**Acta Zoológica Mexicana (nueva serie)**, 2026, Volumen 42, 1–9.
https://doi.org/10.21829/azm.2026.4212793
https://zoobank.org/urn:lsid:zoobank.org:pub:475FFB97-A671-461A-8DEE-27CE04F6257D

Original article

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# Interaction network between fleas and medium-sized mammals in an urban reserve in Mexico City

# Red de interacción entre pulgas y mamíferos medianos en una reserva urbana en la Ciudad de México

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Responsible editor: Andrés M. López Pérez

Acta Zoológica Mexicana (nueva serie)

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How to cite:
Glebskiy, Y., Acosta-Gutiérrez, R., Arenas, P., Gil-Alarcón, G., Carrillo-González, G. V., Cano-Santana, Z. (2026) Interaction network between fleas and medium-sized mammals in an urban reserve in Mexico City. *Acta Zoológica Mexicana* (nueva serie), 42, 1–9.

10.21829/azm.2026.4212793
elocation-id: e4212793

Received: 12 August 2025
Accepted: 09 September 2026
Published: 19 October 2026

**ABSTRACT.** Interaction networks between mammals and fleas are a useful tool to predict and monitor disease transmission. However, those networks are lacking for most environments, particularly in urban areas. Therefore, the aim of this article is to build an interaction network between mid-size mammals and fleas in the Pedregal de San Ángel ecological reserve (REPSA), an urban reserve in Mexico City. We pooled information about fleas found on mid-size mammals from six projects carried out between 2019 and 2022. Using these data, we constructed an interaction

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network between fleas and host species. Mammals of REPSA have fewer fleas per host (up to 7.9 on average per host on ringtails, *Bassariscus astutus*) compared to other urban areas. The most common flea, with the highest degree of centrality, was *Ctenocephalides felis*. The rock squirrels (*Otospermophilus variegatus*) appear to be the least connected mammal in the network. We conclude that flea infestation in REPSA is low compared with other urban areas, epidemiological monitoring should be centered on *C. felis* and the diseases transmitted by it, and more studies about rodents are needed.

**Key words:** *Ctenocephalides felis;* opossums; REPSA; ringtails; Siphonaptera

**RESUMEN.** Las redes de interacción entre mamíferos y pulgas son una herramienta útil para monitorear la transmisión de enfermedades. Pero estas redes se desconocen en la mayoría de los ambientes, particularmente en áreas urbanas. Por lo tanto, el objetivo de este artículo es construir una red de interacción entre mamíferos medianos y pulgas en la Reserva Ecológica del Pedregal de San Ángel (REPSA), una reserva urbana en la Ciudad de México. Agrupamos información de pulgas encontradas sobre mamíferos medianos de seis proyectos realizados entre 2019 y 2022. Con base en estos datos, construimos una red de interacciones entre pulgas y hospederos. Los mamíferos de la REPSA tienen pocas pulgas por hospedero (con un máximo de 7.9 en promedio en los cacomixtles; *Bassariscus astutus*), en comparación con otras áreas urbanas. La pulga más común y con mayor conectividad fue *Ctenocephalides felis*. El ardillón (*Otospermophilus variegatus*) es el mamífero menos conectado en la red. Concluimos que la infestación en nuestro sitio de estudio es baja en comparación con otras áreas urbanas, los monitoreos epidemiológicos deben concentrarse en *C. felis* y las enfermedades que esta pueda transmitir y que se requieren más estudios sobre roedores.

**Palabras clave**: Cacomixtles; *Ctenocephalides felis*; REPSA; Siphonaptera; tlacuaches

## INTRODUCTION

Fleas (Siphonaptera) are common ectoparasites that are vectors for a great variety of diseases, including zoonoses (typhus, *Bartonella*, and tungiasis, among others), most famously the Black Plague caused by *Yersinia pestis* (Bitam *et al*., 2010). At the same time, fleas can also impact the hosts by themselves as they consume blood and decrease the overall fitness of animals (Devevey *et al*., 2008).

Interaction networks are an effective way to study fleas and potential pathways for disease transmission. This approach has been successfully used to study small mammals in Brazil (Sponchiado *et al*., 2015, Mendonça *et al*., 2020), among other examples. Those interaction networks have the potential to predict disease transmission between species, which is useful for wildlife management and prevention of zoonoses. However, most of the studies using the network analysis approach have been conducted in small mammals in natural areas (Sponchiado *et al*., 2015, Mendonça *et al*., 2020). In Mexico there are few network studies between fleas and mid-size mammals (Dzul-Rosado *et al*., 2021); also, studies of flea-host networks are scarce in urban areas (but see Dzul-Rosado *et al*., 2021). This is an important knowledge gap since mid-size animals and their ectoparasites could be reservoirs and vectors of zoonotic diseases, and urban species are of special concern for human health due to their close interaction with pets and the human population (Mackenstedt *et al*., 2015).

In particular, there are several mid-size animals in Mexico City (Hortelano-Moncada *et al*., 2009, Guevara-López *et al*., 2016) that could be hosts of many diseases (Romero *et al*., 2015, Camacho-Giles *et al*., 2024), but there are no studies about the flea-host networks related to those mid-size animals. Therefore, the aim of this article is to study the interaction network of fleas and mid-size mammals in an urban natural reserve in Mexico City.

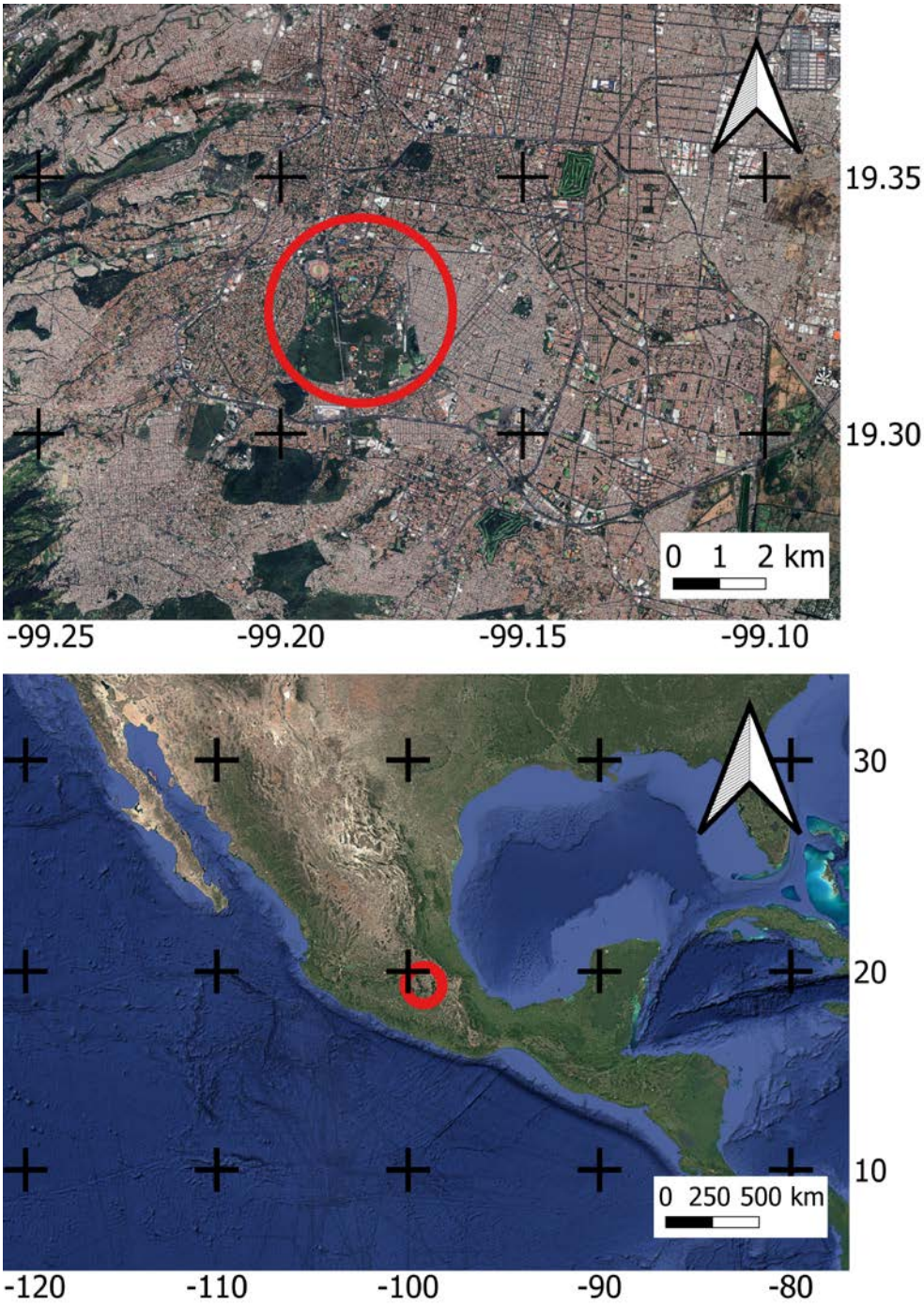



**Figure 1**. The area of sample collection is inside the red circle. Notice that that area of collection is completely surrounded by urban areas.

## MATERIALS AND METHODS

**Location**. This study was performed in and around the Pedregal de San Ángel Ecological Reserve (REPSA by its acronyms in Spanish), located inside the southern portion of Mexico City (Figure 1). This area is composed of several fragments of natural vegetation of xerophytic shrubs covering a total of 237.3 ha (at the time of collection; Lot & Camarena, 2009). REPSA is home to 33 species of native and four exotic mammals (Hortelano-Moncada *et al*., 2009), of which the opossum, *Didelphis virginiana* Allen, 1900, rock squirrel, *Otospermophilus variegatus* (Erxleben, 1777), gray fox, *Urocyon cinereoargenteus* Schreber, 1775, ringtail cat, *Bassariscus astutus* (Lichtenstein, 1830), dog, *Canis familiaris* Linnaeus, 1758, and cat, *Felis catus* Linnaeus, 1758 were considered in this study (based on their size and sample availability).

**Sample collection**. The data for this study was not collected as a single standardized monitoring but rather as a pooling of several projects. The fleas for this study were collected from mammals that were treated at the Wildlife Care Center by the REPSA veterinary team and during several independent studies performed between 2019 and 2022 (for details on those projects, see Glebskiy *et al*. 2022, Carrillo-González 2024, Glebskiy *et al*. 2025a, and Glebskiy *et al*. 2025b). Handling and collection methods varied, and since individuals with no connections are not represented in the interaction networks, only animals with at least one collected flea were considered. The fleas were collected and stored in 70% alcohol until identification. Then they were mounted in slides following the procedures described by Smit (1957) and identified using the keys and descriptions provided by Acosta & Morrone (2003), Salceda-Sánchez (2004), and Traub (1950).

**Statistics**. A bipartite interaction network between fleas and mid-size mammals (weighted by abundance) was constructed using the bipartite package in R, and the connectance (shows how connected the network is, ranging from 0, meaning no connections, to 1, meaning all possible connections) and weighted nestedness (which calculates nestedness considering the frequency of interactions) of the network were calculated (Dormann *et al*., 2009). The interaction network is based on the number of interactions, and it is not affected by the number of fleas found or the effort of collection for each individual animal.

## RESULTS

A total of 404 fleas belonging to 8 species (20 fleas were identified only to genus or family level; see Figure 2) were collected from 111 mammals of six species. The most abundant mammal was the opossum; ringtail cats had the highest intensity of infestation of all mammals (7.9 fleas per infected host), followed closely by the rock squirrels (6.3 fleas per infected host; see Table 1). The most abundant flea was *Ctenocephalides felis* (83.9%, 339 individuals), and it was found in four of the six host species (Figure 2).

In the analysis of interaction networks, two fleas, *Ctenocephalides felis* (Bouche, 1835) and *Echidnophaga gallinacea* (Westwood, 1875), were connected to four of the six mammalian species, and three of these were shared. *E. gallinacea* has the lowest specificity index with 0.41 (node specialization index; Dorman *et al*. 2009). The network connectance is 0.3 and the weighted nestedness is 0.42.

**Table 1**. Number of fleas for each mammal species and flea intensity, total and for each species of flea in REPSA, Mexico City. For this study animals with no fleas were not considered. *C. f.: Ctenocephalides felis, E.g.: Echidnophaga gallinacean, P.s.: Pulex simulans, O.n.: Orchopeas neotomae, O.m.: Oropsylla montanus, E.gl.: Euhoplopsyllus glacialis, P.p.: Plusaetis parus, P.s.: Plusaetis sibynus.*

| Host species | Number of individuals | Total fleas | Fleas per infested host (± standard deviation) | Intensity of each flea infection | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | ***C.f.*** | ***E.g.*** | ***P.s.*** | ***O.n.*** | ***O.m.*** | ***E.gl.*** | ***P.p.*** | ***P.s.*** |
| *Bassariscus astutus* | 10 | 79 | 7.9 ± 12.7 | 6.6 ± 11.3 | 2.8 ± 2.2 | 3 ± 0 | 1 ± 0 | 0 | 0 | 0 | 0 |
| *Canis familiaris* | 1 | 1 | 1 ± 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Didelphis virginiana* | 92 | 297 | 3.2 ± 3.1 | 3 ± 2.9 | 1.8 ± 1.1 | 0 | 0 | 0 | 0 | 1 ± 0 | 1.3 ± 0.4 |
| *Felis catus* | 4 | 6 | 1.5 ± 0.5 | 1.5 ± 0.5 | 2 ± 0 | 0 | 0 | 0 | 1 ± 0 | 0 | 0 |
| *Ortospermophilus variegatus* | 3 | 19 | 6.3 ± 6.1 | 0 | 10 ± 0 | 0 | 0 | 2 ± 0 | 0 | 0 | 0 |
| *Urocyon cinereoargenteus* | 1 | 2 | 2 ± 0 | 2 ± 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

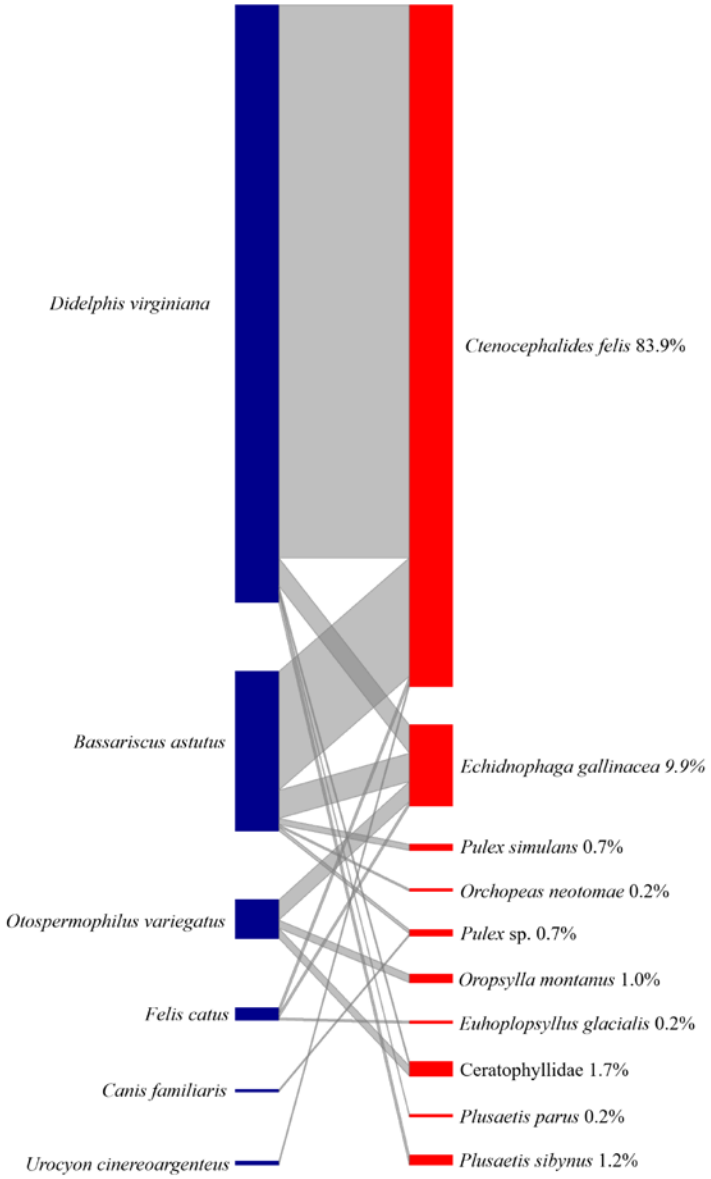



**Figure 2**. Interaction network between mid-size mammals and fleas (including the percentage of fleas collected in this study) in REPSA, Mexico City.

## DISCUSSION

The most common and connected fleas of the network are *Ctenocephalides felis* and *Echidnophaga gallinacea* (Figure 2); this is consistent with Pacheco-Coronel (2010), who found that those species are common in REPSA. These species are common parasites of opossums, which were the most common host in our study (Hernández-Camacho *et al*., 2014, Krueger *et al*., 2016), and are host-generalists (Bitam *et al*. 2010). Those fleas have been reported as vectors for several diseases, such as murine typhus and Rickettsia, among others (Bitam *et al*., 2010, Santoyo-Colín *et al*., 2021, Wu *et al*., 2023); therefore, special attention should be given to zoonoses transmitted by those fleas since they can easily move between animal species due to their connectivity and abundance.

Ringtails and rock squirrels (7.9 and 6.3 fleas per host) were the most infested hosts (Table 1); however, those abundances are relatively low when compared with other studies in urban areas. For example, Penicks *et al*. (2020) found values as high as 69.5 fleas per host in Orange County, California. Interestingly, this value was found for Virginia opossums, and we found only 3.2 fleas per host for the same species. This suggests that midsize animals in REPSA tend to have fewer fleas. Although it also could be related to the fact that most of the animals in this study were handled for purposes other than sample collection, such as medical attention, rehabilitation, or relocation, and this could have led us to underestimate the abundance of fleas. However, other studies in the area show results similar to ours: Pacheco-Coronel (2010), who found average abundances of 8.81 fleas per host for opossums, 6.49 for cats, 2.6 for ringtails, and 1.86 for dogs in the REPSA, and Santoyo-Colín, *et al*. (2021), who found 4.5 fleas per opossum in Mexico City.

From the interaction network, we can observe that rock squirrels appear to separate from the rest of the network and are connected only by *E. gallinacea* (we were unable to identify Ceratophyllidae at a species level; therefore, it is not clear if this connection is valid). These data are similar to those of Martínez-Flores (2013), who found that *Oropsylla montanus* and *E. gallinacea* are the main parasites of rock squirrels. Rock squirrels were the smallest host and the only rodents that were considered in our study, and this suggests that the Rodentia family might have a distinct composition of fleas in our study location. The lack of more rodent species in our study is due to the fact that most studies in our location concentrate on midsize mammals (Pacheco-Coronel, 2010, Glebskiy *et al*., 2021, Carrillo-González, 2024), and small species have been mostly neglected. This is an important knowledge gap since in Mexico *C. felis* has reports of *Rickettsia felis* in rodents (Peniche-Lara *et al*., 2015), and in other countries it has been recorded in *Rattus rattus* and *R. norvegicus* (Psaroulaki *et al*., 2006). Additionally, *Bartonella* has been registered in *Echidnophaga gallinacea* in rodents (Fernández-González *et al*., 2016). Therefore, we recommend performing studies about the parasites of rodents in this location.

Overall our results suggest that midsize animals of REPSA have few fleas per host in comparison with other locations. The most important flea is *Ctenocephalides felis,* and studies of rodent fleas in this area are needed.

**ACKNOWLEDGMENTS.** We are thankful to H.M. Pérez Escobedo and I. Castellanos Vargas for technical support. This project was partially financially supported by PAPIIT grant IN212121 (El efecto de la urbanización sobre el tlacuache *Didelphis virginiana* en un matorral xerófilo de la Ciudad de México) to ZCS.

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