A web of parasite links revealed by metabarcoding

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Running head: Multi-parasite networks

Abstract

Introduction

* Why is parasite sharing important?
* Problems previously (methods, can’t differentiate). Work based on species records.
* Our solution
* General hypotheses and patterns of interest
  + Species richness based on host attributes
    - Specific directional hypotheses
  + Connections – what predicts who is linked to whom?
    - Specific directional hypotheses
  + Compare these to database methods

Methods

* Field sampling
* Extractions
* PCR (qPCR and PCR)
* Sequencing
* Bioinformatics
* Additional filtering
* Database/lit search methods
* Statistics

Results

Discussion

* Important concession that this is more *likely* links – can’t definitively say if sharing is true
* Emphasize need for better parasite archiving and genetic resources (point about preservation)

References

Figure 1: Some sort of breakdown by species – could also have a table summarizing the steps (how many samples we started and ended with)

Figure 2: Correlations between OTU richness and host attributes

Figure 3: NMDS plot of psite communities (this could also potentially be a PCA that aggregates within species and then uses some sort of species metrics)

Figure 4. Network of connections with specific network metrics as hypothesized above.