THERYA, 2024, Vol. 15 (3): 255-257 DOI: 10.12933/therya-24-6158 ISSN 2007-3364

Editorial

Advances and limitations in the trophic ecology of bats in Mexico

Diet studies are essential for understanding ecology, evolutionary biology, and informing ecosystem management and restoration (Nielsen *et al.* 2018). The study of feeding and competitive interactions in bats is considered crucial for understanding their ecology in a rapidly changing environment (Salinas-Ramos *et al.* 2020). Nonetheless, studying the bat guild with the greatest species richness, which preys on the largest number of species on the planet in one of the megadiverse countries is a challenge that few researchers have considered, but it must be addressed.

In recent years, there has been a recurring theme in the study of trophic ecology, focusing on the characteristics of bats and their food sources. This approach aims to understand better trophic specialization, particularly in the context of predator-prey interactions between bats and arthropods. These type of studies approach has been made possible mainly by the high level of resolution offered by diet analyses based on high-throughput mtDNA sequencing. Some previous studies had considered this analysis perspective based on diet visually identifying.

However, they were limited in identifying the prey at higher taxonomic levels (*e. g.*, subclass, order, suborder, etc.). Studies in which the presses were classified based on traits such as their hearing ability, hardness, or flight capacity, but with limited precision due to the resolution in taxonomic identification (*e. g.* Bogdanowicz *et al.* 1999; Segura-Trujillo *et al.* 2016). Limited identification resolution regarding the diet composition of arthropodophagous bats has been achieved since pioneering work of Clare (2009). Since then, the studies addressing the trophic theme in different species of bats that prey on arthropods have increased worldwide. However, challenges in studying the trophic ecology of bats persist. Although studies on the molecular identification of arthropod-predating bats' diets have increased globally in the last decade, however, few studies have been conducted in México. The first DNA barcode-based study conducted in México described the diet and trophic overlap of three species of Mormoopidos (*P. davyi*, *P. personatus*, and *P. parnellii*) in Chamela, Jalisco (Salinas-Ramos *et al.* 2015; Figure 1).

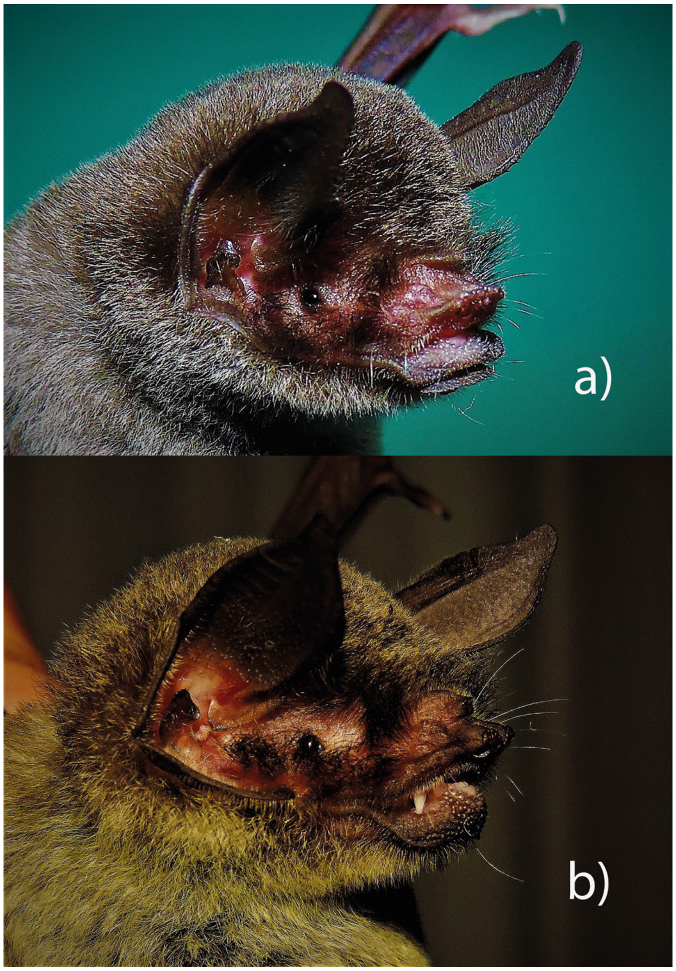

Figure 1. Photographs of two species of Mustached bats, a) *Pteronotus personatus* and b) *Pteronotus parnellii*, currently considered two different species distributed in Mexico, *Pteronotus mexicanus* and *Pteronotus mesoamericanus*. (Photographs by Cintya A. Segura-Trujillo).

Later, 20 species of Mexican bats were researched (*Peropteryx macrotis, Balantiopteryx plicata, Rhynchonycteris naso, Saccopteryx bilineata, Pteronotus mexicanus, Pteronotus mesoamericanus, Pteronotus fulvus, Mormoops megalophylla, Molossus rufus, Nyctinomops laticaudatus, Natalus mexicanus, Macrotus californicus, M. waterhousii, Myotis velifer, M. melanorhinus, M. pilosatibialis, Rhogeessa parvula, R. aeneus, R. tumida,* and *Neoeptesicus furinalis*; Figure 2 and 3), focused in detailing their taxonomic composition and prey traits to describe their trophic segregation and predator-prey interaction based on functional characteristics (Segura-Trujillo *et al.* 2022, 2024). Research on the trophic ecology of arthropod-eating bats in México is currently limited, both by direct identification methods and by molecular analysis of their excreta. It can be difficult to accurately describe the diet of bats in this trophic group because their primary food source, arthropods, is so diverse. To identify the specific types of arthropods they consume, we need information from scientific collections and digital databases such as GenBank, which allow us to identify a larger proportion of their prey at more detailed taxonomic levels.

However, taxonomic identification is only the basis, as it is essential to classify prey based on their functional traits. These traits are helpful for defining interactions with bats or identifying whether bats are preying on species relevant to agriculture or human health. One example, in the case of moths, which are the preferred food of bats, it is difficult to detect them visually in bat droppings due to the low keratin content of their bodies. As a result, their remains are largely broken-down during digestion, making their identification at suborder levels difficult. In research using high-throughput sequencing, most moths can be identified at the family level. However, it is difficult to identify them at the genus or species level because there are not enough sequences of moths from México in GenBank to accurately identify their exact species. In some cases, moths can be identified at the species level when they are of agricultural interest. For example, moths such as *Helicoverpa* sp., *Spodoptera* sp., and *Plutella xylostella*, whose larvae are significant pests in agriculture, have been found in the diet of bats. This is possible because reference sequences for comparison and identification are available, thanks to their importance in the agricultural economy.

Figure 2. Some species' diets have been described through molecular studies in México. a) Black mastiff bat *Molossus rufus*, b) Proboscis bat *Rhynchonycteris naso*, c) Hairy-legged myotis *Myotis pilosatibialis*, and d) Lesser dog-like bat *Peropteryx macrotis* (Photographs by Cintya A. Segura-Trujillo).

Figure 3. Species' diets have been described through molecular studies in México. a) Little yellow bat *Rhogeessa parvula*, b) Black-winged little yellow bat *R. tumida*, (Photographs by Cintya A. Segura-Trujillo).

In this scenario, we have encountered several significant limitations when conducting research in this field. These include limited funding, lack of infrastructure, and the requirement for collaboration with specialist entomologists. Specifically, when it comes to determining diet through molecular studies, there is a need to expand genetic reference databases to Mexican arthropods. In recent years, bats have become one of the most widespread mammals to study. They have gone from being one of the most mythologized animals to one of mammalogists' favorites. Despite this, we still largely ignore their trophic interactions, their importance as pest biocontrol agents, and their vulnerability to the eradication of their prey. Therefore, an invitation to reflect is made to develop strategies for increasing studies on bats' trophic ecology in México.

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