Biota Grant

Aim1: Conduct a thorough conservation status re-assessment for Madagascar’s three pteropodids

Objective1.3: Quantify dispersal and connectivity between fruit bat sub-populations spanning five diverse Madagascar eco-regions.

* Anticipate largescale genetic panmixia
* GPS telemetry approaches will show highly localized behavior for all three bat species
* Though localized preferences may not be sufficient to provide genetic structure, they may still provide refugia to shape metapopulation dynamics and play an important role in pathogen dispersal for these key reservoirs for human disease

Approach

* At each of 5 ecoregion sites
  + A subset of juvenile bats twill be fitted with VHF telemetry to determine survival rates, then followed for one year to estimate survival rates
    - 30 per species
  + Subset of adult *P. rufus* will be fit with GPS telemetry devices to support connectivity estimates
    - 2 adult F 2 adult M from each ecoregion

Budget

* 90x ATS telemetry tags @ $150 each + 1x ATS radio receiver
* 20x Microwave telemetry tags @ $3000 each

General Notes

* ATS tags need to be at a location sampled monthly aka our three normal sites
  + *P rufus*, *R madagascariensis*, *E dupreanum*
* GPS tags can be put anywhere and remain functional for up to one year
  + 2 M 2 F from each of 5 *P rufus* locations
  + *Eidolon dupreanum* at Angovokely
    - Never been tracked before, two known sites, maternal roost
    - Angavokely virus is interesting
  + *P rufus* in valley
    - Most threatened
    - Known metapopulation dynamics
  + Should split M and F, only adults
* Data from this won’t be available until up to one year after setting out tags, so will need to do modeling in the meantime for final chapter
* What is the most interesting to model?
  + Movement ecology and disease dynamics

GPS tags

* Longest 539 days, average F 93, average M 139
* Tracks using Google Earth and ArcMAP10
* Minimum convex polygons (MCPs) to determine homeranges
* Foraging areas: analyzed utilization distribution discontinuities
  + MCP area against percentage inclusion of fixes
  + Using Ranges 7
* Identify roosting sites
* Fixes – reads of data

\*evidence of direct movement between different caves and have found that there is genetic similarity between viruses detected in geographically distant locations

\*spp exists as a large metapopulation with virus circulation over broad geographic ranges

\*plowright suggested metapopulation dynamics were necessary for HeV persistence in Australian pteropodids

\*movement between colonies within the period short enough for infection to occur and for a bat to become infectious

* Small paper just on movement stats
  + Pteropus spp have been done a lot
* Connectivity estimates for modeling paper
* Test maximum bounds of Pteropus movement to get an idea of panmixia of Madagascar
* Comparison of connectivity between species