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**Bugs in the Blood: Exploring Trypanosoma Dynamics in Mexican Free-Tailed Bats**

Nearly all mammals are susceptible to infection by trypanosomes, a genus of vector-borne protozoan parasites, with *Trypanosoma cruzi*, the etiological agent of Chagas Disease, posing significant human health risks among endemic countries within the Western Hemisphere. Seventy million people are at risk of infection with symptoms manifesting among the cardiac, gastrointestinal, and neurological systems. While *T. cruzi* has recently been documented in Oklahoma among mammals including canines, raccoons, and bats, research concerning sylvatic transmission in the state is limited. Mexican free-tailed bats (*Tadarida brasiliensis*) are the most abundant bat within the Western Hemisphere, forming the largest colony of mammals in the world. These bats encounter areas endemic to *T. cruzi* during their yearly migration from Mexico through the southwestern United States, where they form large congregations at summer maternity and bachelor roosts in Oklahoma. Additionally, *T. cruzi* is closely related to bat-restricted *Trypanosoma* spp., and the original hosts of these parasites were likely bats. Migratory behaviors of these bats, along with their long lifespans and shared coevolutionary history with the parasite, implicate them as playing a key role in parasite transmission. While *T. cruzi* is merely one of over a hundred *Trypanosoma* species infectious to mammals, this research provides insight into the transmission dynamics of overlooked trypanosomes among wildlife populations. During monthly sampling trips from 2022-2024, we collected blood and morphometric data from over 400 Mexican free-tailed bats at two roosts in northwestern Oklahoma. PCR targeting the *ssrRNA* gene shared across mammalian trypanosomes and subsequent gel electrophoresis confirmed *Trypanosoma* spp. infection in at least 8% of bats. We further tested how infection risk varied by reproductive status, age, sex, year, and sampling month using generalized additive models. Positive samples were sequenced at the NCSU Genomic Sciences Laboratory to confirm infection, identifying at least *Trypanosoma dionisii*, which shares a close evolutionary relationship with *T. cruzi*. Evaluating the drivers and diversity of trypanosome infection among these migratory bats will provide insight into host-parasite dynamics and the endemicity of the parasite within the southwestern United States.