ3037	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH04	MACN-Bar-Ins-ct 07433	ANTI563-16	MOTU-77	BOLD:ADJ3037	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH04	MACN-bar-ins-ct 07692	ANTI805-17	MOTU-69	BOLD:ADJ3843	658[0n]	Uritorco, Córdoba	Worker
Hypoponera PEH05	MACN-bar-ins-ct 07003	ANTPI604-16	MOTU-43	BOLD:ADE0472	628[0n]	Herradura, Formosa	Worker
Hypoponera PEH06	MACN-Bar-Ins-ct 07414	ANTI544-16	MOTU-52	BOLD:ADF8922	638[0n]	San Ignacio, Misiones	Worker
Hypoponera PEH06	MACN-bar-ins-07443	ANTI573-16	MOTU-52	BOLD:ADF8922	658[0n]	Osununú PR, Misiones	Dealated queen
Hypoponera PEH06	MACN-Bar-Ins-ct 07361	ANTI491-16	MOTU-52	BOLD:ADF8922	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH06	MACN-Bar-Ins-ct 07397	ANTI527-16	MOTU-52	BOLD:ADF8922	658[0n]	San Ignacio, Misiones	Worker
Hypoponera PEH06	MACN-Bar-Ins-ct 07427	ANTI557-16	MOTU-52	BOLD:ADF8922	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH06	MACN-Bar-Ins-ct 07435	ANTI565-16	MOTU-52	BOLD:ADF8922	658[0n]	Osununú PR, Misiones	Worker
Hypoponera PEH07	MACN-bar-ins-ct 07649	ANTI775-17	MOTU-70	BOLD:ACE3452	620[0n]	Sierra del Tigre, Tandil	Worker
Hypoponera PEH07	MACN-bar-ins-07502	ANTI632-16	MOTU-54	BOLD:AAA9087	658[0n]	Campo de los Alisos NP, Tucumán	Worker
Hypoponera PEH08	MACN-bar-ins-ct 07763	ANTI865-17	MOTU-66	BOLD:ADJ4912	637[0n]	Costanera Sur, Buenos Aires	Worker
Hypoponera PEH08	MACN-bar-ins-ct 07776	ANTI877-17	MOTU-66	BOLD:ADJ4912	637[0n]	Costanera Sur, Buenos Aires	Worker
Hypoponera PEH08	MACN-bar-ins-ct 07778	ANTI879-17	MOTU-66	BOLD:ADJ4912	637[0n]	Costanera Sur, Buenos Aires	Worker
Hypoponera PEH08	MACN-bar-ins-ct 07782	ANTI883-17	MOTU-66	BOLD:ADJ4912	637[0n]	Costanera Sur, Buenos Aires	Worker
Hypoponera PEH08	MACN-bar-ins-07483	ANTI613-16	MOTU-29	BOLD:ADG2585	658[0n]	Calilegua, Jujuy	Worker
Hypoponera schmalzi	MACN-bar-ins-ct 06883	ANTPI484-15			0	Iguazú NP, Misiones	Worker
Hypoponera schmalzi	MACN-bar-ins-ct 06885	ANTPI486-15			0	Iguazú NP, Misiones	Worker
Hypoponera trigona	MACN-Bar-Ins-5447	ANTI005-14			0	Formosa NR, Formosa	Worker
Hypoponera trigona	MACN-bar-ins-ct 06938	ANTPI539-15			0	Iguazú NP, Misiones	Worker
Hypoponera trigona	MACN-bar-ins-ct 06951	ANTPI552-15			0	Iguazú NP, Misiones	Worker
Hypoponera trigona	T3W52008PNIB08	ANTPI020-10			0	Iguazú NP, Misiones	Worker
Hypoponera trigona	T4W12008PNIH08	ANTPI092-10			0	Iguazú NP, Misiones	Worker
Hypoponera trigona	MACN-bar-ins-ct 06428	ANTI131-15	MOTU-1	BOLD:AAU1873	632[0n]	Iguazú NP, Misiones	Worker
Hypoponera trigona	MACN-bar-ins-07448	ANTI578-16	MOTU-1	BOLD:AAU1873	658[0n]	Iguazú NP, Misiones	Worker

Hypoponera trigona	MACN-bar-ins-ct 06430	ANTI133-15	MOTU-1	BOLD:AAU1873	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera trigona	MACN-bar-ins-ct 06432	ANTI135-15	MOTU-37	BOLD:ACZ4059	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera trigona	MACN-Bar-Ins-ct 06828	ANTPI429-15	MOTU-45	BOLD:ACZ3162	658[0n]	Iguazú NP, Misiones	Worker
Hypoponera trigona	T3W5A2008PNIB06	ANTPI018-10	MOTU-1	BOLD:AAU1873	658[1n]	Iguazú NP, Misiones	Worker
Leptogenys bohlsi	MACN-Bar-Ins-ct 00359	ANTI191-15			0	Formosa NR, Formosa	Worker
Leptogenys iheringi	MACN-bar-ins-ct 07007	ANTPI608-16	MOTU-49	BOLD:ADE4308	658[0n]	Iguazú NP, Misiones	Worker
Neoponera	MACN-bar-ins-07462	ANTI592-16			0	Iguazú NP, Misiones	Worker
Neoponera	MACN-Bar-Ins-ct 07543	ANTI674-17			0	Copo NP, Santiago del Estero	Worker
Neoponera	MACN-Bar-Ins-ct 07551	ANTI682-17			0	Copo NP, Santiago del Estero	Worker
Neoponera	MACN-Bar-Ins-ct 07347	ANTI477-16			0	CIAR, Misiones	Dealated queen
Neoponera	MACN-bar-ins-ct 07758	ANTI860-17			0	Iguazú NP, Misiones	Dealated queen
Neoponera	MACN-bar-ins-07526	ANTI657-16		BOLD:AAZ3349	371[0n]	Iguazú NP, Misiones	Worker
Neoponera	MACN-bar-ins-ct 07730	ANTI834-17	MOTU-25	BOLD:ACX7584	633[0n]	Iguazú NP, Misiones	Dealated queen
Neoponera	MACN-bar-ins-07459	ANTI589-16	MOTU-17	BOLD:ACM2898	658[0n]	Iguazú NP, Misiones	Dealated queen
Neoponera	MACN-bar-ins-07472	ANTI602-16	MOTU-74	BOLD:ACN1772	658[0n]	Iguazú NP, Misiones	alated queen
Neoponera	MACN-bar-ins-07482	ANTI612-16	MOTU-17	BOLD:ACM2898	658[0n]	Calilegua NP, Jujuy	Dealated queen
Neoponera	MACN-bar-ins-07529	ANTI660-16	MOTU-39	BOLD:AAW5111	658[0n]	Iguazú NP, Misiones	Dealated queen
Neoponera	MACN-bar-ins-07535	ANTI666-16	MOTU-39	BOLD:AAW5111	658[0n]	Iguazú NP, Misiones	Dealated queen
Neoponera	MACN-Bar-Ins-ct 02564	INSAR738-11	MOTU-9	BOLD:ABV2684	658[0n]	Iguazú NP, Misiones	Male
Neoponera	MACN-Bar-Ins-ct 02572	INSAR745-11	MOTU-10	BOLD:ABV2663	658[0n]	Iguazú NP, Misiones	Male
Neoponera	MACN-bar-ins-ct 06970	ANTPI571-16	MOTU-19	BOLD:AAB7675	658[0n]	Osununú PR, Misiones	Male
Neoponera	MACN-Bar-Ins-ct 07371	ANTI501-16	MOTU-17	BOLD:ACM2898	658[0n]	Osununú PR, Misiones	Dealated queen

Neoponera	MACN-Bar-Ins-ct 07364	ANTI494-16	MOTU-23	BOLD:ACO0372	658[1n]	Osununú PR, Misiones	Male
Neoponera aenescens	MACN-bar-ins-ct 07672	ANTI790-17	MOTU-63	BOLD:ADJ2470	658[0n]	Tiraxis, Jujuy	Worker
Neoponera aenescens	MACN-bar-ins-ct 07686	ANTI800-17	MOTU-63	BOLD:ADJ2470	658[0n]	Tiraxis, Jujuy	Worker
Neoponera aenescens	MACN-bar-ins-ct 07689	ANTI803-17	MOTU-63	BOLD:ADJ2470	658[0n]	Tiraxis, Jujuy	Worker
Neoponera aenescens	MACN-bar-ins-ct 07715	ANTI820-17	MOTU-63	BOLD:ADJ2470	658[0n]	Tiraxis, Jujuy	Worker
Neoponera aenescens	MACN-bar-ins-ct 07791	ANTI892-17	MOTU-63	BOLD:ADJ2470	658[0n]	Tiraxis, Jujuy	Worker
Neoponera bactronica	MACN-bar-ins-ct 07540.	ANTI831-17	MOTU-39	BOLD:AAW5111	628[0n]	Copo NP, Santiago del Estero	Worker
Neoponera bactronica	MACN-bar-ins-07514	ANTI645-16	MOTU-39	BOLD:AAW5111	658[0n]	Iguazú NP, Misiones	Worker
Neoponera bactronica	MACN-bar-ins-ct 06396	ANTI099-15	MOTU-39	BOLD:AAW5111	658[0n]	Iguazú NP, Misiones	Worker
Neoponera bactronica	MACN-bar-ins-ct 06464	ANTI167-15	MOTU-39	BOLD:AAW5111	658[0n]	Santo Tome, Corrientes	Dealated queen
Neoponera bactronica	MACN-bar-ins-ct 06471	ANTI174-15	MOTU-39	BOLD:AAW5111	658[0n]	Santo Tome, Corrientes	Worker
Neoponera bactronica	MACN-bar-ins-ct 07029	ANTPI630-16	MOTU-39	BOLD:AAW5111	658[0n]	Cmte. Andresito, Misiones	Worker
Neoponera bactronica	MACN-Bar-Ins-ct 07149	ANTI279-16	MOTU-39	BOLD:AAW5111	658[0n]	Cmte. Andresito, Misiones	Worker
Neoponera bactronica	MACN-Bar-Ins-ct 07536	ANTI667-17	MOTU-39	BOLD:AAW5111	658[0n]	Copo NP, Santiago del Estero	Worker
Neoponera bactronica	MACN-bar-ins-ct 07697	ANTI809-17	MOTU-39	BOLD:AAW5111	658[0n]	Iguazú NP, Misiones	Worker
Neoponera crenata	MACN-Bar-Ins-ct 06779	ANTPI380-15			0	Iguazú NP, Misiones	Worker
Neoponera crenata	MACN-bar-ins-ct 06891	ANTPI492-15			0	Iguazú NP, Misiones	Worker
Neoponera crenata	MACN-bar-ins-ct 06943	ANTPI544-15			0	Iguazú NP, Misiones	Worker
Neoponera crenata	MACN-Bar-Ins-5559	ANTPI305-14	MOTU-25	BOLD:ACX7584	614[0n]	CIAR, Misiones	Worker
Neoponera crenata	MACN-Bar-Ins-5548	ANTPI294-14	MOTU-9	BOLD:ABV2684	658[0n]	CIAR, Misiones	Worker
Neoponera crenata	MACN-bar-ins-ct 06398	ANTI101-15	MOTU-25	BOLD:ACX7584	658[0n]	Iguazú NP, Misiones	Worker
Neoponera crenata	MACN-bar-ins-ct 06416	ANTI119-15	MOTU-25	BOLD:ACX7584	658[0n]	Iguazú NP, Misiones	Worker
Neoponera crenata	MACN-Bar-Ins-ct 06809	ANTPI410-15	MOTU-9	BOLD:ABV2684	658[0n]	Iguazú NP, Misiones	Worker
Neoponera crenata	MACN-Bar-Ins-ct 07343	ANTI473-16	MOTU-25	BOLD:ACX7584	658[0n]	CIAR, Misiones	Worker
Neoponera crenata	MACN-Bar-Ins-ct 07387	ANTI517-16	MOTU-25	BOLD:ACX7584	658[0n]	Osununú PR, Misiones	Worker
Neoponera crenata	MACN-Bar-Ins-ct 07395	ANTI525-16	MOTU-9	BOLD:ABV2684	658[0n]	Osununú PR, Misiones	Worker
Neoponera crenata	MACN-Bar-Ins-ct 07424	ANTI554-16	MOTU-25	BOLD:ACX7584	658[0n]	Osununú PR, Misiones	Worker

Neoponera crenata	MACN-bar-ins-ct 07638	ANTI767-17	MOTU-25	BOLD:ACX7584	658[0n]	Iguazú NP, Misiones	Worker
Neoponera crenata	MACN-bar-ins-ct 07761	ANTI863-17	MOTU-9	BOLD:ABV2684	658[0n]	Iguazú NP, Misiones	Worker
Neoponera curvinodis	MACN-bar-ins-07509	ANTI639-16	MOTU-39	BOLD:AAW5111	658[0n]	Iguazú NP, Misiones	Worker
Neoponera curvinodis	MACN-bar-ins-ct 06407	ANTI110-15	MOTU-39	BOLD:AAW5111	658[0n]	Iguazú NP, Misiones	Worker
Neoponera fiebrigi	MACN-bar-ins-ct 07733	ANTI837-17	MOTU-73	BOLD:ADJ0367	615[0n]	Iguazú NP, Misiones	Worker
Neoponera fiebrigi	MACN-bar-ins-07476	ANTI606-16	MOTU-74	BOLD:ACN1772	658[0n]	Iguazú NP, Misiones	Worker
Neoponera fiebrigi	MACN-bar-ins-ct 06401	ANTI104-15	MOTU-74	BOLD:ACN1772	658[0n]	Iguazú NP, Misiones	Worker
Neoponera fiebrigi	MACN-Bar-Ins-ct 07365	ANTI495-16	MOTU-73	BOLD:ADJ0367	658[0n]	Osununú PR, Misiones	Worker
Neoponera fiebrigi	MACN-Bar-Ins-ct 07439	ANTI569-16	MOTU-74	BOLD:ACN1772	658[0n]	Osununú PR, Misiones	Worker
Neoponera fiebrigi	MACN-bar-ins-ct 07766	ANTI868-17	MOTU-73	BOLD:ADJ0367	658[0n]	Iguazú NP, Misiones	Worker
Neoponera marginata	MACN-bar-ins-ct 06486	ANTI189-15			0	Teyu Cuare NP, Misiones	Worker
Neoponera marginata	MACN-Bar-Ins-ct 07316	ANTI446-16			0	CIAR, Misiones	Worker
Neoponera marginata	MACN-Bar-Ins-ct 07360	ANTI490-16			0	Osununú PR, Misiones	Worker
Neoponera marginata	MACN-Bar-Ins-ct 07413	ANTI543-16			0	Osununú PR, Misiones	Worker
Neoponera marginata	MACN-bar-ins-ct 07726	ANTI829-17			0	Copo NP, Santiago del Estero	Worker
Neoponera marginata	MACN-bar-ins-ct 07729	ANTI833-17			0	Copo NP, Santiago del Estero	Worker
Neoponera marginata	MACN-Bar-Ins-5586	ANTPI332-14	MOTU-28	BOLD:ACZ4191	593[0n]	CIAR, Misiones	Worker
Neoponera marginata	MACN-Bar-Ins-5581	ANTPI327-14	MOTU-28	BOLD:ACZ4191	618[3n]	CIAR, Misiones	Worker
Neoponera marginata	MACN-bar-ins-ct 07743	ANTI847-17	MOTU-67	BOLD:ADG7476	640[0n]	Copo NP, Santiago del Estero	Worker
Neoponera marginata	MACN-Bar-Ins-ct 07567	ANTI698-17	MOTU-67	BOLD:ADG7476	658[0n]	Copo NP, Santiago del Estero	Worker
Neoponera moesta	MACN-bar-ins-ct 06989	ANTPI590-16	MOTU-17	BOLD:ACM2898	629[0n]	Osununú PR, Misiones	Worker
Neoponera moesta	BIOUG24141-A02	GMAFP389-15	MOTU-17	BOLD:ACM2898	658[0n]	El Bagual, Formosa	Worker
Neoponera moesta	MACN-Bar-Ins-ct 05145	ANTPI254-13	MOTU-17	BOLD:ACM2898	658[0n]	Iguazú NP, Misiones	Dealated queen
Neoponera moesta	MACN-bar-ins-ct 06414	ANTI117-15	MOTU-17	BOLD:ACM2898	658[0n]	Iguazú NP, Misiones	Worker
Neoponera moesta	MACN-bar-ins-ct 07023	ANTPI624-16	MOTU-17	BOLD:ACM2898	658[0n]	Osununú PR, Misiones	Worker
Neoponera moesta	MACN-Bar-Ins-ct 07355	ANTI485-16	MOTU-17	BOLD:ACM2898	658[0n]	Teyu Cuare NP, Misiones	Worker
Neoponera moesta	MACN-Bar-Ins-ct 07406	ANTI536-16	MOTU-17	BOLD:ACM2898	658[0n]	Osununú PR, Misiones	Worker

Neoponera moesta	MACN-Bar-Ins-ct 07430	ANTI560-16	MOTU-17	BOLD:ACM2898	658[0n]	Osununú PR, Misiones	Worker
Neoponera obscuricornis	MACN-bar-ins-ct 06440	ANTI143-15			144[1n]	Iguazú NP, Misiones	Worker
Neoponera obscuricornis	MACN-bar-ins-ct 06435	ANTI138-15			151[0n]	Iguazú NP, Misiones	Dealated queen
Neoponera obscuricornis	MACN-bar-ins-ct 07017	ANTPI618-16	MOTU-48	BOLD:AAZ3349	613[0n]	Iguazú NP, Misiones	Worker
Neoponera obscuricornis	MACN-bar-ins-ct 07054	ANTPI655-16	MOTU-48	BOLD:AAZ3349	619[0n]	Iguazú NP, Misiones	Worker
Neoponera obscuricornis	MACN-bar-ins-ct 07038	ANTPI639-16	MOTU-48	BOLD:AAZ3349	658[0n]	Iguazú NP, Misiones	Worker
Neoponera PEH01	MACN-bar-ins-07447	ANTI577-16	MOTU-56	BOLD:ADF9605	620[1n]	Iguazú NP, Misiones	Worker
Neoponera verenae	MACN-Bar-Ins-ct 07345	ANTI475-16	MOTU-19	BOLD:AAB7675	638[0n]	CIAR, Misiones	Worker
Neoponera verenae	BIOUG12771-E04	GMARB027-14	MOTU-19	BOLD:AAB7675	658[0n]	CIAR, Misiones	Worker
Neoponera verenae	MACN-Bar-Ins-5592	ANTPI338-14	MOTU-19	BOLD:AAB7675	658[0n]	CIAR, Misiones	Worker
Neoponera verenae	MACN-bar-ins-ct 06487	ANTI190-15	MOTU-19	BOLD:AAB7675	658[0n]	Osununú PR, Misiones	Worker
Neoponera verenae	MACN-bar-ins-ct 06997	ANTPI598-16	MOTU-19	BOLD:AAB7675	658[0n]	Osununú PR, Misiones	Worker
Neoponera verenae	MACN-bar-ins-ct 07004	ANTPI605-16	MOTU-19	BOLD:AAB7675	658[0n]	Osununú PR, Misiones	Worker
Neoponera verenae	MACN-bar-ins-ct 07051	ANTPI652-16	MOTU-19	BOLD:AAB7675	658[0n]	CIAR, Misiones	Worker
Neoponera verenae	MACN-bar-ins-ct 07061	ANTPI662-16	MOTU-19	BOLD:AAB7675	658[0n]	Iguazú NP, Misiones	Worker
Neoponera verenae	MACN-Bar-Ins-ct 07315	ANTI445-16	MOTU-19	BOLD:AAB7675	658[0n]	CIAR, Misiones	Worker
Neoponera verenae	MACN-Bar-Ins-ct 07353	ANTI483-16	MOTU-19	BOLD:AAB7675	658[0n]	Teyu Cuare NP, Misiones	Worker
Neoponera verenae	MACN-Bar-Ins-ct 07400	ANTI530-16	MOTU-19	BOLD:AAB7675	658[0n]	Teyu Cuare NP, Misiones	Worker
Neoponera verenae	MACN-Bar-Ins-ct 07440	ANTI570-16	MOTU-19	BOLD:AAB7675	658[0n]	Teyu Cuare NP, Misiones	Worker
Neoponera villosa	MACN-bar-ins-07446	ANTI576-16	MOTU-16	BOLD:AAZ7290	658[0n]	Iguazú NP, Misiones	Worker
Neoponera villosa	MACN-bar-ins-07451	ANTI581-16	MOTU-16	BOLD:AAZ7290	658[0n]	Iguazú NP, Misiones	Worker
Neoponera villosa	MACN-bar-ins-07460	ANTI590-16	MOTU-16	BOLD:AAZ7290	658[0n]	Iguazú NP, Misiones	Worker
Neoponera villosa	MACN-Bar-Ins-ct 05121	ANTPI242-13	MOTU-16	BOLD:AAZ7290	658[0n]	Iguazú NP, Misiones	Alated queen
Neoponera villosa	MACN-Bar-Ins-ct 05138	ANTPI247-13	MOTU-16	BOLD:AAZ7290	658[0n]	Iguazú NP, Misiones	Worker
Neoponera villosa	MACN-bar-ins-ct 06404	ANTI107-15	MOTU-16	BOLD:AAZ7290	658[0n]	Iguazú NP, Misiones	Worker
Neoponera villosa	MACN-bar-ins-ct 06976	ANTPI577-16	MOTU-16		658[0n]	Cmte. Andresito, Misiones	Worker
Neoponera villosa	MACN-bar-ins-ct 07010	ANTPI611-16	MOTU-16		658[0n]	Cmte. Andresito, Misiones	Worker

Neoponera villosa	MACN-bar-ins-ct 07047	ANTPI648-16	MOTU-16		658[0n]	Cmte. Andresito, Misiones	Worker
Neoponera villosa	MACN-Bar-Ins-ct 07350	ANTI480-16	MOTU-16	BOLD:AAZ7290	658[0n]	Osununú PR, Misiones	Worker
Neoponera villosa	MACN-Bar-Ins-ct 07386	ANTI516-16	MOTU-16	BOLD:AAZ7290	658[0n]	Teyu Cuare NP, Misiones	Worker
Odontomachus	MACN-Bar-Ins-ct 07545	ANTI676-17			0	Copo NP, Santiago del Estero	Worker
Odontomachus	BIOUG12771-E03	GMARB026-14	MOTU-72	BOLD:ACN0629	658[0n]	CIAR, Misiones	Male
Odontomachus bauri	MACN-bar-ins-ct 07764	ANTI866-17	MOTU-58	BOLD:ADG7092	609[0n]	Copo NP, Santiago del Estero	Worker
Odontomachus bauri	MACN-Bar-Ins-ct 07565	ANTI696-17	MOTU-58	BOLD:ADG7092	641[0n]	Copo NP, Santiago del Estero	Worker
Odontomachus bauri	MACN-Bar-Ins-ct 07570	ANTI701-17	MOTU-58	BOLD:ADG7092	658[0n]	Copo NP, Santiago del Estero	Worker
Odontomachus bauri	MACN-Bar-Ins-ct 07573	ANTI704-17	MOTU-58	BOLD:ADG7092	658[0n]	Copo NP, Santiago del Estero	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 07423	ANTI553-16			0	Osununú PR, Misiones	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07631	ANTI762-17			0	Rosario de la Frontera, Salta	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07639	ANTI768-17			0	Rosario de la Frontera, Salta	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07656	ANTI780-17			0	Rosario de la Frontera, Salta	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07660	ANTI783-17			0	Rosario de la Frontera, Salta	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07674	ANTI792-17	MOTU-57	BOLD:ADG5749	572[0n]	Rosario de la Frontera, Salta	Worker
Odontomachus chelifer	MACN-bar-ins-ct 06972	ANTPI573-16	MOTU-3	BOLD:AAV3356	612[0n]	Santo Tome, Corrientes	Worker
Odontomachus chelifer	BIOUG22490-E02	GMAGD107-15	MOTU-3	BOLD:AAV3356	658[0n]	CIAR, Misiones	Male
Odontomachus chelifer	BIOUG25340-C10	GMAFY016-15	MOTU-3	BOLD:AAV3356	658[0n]	El Bagual, Formosa	Male
Odontomachus chelifer	MACN-bar-ins-07473	ANTI603-16	MOTU-3	BOLD:AAV3356	658[0n]	Osununú PR, Misiones	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 05137	ANTPI246-13	MOTU-3	BOLD:AAV3356	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 05141	ANTPI250-13	MOTU-3	BOLD:AAV3356	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus chelifer	MACN-bar-ins-ct 06399	ANTI102-15	MOTU-3	BOLD:AAV3356	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus chelifer	MACN-bar-ins-ct 06417	ANTI120-15	MOTU-3	BOLD:AAV3356	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07002	ANTPI603-16	MOTU-3	BOLD:AAV3356	658[0n]	Cmte. Andresito, Misiones	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07030	ANTPI631-16	MOTU-3	BOLD:AAV3356	658[0n]	Cmte. Andresito, Misiones	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07046	ANTPI647-16	MOTU-3	BOLD:AAV3356	658[0n]	Santo Tome, Corrientes	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 07314	ANTI444-16	MOTU-3	BOLD:AAV3356	658[0n]	CIAR, Misiones	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 07352	ANTI482-16	MOTU-3	BOLD:AAV3356	658[0n]	Osununú PR, Misiones	Worker

Odontomachus chelifer	MACN-Bar-Ins-ct 07362	ANTI492-16	MOTU-3	BOLD:AAV3356	658[0n]	Osununú PR, Misiones	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 07396	ANTI526-16	MOTU-3	BOLD:AAV3356	658[0n]	Osununú PR, Misiones	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 07421	ANTI551-16	MOTU-3	BOLD:AAV3356	658[0n]	Ebco, Corrientes	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 07425	ANTI555-16	MOTU-3	BOLD:AAV3356	658[0n]	Ebco, Corrientes	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 07552	ANTI683-17	MOTU-57	BOLD:ADG5749	658[0n]	Copo NP, Santiago del Estero	Worker
Odontomachus chelifer	MACN-Bar-Ins-ct 07558	ANTI689-17	MOTU-57	BOLD:ADG4860	658[0n]	Copo NP, Santiago del Estero	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07647	ANTI773-17	MOTU-3	BOLD:AAV3356	658[0n]	Itapua, Brasil	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07651	ANTI776-17	MOTU-3	BOLD:AAV3356	658[0n]	Yaboti, Misiones	Worker
Odontomachus chelifer	MACN-bar-ins-ct 07688	ANTI802-17	MOTU-3	BOLD:AAV3356	658[0n]	Yaboti, Misiones	Worker
Odontomachus chelifer	T6P52008PNID10	ANTPI046-10	MOTU-3	BOLD:AAV3356	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus haematodus	MACN-bar-ins-ct 07779	ANTI880-17	MOTU-51	BOLD:ADI8020	572[0n]	Santa Cruz, Bolivia	Worker
Odontomachus haematodus	MACN-bar-ins-ct 07738	ANTI842-17	MOTU-51	BOLD:ADI8020	582[0n]	Santa Cruz, Bolivia	Worker
Odontomachus haematodus	MACN-bar-ins-07470	ANTI600-16	MOTU-51	BOLD:AAK3202	658[0n]	Corrientes	Worker
Odontomachus haematodus	MACN-bar-ins-07479	ANTI609-16	MOTU-51	BOLD:AAK3202	658[0n]	Corrientes	Worker
Odontomachus haematodus	MACN-bar-ins-07520	ANTI651-16	MOTU-51	BOLD:ADI8013	658[0n]	Libertador Gral San Martín, Jujuy	Worker
Odontomachus haematodus	MACN-bar-ins-ct 07040	ANTPI641-16	MOTU-47	BOLD:ADE2501	658[0n]	Puerto Iguazú, Misiones	Worker
Odontomachus haematodus	MACN-Bar-Ins-ct 07139	ANTI269-16	MOTU-47	BOLD:ADE2501	658[0n]	Puerto Iguazú, Misiones	Worker
Odontomachus haematodus	MACN-Bar-Ins-ct 07367	ANTI497-16	MOTU-51	BOLD:AAK3202	658[0n]	Ebco, Corrientes	Worker
Odontomachus haematodus	MACN-Bar-Ins-ct 07373	ANTI503-16	MOTU-51	BOLD:AAK3202	658[0n]	Ebco, Corrientes	Worker
Odontomachus haematodus	MACN-Bar-Ins-ct 07604	ANTI735-17	MOTU-51	BOLD:AAK3202	658[0n]	Santiago del Estero	Worker

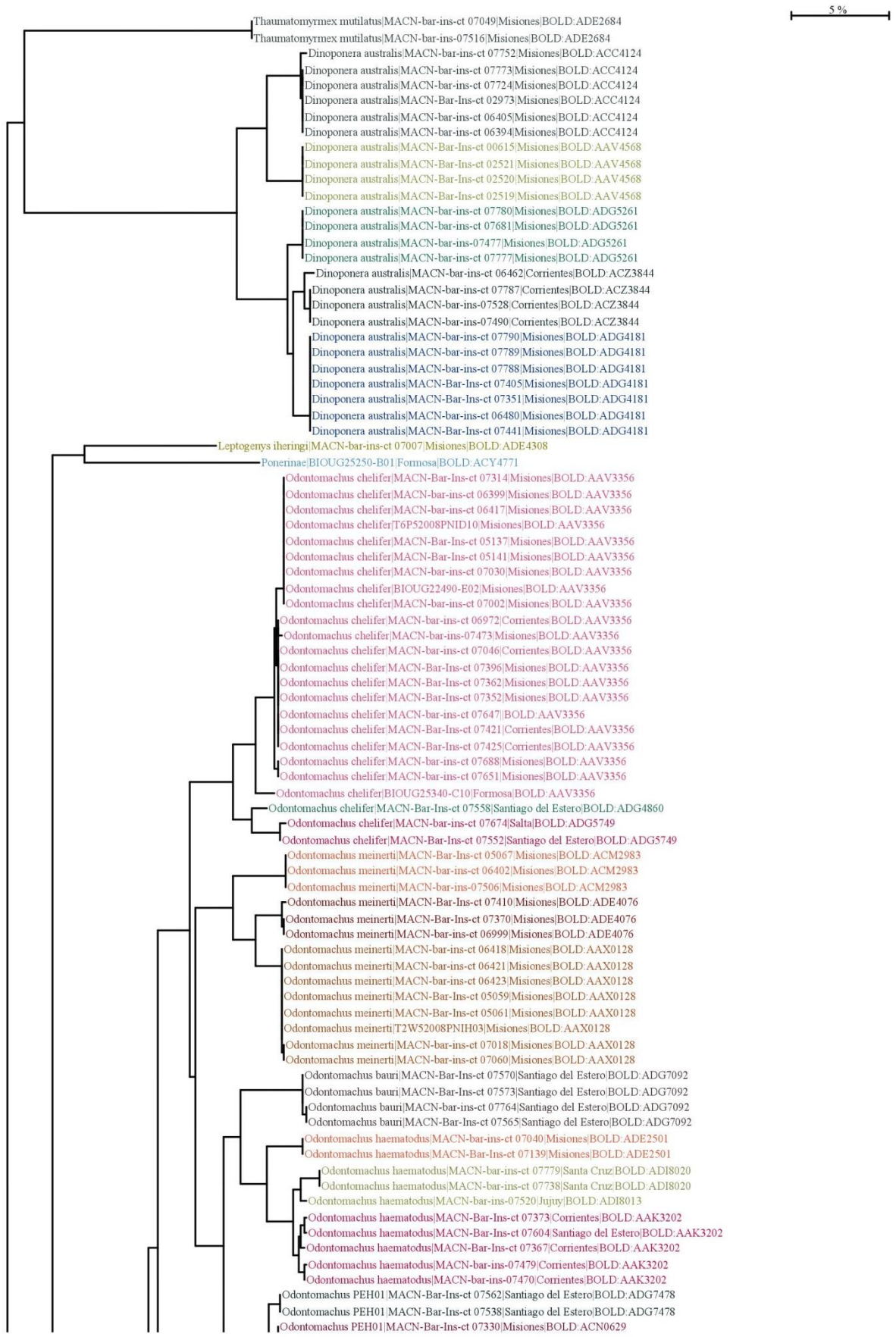
Odontomachus meinerti	MACN-Bar-Ins-ct 05065	ANTPI225-13			0	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-Bar-Ins-ct 05071	ANTPI269-13			0	Misiones	Worker
Odontomachus meinerti	MACN-bar-ins-07506	ANTI636-16	MOTU-14	BOLD:ACM2983	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-Bar-Ins-ct 05059	ANTPI220-13	MOTU-6	BOLD:AAX0128	658[0n]	Iguazú NP, Misiones	Alated queen
Odontomachus meinerti	MACN-Bar-Ins-ct 05061	ANTPI222-13	MOTU-6	BOLD:AAX0128	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-Bar-Ins-ct 05067	ANTPI227-13	MOTU-14	BOLD:ACM2983	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-bar-ins-ct 06402	ANTI105-15	MOTU-14	BOLD:ACM2983	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-bar-ins-ct 06418	ANTI121-15	MOTU-6	BOLD:AAX0128	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-bar-ins-ct 06421	ANTI124-15	MOTU-6	BOLD:AAX0128	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-bar-ins-ct 06423	ANTI126-15	MOTU-6	BOLD:AAX0128	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-bar-ins-ct 06999	ANTPI600-16	MOTU-44	BOLD:ADE4076	658[0n]	Osununú PR, Misiones	Worker
Odontomachus meinerti	MACN-bar-ins-ct 07018	ANTPI619-16	MOTU-6	BOLD:AAX0128	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-bar-ins-ct 07060	ANTPI661-16	MOTU-6	BOLD:AAX0128	658[0n]	Iguazú NP, Misiones	Worker
Odontomachus meinerti	MACN-Bar-Ins-ct 07370	ANTI500-16	MOTU-44	BOLD:ADE4076	658[0n]	San Ignacio, Misiones	Worker
Odontomachus meinerti	MACN-Bar-Ins-ct 07410	ANTI540-16	MOTU-44	BOLD:ADE4076	658[0n]	Osununú PR, Misiones	Worker
Odontomachus meinerti	T2W52008PNIH03	ANTPI087-10	MOTU-6	BOLD:AAX0128	658[0n]	Iguazú NP, Misiones	Dealated queen
Odontomachus PEH01	MACN-bar-ins-ct 06983	ANTPI584-16			0	Osununú PR, Misiones	Worker
Odontomachus PEH01	MACN-Bar-Ins-5624	ANTPI370-14	MOTU-72	BOLD:ACN0629	623[0n]	CIAR, Misiones	Worker
Odontomachus PEH01	MACN-Bar-Ins-ct 07538	ANTI669-17	MOTU-71	BOLD:ADG7478	628[0n]	Copo NP, Santiago del Estero	Worker
Odontomachus PEH01	MACN-Bar-Ins-ct 07325	ANTI455-16	MOTU-72	BOLD:ACN0629	632[0n]	CIAR, Misiones	Worker
Odontomachus PEH01	MACN-Bar-Ins-5557	ANTPI303-14	MOTU-72	BOLD:ACN0629	658[0n]	CIAR, Misiones	Worker
Odontomachus PEH01	MACN-Bar-Ins-5564	ANTPI310-14	MOTU-72	BOLD:ACN0629	658[0n]	CIAR, Misiones	Worker
Odontomachus PEH01	MACN-Bar-Ins-5570	ANTPI316-14	MOTU-72	BOLD:ACN0629	658[0n]	CIAR, Misiones	Worker
Odontomachus PEH01	MACN-bar-ins-ct 07014	ANTPI615-16	MOTU-72	BOLD:ACN0629	658[0n]	Osununú PR, Misiones	Worker
Odontomachus PEH01	MACN-bar-ins-ct 07031	ANTPI632-16	MOTU-72	BOLD:ACN0629	658[0n]	Osununú PR, Misiones	Worker
Odontomachus PEH01	MACN-Bar-Ins-ct 07320	ANTI450-16	MOTU-72	BOLD:ACN0629	658[0n]	CIAR, Misiones	Worker
Odontomachus PEH01	MACN-Bar-Ins-ct 07330	ANTI460-16	MOTU-72	BOLD:ACN0629	658[0n]	CIAR, Misiones	Worker

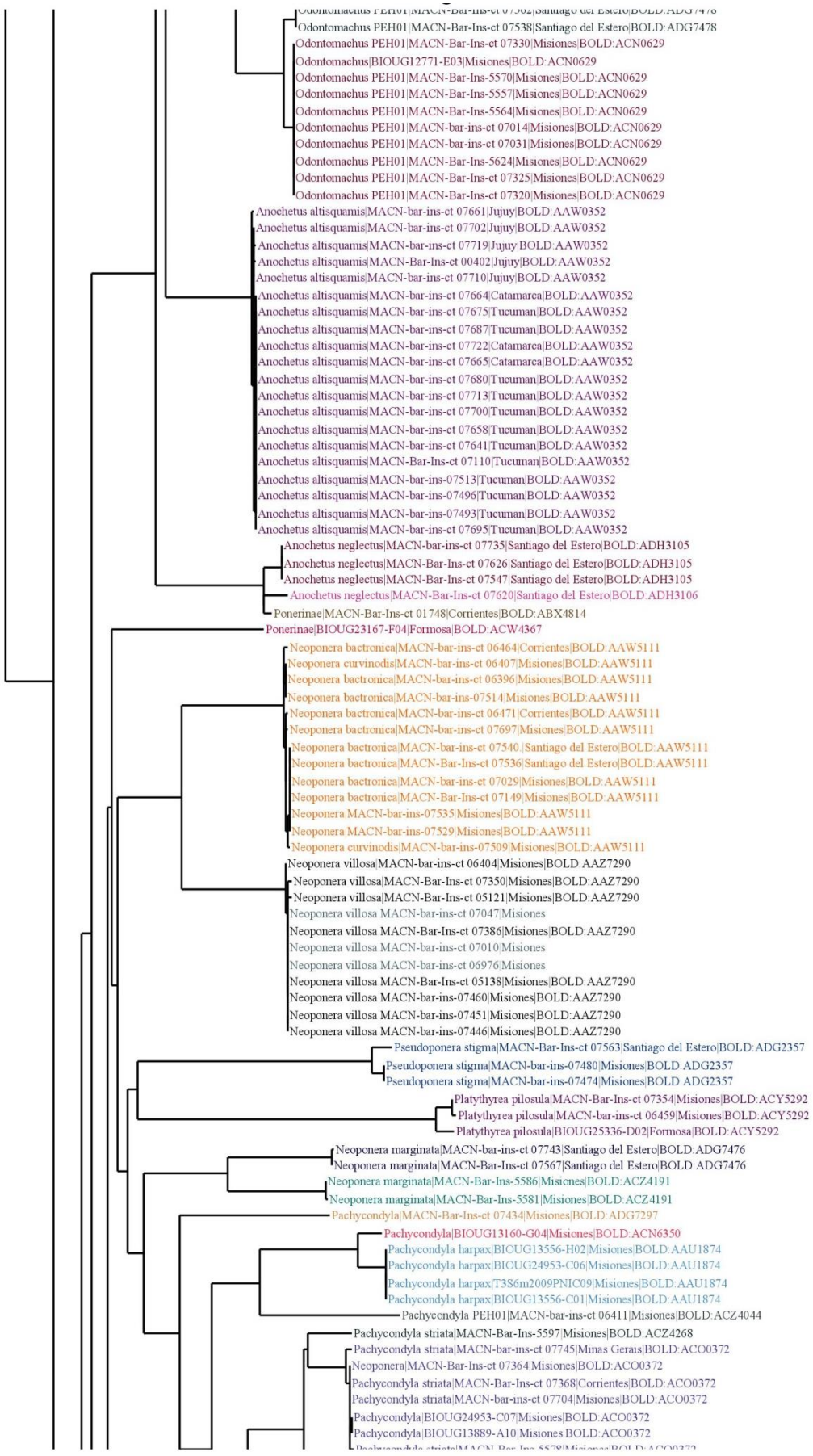
Odontomachus PEH01	MACN-Bar-Ins-ct 07562	ANTI693-17	MOTU-71	BOLD:ADG7478	658[0n]	Copo NP, Santiago del Estero	Worker
Pachycondyla	BIOUG13889-A10	GMARP1219-14	MOTU-23	BOLD:ACO0372	579[0n]	CIAR, Misiones	Alated queen
Pachycondyla	BIOUG24953-C07	GMAGS172-15	MOTU-23	BOLD:ACO0372	621[0n]	CIAR, Misiones	Alated queen
Pachycondyla	BIOUG22759-B01	GMAGB100-15	MOTU-30	BOLD:ACX7645	633[0n]	CIAR, Misiones	Dealated queen
Pachycondyla	BIOUG22759-B02	GMAGB101-15	MOTU-25	BOLD:ACX7584	633[0n]	CIAR, Misiones	Alated queen
Pachycondyla	BIOUG13576-H11	GMARO180-14	MOTU-24	BOLD:ACO0686	637[0n]	CIAR, Misiones	Male
Pachycondyla	BIOUG12827-D06	GMARB126-14	MOTU-74	BOLD:ACN1772	645[0n]	CIAR, Misiones	Alated queen
Pachycondyla	BIOUG12827-D05	GMARB125-14	MOTU-18	BOLD:ACN0120	658[0n]	CIAR, Misiones	Alated queen
Pachycondyla	BIOUG13556-G04	GMARO026-14	MOTU-9	BOLD:ABV2684	658[0n]	CIAR, Misiones	Dealated queen
Pachycondyla	BIOUG14047-C05	GMARU775-14	MOTU-19	BOLD:AAB7675	658[0n]	CIAR, Misiones	Alated queen
Pachycondyla	BIOUG24992-A09	GMAGQ226-15	MOTU-85	BOLD:ADG5761	658[0n]	CIAR, Misiones	Male
Pachycondyla	MACN-Bar-Ins-ct 07434	ANTI564-16	MOTU-50	BOLD:ADG7297	658[0n]	Osununú PR, Misiones	Male
Pachycondyla	BIOUG13160-G04	GMARK050-14	MOTU-21	BOLD:ACN6350	667[0n]	CIAR, Misiones	Male
Pachycondyla constricticeps	MACN-bar-ins-ct 06409	ANTI112-15			0	Iguazú NP, Misiones	Worker
Pachycondyla harpax	BIOUG13556-H02	GMARP009-14	MOTU-2	BOLD:AAU1874	513[0n]	CIAR, Misiones	Male
Pachycondyla harpax	BIOUG13556-C01	GMARN1615-14	MOTU-2	BOLD:AAU1874	658[0n]	CIAR, Misiones	Male
Pachycondyla harpax	BIOUG24953-C06	GMAGS171-15	MOTU-2	BOLD:AAU1874	658[0n]	CIAR, Misiones	Male
Pachycondyla harpax	T3S6m2009PNIC09	ANTPI033-10	MOTU-2	BOLD:AAU1874	658[0n]	Iguazú NP, Misiones	Worker
Pachycondyla PEH01	MACN-bar-ins-ct 06411	ANTI114-15	MOTU-36	BOLD:ACZ4044	658[0n]	Iguazú NP, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 06395	ANTI098-15			0	Ceibas, Entre Ríos	Worker
Pachycondyla striata	MACN-bar-ins-ct 07016	ANTPI617-16			0	Cmte. Andresito, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07069	ANTI199-16			0	Cerro San Javier, Tucumán	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07079	ANTI209-16			0	Cerro San Javier, Tucumán	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07135	ANTI265-16			0	Cerro San Javier, Tucumán	Worker
Pachycondyla striata	MACN-bar-ins-ct 07637	ANTI766-17			0	Yaboti, Misiones	Worker

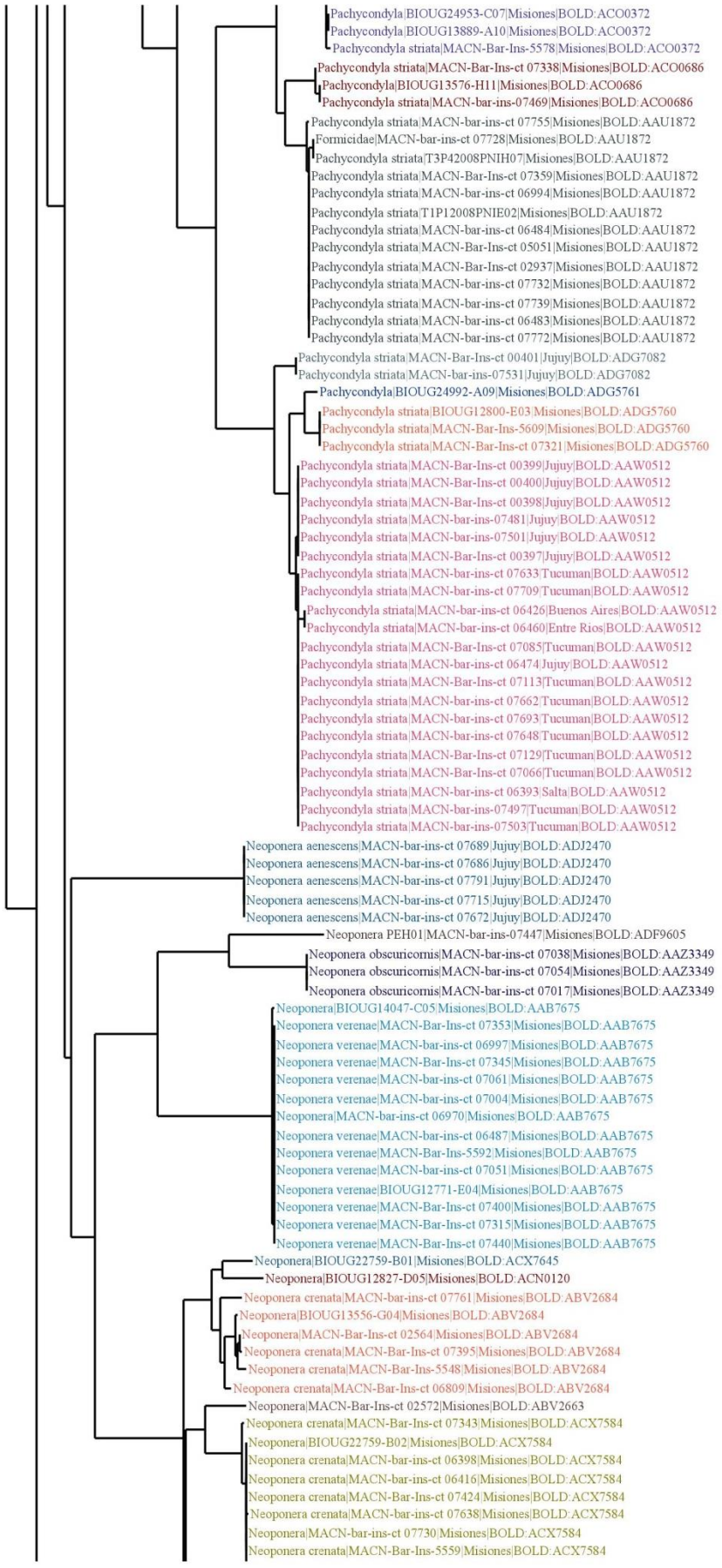
Pachycondyla striata	MACN-bar-ins-ct 07654	ANTI778-17			0	Yaboti, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 05729	INSAR1393-15			0	Iguazú NP, Misiones	Alated queen
Pachycondyla striata	MACN-Bar-Ins-ct 05735	INSAR1399-15			0	Iguazú NP, Misiones	Alated queen
Pachycondyla striata	MACN-Bar-Ins-ct 07129	ANTI259-16	MOTU-84	BOLD:AAW0512	581[0n]	Cerro San Javier, Tucumán	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07066	ANTI196-16	MOTU-84	BOLD:AAW0512	595[0n]	Cerro San Javier, Tucumán	Worker
Pachycondyla striata	MACN-bar-ins-ct 07704	ANTI813-17	MOTU-23	BOLD:ACO0372	625[0n]	Yaboti, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 06483	ANTI186-15	MOTU-4	BOLD:AAU1872	627[0n]	Osununú PR, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07338	ANTI468-16	MOTU-24	BOLD:ACO0686	628[0n]	CIAR, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-5578	ANTPI324-14	MOTU-23	BOLD:ACO0372	629[0n]	CIAR, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 06393	ANTI096-15	MOTU-84	BOLD:AAW0512	632[0n]	El Rey NP, Salta	Worker
Pachycondyla striata	MACN-bar-ins-ct 07755	ANTI857-17	MOTU-4	BOLD:AAU1872	632[0n]	Iguazú NP, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 07745	ANTI848-17	MOTU-23	BOLD:ACO0372	633[0n]	Minas Gerais, Brasil	Worker
Pachycondyla striata	MACN-bar-ins-ct 07709	ANTI815-17	MOTU-84	BOLD:AAW0512	634[0n]	Villa Padre Monti, Tucumán	Worker
Pachycondyla striata	MACN-bar-ins-ct 07739	ANTI843-17	MOTU-4	BOLD:AAU1872	637[0n]	Iguazú NP, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 07772	ANTI873-17	MOTU-4	BOLD:AAU1872	637[0n]	Iguazú NP, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-07469	ANTI599-16	MOTU-24	BOLD:ACO0686	638[0n]	Loreto, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 07732	ANTI836-17	MOTU-4	BOLD:AAU1872	638[0n]	Iguazú NP, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 00398	INSAR371-11	MOTU-84	BOLD:AAW0512	639[0n]	Calilegua NP, Jujuy	Worker
Pachycondyla striata	MACN-bar-ins-ct 07633	ANTI764-17	MOTU-84	BOLD:AAW0512	651[0n]	Cajon, Tucumán	Worker
Pachycondyla striata	BIOUG12800-E03	GMARA1914-14	MOTU-86	BOLD:ADG5760	658[0n]	CIAR, Misiones	Male
Pachycondyla striata	MACN-bar-ins-07481	ANTI611-16	MOTU-84	BOLD:AAW0512	658[0n]	Calilegua NP, Jujuy	Worker
Pachycondyla striata	MACN-bar-ins-07497	ANTI627-16	MOTU-84	BOLD:AAW0512	658[0n]	Campo de los Alisos NP, Tucumán	Worker
Pachycondyla striata	MACN-bar-ins-07501	ANTI631-16	MOTU-84	BOLD:AAW0512	658[0n]	Calilegua NP, Jujuy	Worker
Pachycondyla striata	MACN-bar-ins-07503	ANTI633-16	MOTU-84	BOLD:AAW0512	658[0n]	Campo de los Alisos NP, Tucumán	Worker
Pachycondyla striata	MACN-bar-ins-07531	ANTI662-16	MOTU-83	BOLD:ADG7082	658[0n]	Calilegua NP, Jujuy	Worker
Pachycondyla striata	MACN-Bar-Ins-5597	ANTPI343-14	MOTU-27	BOLD:ACZ4268	658[0n]	CIAR, Misiones	Alated queen
Pachycondyla striata	MACN-Bar-Ins-5609	ANTPI355-14	MOTU-86	BOLD:ADG5760	658[0n]	CIAR, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 00397	INSAR370-11	MOTU-84	BOLD:AAW0512	658[0n]	Calilegua NP, Jujuy	Worker

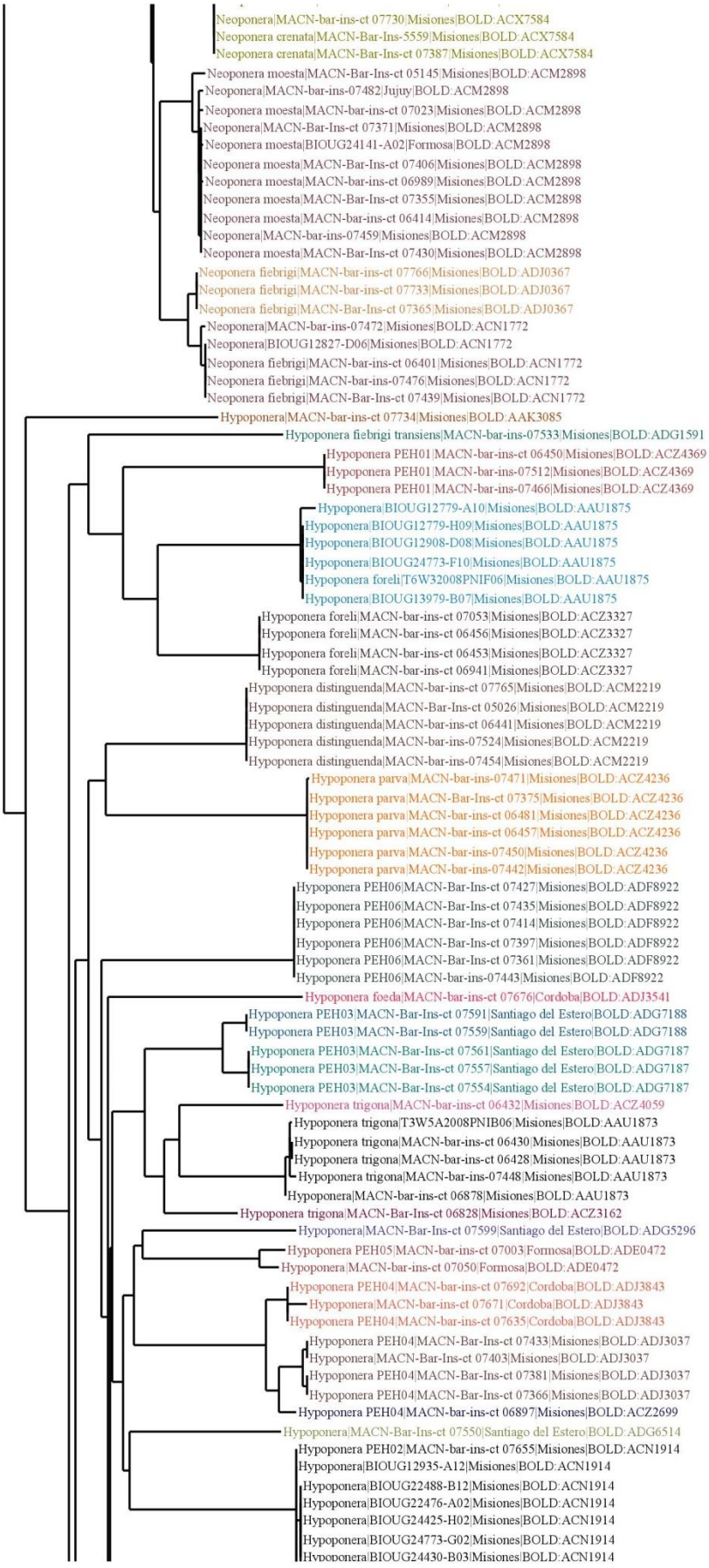
Pachycondyla striata	MACN-Bar-Ins-ct 00399	INSAR372-11	MOTU-84	BOLD:AAW0512	658[0n]	Calilegua NP, Jujuy	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 00400	INSAR373-11	MOTU-84	BOLD:AAW0512	658[0n]	Calilegua NP, Jujuy	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 00401	INSAR374-11	MOTU-83	BOLD:ADG7082	658[0n]	Calilegua NP, Jujuy	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 02937	ANTPI154-12	MOTU-4	BOLD:AAU1872	658[0n]	Iguazú NP, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 05051	ANTPI219-13	MOTU-4	BOLD:AAU1872	658[0n]	Iguazú NP, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 06426	ANTI129-15	MOTU-84	BOLD:AAW0512	658[0n]	Vuelta de Obligado, Buenos Aires	Worker
Pachycondyla striata	MACN-bar-ins-ct 06460	ANTI163-15	MOTU-84	BOLD:AAW0512	658[0n]	Ceibas, Entre Ríos	Worker
Pachycondyla striata	MACN-bar-ins-ct 06474	ANTI177-15	MOTU-84	BOLD:AAW0512	658[0n]	Calilegua NP, Jujuy	Worker
Pachycondyla striata	MACN-bar-ins-ct 06484	ANTI187-15	MOTU-4	BOLD:AAU1872	658[0n]	Osununú PR, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07085	ANTI215-16	MOTU-84	BOLD:AAW0512	658[0n]	Cerro San Javier, Tucumán	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07113	ANTI243-16	MOTU-84	BOLD:AAW0512	658[0n]	Cerro San Javier, Tucumán	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07321	ANTI451-16	MOTU-86	BOLD:ADG5760	658[0n]	CIAR, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 07648	ANTI774-17	MOTU-84	BOLD:AAW0512	658[0n]	Cajon, Tucumán	Worker
Pachycondyla striata	MACN-bar-ins-ct 07662	ANTI785-17	MOTU-84	BOLD:AAW0512	658[0n]	Cajon, Tucumán	Worker
Pachycondyla striata	MACN-bar-ins-ct 07693	ANTI806-17	MOTU-84	BOLD:AAW0512	658[0n]	Villa Padre Monti, Tucumán	Worker
Pachycondyla striata	T3P42008PNIH07	ANTPI091-10	MOTU-4	BOLD:AAU1872	658[0n]	Iguazú NP, Misiones	Worker
Pachycondyla striata	MACN-bar-ins-ct 06994	ANTPI595-16	MOTU-4	BOLD:AAU1872	658[1n]	Cmte. Andresito, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07359	ANTI489-16	MOTU-4	BOLD:AAU1872	658[1n]	San Ignacio, Misiones	Worker
Pachycondyla striata	MACN-Bar-Ins-ct 07368	ANTI498-16	MOTU-23	BOLD:ACO0372	658[1n]	Ebco, Corrientes	Worker
Pachycondyla striata	T1P12008PNIE02	ANTPI050-10	MOTU-4	BOLD:AAU1872	658[1n]	Iguazú NP, Misiones	Worker
Platythyrea pilosula	BIOUG25336-D02	GMAFV080-15	MOTU-38	BOLD:ACY5292	624[0n]	El Bagual, Formosa	Alated queen
Platythyrea pilosula	MACN-bar-ins-ct 06459	ANTI162-15	MOTU-38	BOLD:ACY5292	658[0n]	Iguazú NP, Misiones	Worker
Platythyrea pilosula	MACN-Bar-Ins-ct 07354	ANTI484-16	MOTU-38	BOLD:ACY5292	658[0n]	Osununú PR, Misiones	Alated queen
Ponerinae	BIOUG23334-E10	GMAFF493-15	MOTU-22	BOLD:ACM9912	603[0n]	El Bagual, Formosa	Male
Ponerinae	MACN-Bar-Ins-ct 01748	MBUIN698-12	MOTU-11	BOLD:ABX4814	626[0n]	Mburucuya PN, Corrientes	Male
Ponerinae	MACN-bar-ins-ct 07728	ANTI832-17	MOTU-4	BOLD:AAU1872	627[0n]	Iguazú NP, Misiones	Male
Ponerinae	BIOUG13316-F03	GMARJ1825-14	MOTU-22	BOLD:ACM9912	636[0n]	CIAR, Misiones	Alated queen
Ponerinae	BIOUG22476-B01	GMAGA706-15	MOTU-32	BOLD:ACV2779	658[0n]	CIAR, Misiones	Alated queen

Ponerinae	BIOUG24430-A01	GMAGZ175-15	MOTU-33	BOLD:ACX3395	658[0n]	CIAR, Misiones	Male
Ponerinae	BIOUG24734-D11	GMAGX096-15	MOTU-32	BOLD:ACV2779	658[0n]	CIAR, Misiones	Alated queen
Ponerinae	BIOUG25250-B01	GMAFT555-15	MOTU-34	BOLD:ACY4771	658[0n]	El Bagual, Formosa	Male
Ponerinae	BIOUG23167-F04	GMAFA491-15	MOTU-35	BOLD:ACW4367	667[0n]	El Bagual, Formosa	Male
Pseudoponera stigma	MACN-bar-ins-07474	ANTI604-16	MOTU-55	BOLD:ADG2357	658[0n]	Iguazú NP, Misiones	Worker
Pseudoponera stigma	MACN-bar-ins-07480	ANTI610-16	MOTU-55	BOLD:ADG2357	658[0n]	Iguazú NP, Misiones	Worker
Pseudoponera stigma	MACN-Bar-Ins-ct 07563	ANTI694-17	MOTU-55	BOLD:ADG2357	658[0n]	Copo NP, Santiago del Estero	Alated queen
Rasopone lunaris	MACN-bar-ins-ct 05032	ANTI893-17			0	Iguazú NP, Misiones	Worker
Thaumatomyrmex mutilatus	MACN-bar-ins-ct 06984	ANTPI585-16		BOLD:ADE2684	422[1n]	Osununú PR, Misiones	Worker
Thaumatomyrmex mutilatus	MACN-bar-ins-07516	ANTI647-16	MOTU-46	BOLD:ADE2684	658[0n]	Osununú PR, Misiones	Worker
Thaumatomyrmex mutilatus	MACN-bar-ins-ct 07049	ANTPI650-16	MOTU-46	BOLD:ADE2684	658[0n]	Osununú PR, Misiones	Worker


5 %
Thaumatomyrmex mutilatus|MACN-bar-ins-ct 07049|Misiones|BOLD:ADE2684
Thaumatomyrmex mutilatus|MACN-bar-ins-07516|Misiones|BOLD:ADE2684
Dinoponera australis|MACN-bar-ins-ct 07752|Misiones|BOLD:ACC4124
Dinoponera australis|MACN-bar-ins-ct 07773|Misiones|BOLD:ACC4124
Dinoponera australis|MACN-bar-ins-ct 07724|Misiones|BOLD:ACC4124
Dinoponera australis|MACN-Bar-Ins-ct 02973|Misiones|BOLD:ACC4124
Dinoponera australis|MACN-bar-ins-ct 06405|Misiones|BOLD:ACC4124
Dinoponera australis|MACN-bar-ins-ct 06394|Misiones|BOLD:ACC4124
Dinoponera australis|MACN-Bar-Ins-ct 00615|Misiones|BOLD:AAV4568
Dinoponera australis|MACN-Bar-Ins-ct 02521|Misiones|BOLD:AAV4568
Dinoponera australis|MACN-Bar-Ins-ct 02520|Misiones|BOLD:AAV4568
Dinoponera australis|MACN-Bar-Ins-ct 02519|Misiones|BOLD:AAV4568
Dinoponera australis|MACN-bar-ins-ct 07780|Misiones|BOLD:ADG5261
Dinoponera australis|MACN-bar-ins-ct 07681|Misiones|BOLD:ADG5261
Dinoponera australis|MACN-bar-ins-07477|Misiones|BOLD:ADG5261
Dinoponera australis|MACN-bar-ins-ct 07777|Misiones|BOLD:ADG5261
Dinoponera australis|MACN-bar-ins-ct 06462|Corrientes|BOLD:ACZ3844
Dinoponera australis|MACN-bar-ins-ct 07787|Corrientes|BOLD:ACZ3844
Dinoponera australis|MACN-bar-ins-07528|Corrientes|BOLD:ACZ3844
Dinoponera australis|MACN-bar-ins-07490|Corrientes|BOLD:ACZ3844
Dinoponera australis|MACN-bar-ins-ct 07790|Misiones|BOLD:ADG4181
Dinoponera australis|MACN-bar-ins-ct 07789|Misiones|BOLD:ADG4181
Dinoponera australis|MACN-bar-ins-ct 07788|Misiones|BOLD:ADG4181
Dinoponera australis|MACN-Bar-Ins-ct 07405|Misiones|BOLD:ADG4181
Dinoponera australis|MACN-Bar-Ins-ct 07351|Misiones|BOLD:ADG4181
Dinoponera australis|MACN-bar-ins-ct 06480|Misiones|BOLD:ADG4181
Dinoponera australis|MACN-Bar-Ins-ct 07441|Misiones|BOLD:ADG4181
Leptogenys iheringi|MACN-bar-ins-ct 07007|Misiones|BOLD:ADE4308
Ponerinae|BIOUG25250-B01|Formosa|BOLD:ACY4771
Odontomachus chelifer|MACN-Bar-Ins-ct 07314|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 06399|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 06417|Misiones|BOLD:AAV3356
Odontomachus chelifer|T6P52008PNID10|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-Bar-Ins-ct 05137|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-Bar-Ins-ct 05141|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 07030|Misiones|BOLD:AAV3356
Odontomachus chelifer|BIOUG22490-E02|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 07002|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 06972|Corrientes|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-07473|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 07046|Corrientes|BOLD:AAV3356
Odontomachus chelifer|MACN-Bar-Ins-ct 07396|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-Bar-Ins-ct 07362|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-Bar-Ins-ct 07352|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 07647|BOLD:AAV3356
Odontomachus chelifer|MACN-Bar-Ins-ct 07421|Corrientes|BOLD:AAV3356
Odontomachus chelifer|MACN-Bar-Ins-ct 07425|Corrientes|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 07688|Misiones|BOLD:AAV3356
Odontomachus chelifer|MACN-bar-ins-ct 07651|Misiones|BOLD:AAV3356
Odontomachus chelifer|BIOUG25340-C10|Formosa|BOLD:AAV3356
Odontomachus chelifer|MACN-Bar-Ins-ct 07558|Santiago del Estero|BOLD:ADG4860
Odontomachus chelifer|MACN-bar-ins-ct 07674|Salta|BOLD:ADG5749
Odontomachus chelifer|MACN-Bar-Ins-ct 07552|Santiago del Estero|BOLD:ADG5749
Odontomachus meinerti|MACN-Bar-Ins-ct 05067|Misiones|BOLD:ACM2983
Odontomachus meinerti|MACN-bar-ins-ct 06402|Misiones|BOLD:ACM2983
Odontomachus meinerti|MACN-bar-ins-07506|Misiones|BOLD:ACM2983
Odontomachus meinerti|MACN-Bar-Ins-ct 07410|Misiones|BOLD:ADE4076
Odontomachus meinerti|MACN-Bar-Ins-ct 07370|Misiones|BOLD:ADE4076
Odontomachus meinerti|MACN-bar-ins-ct 06999|Misiones|BOLD:ADE4076
Odontomachus meinerti|MACN-bar-ins-ct 06418|Misiones|BOLD:AAX0128
Odontomachus meinerti|MACN-bar-ins-ct 06421|Misiones|BOLD:AAX0128
Odontomachus meinerti|MACN-bar-ins-ct 06423|Misiones|BOLD:AAX0128
Odontomachus meinerti|MACN-Bar-Ins-ct 05059|Misiones|BOLD:AAX0128
Odontomachus meinerti|MACN-Bar-Ins-ct 05061|Misiones|BOLD:AAX0128
Odontomachus meinerti|T2W52008PNIH03|Misiones|BOLD:AAX0128
Odontomachus meinerti|MACN-bar-ins-ct 07018|Misiones|BOLD:AAX0128
Odontomachus meinerti|MACN-bar-ins-ct 07060|Misiones|BOLD:AAX0128
Odontomachus bauri|MACN-Bar-Ins-ct 07570|Santiago del Estero|BOLD:ADG7092
Odontomachus bauri|MACN-Bar-Ins-ct 07573|Santiago del Estero|BOLD:ADG7092
Odontomachus bauri|MACN-bar-ins-ct 07764|Santiago del Estero|BOLD:ADG7092
Odontomachus bauri|MACN-Bar-Ins-ct 07565|Santiago del Estero|BOLD:ADG7092
Odontomachus haematodus|MACN-bar-ins-ct 07040|Misiones|BOLD:ADE2501
Odontomachus haematodus|MACN-Bar-Ins-ct 07139|Misiones|BOLD:ADE2501
Odontomachus haematodus|MACN-bar-ins-ct 07779|Santa Cruz|BOLD:ADI8020
Odontomachus haematodus|MACN-bar-ins-ct 07738|Santa Cruz|BOLD:ADI8020
Odontomachus haematodus|MACN-bar-ins-07520|Jujuy|BOLD:ADI8013
Odontomachus haematodus|MACN-Bar-Ins-ct 07373|Corrientes|BOLD:AAK3202
Odontomachus haematodus|MACN-Bar-Ins-ct 07604|Santiago del Estero|BOLD:AAK3202
Odontomachus haematodus|MACN-Bar-Ins-ct 07367|Corrientes|BOLD:AAK3202
Odontomachus haematodus|MACN-bar-ins-07479|Corrientes|BOLD:AAK3202
Odontomachus haematodus|MACN-bar-ins-07470|Corrientes|BOLD:AAK3202
Odontomachus PEH01|MACN-Bar-Ins-ct 07562|Santiago del Estero|BOLD:ADG7478
Odontomachus PEH01|MACN-Bar-Ins-ct 07538|Santiago del Estero|BOLD:ADG7478
Odontomachus PEH01|MACN-Bar-Ins-ct 07330|Misiones|BOLD:ACN0629


Odontomachus PEH01|MACN-Bar-Ins-ct 07538|Santiago del Estero|BOLD:ADG7478
Odontomachus PEH01|MACN-Bar-Ins-ct 07330|Misiones|BOLD:ACN0629
Odontomachus|BIOUG12771-E03|Misiones|BOLD:ACN0629
Odontomachus PEH01|MACN-Bar-Ins-5570|Misiones|BOLD:ACN0629
Odontomachus PEH01|MACN-Bar-Ins-5557|Misiones|BOLD:ACN0629
Odontomachus PEH01|MACN-Bar-Ins-5564|Misiones|BOLD:ACN0629
Odontomachus PEH01|MACN-bar-ins-ct 07014|Misiones|BOLD:ACN0629
Odontomachus PEH01|MACN-bar-ins-ct 07031|Misiones|BOLD:ACN0629
Odontomachus PEH01|MACN-Bar-Ins-5624|Misiones|BOLD:ACN0629
Odontomachus PEH01|MACN-Bar-Ins-ct 07325|Misiones|BOLD:ACN0629
Odontomachus PEH01|MACN-Bar-Ins-ct 07320|Misiones|BOLD:ACN0629
Anochetus altisquamis|MACN-bar-ins-ct 07661|Jujuy|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07702|Jujuy|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07719|Jujuy|BOLD:AAW0352
Anochetus altisquamis|MACN-Bar-Ins-ct 00402|Jujuy|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07710|Jujuy|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07664|Catamarca|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07675|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07687|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07722|Catamarca|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07665|Catamarca|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07680|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07713|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07700|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07658|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07641|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-Bar-Ins-ct 07110|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-07513|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-07496|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-07493|Tucuman|BOLD:AAW0352
Anochetus altisquamis|MACN-bar-ins-ct 07695|Tucuman|BOLD:AAW0352
Anochetus neglectus|MACN-bar-ins-ct 07735|Santiago del Estero|BOLD:ADH3105
Anochetus neglectus|MACN-Bar-Ins-ct 07626|Santiago del Estero|BOLD:ADH3105
Anochetus neglectus|MACN-Bar-Ins-ct 07547|Santiago del Estero|BOLD:ADH3105
Anochetus neglectus|MACN-Bar-Ins-ct 07620|Santiago del Estero|BOLD:ADH3106
Ponerinae|MACN-Bar-Ins-ct 01748|Corrientes|BOLD:ABX4814
Ponerinae|BIOUG23167-F04|Formosa|BOLD:ACW4367
Neoponera bactronica|MACN-bar-ins-ct 06464|Corrientes|BOLD:AAW5111
Neoponera curvinodis|MACN-bar-ins-ct 06407|Misiones|BOLD:AAW5111
Neoponera bactronica|MACN-bar-ins-ct 06396|Misiones|BOLD:AAW5111
Neoponera bactronica|MACN-bar-ins-07514|Misiones|BOLD:AAW5111
Neoponera bactronica|MACN-bar-ins-ct 06471|Corrientes|BOLD:AAW5111
Neoponera bactronica|MACN-bar-ins-ct 07697|Misiones|BOLD:AAW5111
Neoponera bactronica|MACN-bar-ins-ct 07540 |Santiago del Estero|BOLD:AAW5111
Neoponera bactronica|MACN-Bar-Ins-ct 07536|Santiago del Estero|BOLD:AAW5111
Neoponera bactronica|MACN-bar-ins-ct 07029|Misiones|BOLD:AAW5111
Neoponera bactronica|MACN-Bar-Ins-ct 07149|Misiones|BOLD:AAW5111
Neoponera|MACN-bar-ins-07535|Misiones|BOLD:AAW5111
Neoponera|MACN-bar-ins-07529|Misiones|BOLD:AAW5111
Neoponera curvinodis|MACN-bar-ins-07509|Misiones|BOLD:AAW5111
Neoponera villosa|MACN-bar-ins-ct 06404|Misiones|BOLD:AAZ7290
Neoponera villosa|MACN-Bar-Ins-ct 07350|Misiones|BOLD:AAZ7290
Neoponera villosa|MACN-Bar-Ins-ct 05121|Misiones|BOLD:AAZ7290
Neoponera villosa|MACN-bar-ins-ct 07047|Misiones
Neoponera villosa|MACN-Bar-Ins-ct 07386|Misiones|BOLD:AAZ7290
Neoponera villosa|MACN-bar-ins-ct 07010|Misiones
Neoponera villosa|MACN-bar-ins-ct 06976|Misiones
Neoponera villosa|MACN-Bar-Ins-ct 05138|Misiones|BOLD:AAZ7290
Neoponera villosa|MACN-bar-ins-07460|Misiones|BOLD:AAZ7290
Neoponera villosa|MACN-bar-ins-07451|Misiones|BOLD:AAZ7290
Neoponera villosa|MACN-bar-ins-07446|Misiones|BOLD:AAZ7290
Pseudoponera stigma|MACN-Bar-Ins-ct 07563|Santiago del Estero|BOLD:ADG2357
Pseudoponera stigma|MACN-bar-ins-07480|Misiones|BOLD:ADG2357
Pseudoponera stigma|MACN-bar-ins-07474|Misiones|BOLD:ADG2357
Platythyrea pilosula|MACN-Bar-Ins-ct 07354|Misiones|BOLD:ACY5292
Platythyrea pilosula|MACN-bar-ins-ct 06459|Misiones|BOLD:ACY5292
Platythyrea pilosula|BIOUG25336-D02|Formosa|BOLD:ACY5292
Neoponera marginata|MACN-bar-ins-ct 07743|Santiago del Estero|BOLD:ADG7476
Neoponera marginata|MACN-Bar-Ins-ct 07567|Santiago del Estero|BOLD:ADG7476
Neoponera marginata|MACN-Bar-Ins-5586|Misiones|BOLD:ACZ4191
Neoponera marginata|MACN-Bar-Ins-5581|Misiones|BOLD:ACZ4191
Pachycondyla|MACN-Bar-Ins-ct 07434|Misiones|BOLD:ADG7297
Pachycondyla|BIOUG13160-G04|Misiones|BOLD:ACN6350
Pachycondyla harpax|BIOUG13556-H02|Misiones|BOLD:AAU1874
Pachycondyla harpax|BIOUG24953-C06|Misiones|BOLD:AAU1874
Pachycondyla harpax|T3S6m2009PNIC09|Misiones|BOLD:AAU1874
Pachycondyla harpax|BIOUG13556-C01|Misiones|BOLD:AAU1874
Pachycondyla PEH01|MACN-bar-ins-ct 06411|Misiones|BOLD:ACZ4044
Pachycondyla striata|MACN-Bar-Ins-5597|Misiones|BOLD:ACZ4268
Pachycondyla striata|MACN-bar-ins-ct 07745|Minas Gerais|BOLD:ACO0372
Neoponera|MACN-Bar-Ins-ct 07364|Misiones|BOLD:ACO0372
Pachycondyla striata|MACN-Bar-Ins-ct 07368|Corrientes|BOLD:ACO0372
Pachycondyla striata|MACN-bar-ins-ct 07704|Misiones|BOLD:ACO0372
Pachycondyla|BIOUG24953-C07|Misiones|BOLD:ACO0372
Pachycondyla|BIOUG13889-A10|Misiones|BOLD:ACO0372


Pachycondyla|BIOUG24953-C07|Misiones|BOLD:ACO0372
Pachycondyla|BIOUG13889-A10|Misiones|BOLD:ACO0372
Pachycondyla striata|MACN-Bar-Ins-5578|Misiones|BOLD:ACO0372
Pachycondyla striata|MACN-Bar-Ins-ct 07338|Misiones|BOLD:ACO0686
Pachycondyla|BIOUG13576-H11|Misiones|BOLD:ACO0686
Pachycondyla striata|MACN-bar-ins-07469|Misiones|BOLD:ACO0686
Pachycondyla striata|MACN-bar-ins-ct 07755|Misiones|BOLD:AAU1872
Formicidae|MACN-bar-ins-ct 07728|Misiones|BOLD:AAU1872
Pachycondyla striata|T3P42008PNIH07|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-Bar-Ins-ct 07359|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-bar-ins-ct 06994|Misiones|BOLD:AAU1872
Pachycondyla striata|T1P12008PNIE02|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-bar-ins-ct 06484|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-Bar-Ins-ct 05051|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-Bar-Ins-ct 02937|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-bar-ins-ct 07732|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-bar-ins-ct 07739|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-bar-ins-ct 06483|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-bar-ins-ct 07772|Misiones|BOLD:AAU1872
Pachycondyla striata|MACN-Bar-Ins-ct 00401|Jujuy|BOLD:ADG7082
Pachycondyla striata|MACN-bar-ins-07531|Jujuy|BOLD:ADG7082
Pachycondyla|BIOUG24992-A09|Misiones|BOLD:ADG5761
Pachycondyla striata|BIOUG12800-E03|Misiones|BOLD:ADG5760
Pachycondyla striata|MACN-Bar-Ins-5609|Misiones|BOLD:ADG5760
Pachycondyla striata|MACN-Bar-Ins-ct 07321|Misiones|BOLD:ADG5760
Pachycondyla striata|MACN-Bar-Ins-ct 00399|Jujuy|BOLD:AAW0512
Pachycondyla striata|MACN-Bar-Ins-ct 00400|Jujuy|BOLD:AAW0512
Pachycondyla striata|MACN-Bar-Ins-ct 00398|Jujuy|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-07481|Jujuy|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-07501|Jujuy|BOLD:AAW0512
Pachycondyla striata|MACN-Bar-Ins-ct 00397|Jujuy|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 07633|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 07709|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 06426|Buenos Aires|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 06460|Entre Rios|BOLD:AAW0512
Pachycondyla striata|MACN-Bar-Ins-ct 07085|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 06474|Jujuy|BOLD:AAW0512
Pachycondyla striata|MACN-Bar-Ins-ct 07113|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 07662|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 07693|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 07648|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-Bar-Ins-ct 07129|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-Bar-Ins-ct 07066|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-ct 06393|Salta|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-07497|Tucuman|BOLD:AAW0512
Pachycondyla striata|MACN-bar-ins-07503|Tucuman|BOLD:AAW0512
Neoponera aenescens|MACN-bar-ins-ct 07689|Jujuy|BOLD:ADJ2470
Neoponera aenescens|MACN-bar-ins-ct 07686|Jujuy|BOLD:ADJ2470
Neoponera aenescens|MACN-bar-ins-ct 07791|Jujuy|BOLD:ADJ2470
Neoponera aenescens|MACN-bar-ins-ct 07715|Jujuy|BOLD:ADJ2470
Neoponera aenescens|MACN-bar-ins-ct 07672|Jujuy|BOLD:ADJ2470
Neoponera PEH01|MACN-bar-ins-07447|Misiones|BOLD:ADF9605
Neoponera obscuricornis|MACN-bar-ins-ct 07038|Misiones|BOLD:AAZ3349
Neoponera obscuricornis|MACN-bar-ins-ct 07054|Misiones|BOLD:AAZ3349
Neoponera obscuricornis|MACN-bar-ins-ct 07017|Misiones|BOLD:AAZ3349
Neoponera|BIOUG14047-C05|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-Bar-Ins-ct 07353|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-bar-ins-ct 06997|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-Bar-Ins-ct 07345|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-bar-ins-ct 07061|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-bar-ins-ct 07004|Misiones|BOLD:AAB7675
Neoponera|MACN-bar-ins-ct 06970|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-bar-ins-ct 06487|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-Bar-Ins-5592|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-bar-ins-ct 07051|Misiones|BOLD:AAB7675
Neoponera verenae|BIOUG12771-E04|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-Bar-Ins-ct 07400|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-Bar-Ins-ct 07315|Misiones|BOLD:AAB7675
Neoponera verenae|MACN-Bar-Ins-ct 07440|Misiones|BOLD:AAB7675
Neoponera|BIOUG22759-B01|Misiones|BOLD:ACX7645
Neoponera|BIOUG12827-D05|Misiones|BOLD:ACN0120
Neoponera crenata|MACN-bar-ins-ct 07761|Misiones|BOLD:ABV2684
Neoponera|BIOUG13556-G04|Misiones|BOLD:ABV2684
Neoponera|MACN-Bar-Ins-ct 02564|Misiones|BOLD:ABV2684
Neoponera crenata|MACN-Bar-Ins-ct 07395|Misiones|BOLD:ABV2684
Neoponera crenata|MACN-Bar-Ins-5548|Misiones|BOLD:ABV2684
Neoponera crenata|MACN-Bar-Ins-ct 06809|Misiones|BOLD:ABV2684
Neoponera|MACN-Bar-Ins-ct 02572|Misiones|BOLD:ABV2663
Neoponera crenata|MACN-Bar-Ins-ct 07343|Misiones|BOLD:ACX7584
Neoponera|BIOUG22759-B02|Misiones|BOLD:ACX7584
Neoponera crenata|MACN-bar-ins-ct 06398|Misiones|BOLD:ACX7584
Neoponera crenata|MACN-bar-ins-ct 06416|Misiones|BOLD:ACX7584
Neoponera crenata|MACN-Bar-Ins-ct 07424|Misiones|BOLD:ACX7584
Neoponera crenata|MACN-bar-ins-ct 07638|Misiones|BOLD:ACX7584
Neoponera|MACN-bar-ins-ct 07730|Misiones|BOLD:ACX7584
Neoponera crenata|MACN-Bar-Ins-5559|Misiones|BOLD:ACX7584


Neoponera|MACN-bar-ins-ct 07730|Misiones|BOLD:ACX7584
Neoponera crenata|MACN-Bar-Ins-5559|Misiones|BOLD:ACX7584
Neoponera crenata|MACN-Bar-Ins-ct 07387|Misiones|BOLD:ACX7584
Neoponera moesta|MACN-Bar-Ins-ct 05145|Misiones|BOLD:ACM2898
Neoponera|MACN-bar-ins-07482|Jujuy|BOLD:ACM2898
Neoponera moesta|MACN-bar-ins-ct 07023|Misiones|BOLD:ACM2898
Neoponera|MACN-Bar-Ins-ct 07371|Misiones|BOLD:ACM2898
Neoponera moesta|BIOUG24141-A02|Formosa|BOLD:ACM2898
Neoponera moesta|MACN-Bar-Ins-ct 07406|Misiones|BOLD:ACM2898
Neoponera moesta|MACN-bar-ins-ct 06989|Misiones|BOLD:ACM2898
Neoponera moesta|MACN-Bar-Ins-ct 07355|Misiones|BOLD:ACM2898
Neoponera moesta|MACN-bar-ins-ct 06414|Misiones|BOLD:ACM2898
Neoponera|MACN-bar-ins-07459|Misiones|BOLD:ACM2898
Neoponera moesta|MACN-Bar-Ins-ct 07430|Misiones|BOLD:ACM2898
Neoponera fiebrigi|MACN-bar-ins-ct 07766|Misiones|BOLD:ADJ0367
Neoponera fiebrigi|MACN-bar-ins-ct 07733|Misiones|BOLD:ADJ0367
Neoponera fiebrigi|MACN-Bar-Ins-ct 07365|Misiones|BOLD:ADJ0367
Neoponera|MACN-bar-ins-07472|Misiones|BOLD:ACN1772
Neoponera|BIOUG12827-D06|Misiones|BOLD:ACN1772
Neoponera fiebrigi|MACN-bar-ins-ct 06401|Misiones|BOLD:ACN1772
Neoponera fiebrigi|MACN-bar-ins-07476|Misiones|BOLD:ACN1772
Neoponera fiebrigi|MACN-Bar-Ins-ct 07439|Misiones|BOLD:ACN1772
Hypoponera|MACN-bar-ins-ct 07734|Misiones|BOLD:AAK3085
Hypoponera fiebrigi transiens|MACN-bar-ins-07533|Misiones|BOLD:ADG1591
Hypoponera PEH01|MACN-bar-ins-ct 06450|Misiones|BOLD:ACZ4369
Hypoponera PEH01|MACN-bar-ins-07512|Misiones|BOLD:ACZ4369
Hypoponera PEH01|MACN-bar-ins-07466|Misiones|BOLD:ACZ4369
Hypoponera|BIOUG12779-A10|Misiones|BOLD:AAU1875
Hypoponera|BIOUG12779-H09|Misiones|BOLD:AAU1875
Hypoponera|BIOUG12908-D08|Misiones|BOLD:AAU1875
Hypoponera|BIOUG24773-F10|Misiones|BOLD:AAU1875
Hypoponera foreli|T6W32008PNIF06|Misiones|BOLD:AAU1875
Hypoponera|BIOUG13979-B07|Misiones|BOLD:AAU1875
Hypoponera foreli|MACN-bar-ins-ct 07053|Misiones|BOLD:ACZ3327
Hypoponera foreli|MACN-bar-ins-ct 06456|Misiones|BOLD:ACZ3327
Hypoponera foreli|MACN-bar-ins-ct 06453|Misiones|BOLD:ACZ3327
Hypoponera foreli|MACN-bar-ins-ct 06941|Misiones|BOLD:ACZ3327
Hypoponera distinguenda|MACN-bar-ins-ct 07765|Misiones|BOLD:ACM2219
Hypoponera distinguenda|MACN-Bar-Ins-ct 05026|Misiones|BOLD:ACM2219
Hypoponera distinguenda|MACN-bar-ins-ct 06441|Misiones|BOLD:ACM2219
Hypoponera distinguenda|MACN-bar-ins-07524|Misiones|BOLD:ACM2219
Hypoponera distinguenda|MACN-bar-ins-07454|Misiones|BOLD:ACM2219
Hypoponera parva|MACN-bar-ins-07471|Misiones|BOLD:ACZ4236
Hypoponera parva|MACN-Bar-Ins-ct 07375|Misiones|BOLD:ACZ4236
Hypoponera parva|MACN-bar-ins-ct 06481|Misiones|BOLD:ACZ4236
Hypoponera parva|MACN-bar-ins-ct 06457|Misiones|BOLD:ACZ4236
Hypoponera parva|MACN-bar-ins-07450|Misiones|BOLD:ACZ4236
Hypoponera parva|MACN-bar-ins-07442|Misiones|BOLD:ACZ4236
Hypoponera PEH06|MACN-Bar-Ins-ct 07427|Misiones|BOLD:ADF8922
Hypoponera PEH06|MACN-Bar-Ins-ct 07435|Misiones|BOLD:ADF8922
Hypoponera PEH06|MACN-Bar-Ins-ct 07414|Misiones|BOLD:ADF8922
Hypoponera PEH06|MACN-Bar-Ins-ct 07397|Misiones|BOLD:ADF8922
Hypoponera PEH06|MACN-Bar-Ins-ct 07361|Misiones|BOLD:ADF8922
Hypoponera PEH06|MACN-bar-ins-07443|Misiones|BOLD:ADF8922
Hypoponera foeda|MACN-bar-ins-ct 07676|Cordoba|BOLD:ADJ3541
Hypoponera PEH03|MACN-Bar-Ins-ct 07591|Santiago del Estero|BOLD:ADG7188
Hypoponera PEH03|MACN-Bar-Ins-ct 07559|Santiago del Estero|BOLD:ADG7188
Hypoponera PEH03|MACN-Bar-Ins-ct 07561|Santiago del Estero|BOLD:ADG7187
Hypoponera PEH03|MACN-Bar-Ins-ct 07557|Santiago del Estero|BOLD:ADG7187
Hypoponera PEH03|MACN-Bar-Ins-ct 07554|Santiago del Estero|BOLD:ADG7187
Hypoponera trigona|MACN-bar-ins-ct 06432|Misiones|BOLD:ACZ4059
Hypoponera trigona|T3W5A2008PNIB06|Misiones|BOLD:AAU1873
Hypoponera trigona|MACN-bar-ins-ct 06430|Misiones|BOLD:AAU1873
Hypoponera trigona|MACN-bar-ins-ct 06428|Misiones|BOLD:AAU1873
Hypoponera trigona|MACN-bar-ins-07448|Misiones|BOLD:AAU1873
Hypoponera|MACN-bar-ins-ct 06878|Misiones|BOLD:AAU1873
Hypoponera trigona|MACN-Bar-Ins-ct 06828|Misiones|BOLD:ACZ3162
Hypoponera|MACN-Bar-Ins-ct 07599|Santiago del Estero|BOLD:ADG5296
Hypoponera PEH05|MACN-bar-ins-ct 07003|Formosa|BOLD:ADE0472
Hypoponera|MACN-bar-ins-ct 07050|Formosa|BOLD:ADE0472
Hypoponera PEH04|MACN-bar-ins-ct 07692|Cordoba|BOLD:ADJ3843
Hypoponera|MACN-bar-ins-ct 07671|Cordoba|BOLD:ADJ3843
Hypoponera PEH04|MACN-bar-ins-ct 07635|Cordoba|BOLD:ADJ3843
Hypoponera PEH04|MACN-Bar-Ins-ct 07433|Misiones|BOLD:ADJ3037
Hypoponera|MACN-Bar-Ins-ct 07403|Misiones|BOLD:ADJ3037
Hypoponera PEH04|MACN-Bar-Ins-ct 07381|Misiones|BOLD:ADJ3037
Hypoponera PEH04|MACN-Bar-Ins-ct 07366|Misiones|BOLD:ADJ3037
Hypoponera PEH04|MACN-bar-ins-ct 06897|Misiones|BOLD:ACZ2699
Hypoponera|MACN-Bar-Ins-ct 07550|Santiago del Estero|BOLD:ADG6514
Hypoponera PEH02|MACN-bar-ins-ct 07655|Misiones|BOLD:ACN1914
Hypoponera|BIOUG12935-A12|Misiones|BOLD:ACN1914
Hypoponera|BIOUG22488-B12|Misiones|BOLD:ACN1914
Hypoponera|BIOUG22476-A02|Misiones|BOLD:ACN1914
Hypoponera|BIOUG24425-H02|Misiones|BOLD:ACN1914
Hypoponera|BIOUG24773-G02|Misiones|BOLD:ACN1914
Hypoponera|BIOUG24430-B03|Misiones|BOLD:ACN1914

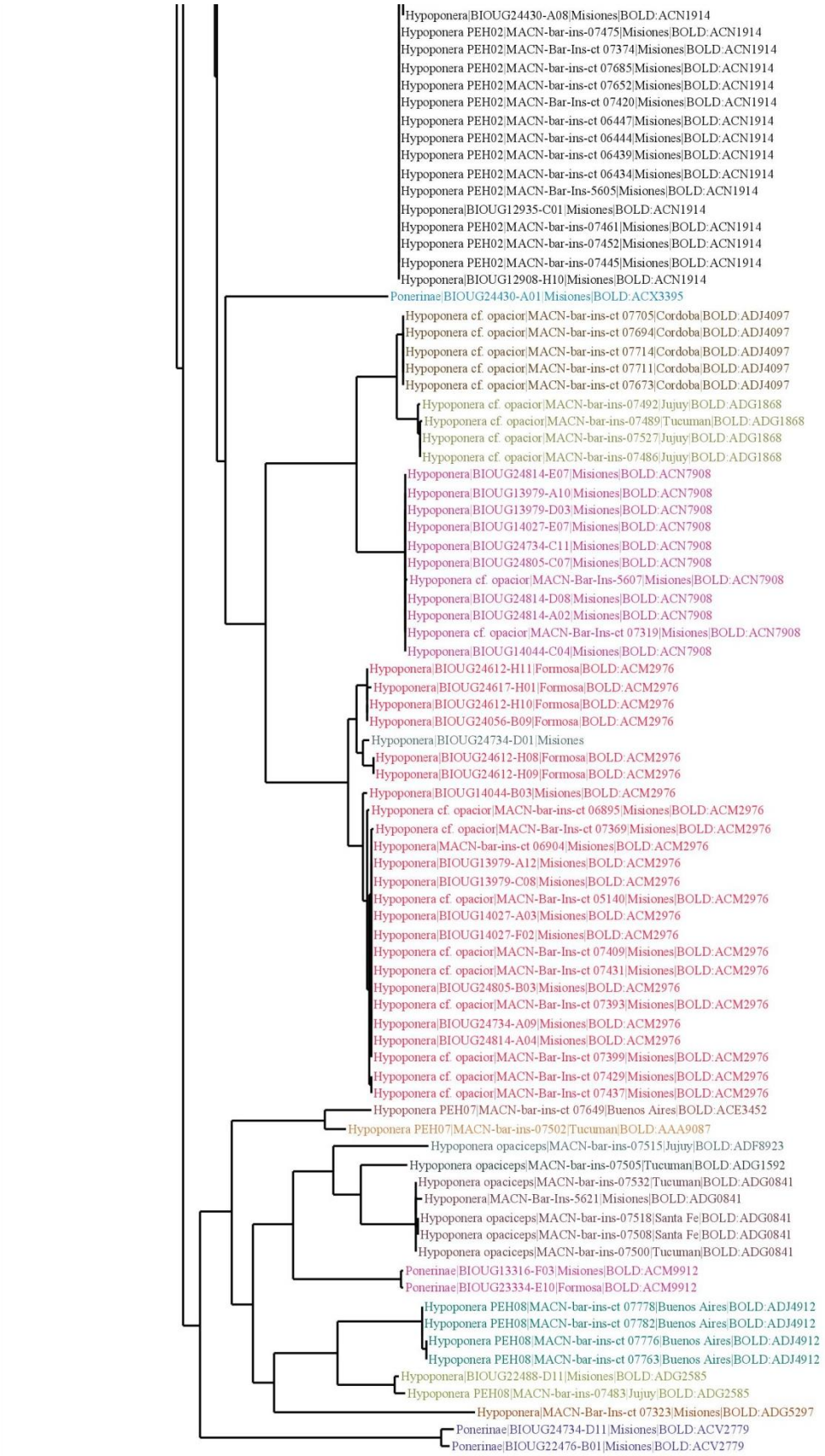


Fig S2.1 Neighbor-Joining (NJ) tree of 417 COI sequences of ponerine ants computed with a K2P substitution model and the Taxon ID tree tool on BOLD. Identified taxon, Sample ID, province and BIN code is provided for each of the specimens. Tree is colored according different BINs.

Appendix Chapter III

Table S3.1 Summary of 623 specimens processed for this study. For each individual, we provide the Sample and Process IDs along with the year of collection. For those individuals that were successfully sequenced we provide information on the length of the COI sequence together with the GenBank accession numbers and BIN information. (A) new record for INP checklist (*) new record for Misiones province, (**) new record for Argentina

Identification	Sample ID	Process ID	GenBank	BIN	Sequence length (bp)	Collection year
Acanthostichus brevicornis	T6S6a2009PNIG02	ANTPI074-10	MF925975	BOLD:ABU8923	600[0n]	2009
Acanthostichus brevicornis	T2S16a2008PNIC11	ANTPI035-10			0	2008
Acanthostichus brevicornis	MACN-Bar-Ins-ct 04968	ANTPI268-13			0	2009
Acanthostichus brevicornis	T6S6m2009PNIF05	ANTPI065-10			0	2009
Acanthostichus quadratus	MACN-bar-ins-ct 06431	ANTI134-15	MF925767	BOLD:ACZ3360	658[0n]	2015
Acanthostichus quadratus	MACN-bar-ins-ct 06922	ANTPI523-15	MF926028	BOLD:ACZ3360	658[0n]	2015
Acromyrmex hispidus	MACN-bar-ins-ct 06961	ANTPI562-15			0	1998
Acromyrmex laticeps	MACN-Bar-Ins-ct 04979	ANTPI193-13			0	2011
Acromyrmex subterraneus (A)	MACN-Bar-Ins-ct 06796	ANTPI397-15			0	1998
Acromyrmex subterraneus (A)	MACN-Bar-Ins-ct 06832	ANTPI433-15			0	1999
Acromyrmex subterraneus (A)	MACN-Bar-Ins-ct 06842	ANTPI443-15			0	1999
Acromyrmex subterraneus (A)	MACN-bar-ins-ct 06478	ANTI181-15			0	2015
Apterostigma PEH01	MACN-bar-ins-ct 06479	ANTI182-15	MF925927	BOLD:ACZ3911	603[0n]	2015
Apterostigma PEH02	MACN-bar-ins-ct 06468	ANTI171-15	MF925864	BOLD:ACZ4237	658[0n]	2015
Apterostigma PEH02	MACN-bar-ins-ct 06482	ANTI185-15	MF925785	BOLD:ACZ4237	658[0n]	2015
Apterostigma PEH02	MACN-Bar-Ins-ct 06782	ANTPI383-15			0	1999
Apterostigma PEH02	MACN-Bar-Ins-ct 06805	ANTPI406-15			0	1999
Apterostigma PEH02	MACN-Bar-Ins-ct 06836	ANTPI437-15			0	1999
Apterostigma PEH02	MACN-Bar-Ins-ct 06846	ANTPI447-15			0	1999
Atta sexdens	MACN-Bar-Ins-ct 06814	ANTPI415-15	MF925972	BOLD:ABV3852	658[0n]	1998
Atta sexdens	MACN-Bar-Ins-ct 06860	ANTPI461-15	MF925770	BOLD:ABV3852	658[0n]	1998
Atta sexdens	MACN-Bar-Ins-ct 02514	INSAR655-11	MF925924	BOLD:ABV3852	658[0n]	2011
Atta sexdens	MACN-Bar-Ins-ct 02515	INSAR656-11	MF925939	BOLD:ABV3852	658[0n]	2011
Atta sexdens	MACN-Bar-Ins-ct 02517	INSAR658-11	MF925806	BOLD:ABV3852	658[0n]	2011
Atta sexdens	MACN-Bar-Ins-ct 02912	ANTPI129-12	MF925926	BOLD:ACC4094	658[0n]	2011
Atta sexdens	MACN-Bar-Ins-ct 04974	ANTPI191-13	MF925819	BOLD:ACC4094	658[0n]	2011
Atta sexdens	MACN-bar-ins-ct 06443	ANTI146-15	MF925797	BOLD:ACZ4391	658[0n]	2015
Atta sexdens	MACN-Bar-Ins-ct 02516	INSAR657-11			658[0n]	2011
Atta sexdens	MACN-bar-ins-ct 06958	ANTPI559-15			0	2015
Azteca adrepens	MACN-Bar-Ins-ct 04976	ANTPI192-13	MF925946	BOLD:ACM2309	658[0n]	2011

Azteca adrepens	MACN-Bar-Ins-ct 04982	ANTPI194-13	MF925771	BOLD:ACM2309	658[0n]	2011
Azteca adrepens	MACN-bar-ins-ct 06918	ANTPI519-15	MF925892	BOLD:ACM2309	658[0n]	2011
Azteca adrepens	MACN-Bar-Ins-ct 04980	ANTPI271-13			0	2011
Azteca alfari	MACN-Bar-Ins-ct 02915	ANTPI132-12			0	2009
Basiceros disciger	MACN-bar-ins-ct 06959	ANTPI560-15			658[0n]	1998
Brachymyrmex antennatus	T4S10a2009PNIE04	ANTPI052-10	MF925990	BOLD:AAU4116	658[0n]	2009
Brachymyrmex antennatus	MACN-Bar-Ins-ct 04984	ANTPI196-13			0	2009
Brachymyrmex aphidicola	T3S12A2009PNIG10	ANTPI082-10	MF925827	BOLD:AAU4115	658[0n]	2009
Brachymyrmex aphidicola	T3S12m2009PNIC08	ANTPI032-10	MF925929	BOLD:AAU4115	658[0n]	2009
Brachymyrmex aphidicola	MACN-Bar-Ins-ct 06801	ANTPI402-15			0	1999
Brachymyrmex aphidicola	T3P42008PNIH09	ANTPI093-10			0	2008
Brachymyrmex aphidicola	T3W52008PNID06	ANTPI042-10			0	2008
Brachymyrmex aphidicola	T6S4a2009PNID09	ANTPI045-10			0	2009
Brachymyrmex cordemoyi	MACN-Bar-Ins-ct 02950	ANTPI167-12	MF925761	BOLD:ACC4473	658[0n]	2011
Brachymyrmex cordemoyi	MACN-Bar-Ins-ct 02961	ANTPI178-12	MF925900	BOLD:ACC4473	658[0n]	2011
Brachymyrmex cordemoyi	MACN-Bar-Ins-ct 02970	ANTPI187-12	MF925855	BOLD:ACC4473	658[0n]	2011
Brachymyrmex cordemoyi	MACN-Bar-Ins-ct 04983	ANTPI195-13	MF925989	BOLD:ACC4473	658[0n]	2011
Brachymyrmex cordemoyi	MACN-bar-ins-ct 06912	ANTPI513-15			0	2005
Brachymyrmex cordemoyi	MACN-bar-ins-ct 06936	ANTPI537-15			0	2005
Brachymyrmex cordemoyi	MACN-bar-ins-ct 06952	ANTPI553-15			0	2005
Brachymyrmex PEH01	MACN-Bar-Ins-ct 06781	ANTPI382-15			0	1999
Brachymyrmex PEH01	MACN-Bar-Ins-ct 06822	ANTPI423-15			0	1999
Brachymyrmex PEH01	MACN-Bar-Ins-ct 06863	ANTPI464-15			0	1999
Camponotus	MACN-Bar-Ins-ct 634	INSAR509-11		BOLD:AAI3890	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 02968	ANTPI185-12		BOLD:AAI3891	658[0n]	2011
Camponotus	MACN-Bar-Ins-ct 621	INSAR497-11		BOLD:AAW7847	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 622	INSAR498-11		BOLD:AAW7847	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 623	INSAR499-11		BOLD:AAW7847	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 624	INSAR500-11		BOLD:AAW7847	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 632	INSAR508-11		BOLD:AAW7847	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 635	INSAR510-11		BOLD:AAW7847	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 614	INSAR491-11		BOLD:AAZ4158	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 637	INSAR512-11		BOLD:AAZ4158	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 616	INSAR492-11		BOLD:AAZ4159	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 617	INSAR493-11		BOLD:AAZ4159	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 618	INSAR494-11		BOLD:AAZ4159	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 619	INSAR495-11		BOLD:AAZ4159	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 625	INSAR501-11		BOLD:AAZ4159	658[0n]	2010

Camponotus	MACN-Bar-Ins-ct 631	INSAR507-11		BOLD:AAZ4159	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 636	INSAR511-11		BOLD:AAZ4159	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 00613	INSAR137-11		BOLD:ABY9693	658[0n]	2010
Camponotus	MACN-Bar-Ins-ct 02539	INSAR716-11		BOLD:ABY9693	658[0n]	2011
Camponotus	MACN-Bar-Ins-ct 00633	INSAR139-11			403[0n]	2010
Camponotus	MACN-Bar-Ins-ct 05001	ANTPI203-13			0	2011
Camponotus	MACN-Bar-Ins-ct 05733	INSAR1397-15			0	2014
Camponotus atriceps	MACN-Bar-Ins-ct 628	INSAR504-11	MF925795	BOLD:AAW0798	658[0n]	2010
Camponotus atriceps	MACN-Bar-Ins-ct 629	INSAR505-11	MF925921	BOLD:AAW0798	658[0n]	2010
Camponotus atriceps	MACN-Bar-Ins-ct 02910	ANTPI127-12			0	2008
Camponotus atriceps	T6P52008PNIE05	ANTPI053-10			0	2008
Camponotus brasiliensis (**)	MACN-bar-ins-ct 06454	ANTI157-15	MF925780	BOLD:ACZ3824	658[0n]	2015
Camponotus brasiliensis (**)	MACN-bar-ins-ct 06903	ANTPI504-15			0	2015
Camponotus cf. landolti	T6P12008PNID07	ANTPI043-10	MF926048	BOLD:AAW7847	658[0n]	2008
Camponotus cf. landolti	T6P22008PNID01	ANTPI037-10	MF925805	BOLD:AAW7847	658[0n]	2008
Camponotus cf. landolti	MACN-Bar-Ins-ct 02892	ANTPI109-12	MF926044	BOLD:AAW7847	658[0n]	2011
Camponotus cf. landolti	MACN-Bar-Ins-ct 02906	ANTPI123-12	MF925749	BOLD:AAW7847	658[0n]	2011
Camponotus cf. landolti	MACN-Bar-Ins-ct 04999	ANTPI201-13			0	2008
Camponotus cf. landolti	T1P12008PNIF01	ANTPI061-10			0	2008
Camponotus cf. landolti	T1P32008PNIF07	ANTPI067-10			0	2008
Camponotus cf. landolti	T1P52008PNIG11	ANTPI083-10			0	2008
Camponotus cingulatus	MACN-Bar-Ins-ct 02927	ANTPI144-12	MF926037	BOLD:AAZ4159	658[0n]	2011
Camponotus cingulatus	MACN-Bar-Ins-ct 04994	ANTPI197-13	MF925763	BOLD:AAZ4159	658[0n]	2011
Camponotus cingulatus	MACN-Bar-Ins-ct 04996	ANTPI198-13	MF925838	BOLD:AAZ4159	658[0n]	2011
Camponotus cingulatus	MACN-Bar-Ins-ct 04998	ANTPI200-13	MF925815	BOLD:AAZ4159	658[0n]	2011
Camponotus cingulatus	MACN-bar-ins-ct 06429	ANTI132-15	MF925877	BOLD:AAZ4159	658[0n]	2015
Camponotus cingulatus	MACN-bar-ins-ct 06463	ANTI166-15	MF925987	BOLD:AAZ4159	658[0n]	2015
Camponotus cingulatus	MACN-Bar-Ins-ct 04992	ANTPI273-13			0	2008
Camponotus cingulatus	T2P12008PNIE07	ANTPI055-10			0	2008
Camponotus cingulatus	T3P42008PNIG03	ANTPI075-10			0	2008
Camponotus crassus	MACN-Bar-Ins-ct 02880	ANTPI097-12	MF925960	BOLD:AAW1347	658[0n]	2011
Camponotus crassus	MACN-Bar-Ins-ct 02894	ANTPI111-12	MF925917	BOLD:AAW1347	658[0n]	2011
Camponotus crassus	MACN-Bar-Ins-ct 02920	ANTPI137-12	MF925944	BOLD:AAW1347	658[0n]	2011
Camponotus crassus	MACN-Bar-Ins-ct 02951	ANTPI168-12	MF925745	BOLD:AAW1347	650[0n]	2011
Camponotus crassus	MACN-Bar-Ins-ct 04997	ANTPI199-13	MF925933	BOLD:AAW1347	658[0n]	2011
Camponotus crassus	MACN-Bar-Ins-ct 02904	ANTPI121-12			658[0n]	2011
Camponotus depressus	MACN-Bar-Ins-ct 05144	ANTPI253-13			0	2011
Camponotus depressus	MACN-bar-ins-ct 06437	ANTI140-15			0	2015

Camponotus geralensis (A)	MACN-Bar-Ins-ct 626	INSAR502-11	MF925851	BOLD:AAZ4160	658[0n]	2010
Camponotus lespessi	T2P32008PNIC10	ANTPI034-10			285[0n]	2008
Camponotus lespessi	MACN-Bar-Ins-ct 02886	ANTPI103-12			0	2011
Camponotus lespessi	MACN-Bar-Ins-ct 02922	ANTPI139-12			0	2011
Camponotus PEH01	MACN-Bar-Ins-ct 06802	ANTPI403-15	MF925993	BOLD:ABY9693	658[0n]	1999
Camponotus PEH01	MACN-Bar-Ins-ct 06807	ANTPI408-15			0	1999
Camponotus punctulatus	MACN-bar-ins-ct 06960	ANTPI561-15			0	1998
Camponotus renggeri	MACN-Bar-Ins-ct 02948	ANTPI165-12	MF925982	BOLD:ACC4407	658[0n]	2011
Camponotus renggeri	T4P22008PNID04	ANTPI040-10			0	2008
Camponotus rufipes	MACN-bar-ins-ct 06403	ANTI106-15	MF925750	BOLD:AAI3891	658[0n]	2015
Camponotus rufipes	MACN-Bar-Ins-ct 02884	ANTPI101-12	MF925843	BOLD:ACC4111	658[0n]	2011
Camponotus rufipes	MACN-Bar-Ins-ct 02898	ANTPI115-12	MF925831	BOLD:ACC4111	658[0n]	2011
Camponotus rufipes	MACN-Bar-Ins-ct 02964	ANTPI181-12	MF925739	BOLD:ACC4111	658[0n]	2011
Camponotus rufipes	MACN-Bar-Ins-ct 06798	ANTPI399-15			0	1999
Camponotus scissus	MACN-bar-ins-ct 06964	ANTPI565-15			0	1998
Camponotus sericeiventris	T2P42008PNIF04	ANTPI064-10	MF925756	BOLD:AAW7849	658[0n]	2008
Camponotus sericeiventris	MACN-Bar-Ins-ct 02518	INSAR659-11	MF925768	BOLD:AAW7849	658[0n]	2011
Camponotus sericeiventris	MACN-Bar-Ins-ct 02882	ANTPI099-12	MF925868	BOLD:AAW7849	658[0n]	2011
Camponotus sericeiventris	MACN-Bar-Ins-ct 02908	ANTPI125-12	MF925812	BOLD:AAW7849	658[0n]	2011
Camponotus sericeiventris	MACN-Bar-Ins-ct 02916	ANTPI133-12	MF925898	BOLD:AAW7849	658[0n]	2011
Camponotus sericeiventris	MACN-Bar-Ins-ct 02929	ANTPI146-12	MF925862	BOLD:AAW7849	658[0n]	2011
Camponotus sericeiventris	MACN-Bar-Ins-ct 02940	ANTPI157-12	MF925800	BOLD:AAW7849	658[0n]	2011
Camponotus sericeiventris	MACN-Bar-Ins-ct 02972	ANTPI189-12	MF925897	BOLD:AAW7849	658[0n]	2011
Camponotus sericeiventris	MACN-Bar-Ins-ct 05731	INSAR1395-15			0	2014
Camponotus striatus (**)	T6P22008PNIE11	ANTPI059-10	MF926007	BOLD:AAW1349	658[2n]	2008
Camponotus trapezoideus	MACN-bar-ins-ct 06882	ANTPI483-15			0	2015
Carebara brasiliana	MACN-bar-ins-ct 06937	ANTPI538-15	MF925889	BOLD:ACZ3340	658[0n]	2003
Carebara brasiliana	MACN-bar-ins-ct 06949	ANTPI550-15			0	2003
Carebara brevipilosa	MACN-Bar-Ins-ct 06790	ANTPI391-15			0	1999
Carebara brevipilosa	MACN-Bar-Ins-ct 06813	ANTPI414-15			0	1999
Carebara brevipilosa	MACN-Bar-Ins-ct 06831	ANTPI432-15			0	1999
Carebara brevipilosa	MACN-Bar-Ins-ct 06852	ANTPI453-15			0	1999
Carebara brevipilosa	MACN-Bar-Ins-ct 05000	ANTPI202-13			0	2009
Carebara brevipilosa	T5S4a2009PNIF12	ANTPI072-10			0	2009
Carebara brevipilosa	T5S4m2009PNIG04	ANTPI076-10			485[8n]	2009
Cephalotes eduarduli (A)	MACN-bar-ins-ct 06422	ANTI125-15	MF926016	BOLD:ACQ0707	658[0n]	2015
Cephalotes eduarduli (A)	MACN-bar-ins-ct 06967	ANTPI568-16	MF926034	BOLD:ACQ0707	658[0n]	2015
Cephalotes minutus	MACN-bar-ins-ct 06455	ANTI158-15	MF925879	BOLD:ACY4404	658[0n]	2015

Cephalotes pusillus	MACN-Bar-Ins-ct 05151	ANTPI259-13	MF925985	BOLD:ACM2165	658[0n]	2011
Cephalotes pusillus	MACN-Bar-Ins-ct 05153	ANTPI261-13	MF925867	BOLD:ACM2165	658[0n]	2011
Cephalotes pusillus	MACN-Bar-Ins-ct 05004	ANTPI275-13			0	2008
Crematogaster cl. obscurata (**)	MACN-bar-ins-ct 06954	ANTPI555-15			0	2015
Crematogaster corticicola	MACN-bar-ins-ct 06449	ANTI152-15	MF925802	BOLD:ACN2394	658[0n]	2015
Crematogaster corticicola	MACN-bar-ins-ct 06887	ANTPI488-15	MF925980	BOLD:ACN2394	658[0n]	2015
Crematogaster corticicola	MACN-bar-ins-ct 07019	ANTPI620-16	MF926013	BOLD:ACN2394	658[0n]	2016
Crematogaster corticicola	MACN-bar-ins-ct 07057	ANTPI658-16	MF925836	BOLD:ACN2394	658[0n]	2016
Crematogaster crinosa	MACN-bar-ins-ct 06442	ANTI145-15			0	2015
Crematogaster curvispinosa (*)	MACN-bar-ins-ct 06461	ANTI164-15	MF925901	BOLD:ACZ3040	658[0n]	2015
Crematogaster curvispinosa (*)	MACN-bar-ins-ct 06945	ANTPI546-15	MF925943	BOLD:ACZ3040	566[0n]	2015
Crematogaster erecta	MACN-Bar-Ins-ct 05157	ANTPI265-13			0	2008
Crematogaster lutzi (**)	MACN-Bar-Ins-ct 06838	ANTPI439-15	MF925978	BOLD:ACZ3057	545[3n]	1998
Crematogaster lutzi (**)	MACN-Bar-Ins-ct 06803	ANTPI404-15			0	1998
Crematogaster montezumia	MACN-bar-ins-ct 06427	ANTI130-15	MF925904	BOLD:ACZ3938	658[0n]	2015
Crematogaster montezumia	MACN-bar-ins-ct 07013	ANTPI614-16	MF925858	BOLD:ACZ3938	658[0n]	2015
Crematogaster montezumia	MACN-bar-ins-ct 07042	ANTPI643-16	MF925783	BOLD:ACZ3938	658[0n]	2015
Crematogaster nigropilosa	MACN-Bar-Ins-ct 02890	ANTPI107-12	MF925922	BOLD:ACC4305	658[0n]	2011
Crematogaster nigropilosa	MACN-Bar-Ins-ct 02896	ANTPI113-12	MF925905	BOLD:ACC4305	658[0n]	2011
Crematogaster nigropilosa	MACN-Bar-Ins-ct 02942	ANTPI159-12	MF925748	BOLD:ACC4305	658[0n]	2011
Crematogaster nigropilosa	MACN-Bar-Ins-ct 02953	ANTPI170-12	MF925813	BOLD:ACC4305	658[0n]	2011
Crematogaster nigropilosa	MACN-Bar-Ins-ct 06784	ANTPI385-15			0	1999
Crematogaster nigropilosa	T4P12008PNIH01	ANTPI085-10			0	2008
Crematogaster nigropilosa	MACN-Bar-Ins-ct 02924	ANTPI141-12			658[0n]	2011
Crematogaster PEH01	MACN-Bar-Ins-ct 06795	ANTPI396-15			0	1999
Crematogaster PEH01	MACN-Bar-Ins-ct 06830	ANTPI431-15			0	1999
Crematogaster PEH01	MACN-Bar-Ins-ct 06848	ANTPI449-15			0	1999
Crematogaster PEH01	MACN-Bar-Ins-ct 02888	ANTPI105-12			0	2011
Crematogaster PEH01	MACN-bar-ins-ct 06475	ANTI178-15			0	2011
Crematogaster PEH01	MACN-bar-ins-ct 06965	ANTPI566-15			0	2011
Crematogaster PEH02	MACN-Bar-Ins-ct 627	INSAR503-11	MF926025	BOLD:AAZ4161	658[0n]	2010
Crematogaster PEH02	MACN-Bar-Ins-ct 630	INSAR506-11	MF926040	BOLD:AAZ4161	658[0n]	2010
Cylindromyrmex brasiliensis (**)	MACN-bar-ins-ct 07036	ANTPI637-16	MF925940	BOLD:ADE2377	658[0n]	2015
Cyphomyrmex minutus	MACN-Bar-Ins-ct 06788	ANTPI389-15			0	1999
Cyphomyrmex minutus	MACN-Bar-Ins-ct 06792	ANTPI393-15			0	1999
Cyphomyrmex minutus	MACN-Bar-Ins-ct 06815	ANTPI416-15			0	1999
Cyphomyrmex minutus	MACN-Bar-Ins-ct 06826	ANTPI427-15			0	1999
Cyphomyrmex minutus	MACN-Bar-Ins-ct 06833	ANTPI434-15			0	1999

Cyphomyrmex minutus	MACN-bar-ins-ct 06939	ANTPI540-15			0	2015
Cyphomyrmex olitor	MACN-Bar-Ins-ct 06820	ANTPI421-15			0	1999
Cyphomyrmex rimosus	MACN-bar-ins-ct 06420	ANTI123-15	MF925959	BOLD:ACM5106	658[0n]	2015
Dinoponera australis	MACN-Bar-Ins-ct 00615	INSAR138-11	MF925772	BOLD:AAV4568	658[0n]	2010
Dinoponera australis	MACN-Bar-Ins-ct 02519	INSAR660-11	MF926022	BOLD:AAV4568	658[0n]	2011
Dinoponera australis	MACN-Bar-Ins-ct 02520	INSAR661-11	MF925799	BOLD:AAV4568	658[0n]	2011
Dinoponera australis	MACN-Bar-Ins-ct 02521	INSAR662-11	MF925847	BOLD:AAV4568	658[0n]	2011
Dinoponera australis	MACN-Bar-Ins-ct 02973	ANTPI190-12	MF925936	BOLD:ACC4124	658[0n]	2011
Dinoponera australis	MACN-bar-ins-ct 06394	ANTI097-15	MF925893	BOLD:ACC4124	658[0n]	2015
Dinoponera australis	MACN-bar-ins-ct 06405	ANTI108-15	MF926009	BOLD:ACC4124	658[0n]	2015
Dinoponera australis	T6P22008PNID05	ANTPI041-10			0	2008
Dinoponera australis	MACN-Bar-Ins-ct 05752	INSAR1416-15			0	2012
Discothyrea sexarticulata (**)	MACN-Bar-Ins-ct 06804	ANTPI405-15			0	1999
Discothyrea sexarticulata (**)	MACN-Bar-Ins-ct 06865	ANTPI466-15			0	1999
Discothyrea sexarticulata (**)	MACN-Bar-Ins-ct 06872	ANTPI473-15			0	1999
Dolichoderus bispinosus	MACN-Bar-Ins-ct 02959	ANTPI176-12	MF925995	BOLD:ACC4406	658[0n]	2008
Dolichoderus bispinosus	MACN-Bar-Ins-ct 05010	ANTPI270-13	MF925853	BOLD:ACC4406	658[0n]	2008
Dolichoderus bispinosus	MACN-Bar-Ins-ct 05008	ANTPI204-13	MF925886	BOLD:ACC4406	658[0n]	2011
Dolichoderus bispinosus	MACN-Bar-Ins-ct 05152	ANTPI260-13	MF925791	BOLD:ACC4406	658[0n]	2011
Dolichoderus germaini (**)	MACN-bar-ins-ct 06408	ANTI111-15	MF926049	BOLD:ACZ4117	658[0n]	2015
Dolichoderus germaini (**)	MACN-bar-ins-ct 06451	ANTI154-15	MF925890	BOLD:ACZ4117	658[0n]	2015
Dolichoderus lutosus (**)	MACN-bar-ins-ct 06894	ANTPI495-15	MF925909	BOLD:ACZ2733	658[0n]	2015
Dorymyrmex	MACN-Bar-Ins-ct 02580	INSAR751-11		BOLD:ABV2662	658[0n]	2011
Dorymyrmex brunneus	MACN-Bar-Ins-ct 02933	ANTPI150-12	MF925937	BOLD:ACC4210	658[0n]	2008
Dorymyrmex brunneus	MACN-Bar-Ins-ct 02955	ANTPI172-12	MF925849	BOLD:ACC4210	658[0n]	2008
Eciton vagans	MACN-Bar-Ins-ct 600	INSAR486-11	MF925824	BOLD:AAX9809	658[0n]	2010
Eciton vagans	MACN-Bar-Ins-ct 602	INSAR488-11	MF925793	BOLD:AAX9809	658[0n]	2010
Eciton vagans	MACN-Bar-Ins-ct 603	INSAR489-11	MF925920	BOLD:AAX9809	658[0n]	2010
Eciton vagans	MACN-Bar-Ins-ct 604	INSAR490-11	MF925790	BOLD:AAX9809	658[0n]	2010
Eciton vagans	MACN-bar-ins-ct 06452	ANTI155-15	MF925962	BOLD:AAX9809	658[0n]	2015
Eciton vagans	MACN-bar-ins-ct 06879	ANTPI480-15	MF926003	BOLD:AAX9809	649[0n]	2015
Eciton vagans	MACN-Bar-Ins-ct 601	INSAR487-11			0	2010
Ectatomma	MACN-Bar-Ins-ct 02555	INSAR729-11		BOLD:AAX9859	658[0n]	2011
Ectatomma	MACN-Bar-Ins-ct 02573	INSAR746-11		BOLD:AAX9859	658[0n]	2011
Ectatomma brunneum	MACN-bar-ins-ct 06446	ANTI149-15	MF925777	BOLD:ACX3889	658[0n]	2015
Ectatomma edentatum	T2W42008PNIB05	ANTPI017-10	MF925846	BOLD:AAX9859	658[0n]	2008
Ectatomma edentatum	MACN-Bar-Ins-ct 02949	ANTPI166-12	MF925782	BOLD:AAX9859	658[0n]	2011
Ectatomma edentatum	MACN-Bar-Ins-ct 05011	ANTPI205-13	MF925969	BOLD:AAX9859	658[1n]	2011

Ectatomma edentatum	MACN-Bar-Ins-ct 05123	ANTPI243-13	MF925829	BOLD:AAX9859	658[0n]	2011
Ectatomma edentatum	MACN-bar-ins-ct 06433	ANTI136-15	MF925817	BOLD:ACZ3750	658[0n]	2015
Ectatomma edentatum	MACN-Bar-Ins-ct 02931	ANTPI148-12			0	2008
Ectatomma edentatum	T3P52008PNIH06	ANTPI090-10			0	2008
Ectatomminae	MACN-bar-ins-ct 06957	ANTPI558-15		BOLD:ABV2806	658[0n]	2015
Formicinae	MACN-Bar-Ins-ct 02581	INSAR752-11		BOLD:ABV2661	658[0n]	2011
Gnamptogenys haenschi	MACN-bar-ins-ct 06413	ANTI116-15	MF925963	BOLD:ACZ4223	658[0n]	2015
Gnamptogenys hartmani (*)	MACN-bar-ins-ct 06924	ANTPI525-15			0	2015
Gnamptogenys PEH01	MACN-bar-ins-ct 06415	ANTI118-15			0	2015
Gnamptogenys PEH01	MACN-bar-ins-ct 06448	ANTI151-15			0	2015
Gnamptogenys striatula	MACN-Bar-Ins-ct 02944	ANTPI161-12	MF926038	BOLD:ACM2117	658[0n]	2011
Gnamptogenys striatula	MACN-Bar-Ins-ct 05014	ANTPI206-13	MF925896	BOLD:ACM2117	658[0n]	2011
Gnamptogenys striatula	MACN-Bar-Ins-ct 05124	ANTPI244-13	MF925914	BOLD:ACM2117	658[0n]	2011
Gnamptogenys striatula	MACN-Bar-Ins-ct 05149	ANTPI257-13	MF925758	BOLD:ACM2117	658[0n]	2011
Gnamptogenys striatula	MACN-Bar-Ins-ct 05016	ANTPI277-13			0	2008
Gnamptogenys striatula	T5P32008PNIH10	ANTPI094-10			0	2008
Gnamptogenys striatula	MACN-Bar-Ins-ct 02914	ANTPI131-12			0	2011
Gnamptogenys triangularis (*)	MACN-bar-ins-ct 06425	ANTI128-15	MF925778	BOLD:ACZ3490	658[0n]	2015
Gnamptogenys triangularis (*)	MACN-bar-ins-ct 06900	ANTPI501-15	MF926026	BOLD:ACZ3490	658[0n]	2015
Heteroponera dolo	MACN-Bar-Ins-ct 02946	ANTPI163-12	MF926014	BOLD:ACC4116	658[0n]	2011
Heteroponera dolo	MACN-Bar-Ins-ct 05020	ANTPI208-13	MF925951	BOLD:ACC4116	658[0n]	2011
Heteroponera dolo	MACN-bar-ins-ct 06438	ANTI141-15	MF925792	BOLD:ACC4116	649[1n]	2015
Heteroponera dolo	MACN-bar-ins-ct 06472	ANTI175-15	MF926008	BOLD:ACC4116	658[0n]	2015
Heteroponera dolo	MACN-Bar-Ins-ct 05017	ANTPI207-13			0	2011
Heteroponera mayri	MACN-Bar-Ins-ct 06824	ANTPI425-15	MF926021	BOLD:ACZ3308	658[0n]	1998
Heteroponera mayri	MACN-Bar-Ins-ct 06857	ANTPI458-15			0	1998
Heteroponera mayri	MACN-Bar-Ins-ct 06867	ANTPI468-15			0	1998
Heteroponera mayri	MACN-Bar-Ins-ct 06812	ANTPI413-15			0	1999
Heteroponera microps	T5S10m2009PNIE12	ANTPI060-10	MF925787	BOLD:AAV7129	658[0n]	2009
Heteroponera microps	T6S6a2009PNIF08	ANTPI068-10	MF925965	BOLD:AAV7129	658[0n]	2009
Hylomyrma balzani	MACN-bar-ins-ct 06926	ANTPI527-15	MF925822	BOLD:ACZ3727	658[0n]	2015
Hylomyrma balzani	MACN-Bar-Ins-ct 06791	ANTPI392-15			0	1999
Hylomyrma balzani	MACN-Bar-Ins-ct 05095	ANTPI274-13			0	2008
Hylomyrma PEH01	MACN-Bar-Ins-ct 06841	ANTPI442-15			0	1999
Hylomyrma reitteri	MACN-Bar-Ins-ct 06868	ANTPI469-15			0	1998
Hylomyrma reitteri	MACN-Bar-Ins-ct 06799	ANTPI400-15			0	1999
Hylomyrma reitteri	MACN-Bar-Ins-ct 06818	ANTPI419-15			0	1999
Hypoponera	MACN-bar-ins-ct 06878	ANTPI479-15		BOLD:AAU1873	658[0n]	2005

Hypoponera	MACN-bar-ins-ct 06904	ANTPI505-15		BOLD:ACM2976	658[0n]	2003
Hypoponera cf. agilis (**)	MACN-bar-ins-ct 06897	ANTPI498-15	MF926020	BOLD:ACZ2699	651[0n]	2005
Hypoponera cf. agilis (**)	MACN-bar-ins-ct 06929	ANTPI530-15			0	2005
Hypoponera cf. opacior	MACN-bar-ins-ct 06895	ANTPI496-15	MF926018	BOLD:ACM2976	658[0n]	2008
Hypoponera cf. opacior	MACN-Bar-Ins-ct 05140	ANTPI249-13	MF925934	BOLD:ACM2976	658[0n]	2011
Hypoponera cf. opacior	MACN-bar-ins-ct 06888	ANTPI489-15			0	2003
Hypoponera cf. opacior	MACN-bar-ins-ct 06901	ANTPI502-15			0	2005
Hypoponera distinguenda	MACN-Bar-Ins-ct 05026	ANTPI210-13	MF925885	BOLD:ACM2219	658[0n]	2011
Hypoponera distinguenda	MACN-bar-ins-ct 06441	ANTI144-15	MF926019	BOLD:ACM2219	658[0n]	2015
Hypoponera distinguenda	MACN-Bar-Ins-ct 06844	ANTPI445-15			0	1999
Hypoponera distinguenda	T1W32008PNID12	ANTPI048-10			0	2008
Hypoponera distinguenda	MACN-Bar-Ins-ct 05028	ANTPI280-13			0	2015
Hypoponera foreli	T6W32008PNIF06	ANTPI066-10	MF925970	BOLD:AAU1875	658[0n]	2008
Hypoponera foreli	MACN-bar-ins-ct 06941	ANTPI542-15	MF925755	BOLD:ACZ3327	658[0n]	2011
Hypoponera foreli	MACN-bar-ins-ct 06453	ANTI156-15	MF925788	BOLD:ACZ3327	658[0n]	2015
Hypoponera foreli	MACN-bar-ins-ct 06456	ANTI159-15	MF925751	BOLD:ACZ3327	658[0n]	2015
Hypoponera foreli	MACN-bar-ins-ct 07053	ANTPI654-16	MF925844	BOLD:ACZ3327	658[0n]	2016
Hypoponera foreli	MACN-Bar-Ins-ct 06819	ANTPI420-15			0	1998
Hypoponera opaciceps	MACN-bar-ins-ct 06923	ANTPI524-15			0	2003
Hypoponera parva (**)	MACN-bar-ins-ct 06457	ANTI160-15	MF925820	BOLD:ACZ4236	658[0n]	2015
Hypoponera parva (**)	MACN-bar-ins-ct 06481	ANTI184-15	MF926011	BOLD:ACZ4236	658[0n]	2015
Hypoponera parva (**)	MACN-Bar-Ins-ct 06823	ANTPI424-15			0	1999
Hypoponera parva (**)	MACN-Bar-Ins-ct 06850	ANTPI451-15			0	1999
Hypoponera parva (**)	MACN-Bar-Ins-ct 06859	ANTPI460-15			0	1999
Hypoponera parva (**)	MACN-bar-ins-ct 06935	ANTPI536-15			0	2005
Hypoponera parva (**)	MACN-bar-ins-ct 06944	ANTPI545-15			0	2005
Hypoponera PEH01	MACN-bar-ins-ct 06450	ANTI153-15	MF925746	BOLD:ACZ4369	624[0n]	2015
Hypoponera PEH02	MACN-bar-ins-ct 06434	ANTI137-15	MF925808	BOLD:ACN1914	658[0n]	2015
Hypoponera PEH02	MACN-bar-ins-ct 06439	ANTI142-15	MF925801	BOLD:ACN1914	658[0n]	2015
Hypoponera PEH02	MACN-bar-ins-ct 06444	ANTI147-15	MF925789	BOLD:ACN1914	658[0n]	2015
Hypoponera PEH02	MACN-bar-ins-ct 06447	ANTI150-15	MF925923	BOLD:ACN1914	658[0n]	2015
Hypoponera PEH02	MACN-Bar-Ins-ct 06870	ANTPI471-15			0	1999
Hypoponera schmalzi	MACN-bar-ins-ct 06885	ANTPI486-15			0	2003
Hypoponera schmalzi	MACN-bar-ins-ct 06883	ANTPI484-15			0	2005
Hypoponera trigona	T3W5A2008PNIB06	ANTPI018-10	MF925935	BOLD:AAU1873	658[1n]	2008
Hypoponera trigona	MACN-bar-ins-ct 06428	ANTI131-15	MF926047	BOLD:AAU1873	632[0n]	2015
Hypoponera trigona	MACN-bar-ins-ct 06430	ANTI133-15	MF925825	BOLD:AAU1873	658[0n]	2015
Hypoponera trigona	MACN-Bar-Ins-ct 06828	ANTPI429-15	MF925811	BOLD:ACZ3162	658[0n]	1999

Hypoponera trigona	MACN-bar-ins-ct 06432	ANTI135-15	MF925902	BOLD:ACZ4059	658[0n]	2015
Hypoponera trigona	MACN-bar-ins-ct 06938	ANTPI539-15			0	2003
Hypoponera trigona	MACN-bar-ins-ct 06951	ANTPI552-15			0	2003
Hypoponera trigona	T3W52008PNIB08	ANTPI020-10			0	2008
Hypoponera trigona	T4W12008PNIH08	ANTPI092-10			0	2008
Labidus	MACN-Bar-Ins-ct 00605	INSAR129-11			0	2010
Labidus coecus	T3S16m2009PNIC06	ANTPI030-10	MF925821	BOLD:AAE5557	658[0n]	2009
Labidus coecus	T1S6a2009PNID03	ANTPI039-10	MF925887	BOLD:AAU1427	658[0n]	2009
Labidus coecus	T1S8a2009PNIC02	ANTPI026-10	MF925839	BOLD:AAU1427	658[0n]	2009
Labidus coecus	T3S16m2009PNIF10	ANTPI070-10	MF925908	BOLD:AAU1427	658[0n]	2009
Labidus coecus	T5S12A2009PNIG01	ANTPI073-10	MF925992	BOLD:AAU1427	658[0n]	2009
Labidus coecus	T5S4a2009PNIG05	ANTPI077-10	MF926041	BOLD:AAU1427	658[0n]	2009
Labidus coecus	MACN-bar-ins-ct 06400	ANTI103-15	MF925899	BOLD:AAU1427	658[0n]	2015
Labidus coecus	MACN-bar-ins-ct 06874	ANTPI475-15	MF926035	BOLD:AAU1427	658[0n]	2015
Labidus coecus	MACN-Bar-Ins-ct 05025	ANTPI209-13			0	2009
Labidus PEH01	MACN-Bar-Ins-ct 02494	INSAR635-11			421[0n]	2011
Labidus praedator	MACN-Bar-Ins-ct 02493	INSAR634-11	MF925979	BOLD:ABV2652	658[0n]	2011
Labidus praedator	T3P42008PNIE10	ANTPI058-10			0	2008
Labidus praedator	MACN-bar-ins-ct 06397	ANTI100-15			0	2015
Lachnomyrmex plaumanni	MACN-Bar-Ins-ct 06789	ANTPI390-15			0	1999
Lachnomyrmex plaumanni	MACN-Bar-Ins-ct 06851	ANTPI452-15			0	1999
Leptogenys iheringi(**)	MACN-bar-ins-ct 07007	ANTPI608-16	MF925888	BOLD:ADE4308	658[0n]	2016
Linepithema humile	MACN-Bar-Ins-ct 06778	ANTPI379-15			470[0n]	1999
Linepithema humile	MACN-Bar-Ins-ct 06793	ANTPI394-15			0	1999
Linepithema humile	MACN-Bar-Ins-ct 06825	ANTPI426-15			0	1999
Linepithema iniquum	MACN-bar-ins-ct 06928	ANTPI529-15	MF925816	BOLD:ACZ3624	649[0n]	2011
Linepithema iniquum	MACN-Bar-Ins-ct 06783	ANTPI384-15			0	1999
Linepithema iniquum	MACN-Bar-Ins-ct 06797	ANTPI398-15			0	1999
Linepithema micans	MACN-Bar-Ins-ct 02945	ANTPI162-12	MF925743	BOLD:AAD2894	658[0n]	2011
Linepithema micans	MACN-Bar-Ins-ct 02954	ANTPI171-12	MF925766	BOLD:AAD2894	658[0n]	2011
Linepithema micans	MACN-Bar-Ins-ct 02969	ANTPI186-12	MF926029	BOLD:AAD2894	658[0n]	2011
Linepithema micans	MACN-bar-ins-ct 06445	ANTI148-15	MF925981	BOLD:AAD2894	658[0n]	2015
Linepithema micans	MACN-Bar-Ins-ct 05040	ANTPI266-13			0	2011
Linepithema pulex	MACN-Bar-Ins-ct 05035	ANTPI212-13	MF925955	BOLD:AAX5108	658[0n]	2011
Linepithema pulex	MACN-Bar-Ins-ct 06811	ANTPI412-15			0	1999
Linepithema pulex	MACN-Bar-Ins-ct 06835	ANTPI436-15			0	1999
Linepithema pulex	MACN-Bar-Ins-ct 06843	ANTPI444-15			0	1999
Megalomyrmex brandaoi (**)	MACN-Bar-Ins-ct 06840	ANTPI441-15	MF925994	BOLD:ACZ3268	658[0n]	1998
Megalomyrmex megadrifti (*)	T3W52008PNIG09	ANTPI081-10	MF925997	BOLD:ADB2786	567[0n]	2008

Megalomyrmex megadrifti (*)	MACN-Bar-Ins-ct 06794	ANTPI395-15			0	1999
Megalomyrmex megadrifti (*)	MACN-Bar-Ins-ct 06862	ANTPI463-15			0	1999
Megalomyrmex megadrifti (*)	MACN-bar-ins-ct 06906	ANTPI507-15			0	2015
Megalomyrmex miri	MACN-Bar-Ins-ct 06817	ANTPI418-15	MF925983	BOLD:ACZ2861	658[0n]	1999
Megalomyrmex miri	MACN-Bar-Ins-ct 06834	ANTPI435-15			0	1999
Mycetarotes parallelus	MACN-bar-ins-ct 06877	ANTPI478-15	MF925757	BOLD:ACZ2682	658[0n]	2015
Mycocepurus smithii	MACN-Bar-Ins-ct 02901	ANTPI118-12	MF926032	BOLD:ACC4194	658[0n]	2011
Mycocepurus smithii	MACN-Bar-Ins-ct 05045	ANTPI214-13	MF925744	BOLD:ACC4194	658[0n]	2011
Mycocepurus smithii	MACN-bar-ins-ct 06921	ANTPI522-15	MF926042	BOLD:ACC4194	658[0n]	2015
Mycocepurus smithii	MACN-bar-ins-ct 06911	ANTPI512-15			0	2015
Myrmelachista catharinae (**)	MACN-bar-ins-ct 06931	ANTPI532-15	MF925752	BOLD:ACZ2735	658[0n]	2015
Myrmelachista catharinae (**)	MACN-bar-ins-ct 06946	ANTPI547-15	MF926004	BOLD:ACZ2735	658[0n]	2015
Myrmelachista nodigera	MACN-bar-ins-ct 06932	ANTPI533-15	MF925911	BOLD:ACZ2726	658[0n]	2005
Myrmelachista nodigera	MACN-bar-ins-ct 06913	ANTPI514-15			0	2005
Myrmicocrypta foreli	MACN-Bar-Ins-ct 06854	ANTPI455-15			0	1999
Myrmicocrypta foreli	MACN-Bar-Ins-ct 02935	ANTPI152-12			0	2011
Neivamyrmex	MACN-bar-ins-ct 06470	ANTI173-15		BOLD:ACZ3964	658[0n]	2015
Neivamyrmex angustinodis (A)	MACN-Bar-Ins-ct 06808	ANTPI409-15	MF925880	BOLD:ACZ3084	658[0n]	1999
Neivamyrmex angustinodis (A)	MACN-Bar-Ins-ct 06780	ANTPI381-15			0	1999
Neivamyrmex punctaticeps	MACN-Bar-Ins-ct 05034	ANTPI211-13	MF926006	BOLD:ACM2493	658[0n]	2011
Neivamyrmex punctaticeps	MACN-Bar-Ins-ct 05038	ANTPI213-13	MF925828	BOLD:ACM2493	658[0n]	2011
Neivamyrmex punctaticeps	MACN-bar-ins-ct 06419	ANTI122-15	MF925840	BOLD:ACM2493	658[0n]	2015
Neivamyrmex punctaticeps	MACN-bar-ins-ct 06436	ANTI139-15	MF925857	BOLD:ACM2493	658[0n]	2015
Neivamyrmex punctaticeps	MACN-bar-ins-ct 06902	ANTPI503-15	MF925774	BOLD:ACM2493	658[0n]	2015
Neoponera	MACN-Bar-Ins-ct 02572	INSAR745-11		BOLD:ABV2663	658[0n]	2011
Neoponera	MACN-Bar-Ins-ct 02564	INSAR738-11		BOLD:ABV2684	658[0n]	2011
Neoponera bactronica (**)	MACN-bar-ins-ct 06396	ANTI099-15	MF925845	BOLD:AAW5111	658[0n]	2015
Neoponera crenata	MACN-Bar-Ins-ct 06809	ANTPI410-15	MF925832	BOLD:ABV2684	658[0n]	1999
Neoponera crenata	MACN-bar-ins-ct 06398	ANTI101-15	MF925804	BOLD:ACX7584	658[0n]	2015
Neoponera crenata	MACN-bar-ins-ct 06416	ANTI119-15	MF925895	BOLD:ACX7584	658[0n]	2015
Neoponera crenata	MACN-Bar-Ins-ct 06779	ANTPI380-15			0	1999
Neoponera crenata	MACN-bar-ins-ct 06891	ANTPI492-15			0	2005
Neoponera crenata	MACN-bar-ins-ct 06943	ANTPI544-15			0	2005
Neoponera curvinodis (**)	MACN-bar-ins-ct 06407	ANTI110-15	MF925818	BOLD:AAW5111	658[0n]	2015
Neoponera fiebrigi (A)	MACN-bar-ins-ct 06401	ANTI104-15	MF925945	BOLD:ACN1772	658[0n]	2015
Neoponera moesta	MACN-Bar-Ins-ct 05145	ANTPI254-13	MF925968	BOLD:ACM2898	658[0n]	2011
Neoponera moesta	MACN-bar-ins-ct 06414	ANTI117-15	MF925884	BOLD:ACM2898	658[0n]	2015
Neoponera obscuricornis (*)	MACN-bar-ins-ct 07017	ANTPI618-16	MF925964	BOLD:AAZ3349	613[0n]	2015

Neoponera obscuricornis (*)	MACN-bar-ins-ct 07038	ANTPI639-16	MF926036	BOLD:AAZ3349	658[0n]	2015
Neoponera obscuricornis (*)	MACN-bar-ins-ct 07054	ANTPI655-16	MF925794	BOLD:AAZ3349	619[0n]	2016
Neoponera obscuricornis (*)	MACN-bar-ins-ct 06435	ANTI138-15			151[0n]	2015
Neoponera obscuricornis (*)	MACN-bar-ins-ct 06440	ANTI143-15			144[1n]	2015
Neoponera verenae (**)	MACN-bar-ins-ct 07061	ANTPI662-16	MF925961	BOLD:ACN0470	658[0n]	2011
Neoponera villosa	MACN-Bar-Ins-ct 05121	ANTPI242-13	MF925837	BOLD:AAZ7290	658[0n]	2011
Neoponera villosa	MACN-Bar-Ins-ct 05138	ANTPI247-13	MF925948	BOLD:AAZ7290	658[0n]	2011
Neoponera villosa	MACN-bar-ins-ct 06404	ANTI107-15	MF925742	BOLD:AAZ7290	658[0n]	2015
Nesomyrmex asper	MACN-bar-ins-ct 06876	ANTPI477-15	MF925848	BOLD:ACZ2681	658[0n]	2015
Nesomyrmex asper	MACN-bar-ins-ct 06892	ANTPI493-15	MF926039	BOLD:ACZ2681	658[0n]	2015
Nesomyrmex asper	MACN-bar-ins-ct 06934	ANTPI535-15	MF926031	BOLD:ACZ2681	658[0n]	2015
Nesomyrmex tonsuratus (**)	MACN-bar-ins-ct 06909	ANTPI510-15	MF925803	BOLD:ACZ2734	658[0n]	2015
Nylanderia fulva	MACN-bar-ins-ct 06465	ANTI168-15	MF925786	BOLD:ACZ3937	658[0n]	2015
Nylanderia fulva	MACN-Bar-Ins-ct 05046	ANTPI215-13			0	2011
Nylanderia fulva	MACN-Bar-Ins-ct 05050	ANTPI218-13			0	2011
Nylanderia fulva	MACN-Bar-Ins-ct 05060	ANTPI221-13			0	2011
Nylanderia fulva	MACN-bar-ins-ct 06880	ANTPI481-15			0	2011
Nylanderia fulva	MACN-bar-ins-ct 06927	ANTPI528-15			0	2011
Nylanderia fulva	MACN-bar-ins-ct 06942	ANTPI543-15			0	2011
Nylanderia PEH01	MACN-Bar-Ins-ct 05047	ANTPI216-13	MF925807	BOLD:ACM2582	658[0n]	2011
Nylanderia PEH01	MACN-Bar-Ins-ct 06810	ANTPI411-15			0	1999
Nylanderia PEH01	MACN-Bar-Ins-ct 05052	ANTPI267-13			0	2008
Nylanderia PEH01	MACN-Bar-Ins-ct 05062	ANTPI223-13			0	2011
Nylanderia PEH02	MACN-Bar-Ins-ct 05049	ANTPI217-13	MF925872	BOLD:ACM2581	658[0n]	2011
Nylanderia PEH02	MACN-bar-ins-ct 06485	ANTI188-15	MF925931	BOLD:ACM2581	658[0n]	2015
Nylanderia PEH03	T1S12m2009PNIC04	ANTPI028-10			491[8n]	2009
Octostruma balzani	MACN-Bar-Ins-ct 06847	ANTPI448-15			0	1999
Octostruma balzani	MACN-Bar-Ins-ct 06866	ANTPI467-15			0	1999
Octostruma balzani	T1W12008PNID08	ANTPI044-10			0	2008
Octostruma balzani	MACN-bar-ins-ct 06947	ANTPI548-15			0	2015
Octostruma iheringi	T6S6a2009PNIG07	ANTPI079-10	MF925942	BOLD:AAX0010	658[0n]	2009
Octostruma iheringi	T6S8a2009PNIE09	ANTPI057-10			0	2009
Octostruma PEH01	MACN-Bar-Ins-ct 06853	ANTPI454-15	MF926023	BOLD:ACZ2651	658[0n]	1998
Octostruma PEH01	MACN-Bar-Ins-ct 06827	ANTPI428-15			0	1998
Octostruma PEH01	MACN-Bar-Ins-ct 06800	ANTPI401-15			0	1999
Odontomachus chelifer	T6P52008PNID10	ANTPI046-10	MF925976	BOLD:AAV3356	658[0n]	2008
Odontomachus chelifer	MACN-Bar-Ins-ct 05137	ANTPI246-13	MF925881	BOLD:AAV3356	658[0n]	2011
Odontomachus chelifer	MACN-Bar-Ins-ct 05141	ANTPI250-13	MF925876	BOLD:AAV3356	658[0n]	2011
Odontomachus chelifer	MACN-bar-ins-ct 06399	ANTI102-15	MF926046	BOLD:AAV3356	658[0n]	2015

Odontomachus chelifer	MACN-bar-ins-ct 06417	ANTI120-15	MF925784	BOLD:AAV3356	658[0n]	2015
Odontomachus meinerti	T2W52008PNIH03	ANTPI087-10	MF925903	BOLD:AAX0128	658[0n]	2008
Odontomachus meinerti	MACN-Bar-Ins-ct 05059	ANTPI220-13	MF925996	BOLD:AAX0128	658[0n]	2011
Odontomachus meinerti	MACN-Bar-Ins-ct 05061	ANTPI222-13	MF925991	BOLD:AAX0128	658[0n]	2011
Odontomachus meinerti	MACN-bar-ins-ct 06418	ANTI121-15	MF926012	BOLD:AAX0128	658[0n]	2015
Odontomachus meinerti	MACN-bar-ins-ct 06421	ANTI124-15	MF925878	BOLD:AAX0128	658[0n]	2015
Odontomachus meinerti	MACN-bar-ins-ct 06423	ANTI126-15	MF925910	BOLD:AAX0128	658[0n]	2015
Odontomachus meinerti	MACN-bar-ins-ct 07018	ANTPI619-16	MF925779	BOLD:AAX0128	658[0n]	2016
Odontomachus meinerti	MACN-bar-ins-ct 07060	ANTPI661-16	MF926002	BOLD:AAX0128	658[0n]	2016
Odontomachus meinerti	MACN-Bar-Ins-ct 05067	ANTPI227-13	MF926045	BOLD:ACM2983	658[0n]	2008
Odontomachus meinerti	MACN-bar-ins-ct 06402	ANTI105-15	MF925977	BOLD:ACM2983	658[0n]	2015
Odontomachus meinerti	MACN-Bar-Ins-ct 05071	ANTPI269-13			0	2008
Odontomachus meinerti	MACN-Bar-Ins-ct 05065	ANTPI225-13			0	2009
Pachycondyla constricticeps	MACN-bar-ins-ct 06409	ANTI112-15			0	2008
Pachycondyla harpax	T3S6m2009PNIC09	ANTPI033-10	MF925954	BOLD:AAU1874	658[0n]	2009
Pachycondyla PEH01	MACN-bar-ins-ct 06411	ANTI114-15	MF925894	BOLD:ACZ4044	658[0n]	2015
Pachycondyla striata	MACN-Bar-Ins-ct 02937	ANTPI154-12	MF926017	BOLD:AAU1872	658[0n]	2008
Pachycondyla striata	MACN-Bar-Ins-ct 05051	ANTPI219-13	MF925835	BOLD:AAU1872	658[0n]	2008
Pachycondyla striata	T1P12008PNIE02	ANTPI050-10	MF925916	BOLD:AAU1872	658[1n]	2008
Pachycondyla striata	T3P42008PNIH07	ANTPI091-10	MF925918	BOLD:AAU1872	658[0n]	2008
Pachycondyla striata	MACN-Bar-Ins-ct 05729	INSAR1393-15			0	2014
Pachycondyla striata	MACN-Bar-Ins-ct 05735	INSAR1399-15			0	2014
Pheidole	MACN-bar-ins-ct 06948	ANTPI549-15		BOLD:ACM2643	634[0n]	2011
Pheidole	MACN-Bar-Ins-ct 05119	ANTPI278-13			0	2008
Pheidole	T1W12008PNIB09	ANTPI021-10			0	2008
Pheidole	T1W12008PNIB11	ANTPI023-10			0	2008
Pheidole	T3W52008PNIF02	ANTPI062-10			0	2008
Pheidole	T3W52008PNIH11	ANTPI095-10			0	2008
Pheidole	M22009PNIA10	ANTPI010-10			0	2009
Pheidole	T1S16M2009PNIA03	ANTPI003-10			591[2n]	2009
Pheidole	MACN-Bar-Ins-ct 02889	ANTPI106-12			0	2011
Pheidole	MACN-Bar-Ins-ct 02966	ANTPI183-12			0	2011
Pheidole	MACN-Bar-Ins-ct 05116	ANTPI241-13			0	2011
Pheidole alpinensis (*)	MACN-Bar-Ins-ct 02899	ANTPI116-12	MF925760	BOLD:ACC4235	658[0n]	2011
Pheidole alpinensis (*)	MACN-Bar-Ins-ct 02913	ANTPI130-12			0	2011
Pheidole cl. dinophila (**)	MACN-bar-ins-ct 06873	ANTPI474-15			0	2005
Pheidole cl. dinophila (**)	MACN-bar-ins-ct 06886	ANTPI487-15			0	2005
Pheidole cl. dinophila (**)	MACN-bar-ins-ct 06896	ANTPI497-15			0	2008
Pheidole cl. dinophila (**)	MACN-bar-ins-ct 06920	ANTPI521-15			0	2008

Pheidole fimbriata	T4S18A2009PNIA11	ANTPI011-10	MF925883	BOLD:AAU2524	658[0n]	2009
Pheidole fimbriata	T5S4m2009PNIC01	ANTPI025-10	MF925740	BOLD:AAU2524	658[0n]	2009
Pheidole fimbriata	MACN-Bar-Ins-ct 05066	ANTPI226-13	MF925932	BOLD:ACM2608	658[0n]	2011
Pheidole gertrudae	MACN-Bar-Ins-ct 05104	ANTPI282-13			0	2011
Pheidole gertrudae	MACN-Bar-Ins-ct 05110	ANTPI237-13			0	2011
Pheidole mosenopsis	MACN-bar-ins-ct 06898	ANTPI499-15	MF925882	BOLD:AAU2525	658[0n]	2005
Pheidole mosenopsis	T2S4M2009PNIA05	ANTPI005-10	MF925796	BOLD:AAU2525	658[0n]	2009
Pheidole mosenopsis	MACN-bar-ins-ct 06875	ANTPI476-15			0	2005
Pheidole mosenopsis	MACN-bar-ins-ct 06890	ANTPI491-15			0	2005
Pheidole mosenopsis	MACN-bar-ins-ct 06893	ANTPI494-15			0	2005
Pheidole mosenopsis	MACN-bar-ins-ct 06919	ANTPI520-15			168[0n]	2005
Pheidole mosenopsis	T1W12008PNIB04	ANTPI016-10			0	2008
Pheidole obscurithorax	MACN-bar-ins-ct 06956	ANTPI557-15	MF926030	BOLD:ACZ4199	658[0n]	2011
Pheidole PEH01	MACN-Bar-Ins-ct 02883	ANTPI100-12	MF926010	BOLD:ACC4288	658[0n]	2011
Pheidole PEH01	MACN-Bar-Ins-ct 02891	ANTPI108-12	MF925873	BOLD:ACC4288	658[0n]	2011
Pheidole PEH01	MACN-Bar-Ins-ct 02909	ANTPI126-12	MF925928	BOLD:ACC4288	658[0n]	2011
Pheidole PEH01	MACN-Bar-Ins-ct 02923	ANTPI140-12	MF926005	BOLD:ACC4288	658[0n]	2011
Pheidole PEH01	MACN-Bar-Ins-ct 02938	ANTPI155-12	MF925850	BOLD:ACC4288	658[0n]	2011
Pheidole PEH01	MACN-Bar-Ins-ct 02941	ANTPI158-12	MF926033	BOLD:ACC4288	658[0n]	2011
Pheidole PEH01	MACN-Bar-Ins-ct 02956	ANTPI173-12	MF925938	BOLD:ACC4288	658[0n]	2011
Pheidole PEH02	T1S12A2009PNIA08	ANTPI008-10	MF925953	BOLD:AAU4344	658[0n]	2009
Pheidole PEH02	T5S4m2009PNIC03	ANTPI027-10	MF925764	BOLD:AAU4344	658[0n]	2009
Pheidole PEH02	T3S16a2008PNIC12	ANTPI036-10	MF926024	BOLD:AAU4345	658[0n]	2008
Pheidole PEH02	MACN-Bar-Ins-ct 02893	ANTPI110-12	MF926043	BOLD:AAU4345	658[0n]	2011
Pheidole PEH02	MACN-Bar-Ins-ct 02943	ANTPI160-12	MF925967	BOLD:AAU4345	658[0n]	2011
Pheidole PEH02	MACN-Bar-Ins-ct 02965	ANTPI182-12	MF925798	BOLD:AAU4345	658[0n]	2011
Pheidole PEH02	MACN-Bar-Ins-ct 02971	ANTPI188-12	MF925841	BOLD:AAU4345	658[0n]	2011
Pheidole PEH02	T3S16m2009PNIC05	ANTPI029-10			0	2009
Pheidole PEH02	MACN-Bar-Ins-ct 02879	ANTPI096-12			0	2011
Pheidole PEH02	MACN-Bar-Ins-ct 02928	ANTPI145-12	XXXX		0	2011
Pheidole PEH02	MACN-Bar-Ins-ct 02952	ANTPI169-12			658[0n]	2011
Pheidole PEH03	MACN-Bar-Ins-ct 02887	ANTPI104-12	MF925913	BOLD:ACC4180	658[0n]	2011
Pheidole PEH03	MACN-Bar-Ins-ct 02905	ANTPI122-12	MF925907	BOLD:ACC4180	658[0n]	2011
Pheidole PEH03	MACN-Bar-Ins-ct 05080	ANTPI229-13	MF925809	BOLD:ACC4180	658[0n]	2011
Pheidole PEH04	MACN-Bar-Ins-ct 02925	ANTPI142-12	MF925861	BOLD:ACC4354	658[0n]	2011
Pheidole PEH04	MACN-Bar-Ins-ct 02930	ANTPI147-12	MF925925	BOLD:ACC4354	658[0n]	2011
Pheidole PEH04	MACN-Bar-Ins-ct 05112	ANTPI238-13	MF925949	BOLD:ACC4354	658[0n]	2011
Pheidole PEH04	MACN-Bar-Ins-ct 05154	ANTPI262-13	MF925957	BOLD:ACC4354	658[0n]	2011

Pheidole PEH05	MACN-Bar-Ins-ct 731	INSAR540-11	MF925984	BOLD:AAZ4402	658[0n]	2010
Pheidole PEH06	MACN-Bar-Ins-ct 02962	ANTPI179-12	MF925860	BOLD:AAP9302	658[0n]	2011
Pheidole PEH09	MACN-Bar-Ins-ct 02907	ANTPI124-12	MF925823	BOLD:AAL5917	658[0n]	2011
Pheidole PEH09	MACN-Bar-Ins-ct 02921	ANTPI138-12	MF925863	BOLD:AAL5917	658[0n]	2011
Pheidole PEH10	T1S10M2009PNIA01	ANTPI001-10			0	2009
Pheidole PEH11	MACN-Bar-Ins-ct 02902	ANTPI119-12			0	2011
Pheidole PEH12	MACN-bar-ins-ct 06881	ANTPI482-15			0	2005
Pheidole PEH12	MACN-bar-ins-ct 06966	ANTPI567-15			0	2005
Pheidole PEH12	MACN-Bar-Ins-ct 02932	ANTPI149-12			0	2011
Pheidole PEH12	MACN-Bar-Ins-ct 02960	ANTPI177-12			0	2011
Pheidole rudigenis	MACN-bar-ins-ct 06916	ANTPI517-15			0	2003
Pheidole rugatula	MACN-Bar-Ins-ct 02885	ANTPI102-12	MF925830	BOLD:ACC4289	658[0n]	2011
Pheidole rugatula	MACN-Bar-Ins-ct 02934	ANTPI151-12	MF925852	BOLD:ACC4289	658[0n]	2011
Pheidole rugatula	MACN-Bar-Ins-ct 05070	ANTPI228-13	MF925775	BOLD:ACC4289	658[0n]	2011
Pheidole rugatula	MACN-Bar-Ins-ct 05122	ANTPI276-13	MF925859	BOLD:ACC4289	658[0n]	2011
Pheidole sigillata (**)	MACN-Bar-Ins-ct 02897	ANTPI114-12	MF925769	BOLD:ACC4420	658[0n]	2011
Pheidole sigillata (**)	MACN-Bar-Ins-ct 02917	ANTPI134-12	MF925754	BOLD:ACC4420	658[0n]	2011
Pheidole sigillata (**)	MACN-Bar-Ins-ct 02958	ANTPI175-12	MF925875	BOLD:ACC4420	658[0n]	2011
Pheidole sigillata (**)	MACN-Bar-Ins-ct 05081	ANTPI230-13	MF925842	BOLD:ACC4420	658[0n]	2011
Pheidole sigillata (**)	MACN-Bar-Ins-ct 05088	ANTPI233-13	MF926027	BOLD:ACC4420	658[0n]	2011
Pheidole sigillata (**)	T2S2A2009PNIA04	ANTPI004-10			0	2009
Pheidole sigillata (**)	MACN-Bar-Ins-ct 02936	ANTPI153-12			0	2011
Pheidole subarmata	T1S8M2009PNIA02	ANTPI002-10	MF925919	BOLD:AAU4342	658[2n]	2009
Pheidole subarmata	T3S10A2009PNIG12	ANTPI084-10	MF926015	BOLD:AAU4342	658[0n]	2009
Pheidole subarmata	T3S14M2009PNIA06	ANTPI006-10	MF925773	BOLD:AAU4342	658[0n]	2009
Pheidole subarmata	MACN-Bar-Ins-ct 02939	ANTPI156-12	MF925999	BOLD:AAU4342	658[0n]	2011
Pheidole subarmata	MACN-Bar-Ins-ct 02963	ANTPI180-12	MF925930	BOLD:AAU4342	649[0n]	2011
Pheidole subarmata	T3S2A2009PNIA07	ANTPI007-10	MF925781	BOLD:ACM2643	658[0n]	2009
Pheidole subarmata	T3S2a2009PNIE01	ANTPI049-10	MF925741	BOLD:ACM2643	658[0n]	2009
Pheidole subarmata	T3S4a2009PNIC07	ANTPI031-10	MF925958	BOLD:ACM2643	658[0n]	2009
Pheidole subarmata	T4S16A2009PNIH04	ANTPI088-10	MF925870	BOLD:ACM2643	658[0n]	2009
Pheidole subarmata	T4S4M2009PNIA09	ANTPI009-10	MF925874	BOLD:ACM2643	658[0n]	2009
Pheidole subarmata	MACN-Bar-Ins-ct 02881	ANTPI098-12	MF925974	BOLD:ACM2643	658[0n]	2011
Pheidole subarmata	MACN-Bar-Ins-ct 02895	ANTPI112-12	MF925834	BOLD:ACM2643	658[0n]	2011
Pheidole subarmata	MACN-Bar-Ins-ct 02903	ANTPI120-12	MF925956	BOLD:ACM2643	658[0n]	2011
Pheidole subarmata	MACN-Bar-Ins-ct 05064	ANTPI224-13	MF925856	BOLD:ACM2643	658[0n]	2011
Pheidole subarmata	MACN-Bar-Ins-ct 05114	ANTPI239-13	MF925906	BOLD:ACM2643	658[0n]	2011
Pheidole subarmata	T1W12008PNIB03	ANTPI015-10			0	2008
Pheidole subarmata	T1S18M2009PNIG06	ANTPI078-10			0	2009

Pheidole subarmata	T3S10a2009PNIF09	ANTPI069-10			0	2009
Pheidole subarmata	T5S10m2009PNIE06	ANTPI054-10			0	2009
Pheidole subarmata	T5S10m2009PNIE08	ANTPI056-10			0	2009
Pheidole subarmata	MACN-Bar-Ins-ct 02919	ANTPI136-12			0	2011
Platythyrea pilosula (**)	MACN-bar-ins-ct 06459	ANTI162-15	MF925988	BOLD:ACY5292	658[0n]	2015
Pogonomyrmex naegelii	MACN-bar-ins-ct 06469	ANTI172-15	MF925762	BOLD:AAL0334	658[0n]	2015
Pogonomyrmex naegelii	MACN-bar-ins-ct 06915	ANTPI516-15			0	2015
Procryptocerus adlerzi (**)	MACN-Bar-Ins-ct 05142	ANTPI251-13	MF925971	BOLD:ACM2934	658[0n]	2011
Procryptocerus hylaeus	MACN-bar-ins-ct 06410	ANTI113-15	MF925854	BOLD:ACQ7782	658[0n]	2015
Procryptocerus hylaeus	MACN-bar-ins-ct 06412	ANTI115-15	MF925950	BOLD:ACQ7782	658[0n]	2015
Procryptocerus hylaeus	MACN-bar-ins-ct 06950	ANTPI551-15	MF925973	BOLD:ACQ7782	658[0n]	2015
Procryptocerus hylaeus	MACN-bar-ins-ct 06884	ANTPI485-15			0	2015
Procryptocerus regularis	MACN-Bar-Ins-ct 05147	ANTPI255-13	MF925814	BOLD:ACM2933	658[0n]	2011
Pseudomyrmex cf. pupa (**)	MACN-Bar-Ins-ct 05150	ANTPI258-13			0	2011
Pseudomyrmex cf. pupa (**)	MACN-bar-ins-ct 06424	ANTI127-15			0	2015
Pseudomyrmex gracilis	MACN-Bar-Ins-ct 02926	ANTPI143-12	MF925776	BOLD:ACC4398	658[0n]	2011
Pseudomyrmex gracilis	MACN-Bar-Ins-ct 02957	ANTPI174-12			0	2011
Pseudomyrmex gracilis	MACN-Bar-Ins-ct 05087	ANTPI232-13			0	2011
Pseudomyrmex gracilis	MACN-Bar-Ins-ct 05148	ANTPI256-13			0	2011
Pseudomyrmex gracilis	MACN-bar-ins-ct 06406	ANTI109-15			0	2015
Pseudomyrmex PEH01	MACN-Bar-Ins-ct 05139	ANTPI248-13	MF925912	BOLD:ACM3001	658[0n]	2011
Pseudomyrmex PEH02	MACN-bar-ins-ct 06986	ANTPI587-16	MF925810	BOLD:ACM9913	591[1n]	2015
Pseudomyrmex PEH03	MACN-bar-ins-ct 06963	ANTPI564-15			0	1998
Pseudomyrmex phyllophilus	MACN-bar-ins-ct 06962	ANTPI563-15			0	1999
Pseudomyrmex schuppi	MACN-bar-ins-ct 06458	ANTI161-15	MF925765	BOLD:ACV2863	658[0n]	2015
Pseudomyrmex simplex	MACN-bar-ins-ct 06889	ANTPI490-15	MF925966	BOLD:ACZ3034	658[0n]	2015
Pseudomyrmex termitarius (A)	MACN-bar-ins-ct 06908	ANTPI509-15			0	2015
Pseudomyrmex urbanus (A)	MACN-Bar-Ins-ct 02911	ANTPI128-12			0	2011
Rogeria PEH01	MACN-Bar-Ins-ct 06856	ANTPI457-15			0	1999
Rogeria scobinata	MACN-Bar-Ins-ct 06786	ANTPI387-15			0	1999
Rogeria scobinata	MACN-Bar-Ins-ct 06806	ANTPI407-15			0	1999
Rogeria scobinata	MACN-Bar-Ins-ct 06816	ANTPI417-15			0	1999
Rogeria scobinata	MACN-Bar-Ins-ct 06845	ANTPI446-15			0	1999
Solenopsis cf. picea (*)	T1W32008PNIB07	ANTPI019-10			498[4n]	2008
Solenopsis cf. picea (*)	T3W32008PNID02	ANTPI038-10			0	2008
Solenopsis helena (*)	MACN-Bar-Ins-ct 02900	ANTPI117-12	MF925753	BOLD:ACC4227	658[0n]	2011
Solenopsis helena (*)	MACN-Bar-Ins-ct 02918	ANTPI135-12	MF925941	BOLD:ACC4227	658[0n]	2011
Solenopsis helena (*)	MACN-bar-ins-ct 06917	ANTPI518-15			0	2015

Solenopsis iheringi (**)	MACN-Bar-Ins-ct 05105	ANTPI235-13	MF925871	BOLD:AAE8643	658[0n]	2009
Solenopsis iheringi (**)	T1W12008PNIG08	ANTPI080-10			0	2008
Solenopsis iheringi (**)	T1W32008PNIB01	ANTPI013-10			0	2008
Solenopsis iheringi (**)	T1W32008PNIB02	ANTPI014-10			0	2008
Solenopsis iheringi (**)	MACN-bar-ins-ct 06899	ANTPI500-15			0	2015
Solenopsis PEH01	MACN-bar-ins-ct 06955	ANTPI556-15	MF925826	BOLD:ACW4714	627[0n]	2015
Solenopsis PEH02	MACN-bar-ins-ct 06933	ANTPI534-15	MF925866	BOLD:ACZ3333	658[0n]	2015
Solenopsis PEH03	T3W52008PNIA12	ANTPI012-10			0	2008
Solenopsis PEH04	T1W32008PNIB10	ANTPI022-10			658[1n]	2008
Solenopsis PEH04	MACN-Bar-Ins-ct 02947	ANTPI164-12			0	2011
Solenopsis PEH04	MACN-Bar-Ins-ct 02967	ANTPI184-12			0	2011
Solenopsis PEH04	MACN-Bar-Ins-ct 05134	ANTPI279-13			0	2011
Solenopsis PEH06	MACN-Bar-Ins-ct 05107	ANTPI236-13	MF925759	BOLD:ACM2874	658[0n]	2011
Solenopsis PEH06	MACN-Bar-Ins-ct 05115	ANTPI240-13	MF925915	BOLD:ACM2874	658[0n]	2011
Solenopsis PEH06	MACN-Bar-Ins-ct 05083	ANTPI272-13			0	2011
Solenopsis PEH06	MACN-Bar-Ins-ct 05086	ANTPI231-13			0	2011
Solenopsis PEH06	MACN-Bar-Ins-ct 05130	ANTPI245-13			0	2011
Solenopsis PEH06	MACN-Bar-Ins-ct 05131	ANTPI281-13			0	2011
Solenopsis PEH06	MACN-Bar-Ins-ct 05146	ANTPI283-13			0	2011
Solenopsis PEH07	T2S20m2009PNIF03	ANTPI063-10			0	2009
Solenopsis PEH09	T1W32008PNIB12	ANTPI024-10			0	2008
Solenopsis richteri (A)	MACN-bar-ins-ct 06467	ANTI170-15	MF925833	BOLD:ABV0845	658[0n]	2015
Solenopsis richteri (A)	MACN-bar-ins-ct 06925	ANTPI526-15	MF925986	BOLD:ABV0845	658[0n]	2015
Solenopsis richteri (A)	MACN-bar-ins-ct 06930	ANTPI531-15	MF926001	BOLD:ABV0845	658[0n]	2015
Solenopsis richteri (A)	MACN-bar-ins-ct 06978	ANTPI579-16	MF925869	BOLD:ABV0845	658[0n]	2015
Solenopsis richteri (A)	MACN-bar-ins-ct 07001	ANTPI602-16	MF925738	BOLD:ABV0845	658[0n]	2015
Strumigenys	T5W42008PNIH05	ANTPI089-10			0	2008
Strumigenys appretiata	MACN-Bar-Ins-ct 05155	ANTPI263-13			0	2008
Strumigenys appretiata	MACN-bar-ins-ct 06914	ANTPI515-15			0	2008
Strumigenys crassicornis	MACN-Bar-Ins-ct 06785	ANTPI386-15			0	1999
Strumigenys denticulata	MACN-Bar-Ins-ct 06861	ANTPI462-15			0	1999
Strumigenys denticulata	T1W52008PNIH02	ANTPI086-10			0	2008
Strumigenys denticulata	T6W32008PNIF11	ANTPI071-10			0	2008
Strumigenys denticulata	T6W42008PNIE03	ANTPI051-10			0	2008
Strumigenys elongata	MACN-bar-ins-ct 06473	ANTI176-15	MF925891	BOLD:ACZ3541	658[0n]	2015
Strumigenys elongata	MACN-bar-ins-ct 06477	ANTI180-15	MF925998	BOLD:ACZ3541	658[0n]	2015
Strumigenys elongata	MACN-bar-ins-ct 06940	ANTPI541-15	MF925947	BOLD:ACZ3541	658[0n]	2015
Strumigenys elongata	MACN-Bar-Ins-ct 06864	ANTPI465-15			0	1999
Strumigenys elongata	MACN-Bar-Ins-ct 05092	ANTPI234-13			0	2008

Strumigenys louisianae	MACN-Bar-Ins-ct 06829	ANTPI430-15			0	1999
Strumigenys louisianae	T1W32008PNID11	ANTPI047-10			0	2008
Strumigenys ogloblini	MACN-bar-ins-ct 06476	ANTI179-15	MF925865	BOLD:ACZ4305	658[0n]	2015
Strumigenys ogloblini	MACN-Bar-Ins-ct 06839	ANTPI440-15			0	1999
Strumigenys PEH01	MACN-Bar-Ins-ct 06821	ANTPI422-15			0	1999
Strumigenys PEH01	MACN-Bar-Ins-ct 06849	ANTPI450-15			0	1999
Strumigenys PEH01	MACN-Bar-Ins-ct 06855	ANTPI456-15			0	1999
Strumigenys PEH02	MACN-Bar-Ins-ct 06871	ANTPI472-15			0	1999
Tapinoma atriceps	MACN-bar-ins-ct 06905	ANTPI506-15			0	1999
Tapinoma atriceps	MACN-bar-ins-ct 06910	ANTPI511-15			0	1999
Trachymyrmex PEH01	MACN-bar-ins-ct 06953	ANTPI554-15			0	2015
Wasmannia auropunctata	MACN-Bar-Ins-ct 05143	ANTPI252-13	MF925747	BOLD:ACH5104	658[0n]	2011
Wasmannia auropunctata	MACN-Bar-Ins-ct 05156	ANTPI264-13	MF926000	BOLD:ACH5104	658[0n]	2011
Wasmannia rochai	MACN-bar-ins-ct 06907	ANTPI508-15	MF925952	BOLD:ACZ3037	658[0n]	2015
Wasmannia rochai	MACN-Bar-Ins-ct 06787	ANTPI388-15			0	1999
Wasmannia rochai	MACN-Bar-Ins-ct 06837	ANTPI438-15			0	1999
Wasmannia rochai	MACN-Bar-Ins-ct 06858	ANTPI459-15			0	1999
Wasmannia rochai	MACN-Bar-Ins-ct 06869	ANTPI470-15			0	1999

Table S3.2 Summary of the 124 species that constituted the dataset used for the analyses. For each species we report the sampling size (N), the mean and maximum intraspecific distances, and the minimum distance to the nearest neighbor (heterospecific). We also show the correspondence between MOTUs and species boundaries for each clustering algorithm (see Materials and methods for more details). Numbers in brackets after the SPLIT category indicate the number of groups in which the species was divided.

Species (124)	N	Mean distance (% K2P)	Max distance (% K2P)	Min distance to NN	RESL (137)	TCS 95% (136)	ABGD initial partition (125)	ABGD recursive P = 1.29% (132)	ABGD recursive P = 0.28% (136)
Acanthostichus brevicornis	1	NA	NA	8.59	MATCH	MATCH	MATCH	MATCH	MATCH
Acanthostichus quadratus	2	0.00	0.00	8.59	MATCH	MATCH	MATCH	MATCH	MATCH
Apterostigma PEH01	1	NA	NA	15.35	MATCH	MATCH	MATCH	MATCH	MATCH
Apterostigma PEH02	2	0.15	0.15	15.35	MATCH	MATCH	MATCH	MATCH	MATCH
Atta sexdens	8	1.60	2.97	19.42	SPLIT (3)	SPLIT (2)	MATCH	SPLIT (3)	SPLIT (3)
Azteca adrepens	3	0.20	0.30	20.52	MATCH	MATCH	MATCH	MATCH	MATCH
Brachymyrmex antennatus	1	NA	NA	13.52	MATCH	MATCH	MATCH	MATCH	MATCH
Brachymyrmex aphidicola	2	0.00	0.00	10.44	MATCH	MATCH	MATCH	MATCH	MATCH
Brachymyrmex cordemoyi	4	0.00	0.00	10.44	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus atriceps	2	0.00	0.00	11.31	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus brasiliensis	1	NA	NA	18.37	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus cf. landolti	4	0.00	0.00	16.87	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus cingulatus	6	0.05	0.15	15.54	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus crassus	5	0.46	0.78	17.31	MATCH	MATCH	MATCH	MATCH	SPLIT (2)
Camponotus geralensis	1	NA	NA	17.21	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus PEH01	1	NA	NA	11.31	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus renggeri	1	NA	NA	13.22	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus rufipes	4	1.17	2.33	13.22	SPLIT (2)	SPLIT (2)	MATCH	MATCH	MATCH

Camponotus sericeiventris	8	0.04	0.15	17.21	MATCH	MATCH	MATCH	MATCH	MATCH
Camponotus striatus	1	NA	NA	16.93	MATCH	MATCH	MATCH	MATCH	MATCH
Carebara brasiliana	1	NA	NA	20.18	MATCH	MATCH	MATCH	MATCH	MATCH
Cephalotes eduarduli	2	0.00	0.00	17.50	MATCH	MATCH	MATCH	MATCH	MATCH
Cephalotes minutus	1	NA	NA	12.45	MATCH	MATCH	MATCH	MATCH	MATCH
Cephalotes pusillus	2	0.00	0.00	12.45	MATCH	MATCH	MATCH	MATCH	MATCH
Crematogaster corticicola	4	0.00	0.00	14.51	MATCH	MATCH	MATCH	MATCH	MATCH
Crematogaster curvispinosa	2	0.00	0.00	17.41	MATCH	MATCH	MATCH	MATCH	MATCH
Crematogaster lutzi	1	NA	NA	14.51	MATCH	MATCH	MATCH	MATCH	MATCH
Crematogaster montezumia	3	0.00	0.00	17.43	MATCH	MATCH	MATCH	MATCH	MATCH
Crematogaster nigropilosa	4	0.00	0.00	17.28	MATCH	MATCH	MATCH	MATCH	MATCH
Crematogaster PEH02	2	0.00	0.00	19.71	MATCH	MATCH	MATCH	MATCH	MATCH
Cylindromyrmex brasiliensis	1	NA	NA	19.11	MATCH	MATCH	MATCH	MATCH	MATCH
Cyphomyrmex rimosus	1	NA	NA	18.37	MATCH	MATCH	MATCH	MATCH	MATCH
Dinoponera australis	7	2.08	3.64	25.16	SPLIT (2)	SPLIT (2)	MATCH	SPLIT (2)	SPLIT (2)
Dolichoderus bispinosus	4	0.10	0.15	24.54	MATCH	MATCH	MATCH	MATCH	MATCH
Dolichoderus germaini	2	0.00	0.00	22.42	MATCH	MATCH	MATCH	MATCH	MATCH
Dolichoderus lutosus	1	NA	NA	20.16	MATCH	MATCH	MATCH	MATCH	MATCH
Dorymyrmex bruneus	2	0.00	0.00	18.75	MATCH	MATCH	MATCH	MATCH	MATCH
Eciton vagans	6	0.21	0.46	16.44	MATCH	MATCH	MATCH	MATCH	MATCH
Ectatomma brunneum	1	NA	NA	14.95	MATCH	MATCH	MATCH	MATCH	MATCH
Ectatomma edentatum	5	7.57	18.97	14.95	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)
Gnamptogenys haenschi	1	NA	NA	17.78	MATCH	MATCH	MATCH	MATCH	MATCH
Gnamptogenys striatula	4	0.08	0.15	17.83	MATCH	MATCH	MATCH	MATCH	MATCH
Gnamptogenys triangularis	2	0.00	0.00	17.83	MATCH	MATCH	MATCH	MATCH	MATCH
Heteroponera dolo	4	0.81	1.57	9.23	MATCH	MATCH	MATCH	SPLIT (2)	SPLIT (2)
Heteroponera mayri	1	NA	NA	9.23	MATCH	MATCH	MATCH	MATCH	MATCH

Heteroponera microps	2	0.00	0.00	14.71	MATCH	MATCH	MATCH	MATCH	MATCH
Hylomyrma balzani	1	NA	NA	23.59	MATCH	MATCH	MATCH	MATCH	MATCH
Hypoponera agilis	1	NA	NA	14.10	MATCH	MATCH	MATCH	MATCH	MATCH
Hypoponera cf. opacior	2	0.30	0.30	12.98	MATCH	MATCH	MATCH	MATCH	MATCH
Hypoponera distinguenda	2	0.00	0.00	13.01	MATCH	MATCH	MATCH	MATCH	MATCH
Hypoponera foreli	5	4.48	11.20	13.90	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)
Hypoponera parva	2	0.00	0.00	15.20	MATCH	MATCH	MATCH	MATCH	MATCH
Hypoponera PEH01	1	NA	NA	15.54	MATCH	MATCH	MATCH	MATCH	MATCH
Hypoponera PEH02	4	0.00	0.00	12.35	MATCH	MATCH	MATCH	MATCH	MATCH
Hypoponera trigona	5	6.41	9.92	12.35	SPLIT (3)	SPLIT (3)	SPLIT (3)	SPLIT (3)	SPLIT (3)
Labidus coecus	8	2.32	8.12	16.44	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (4)
Labidus praedator	1	NA	NA	17.04	MATCH	MATCH	MATCH	MATCH	MATCH
Leptogenys iheringi	1	NA	NA	17.95	MATCH	MATCH	MATCH	MATCH	MATCH
Linepithema iniquum	1	NA	NA	12.87	MATCH	MATCH	MATCH	MATCH	MATCH
Linepithema micans	4	0.08	0.15	12.87	MATCH	MATCH	MATCH	MATCH	MATCH
Linepithema pulex	1	NA	NA	13.05	MATCH	MATCH	MATCH	MATCH	MATCH
Megalomyrmex brandaoi	1	NA	NA	14.06	MATCH	MATCH	MATCH	MATCH	MATCH
Megalomyrmex megadrifti	1	NA	NA	14.06	MATCH	MATCH	MATCH	MATCH	MATCH
Megalomyrmex miri	1	NA	NA	17.78	MATCH	MATCH	MATCH	MATCH	MATCH
Mycetarotes parallelus	1	NA	NA	20.50	MATCH	MATCH	MATCH	MATCH	MATCH
Mycocepurus smithii	3	0.00	0.00	25.52	MATCH	MATCH	MATCH	MATCH	MATCH
Myrmelachista catharinae	2	0.00	0.00	14.45	MATCH	MATCH	MATCH	MATCH	MATCH
Myrmelachista nodigera	1	NA	NA	14.45	MATCH	MATCH	MATCH	MATCH	MATCH
Neivamyrmex angustinodis	1	NA	NA	21.67	MATCH	MATCH	MATCH	MATCH	MATCH
Neivamyrmex punctaticeps	5	0.00	0.00	21.67	MATCH	MATCH	MATCH	MATCH	MATCH
Neoponera bactronica	1	NA	NA	0.00	MERGE	MERGE	MERGE	MERGE	MERGE
Neoponera crenata	3	3.26	4.88	4.39	SPLIT (2)	SPLIT (2)	MERGE	MERGE	MERGE

Neoponera curvinodis	1	NA	NA	0.00	MERGE	MERGE	MERGE	MERGE	MERGE
Neoponera fiebrigi	1	NA	NA	3.92	MATCH	MATCH	MERGE	MERGE	MERGE
Neoponera moesta	2	0.92	0.92	3.92	MATCH	MATCH	MERGE	MERGE	MERGE
Neoponera obscuricornis	3	0.00	0.00	11.10	MATCH	MATCH	MATCH	MATCH	MATCH
Neoponera verenae	1	NA	NA	11.10	MATCH	MATCH	MATCH	MATCH	MATCH
Neoponera villosa	3	0.20	0.30	9.98	MATCH	MATCH	MATCH	MATCH	MATCH
Nesomyrmex asper	3	0.00	0.00	19.89	MATCH	MATCH	MATCH	MATCH	MATCH
Nesomyrmex tonsuratus	1	NA	NA	20.95	MATCH	MATCH	MATCH	MATCH	MATCH
Nylanderia fulva	1	NA	NA	8.26	MATCH	MATCH	MATCH	MATCH	MATCH
Nylanderia PEH01	1	NA	NA	8.26	MATCH	MATCH	MATCH	MATCH	MATCH
Nylanderia PEH02	2	0.00	0.00	11.12	MATCH	MATCH	MATCH	MATCH	MATCH
Octostruma iheringi	1	NA	NA	20.41	MATCH	MATCH	MATCH	MATCH	MATCH
Octostruma PEH01	1	NA	NA	21.20	MATCH	MATCH	MATCH	MATCH	MATCH
Odontomachus chelifer	5	0.00	0.00	9.55	MATCH	MATCH	MATCH	MATCH	MATCH
Odontomachus meinerti	10	1.96	5.53	9.55	SPLIT (2)	SPLIT (2)	MATCH	SPLIT (2)	SPLIT (2)
Pachycondyla harpax	1	NA	NA	12.82	MATCH	MATCH	MATCH	MATCH	MATCH
Pachycondyla PEH01	1	NA	NA	12.82	MATCH	MATCH	MATCH	MATCH	MATCH
Pachycondyla striata	4	0.15	0.31	15.41	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole alpinensis	1	NA	NA	17.90	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole fimbriata	3	7.06	10.59	20.19	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)	SPLIT (2)
Pheidole mosenopsis	2	0.30	0.30	17.91	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole obscurithorax	1	NA	NA	15.12	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole PEH01	7	0.07	0.15	16.50	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole PEH02	7	2.75	5.91	12.52	SPLIT (2)	SPLIT (2)	MATCH	SPLIT (2)	SPLIT (2)
Pheidole PEH03	3	0.10	0.15	16.64	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole PEH04	4	0.00	0.00	16.09	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole PEH05	1	NA	NA	16.09	MATCH	MATCH	MATCH	MATCH	MATCH

Pheidole PEH06	1	NA	NA	15.12	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole PEH09	2	0.00	0.00	12.52	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole rugatula	4	0.00	0.00	18.67	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole sigillata	5	0.24	0.61	18.68	MATCH	MATCH	MATCH	MATCH	MATCH
Pheidole subarmata	15	1.09	2.19	17.99	SPLIT (2)	SPLIT (2)	MATCH	SPLIT (2)	SPLIT (2)
Platythyrea pilosula	1	NA	NA	22.18	MATCH	MATCH	MATCH	MATCH	MATCH
Pogonomyrmex naegelii	1	NA	NA	21.18	MATCH	MATCH	MATCH	MATCH	MATCH
Procryptocerus adlerzi	1	NA	NA	16.17	MATCH	MATCH	MATCH	MATCH	MATCH
Procryptocerus hylaeus	3	0.20	0.30	17.91	MATCH	MATCH	MATCH	MATCH	MATCH
Procryptocerus regularis	1	NA	NA	16.17	MATCH	MATCH	MATCH	MATCH	MATCH
Pseudomyrmex gracilis	1	NA	NA	5.84	MATCH	MATCH	MERGE	MERGE	MERGE
Pseudomyrmex PEH01	1	NA	NA	16.21	MATCH	MATCH	MATCH	MATCH	MATCH
Pseudomyrmex PEH02	1	NA	NA	5.84	MATCH	MATCH	MERGE	MERGE	MERGE
Pseudomyrmex schuppi	1	NA	NA	21.60	MATCH	MATCH	MATCH	MATCH	MATCH
Pseudomyrmex simplex	1	NA	NA	16.21	MATCH	MATCH	MATCH	MATCH	MATCH
Solenopsis helena	2	0.00	0.00	17.10	MATCH	MATCH	MATCH	MATCH	MATCH
Solenopsis iheringi	1	NA	NA	19.49	MATCH	MATCH	MATCH	MATCH	MATCH
Solenopsis PEH01	1	NA	NA	4.67	MATCH	MATCH	MERGE	MERGE	MERGE
Solenopsis PEH02	1	NA	NA	18.86	MATCH	MATCH	MATCH	MATCH	MATCH
Solenopsis PEH06	2	0.00	0.00	4.67	MATCH	MATCH	MERGE	MERGE	MERGE
Solenopsis richteri	5	0.00	0.00	17.10	MATCH	MATCH	MATCH	MATCH	MATCH
Strumigenys elongata	3	0.20	0.30	17.45	MATCH	MATCH	MATCH	MATCH	MATCH
Strumigenys ogloblini	1	NA	NA	17.45	MATCH	MATCH	MATCH	MATCH	MATCH
Wasmannia auropunctata	2	0.00	0.00	19.38	MATCH	MATCH	MATCH	MATCH	MATCH
Wasmannia rochai	1	NA	NA	19.53	MATCH	MATCH	MATCH	MATCH	MATCH

Table S3.3 Results of the TCS analyses for a range of ten parsimony limit (i.e. cut-off) values.

Parsimony probability	Maximum connection steps	Subnetworks
90%	16	133
91%	15	134
92%	14	135
93%	13	135
94%	12	136
95%	11	136
96%	9	136
97%	8	138
98%	6	138
99%	4	140

Table S3.4 Results of the ABGD analyses for two distances metrics (p-distance and K2P), two relative gap values (X = 0.8 and X = 1) and a range of prior intraspecific divergence (P) values between 0.1% and 10%.

Distance model	X	Partition	Prior intraspecific divergence (P, %)									
			0.1	0.17	0.28	0.46	0.77	1.29	2.15	3.59	5.99	10
p-distance	1	Initial	125	125	125	125	125	125	125	125	125	1
		Recursive	147	135	135	135	132	132	128	127	125	1
	0.8	Initial	125	125	125	125	125	125	125	125	125	1
		Recursive	157	140	140	139	136	136	132	130	125	
K2P	1	Initial	125	125	125	125	125	125	125	125	125	1
		Recursive	147	135	135	135	132	132	128	128	125	1
	0.8	Initial	125	125	125	125	125	125	125	125	125	1
		Recursive	157	140	140	139	136	136	132	131	125	1

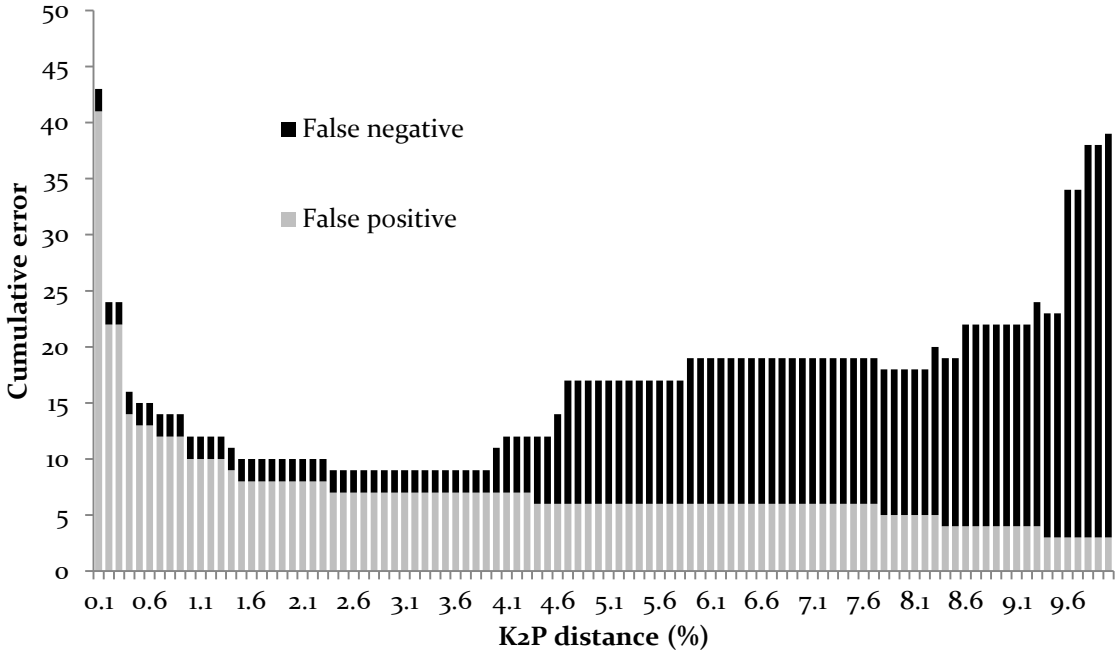


Fig S3.1 Histogram of threshold optimization method reporting the frequencies of false-positive and false-negative identifications across thresholds values from 0.1% to 10%.

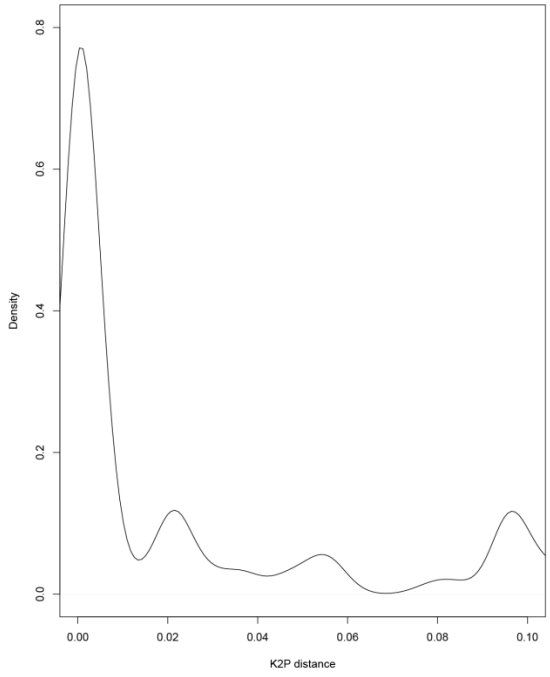


Fig S3.2 Density plot of genetic distances generated by the function 'localMinima' in SPIDER.

Fig S3.3 Morphological differences between the two MOTUs of *Ectatomma edentatum* (left: MACN-Bar-Ins-ct 5123, right: MACN-Bar- Ins-ct 6433).

Appendix Chapter IV

Supplementary material

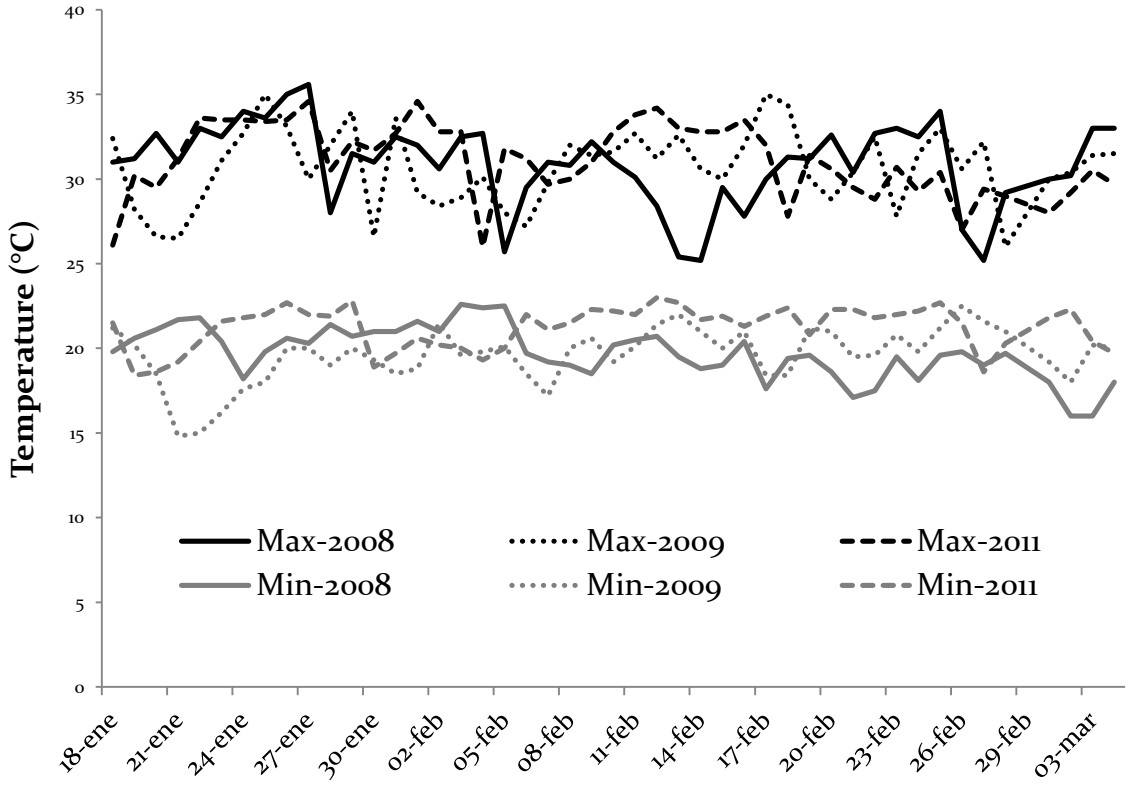


Fig S4.1 Temperature (Maximum and minimum) in the course of January 18th to March 4th. In this period we sampled ants with pitfalls and litter samples (2008), subterranean baits (2009) and surface baiting (2011). The precipitation during this period was similar, averaging 10.9 ± 4 mm for the three years.

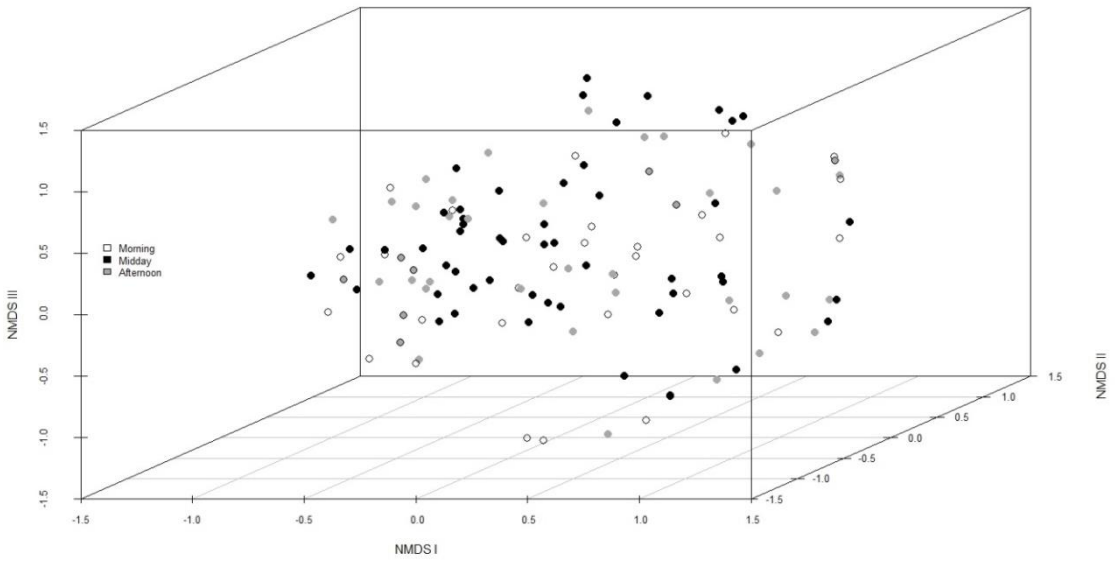


Fig S4.2 Ordination of ant community collected by surface baits collected at Morning (white), Midday (black) and Afternoon (gray). The ordination was performed by a non-metric multidimensional scaling (NMDS) analysis using the Jaccard similarity index (Stress= 0.20).

Table S4.1 Detail of the samples used for stable isotope analysis. Voucher specimens for some samples were included for DNA Barcode analysis to improve their taxonomical identification, for these samples, the associated Sample ID is shown.

Sample code	Class	Taxonomic group	Locality	δ13C	δ15N	DNA Barcode Sample ID
iso_029	Apogonia	Poaceae	INP	-13.63	2.11	
iso_352	Apogonia	*Setaria sulcata*	INP	-13.74	4.50	
iso_209	Arachnida	Araneae	OPR	-26.72	8.81	
iso_211	Arachnida	Araneae	INP	-24.81	11.50	
iso_214	Arachnida	Araneae	INP	-26.43	4.19	
iso_226	Arachnida	Araneae	INP	-26.44	10.84	
iso_370	Arachnida	Araneae	INP	-20.29	10.74	
iso_091	Arachnida	*Araneus venatrix*	OPR	-25.93	7.23	
iso_212	Arachnida	*Castianeira* sp	OPR	-24.84	10.39	
iso_213	Arachnida	*Castianeira* sp	INP	-29.28	5.81	
iso_385	Arachnida	Corinnidae	INP	-25.49	12.08	
iso_386	Arachnida	Corinnidae	INP	-26.55	9.61	
iso_389	Arachnida	Corinnidae	INP	-25.04	12.96	
iso_043	Arachnida	*Cryptogeobiidae*	INP	-25.35	13.73	
iso_046	Arachnida	*Discocyrtus cornytus*	INP	-26.67	7.15	
iso_039	Arachnida	*Discocyrtus prospicuus*	INP	-25.52	8.40	
iso_040	Arachnida	*Discocyrtus prospicuus*	INP	-26.62	9.31	

iso_042	Arachnida	*Discocyrtus prospicuus*	INP	-25.72	8.70	
iso_050	Arachnida	*Discocyrtus prospicuus*	INP	-25.84	9.66	
iso_051	Arachnida	*Discocyrtus prospicuus*	INP	-26.47	9.61	
iso_049	Arachnida	*Eusarcus hastatus*	INP	-24.29	9.16	
iso_388	Arachnida	*Eustiromastix* sp.	INP	-26.32	9.15	
iso_093	Arachnida	Gasteracantha cancriformis	OPR	-23.12	7.62	
iso_068	Arachnida	Ixodida	INP	-23.99	13.43	
iso_075	Arachnida	Ixodida	INP	-21.67	11.65	
iso_095	Arachnida	Lycosinae	OPR	-24.15	9.21	
iso_248	Arachnida	Lycosinae	OPR	-24.85	8.52	
iso_207	Arachnida	*Myrmecotypus* sp	INP	-26.70	6.93	
iso_066	Arachnida	*Nephila* sp	OPR	-24.61	6.27	
iso_044	Arachnida	*Ogloblinia loretoensis*	INP	-25.54	11.06	
iso_045	Arachnida	*Ogloblinia loretoensis*	INP	-26.26	9.92	
iso_047	Arachnida	*Ogloblinia loretoensis*	INP	-26.61	10.45	
iso_048	Arachnida	*Ogloblinia loretoensis*	INP	-24.73	7.88	
iso_144	Arachnida	Opiliones	INP	-27.05	8.87	
iso_067	Arachnida	*Parawixia audax*	INP	-24.10	8.29	
iso_077	Arachnida	*Phiale guttata*	INP	-25.58	9.57	
iso_210	Arachnida	Salticidae	OPR	-25.44	10.71	
iso_390	Arachnida	Salticidae	INP	-27.46	7.99	
iso_307	Arachnida	*Sphecotypus* sp	INP	-27.07	9.53	
iso_076	Arachnida	*Thiodina* sp	OPR	-25.53	9.13	
iso_235	Arachnida	*Viracucha* sp	OPR	-24.76	17.25	
iso_405	Chilopoda		INP	-23.83	8.08	
iso_413	Chilopoda		INP	-24.59	13.31	
iso_104	Diplopoda		OPR	-23.85	4.65	
iso_106	Diplopoda		INP	-24.78	1.23	
iso_107	Diplopoda		INP	-23.21	6.90	
iso_108	Diplopoda		INP	-26.30	5.47	
iso_103	Diplopoda		INP	-24.02	10.81	
iso_002N	Eudicotyledoneae	Leguminosae	OPR	-28.12	-0.30	
iso_222	Formicidae	*Neoponera crenata*	INP	-28.87	6.72	MACN-bar-ins-ct 06416
iso_434	Formicidae	*Neoponera crenata*	INP	-26.47	13.88	MACN-bar-ins-ct 07761
iso_114	Formicidae	*Neoponera obscuricornis*	INP	-23.96	9.95	
iso_254	Formicidae	*Neoponera obscuricornis*	INP	-24.41	7.63	MACN-bar-ins-07462
iso_258	Formicidae	*Neoponera obscuricornis*	INP	-24.87	9.26	MACN-bar-ins-ct 06440
iso_378	Formicidae	*Neoponera obscuricornis*	INP	-25.73	11.35	
iso_421	Formicidae	*Neoponera obscuricornis*	INP	-24.20	10.69	
iso_423	Formicidae	*Neoponera obscuricornis*	INP	-25.58	9.88	
iso_099	Formicidae	*Odontomachus chelifer*	INP	-25.96	10.85	
iso_100	Formicidae	*Odontomachus*	INP	-26.15	10.26	

		chelifer				
iso_244	Formicidae	*Odontomachus chelifer*	INP	-26.72	9.44	
iso_245	Formicidae	*Odontomachus chelifer*	INP	-24.89	10.07	
iso_247	Formicidae	*Odontomachus chelifer*	INP	-26.44	9.19	
iso_249	Formicidae	*Odontomachus chelifer*	INP	-26.31	8.31	
iso_403	Insecta	*Acanthocephala* sp	INP	-28.06	4.36	
iso_326	Insecta	*Acanthostichus quadratus*	INP	-25.31	11.26	MACN-bar-ins-ct 06431
iso_368	Insecta	*Acanthostichus quadratus*	INP	-26.29	11.20	MACN-bar-ins-07521
iso_272	Insecta	*Acromyrmex laticeps*	INP	-26.23	5.98	
iso_217	Insecta	*Acromyrmex subterraneus*	OPR	-24.97	4.93	MACN-Bar-Ins-ct 07392
iso_358	Insecta	*Acromyrmex subterraneus*	INP	-26.85	7.84	MACN-bar-ins-07523
iso_394	Insecta	Apidae	INP	-24.68	5.36	
iso_191	Insecta	*Apterostigma pilosum* group	OPR	-24.36	8.84	MACN-Bar-Ins-ct 07398
iso_231	Insecta	*Atta sexdens*	INP	-25.93	6.02	MACN-bar-ins-ct 06443
iso_201	Insecta	*Atta vollenweideri*	OPR	-26.38	1.55	MACN-Bar-Ins-ct 07389
iso_055	Insecta	Belostomatidae	INP	-36.69	3.80	
iso_056	Insecta	Belostomatidae	OPR	-25.51	8.48	
iso_097	Insecta	Blattodea	OPR	-23.30	4.52	
iso_122	Insecta	Blattodea	INP	-28.49	-6.33	
iso_123	Insecta	Blattodea	INP	-28.29	-6.41	
iso_126	Insecta	Blattodea	OPR	-23.74	7.20	
iso_418	Insecta	Blattodea	INP	-24.98	6.08	
iso_373	Insecta	*Brachygastra* sp	INP	-25.78	7.35	MACN-bar-ins-07517
iso_195	Insecta	*Brachymyrmex termitophilus*	OPR	-24.16	9.11	MACN-Bar-Ins-ct 07418
iso_223	Insecta	*Camponotus bonaerensis*	OPR	-25.94	3.61	MACN-Bar-Ins-ct 07426
iso_367	Insecta	*Camponotus bonaerensis*	OPR	-26.09	4.99	MACN-bar-ins-ct 07033; MACN-bar-ins-ct 07009
iso_275	Insecta	*Camponotus cingulatus*	OPR	-24.81	2.89	MACN-Bar-Ins-ct 07401
iso_270	Insecta	*Camponotus crassus*	OPR	-24.93	3.23	MACN-Bar-Ins-ct 07382
iso_356	Insecta	*Camponotus lespessi*	INP	-25.07	7.45	MACN-bar-ins-07522
iso_200	Insecta	*Camponotus PEH02*	INP	-25.35	3.77	MACN-bar-ins-07458
iso_294	Insecta	*Camponotus punctulatus*	OPR	-22.64	4.27	
iso_224	Insecta	*Camponotus renggeri*	OPR	-24.24	5.18	MACN-Bar-Ins-ct 07388
iso_215	Insecta	*Camponotus rufipes*	INP	-24.57	3.75	MACN-bar-ins-ct 06403
iso_280	Insecta	*Camponotus rufipes*	INP	-25.74	7.96	
iso_360	Insecta	*Camponotus sericeiventris*	INP	-26.59	6.50	
iso_372	Insecta	*Camponotus sericeiventris*	INP	-25.79	4.79	
iso_290	Insecta	*Cephalotes clypeatus*	OPR	-25.16	5.30	
iso_188	Insecta	*Ceraia* sp	OPR	-25.10	3.20	
ISO_052	Insecta	Cicadidae	OPR	-24.69	-0.88	

iso_054	Insecta	Cicadidae	INP	-28.96	2.39	
iso_399	Insecta	Cicadidae	INP	-26.45	8.21	
iso_128	Insecta	Coleoptera	OPR	-23.07	4.65	
iso_140	Insecta	Coleoptera	OPR	-26.14	4.30	
iso_142	Insecta	Coleoptera	OPR	-23.62	4.33	
iso_396	Insecta	Coleoptera	INP	-27.42	4.25	
iso_404	Insecta	Coleoptera	INP	-24.42	11.41	
iso_408	Insecta	Coleoptera	INP	-24.43	4.56	
iso_414	Insecta	Coleoptera	INP	-25.97	5.97	
iso_061	Insecta	Coreidae	OPR	-25.50	5.89	
iso_065	Insecta	Coreidae	INP	-28.12	4.02	
iso_397	Insecta	Coreidae	INP	-27.87	5.71	
iso_412	Insecta	Coreidae	INP	-27.95	5.96	
iso_196	Insecta	*Crematogaster* cl. *rochai*	INP	-26.85	7.17	MACN-Bar-Ins-ct 07444
iso_288	Insecta	*Crematogaster montezumia*	INP	-27.00	5.54	MACN-bar-ins-ct 06427
iso_302	Insecta	*Crematogaster obscurata*	OPR	-22.51	5.66	MACN-Bar-Ins-ct 07416
iso_132	Insecta	Curculionidae	OPR	-24.61	2.26	
iso_116	Insecta	*Dinoponera australis*	OPR	-26.21	9.51	
iso_117	Insecta	*Dinoponera australis*	OPR	-21.01	7.56	MACN-Bar-Ins-ct 07441
iso_159	Insecta	*Dinoponera australis*	OPR	-26.47	10.23	
iso_161	Insecta	*Dinoponera australis*	OPR	-21.00	8.34	
iso_162	Insecta	*Dinoponera australis*	OPR	-27.39	9.58	
iso_168	Insecta	*Dinoponera australis*	OPR	-26.83	8.37	
iso_232	Insecta	*Dinoponera australis*	INP	-27.06	12.54	
iso_234	Insecta	*Dinoponera australis*	INP	-26.33	11.44	
iso_236	Insecta	*Dinoponera australis*	INP	-26.88	11.80	
iso_371	Insecta	*Dinoponera australis*	INP	-26.29	9.93	
iso_374	Insecta	*Dinoponera australis*	INP	-27.14	12.69	
iso_074	Insecta	Diptera	OPR	-25.83	7.84	
iso_038	Insecta	*Discocyrtus prospicuus*	OPR	-26.16	7.96	
iso_041	Insecta	*Discocyrtus prospicuus*	OPR	-25.73	6.27	
iso_357	Insecta	*Dolichoderus bispinosus*	INP	-26.99	6.44	MACN-bar-ins-07510
iso_219	Insecta	*Eciton vagans*	INP	-25.75	13.10	MACN-bar-ins-ct 06452
iso_233	Insecta	*Eciton vagans*	OPR	-25.84	10.05	
iso_384	Insecta	*Eciton vagans*	OPR	-24.99	11.06	MACN-bar-ins-ct 06990
iso_382	Insecta	*Ectatomma* sp	INP	-25.30	11.60	
iso_131	Insecta	Erotylidae	OPR	-24.49	9.44	
iso_379	Insecta	*Gnamptogenys striatula*	INP	-25.51	11.81	
iso_291	Insecta	*Gnamptogenys tryangularis*	INP	-25.08	11.26	MACN-bar-ins-ct 06425
iso_186	Insecta	Gomphocerinae	INP	-15.30	5.99	

iso_184	Insecta	Grylloidea	OPR	-25.30	6.07	
iso_185	Insecta	Grylloidea	INP	-25.36	5.62	
iso_187	Insecta	Grylloidea	OPR	-22.71	5.51	
iso_395	Insecta	Grylloidea	INP	-16.68	12.80	
iso_398	Insecta	Grylloidea	INP	-25.37	9.67	
iso_063	Insecta	Hemiptera	OPR	-27.12	2.86	
iso_094	Insecta	Hemiptera	OPR	-25.98	10.76	
iso_127	Insecta	Hemiptera	OPR	-27.08	4.93	
iso_130	Insecta	Hemiptera	INP	-31.71	3.80	
iso_133	Insecta	Hemiptera	INP	-26.91	3.12	
iso_152	Insecta	Hemiptera	INP	-27.78	4.77	
iso_415	Insecta	Hemiptera	INP	-27.54	11.96	
iso_199	Insecta	*Heteroponera dolo*	INP	-22.02	7.81	MACN-Bar-Ins-ct 06438
iso_292	Insecta	*Hypoponera* cf. *agilis*	OPR	-23.36	6.89	MACN-Bar-Ins-ct 07433
iso_271	Insecta	*Hypoponera* cf. *opacior*	INP	-25.16	9.47	
iso_284	Insecta	*Hypoponera* cf. *opacior*	INP	-25.17	11.49	
iso_316	Insecta	*Hypoponera* cf. *opacior*	OPR	-26.80	9.63	MACN-Bar-Ins-ct 07431, MACN-Bar-Ins-ct 07393
iso_317	Insecta	*Hypoponera* cf. *opacior*	OPR	-24.63	9.26	MACN-Bar-Ins-ct 07399, MACN-Bar-Ins-ct 07409
iso_221	Insecta	*Hypoponera distinguenda*	INP	-24.32	11.04	MACN-bar-ins-ct 06441
iso_225	Insecta	*Hypoponera distinguenda*	INP	-25.42	12.64	MACN-bar-ins-07454
iso_277	Insecta	*Hypoponera distinguenda*	INP	-23.64	11.40	MACN-bar-ins-07524
iso_281	Insecta	*Hypoponera distinguenda*	INP	-24.70	11.10	
iso_298	Insecta	*Hypoponera distinguenda*	INP	-23.69	11.24	
iso_319	Insecta	*Hypoponera distinguenda*	INP	-24.14	11.37	
iso_380	Insecta	*Hypoponera distinguenda*	INP	-25.59	13.31	MACN-bar-ins-ct 07765
iso_315	Insecta	*Hypoponera foreli*	INP	-24.34	11.50	
iso_293	Insecta	*Hypoponera parva*	INP	-25.12	15.96	MACN-bar-ins-ct 06457
iso_297	Insecta	*Hypoponera parva*	OPR	-24.13	12.13	MACN-bar-ins-07453
iso_299	Insecta	*Hypoponera parva*	OPR	-24.36	10.87	MACN-bar-ins-07442
iso_331	Insecta	*Hypoponera parva*	INP	-24.06	11.47	MACN-bar-ins-07450
iso_197	Insecta	*Hypoponera* PEH02	INP	-24.01	9.72	
iso_296	Insecta	*Hypoponera* PEH02	OPR	-24.29	10.03	MACN-Bar-Ins-ct 07420
iso_318	Insecta	*Hypoponera* PEH02	OPR	-23.30	11.48	
iso_320	Insecta	*Hypoponera* PEH02	OPR	-24.25	9.59	MACN-bar-ins-07445
iso_324	Insecta	*Hypoponera* PEH02	INP	-23.54	11.60	MACN-bar-ins-07461
iso_327	Insecta	*Hypoponera* PEH02	INP	-24.08	10.42	MACN-bar-ins-07475
iso_364	Insecta	*Hypoponera* PEH02	OPR	-25.04	12.26	
iso_273	Insecta	*Hypoponera trigona*	INP	-25.25	11.69	
iso_282	Insecta	*Hypoponera trigona*	INP	-24.38	9.98	
iso_283	Insecta	*Hypoponera trigona*	INP	-25.26	9.99	
iso_285	Insecta	*Hypoponera trigona*	INP	-25.39	10.94	MACN-bar-ins-07448

iso_160	Insecta	Ichneumonidae	INP	-27.00	10.41	
iso_163	Insecta	Ichneumonidae	INP	-25.58	10.72	
iso_079	Insecta	Isoptera	INP	-27.69	3.17	
iso_080	Insecta	Isoptera	OPR	-25.56	1.65	
iso_083	Insecta	Isoptera	OPR	-14.87	4.16	
iso_085	Insecta	Isoptera	INP	-26.90	1.44	
iso_086	Insecta	Isoptera	OPR	-25.18	3.60	
iso_087	Insecta	Isoptera	OPR	-25.96	1.57	
iso_369	Insecta	Isoptera	INP	-29.82	6.09	
iso_190	Insecta	*Labidus coecus*	INP	-25.76	10.62	MACN-bar-ins-ct 06400
iso_262	Insecta	*Labidus coecus*	OPR	-25.84	10.81	MACN-Bar-Ins-ct 07415
iso_365	Insecta	*Labidus coecus*	OPR	-26.58	10.31	
iso_218	Insecta	*Labidus praedator*	OPR	-25.88	9.88	MACN-Bar-Ins-ct 07380
iso_264	Insecta	*Labidus praedator*	INP	-25.97	9.75	
iso_266	Insecta	*Labidus praedator*	INP	-26.87	10.37	MACN-bar-ins-ct 06397
iso_361	Insecta	*Labidus praedator*	INP	-26.33	13.26	
iso_118	Insecta	Lepidoptera	OPR	-25.96	5.12	
iso_119	Insecta	Lepidoptera	OPR	-26.57	4.45	
iso_124	Insecta	Lepidoptera	OPR	-28.68	1.91	
iso_129	Insecta	Lepidoptera	INP	-34.15	1.82	
iso_393	Insecta	Lepidoptera	INP	-24.30	11.89	
iso_409	Insecta	Lepidoptera	INP	-30.70	10.86	
iso_420	Insecta	Lepidoptera	INP	-30.01	8.01	
iso_407	Insecta	*Linepithema* sp	INP	-25.97	10.76	
iso_073	Insecta	Machilidae	INP	-29.73	0.02	
iso_406	Insecta	Mantispidae	INP	-26.82	8.86	
iso_060	Insecta	Mantodea	OPR	-25.20	6.27	
iso_064	Insecta	Mantodea	INP	-26.05	5.48	
iso_416	Insecta	Mantodea	INP	-25.64	8.97	
iso_151	Insecta	Megachilidae	INP	-22.48	4.19	
iso_062	Insecta	*Montina* sp	OPR	-27.90	8.04	
iso_125	Insecta	Mutilidae	OPR	-26.71	8.95	
iso_148	Insecta	Mutilidae	OPR	-18.29	8.19	
iso_387	Insecta	Mutilidae	INP	-26.54	2.83	
iso_268	Insecta	*Neivamyrmex* (males)	INP	-25.81	9.11	MACN-bar-ins-ct 06470
iso_176	Insecta	*Neoconocephalus* sp	INP	-21.92	4.55	
iso_178	Insecta	*Neoconocephalus* sp	INP	-26.41	6.14	
iso_121	Insecta	*Neocorynura* sp	OPR	-24.56	3.88	MACN-Bar-Ins-7463
iso_156	Insecta	*Neocorynura sp*	OPR	-25.52	2.74	MACN-Bar-Ins-7463
iso_261	Insecta	*Neoponera bactronica*	INP	-26.03	7.87	MACN-bar-ins-07514
iso_295	Insecta	*Neoponera crenata*	INP	-27.39	10.31	
iso_430	Insecta	*Neoponera curvinodis*	INP	-25.42	10.51	MACN-bar-ins-07529
iso_286	Insecta	*Neoponera fiebrigi*	INP	-27.23	6.56	
iso_306	Insecta	*Neoponera fiebrigi*	INP	-26.91	6.46	MACN-bar-ins-07476
iso_309	Insecta	*Neoponera fiebrigi*	OPR	-26.84	5.61	

iso_174	Insecta	*Neoponera marginata*	OPR	-24.45	14.22	
iso_238	Insecta	*Neoponera marginata*	OPR	-24.76	11.99	MACN-Bar-Ins-ct 07413
iso_311	Insecta	*Neoponera marginata*	OPR	-24.97	14.28	MACN-bar-ins-ct 06486
iso_312	Insecta	*Neoponera marginata*	OPR	-25.21	13.72	
iso_313	Insecta	*Neoponera marginata*	OPR	-24.93	14.18	MACN-Bar-Ins-ct 07360
iso_314	Insecta	*Neoponera marginata*	OPR	-25.13	11.67	
iso_115	Insecta	*Neoponera moesta*	OPR	-27.19	8.37	
iso_308	Insecta	*Neoponera moesta*	OPR	-27.48	7.84	
iso_433	Insecta	*Neoponera moesta*	OPR	-27.36	5.96	MACN-bar-ins-ct 07023
iso_229	Insecta	*Neoponera verenae*	OPR	-25.60	6.07	MACN-Bar-Ins-ct 07353, MACN-Bar-Ins-ct 07400
iso_239	Insecta	*Neoponera verenae*	OPR	-26.30	7.60	MACN-Bar-Ins-ct 07440
iso_243	Insecta	*Neoponera verenae*	OPR	-24.91	6.36	
iso_422	Insecta	*Neoponera verenae*	OPR	-26.06	8.87	
iso_111	Insecta	*Neoponera villosa*	OPR	-27.60	7.84	
iso_112	Insecta	*Neoponera villosa*	OPR	-26.14	8.19	
iso_113	Insecta	*Neoponera villosa*	OPR	-26.31	8.44	
iso_172	Insecta	*Neoponera villosa*	OPR	-25.83	8.81	MACN-Bar-Ins-ct 07350
iso_173	Insecta	*Neoponera villosa*	OPR	-26.86	8.68	
iso_251	Insecta	*Neoponera villosa*	INP	-26.17	7.54	MACN-bar-ins-07446
iso_257	Insecta	*Neoponera villosa*	INP	-25.67	9.62	MACN-bar-ins-07451
iso_260	Insecta	*Neoponera villosa*	INP	-24.68	9.21	
iso_267	Insecta	*Neoponera villosa*	INP	-26.28	7.25	MACN-bar-ins-07460
iso_424	Insecta	*Neoponera villosa*	INP	-27.51	6.43	
iso_425	Insecta	*Neoponera villosa*	INP	-25.83	9.19	
iso_426	Insecta	*Neoponera villosa*	INP	-25.82	8.71	
iso_427	Insecta	*Neoponera villosa*	INP	-26.20	7.93	
iso_428	Insecta	*Neoponera villosa*	INP	-26.39	7.96	
iso_429	Insecta	*Neoponera villosa*	INP	-27.21	5.86	
iso_205	Insecta	*Nylanderia* sp	INP	-25.49	10.23	MACN-bar-ins-ct 06465
iso_376	Insecta	*Nylanderia* sp	INP	-25.62	10.74	
iso_057	Insecta	Odonata	OPR	-19.83	9.85	
iso_228	Insecta	*Odontomachus chelifer*	OPR	-25.06	9.88	
iso_230	Insecta	*Odontomachus chelifer*	OPR	-23.66	9.14	MACN-Bar-Ins-ct 07362
iso_240	Insecta	*Odontomachus chelifer*	OPR	-27.16	8.53	MACN-Bar-Ins-ct 07423
iso_241	Insecta	*Odontomachus chelifer*	OPR	-25.13	7.56	
iso_242	Insecta	*Odontomachus chelifer*	OPR	-25.33	9.61	MACN-Bar-Ins-ct 07352
iso_246	Insecta	*Odontomachus chelifer*	INP	-27.23	9.71	
iso_253	Insecta	*Odontomachus chelifer*	OPR	-25.00	5.14	
iso_259	Insecta	*Odontomachus chelifer*	OPR	-25.21	8.41	MACN-Bar-Ins-ct 07396
iso_227	Insecta	*Odontomachus meinerti*	OPR	-26.20	11.79	

iso_269	Insecta	*Odontomachus meinerti*	OPR	-24.15	8.77	MACN-Bar-Ins-ct 07410
iso_300	Insecta	*Odontomachus meinerti*	INP	-24.10	9.70	MACN-bar-ins-07506
iso_301	Insecta	*Odontomachus meinerti*	INP	-22.59	12.14	
iso_303	Insecta	*Odontomachus meinerti*	INP	-24.44	11.50	
iso_304	Insecta	*Odontomachus meinerti*	INP	-25.91	12.71	MACN-bar-ins-ct 06402
iso_305	Insecta	*Odontomachus meinerti*	INP	-24.85	10.75	
iso_325	Insecta	*Odontomachus meinerti*	OPR	-24.83	8.77	
iso_363	Insecta	*Odontomachus meinerti*	OPR	-25.13	11.20	
iso_377	Insecta	*Odontomachus meinerti*	INP	-25.56	12.25	MACN-bar-ins-ct 07018
iso_332	Insecta	*Odontomachus* PEH01	OPR	-17.69	7.53	MACN-bar-ins-ct 06983
iso_274	Insecta	*Pachycondyla harpax*	OPR	-22.99	13.40	
iso_276	Insecta	*Pachycondyla harpax*	OPR	-25.89	11.60	
iso_278	Insecta	*Pachycondyla harpax*	OPR	-24.67	7.46	
iso_102	Insecta	*Pachycondyla striata*	OPR	-25.50	7.04	
iso_109	Insecta	*Pachycondyla striata*	OPR	-25.52	10.01	MACN-Bar-Ins-ct 07359
iso_110	Insecta	*Pachycondyla striata*	OPR	-25.71	8.36	
iso_169	Insecta	*Pachycondyla striata*	OPR	-26.35	8.20	
iso_170	Insecta	*Pachycondyla striata*	OPR	-24.82	8.28	
iso_171	Insecta	*Pachycondyla striata*	OPR	-25.01	5.25	
iso_216	Insecta	*Pachycondyla striata*	INP	-26.08	10.18	
iso_237	Insecta	*Pachycondyla striata*	INP	-25.38	10.55	
iso_250	Insecta	*Pachycondyla striata*	INP	-26.36	12.54	
iso_252	Insecta	*Pachycondyla striata*	INP	-26.99	9.44	
iso_255	Insecta	*Pachycondyla striata*	INP	-25.86	9.76	MACN-bar-ins-ct 07755
iso_256	Insecta	*Pachycondyla striata*	INP	-26.85	9.52	
iso_375	Insecta	*Pachycondyla striata*	INP	-25.21	12.69	
iso_383	Insecta	*Pachycondyla striata*	INP	-26.11	11.17	
iso_175	Insecta	*Parascopas sanguineus*	INP	-26.35	4.17	
iso_137	Insecta	Passalidae	OPR	-24.00	4.08	
iso_145	Insecta	Passalidae	OPR	-24.58	5.91	
iso_400	Insecta	Pentatomidae	INP	-28.05	2.00	
iso_401	Insecta	Pentatomidae	INP	-26.13	1.53	
iso_402	Insecta	Pentatomidae	INP	-27.01	2.99	
iso_058	Insecta	*Pepsis* sp	OPR	-24.58	10.71	
iso_059	Insecta	*Pepsis* sp	INP	-27.87	10.16	
iso_410	Insecta	Phaneropteridae	INP	-25.88	5.38	
iso_417	Insecta	Phaneropteridae	INP	-26.57	8.19	
iso_180	Insecta	Phaneropterinae	OPR	-25.51	7.76	

iso_181	Insecta	Phasmatodea	OPR	-25.51	2.52	
iso_182	Insecta	Phasmatodea	OPR	-28.57	7.00	
iso_192	Insecta	*Pheidole dinophila*	INP	-26.44	9.58	MACN-Bar-Ins-ct 07404, MACN-Bar-Ins-ct 07428
iso_193	Insecta	*Pheidole dinophila*	INP	-24.14	8.83	
iso_263	Insecta	*Pheidole dinophila*	INP	-23.69	10.01	MACN-Bar-Ins-ct 07383
iso_366	Insecta	*Pheidole dinophila*	OPR	-26.54	9.60	MACN-Bar-Ins-ct 07377, MACN-Bar-Ins-ct 07389, MACN-Bar-Ins-ct 07419
iso_362	Insecta	*Pheidole fimbriata*	INP	-27.01	8.51	MACN-bar-ins-07511
iso_287	Insecta	*Pheidole* PEH06	OPR	-24.20	7.87	MACN-Bar-Ins-ct 07436, MACN-Bar-Ins-ct 07378
iso_194	Insecta	*Pheidole rugatula*	OPR	-25.24	9.71	MACN-Bar-Ins-ct 07408, MACN-Bar-Ins-ct 07432
iso_432	Insecta	*Platythyrea pilosula*	INP	-24.26	14.37	
iso_289	Insecta	*Pogonomyrmex naegelli*	INP	-21.85	5.54	MACN-bar-ins-ct 06469
iso_072	Insecta	*Polistes* sp	INP	-26.61	6.43	
iso_153	Insecta	*Polistes* sp	INP	-26.36	7.62	
iso_155	Insecta	*Polistes* sp	OPR	-25.27	6.69	
iso_158	Insecta	*Polistes* sp	OPR	-26.66	7.52	
iso_150	Insecta	*Polybia* sp	INP	-27.10	7.11	
iso_202	Insecta	*Procryptocerus hylaeus*	INP	-26.85	3.16	MACN-bar-ins-ct 06410; MACN-bar-ins-ct 06884; MACN-bar-ins-ct 06412
iso_203	Insecta	*Pseudomyrmex gracilis*	INP	-25.42	6.49	MACN-bar-ins-ct 06406; MACN-bar-ins-07465
iso_189	Insecta	*Ronderosia bergii*	INP	-30.55	3.38	
iso_139	Insecta	Rutelinae	OPR	-24.71	4.12	
iso_183	Insecta	*Scaphura* sp	OPR	-25.89	4.14	
iso_419	Insecta	*Scaphura* sp	INP	-26.13	5.40	
iso_134	Insecta	Scarabaeidae	OPR	-24.44	11.67	
iso_146	Insecta	Scarabaeidae	INP	-28.82	5.93	
iso_147	Insecta	Scarabaeidae	OPR	-26.08	6.30	
iso_141	Insecta	Scarabeidae	OPR	-24.55	12.66	
iso_392	Insecta	Scarabeidae	INP	-27.30	6.84	
iso_206	Insecta	*Solenopsis richteri*	INP	-18.99	9.44	MACN-bar-ins-ct 06467
iso_135	Insecta	Sphingidae	OPR	-29.82	6.93	
iso_136	Insecta	Sphingidae	OPR	-28.48	5.21	
iso_177	Insecta	*Staleochlora* sp	OPR	-25.03	5.27	
iso_157	Insecta	Stratiomyiidae	OPR	-24.55	4.62	
iso_071	Insecta	*Synoeca sp*	INP	-26.54	3.60	
iso_149	Insecta	Tenebrionidae	INP	-23.92	3.30	
iso_089	Insecta	*Trigona spinipes*	OPR	-24.40	4.61	MACN-bar-ins-07449
iso_090	Insecta	*Trigona spinipes*	OPR	-24.07	4.97	
iso_154	Insecta	*Trigona spinipes*	OPR	-23.63	4.87	
iso_198	Insecta	*Wasmannia auropunctata*	OPR	-24.92	8.73	MACN-Bar-Ins-ct 07391
iso_381	Insecta	*Wasmannia rochai*	INP	-25.92	10.74	
iso_391	Insecta	*Zelus* sp	INP	-25.99	9.23	
iso_012	Liliopsida	*Aechmea distichantha*	INP	-15.84	1.21	
iso_338	Liliopsida	*Billbergia nutans*	INP	-16.53	0.57	
iso_009	Liliopsida	*Chusquea ramossisima*	INP	-30.14	6.24	
iso_334	Liliopsida	*Chusquea*	INP	-29.83	3.10	

		ramossisima			
iso_034	Liliopsida	*Commelina erecta*	OPR	-29.72	-0.63
iso_349	Liliopsida	*Ctenanthe casupoides*	INP	-34.58	5.69
iso_336	Liliopsida	*Cyperus* sp.	INP	-30.95	-0.70
iso_351	Liliopsida	*Dichorisandra hexandra*	INP	-31.25	3.20
iso_005	Liliopsida	*Euterpe edulis*	INP	-34.29	1.62
iso_344	Liliopsida	Euterpe edulis	INP	-36.07	4.36
iso_011	Liliopsida	*Heliconia acuminata*	INP	-29.79	3.70
iso_347	Liliopsida	*Olyra* sp	INP	-35.58	4.15
iso_337	Liliopsida	*Philodendron bipinnatifidum*	INP	-30.21	2.86
iso_006	Liliopsida	Poaceae	OPR	-12.99	4.83
iso_007	Liliopsida	*Pseudananas sagenarius*	OPR	-16.45	2.34
iso_350	Magnoliopsida	*Acalypha* sp	INP	-30.84	4.97
iso_003N	Magnoliopsida	*Acanthaceae*	OPR	-30.17	1.90
iso_333	Magnoliopsida	*Alchornea glandulosa*	INP	-30.74	2.65
iso_340	Magnoliopsida	*Cecropia pachystachya*	INP	-32.33	3.75
iso_335	Magnoliopsida	*Elephantopus mollis*	INP	-31.37	1.88
iso_001N	Magnoliopsida	*Faramea cyanea*	OPR	-32.04	1.53
iso_008	Magnoliopsida	*Faramea cyanea*	OPR	-32.95	1.50
iso_015	Magnoliopsida	*Faramea cyanea*	OPR	-33.68	1.70
iso_014	Magnoliopsida	*Ficus luxeoteana*	INP	-29.89	1.45
iso_016	Magnoliopsida	*Ficus luxeoteana*	INP	-31.71	2.15
iso_348	Magnoliopsida	*Geophila macropoda*	INP	-33.71	2.69
iso_026	Magnoliopsida	*Hydrocotyle* sp	INP	-34.77	-2.58
iso_023	Magnoliopsida	*Miconia collatata*	INP	-33.19	3.45
iso_355	Magnoliopsida	*Miconia discolor*	INP	-33.26	4.53
iso_339	Magnoliopsida	*Nectandra lanceola*	INP	-32.02	1.92
iso_032	Magnoliopsida	*Nectandra megapotamica*	INP	-35.44	1.48
iso_019	Magnoliopsida	*Oxalis rhombeo-ovata*	INP	-35.16	4.42
iso_354	Magnoliopsida	*Oxalis rhombeo-ovata*	INP	-34.52	5.60
iso_343	Magnoliopsida	*Parapiptadenia rigida*	INP	-31.31	2.02
iso_018	Magnoliopsida	*Pavonia sepium*	INP	-31.91	3.97
iso_035	Magnoliopsida	*Piper hispidun*	INP	-32.90	0.92
iso_013	Magnoliopsida	*Plinia rivularis*	INP	-32.87	5.18
iso_036	Magnoliopsida	*Qualea cordata*	OPR	-27.54	0.81
iso_342	Magnoliopsida	*Rhipsalis crusiforme*	INP	-18.68	2.03
iso_346	Magnoliopsida	*Sorocea bonplandii*	INP	-31.38	4.91
iso_033	Magnoliopsida	*Tetracera oblongata*	INP	-29.89	2.86
iso_353	Magnoliopsida	*Trichilia clausseni*	INP	-31.30	5.95
iso_088	Oligochaeta	Annelidae	OPR	-25.59	6.91
iso_025	Polypodiopsida	*Didymochlaena truncatula*	INP	-33.46	3.04

iso_345	Polypodiopsida	*Thelypteris* sp	INP	-36.23	1.51
iso_028	Pteridopsida	*Doryopteris nobilis*	INP	-33.59	0.40
Iso_037	Pteridopsida	*Doryopteris novilis*	INP	-33.30	0.14
iso_017		Plantae	OPR	-27.83	2.38
iso_031		Plantae	INP	-33.05	1.11

Appendix Chapter V

Appendix 5.1

Function “calc_areas” use for the calculation of the area in sofward GNU Octave.

```
function calc_areas(archivo)
        pkg load image
        im = imread(archivo);
        bw = rgb2gray(im) < 240;
        datos = regionprops(bw, "Area", "BoundingBox");
        N = length(datos);
        squadness = zeros(1, N);
        for i=1:N
                area = datos(i).Area;
                box = datos(i).BoundingBox;
                squadness(i) = area / (box(3)*box(4));
        end
        [x, ix] = max(squadness);
        area_metro = datos(ix).Area;
        for i=1:N
                subplot(1,N,i);
                area = datos(i).Area;
                box = datos(i).BoundingBox;
                imshow(imcrop(~bw, box));
                title(sprintf("area = %d px, %.2f m^2", area, area/area_metro));
        end
endfunction
```

Appendix 5.2

D. australis nest estructure

Colonies usually had 2 entrances. These entrances normally merged into a single gallery at 15 cm below the soil surface, which led to the nest chambers. Excavated colonies had between 4 - 8 chambers. The deepest chambers usually were separated of remaining chambers by a long corridor. Maximum deep was always between 86-90 cm (Fig S5.2.1).

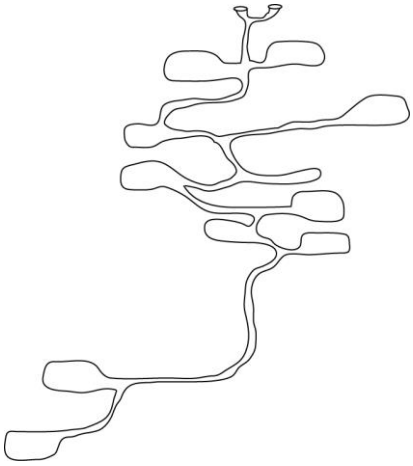


Fig S5.2.1 General drawing of a colony of *D. australis* based on 4 excavated nest in Iguazú National Park.

Some deep chambers were used as refuse deposits. In this chambers coleoptera and diptera larva were found (Fig S5.2.2-Fig S5.2.3). Usually colonies in Iguazú were occupied by another ant (*Pheidole dinophila*). Also cockroaches, snails (*Leptinaria* n. sp.), spiders (*Falconina* n. sp), coleopterans, millipedes and lepidopterans were found associated with *D. australis* nest (Fig S5.2.4-S5.2.8).

Fig S5.4.2. Coleoptera. Collection number MACN-bar-ins-ct 07642 and MACN-bar-ins-ct 07703 (imaged specimen), all were associated to BIN BOLD:ADI9903

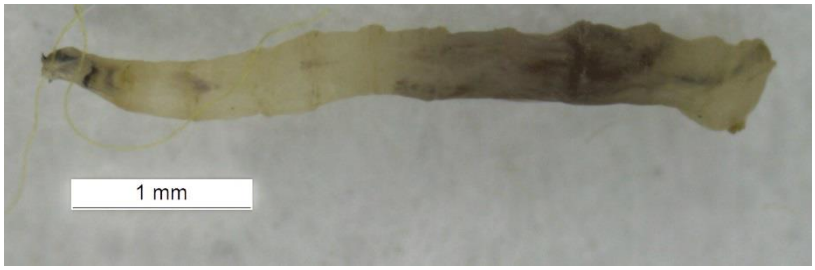


Fig S5.4.3. Diptera. Collection number MACN-bar-ins-ct 07708, MACN-bar-ins-ct 07712 (imaged specimen) and MACN-bar-ins-ct 07653, all were associated to BIN BOLD:ADJ1334

Fig S5.4.4. *Falconina* n. sp. General habitus of female (left) and male (right). Collection number MACN-Ar 38374 and MACN-Ar 38375 respectly.

Fig S5.4.5. Lepidoptera larva. Collection number MACN-bar-ins-ct 07663, MACN-bar-ins-ct 07668 and MACN-bar-ins-ct 07683 (imaged specimen), all were associated with BIN BOLD:ADJ4777.

Fig S5.4.6. Left: *Leptinaria* sp (Subulinidae). Right: Diplopoda, collection number MACN-bar-ins-ct 07667 associated with BIN BOLD:ADI6959.

Fig S5.4.7. Right: Blattodea. Collection number MACN-bar-ins-ct 07650 (imaged specimen), MACN-bar-ins-ct 07670, MACN-bar-ins-ct 07677, MACN-bar-ins-ct 07682, MACN-bar-ins-ct 07691, MACN-bar-ins-ct 07698 and MACN-bar-ins-ct 07718. All were associated to BIN BOLD:ADI9304 Left: Coleoptera. Collection number MACN-bar-ins-ct 07636, MACN-bar-ins-ct 07659, MACN-bar-ins-ct 07669, MACN-bar-ins-ct 07684 (imaged specimen), MACN-bar-ins-ct 07707. All associated with BIN BOLD:ADI8219

Fig S5.4.8. Coleoptera. Collection number MACN-bar-ins-ct 07644.