Interactions between *Pseudogymnoascus destructans*, bat immunity, and ectoparasite-mediated transmission of blood parasites

Bats provide essential ecosystem services while hosting diverse parasites and pathogens of relevance to conservation and One Health. Emerging fungal diseases such as white-nose syndrome, caused by *Pseudogymnoascus destructans*, may disrupt host immunity and alter susceptibility to co-infections. However, interactions among fungal pathogens, ectoparasites, and haemoparasites remain poorly understood, particularly in tropical systems and at wildlife–human interfaces where anthropogenic pressures may reshape transmission dynamics.

We are conducting an ongoing disease ecology study in Cusuco National Park and the adjacent community of Buenos Aires, Honduras. This protected-area/community interface is characterised by ecotourism, livestock presence, and deforestation, creating opportunities for altered host condition and pathogen exchange. Free-ranging bats are sampled using mist nets and harp traps to assess body condition, ectoparasite burden, and infection status. Focal species include the common vampire bat, *Desmodus rotundus*, and *Bauerus dubiaquercus*, a Near Threatened species.

Individuals are examined for ectoparasites (bat flies, mites, ticks), screened for haemoparasites including trypanosomes and haemosporidians via blood samples and molecular methods, and assessed for fungal pathogens including *P. destructans* and cuticular fungi of the order Laboulbeniales. We test four hypotheses: (1) *P. destructans* infection is associated with altered ectoparasite intensity; (2) *P. destructans* infection is associated with altered susceptibility to haemoparasites, consistent with immune-mediated trade-offs; (3) ectoparasites can serve as surveillance tools for haemoparasite detection; and (4) Laboulbeniales infection is negatively associated with haemoparasite prevalence, suggesting a role in limiting pathogen transmission.

Sample processing and molecular screening are ongoing. Planned analyses will quantify parasite prevalence, co-infection patterns, and associations among fungal infection, ectoparasite burden, and haemoparasite status across the protected area/community gradient, including detection of haemoparasites within collected ectoparasites. Generalized linear mixed models will evaluate associations between infection status, parasite intensity, and host body condition, accounting for species identity and sampling location. Co-infection networks will characterise parasite community structure across the wildlife–human interface. This study will generate baseline data for long-term surveillance and inform One Health risk assessment in anthropogenically changing landscapes.