

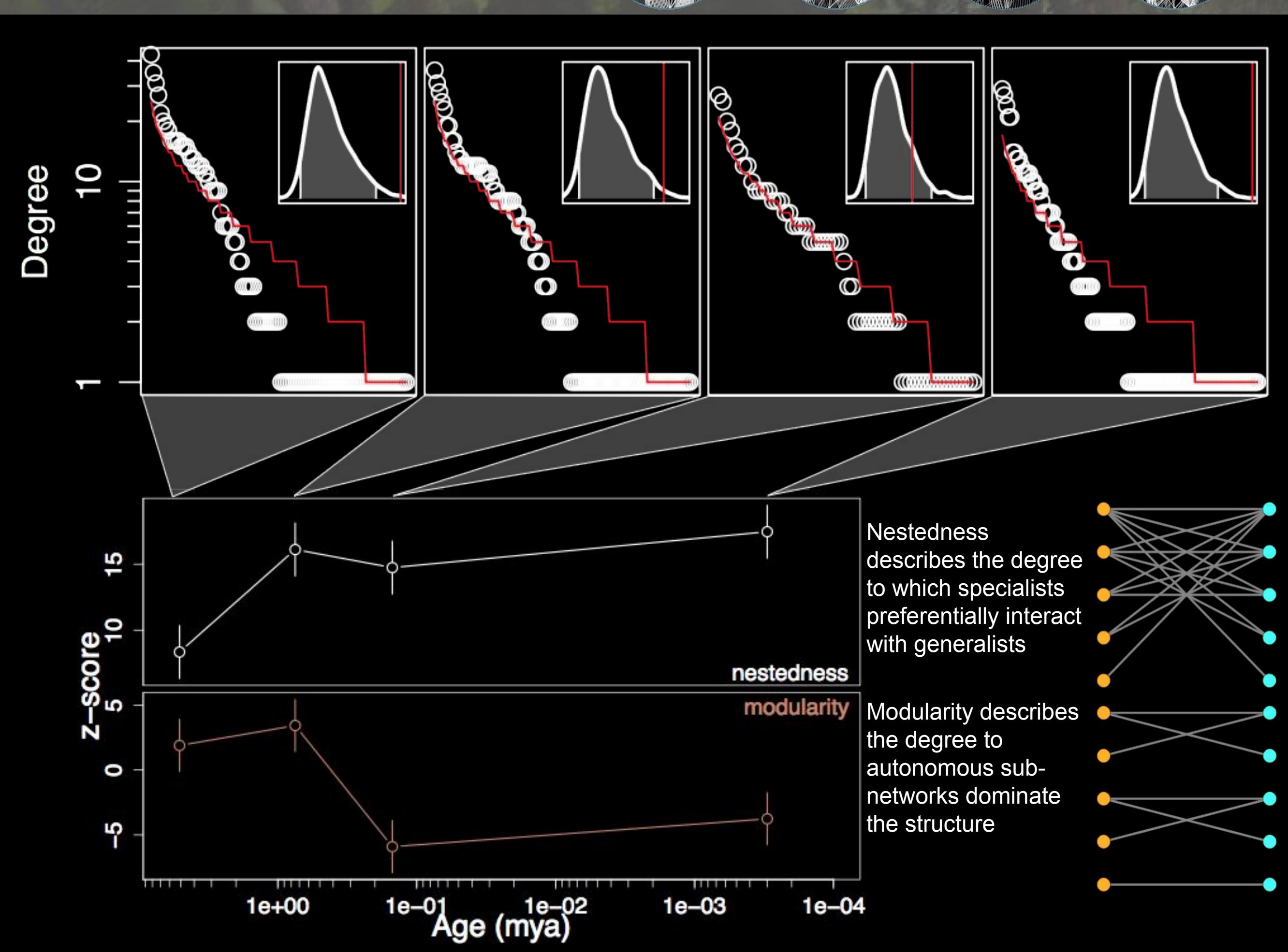
Integrating Ecology and Evolution Using the Dynamic Landscape of Hawaii

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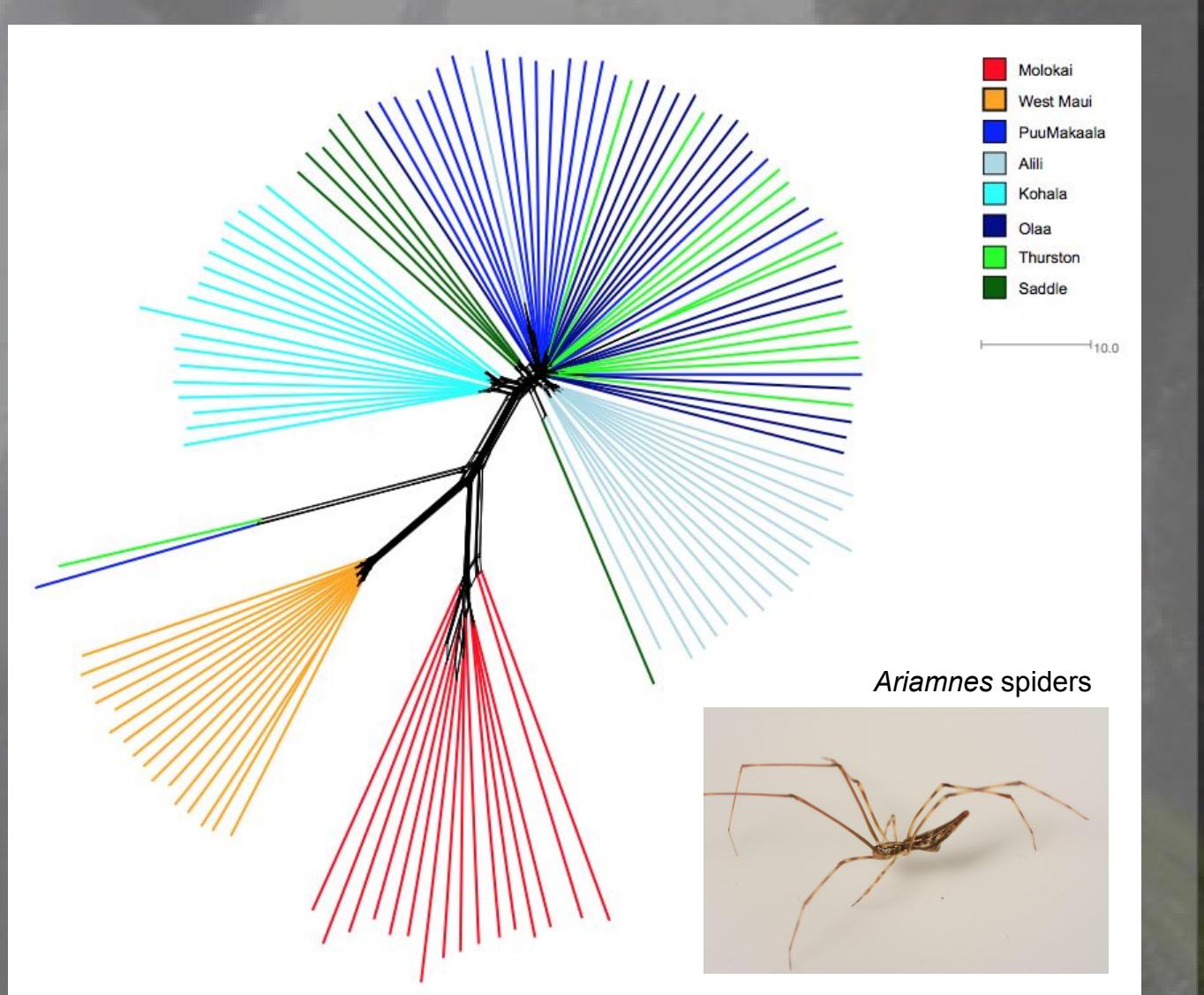
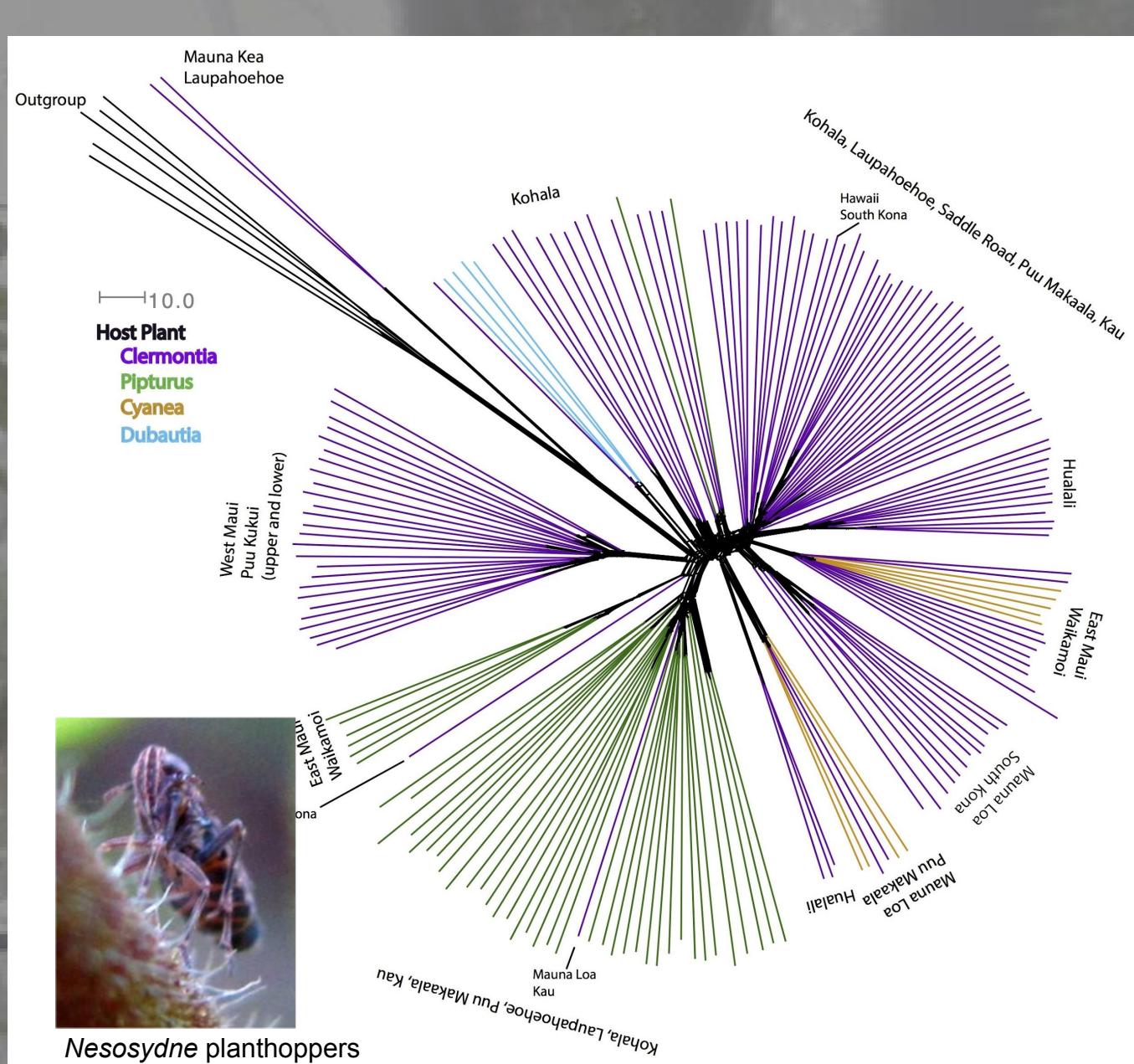
Understanding the origins of biodiversity requires disentangling the influence of evolutionary/historical processes from ecological processes. What makes this difficult is that ecological and evolutionary processes form a spatiotemporal continuum; while we can observe and test local ecological phenomena, we must infer past evolutionary processes from current observations. Remote island archipelagoes, in particular those with well defined chronologies, provide an opportunity to synthesize ecology and evolution. We use the Hawaiian Archipelago as a natural experiment to address a fundamental question in biodiversity—how do ecological processes (e.g. colonization and ecological fitting) interact to give rise to larger and longer term processes of adaptation and species diversification?

Food webs

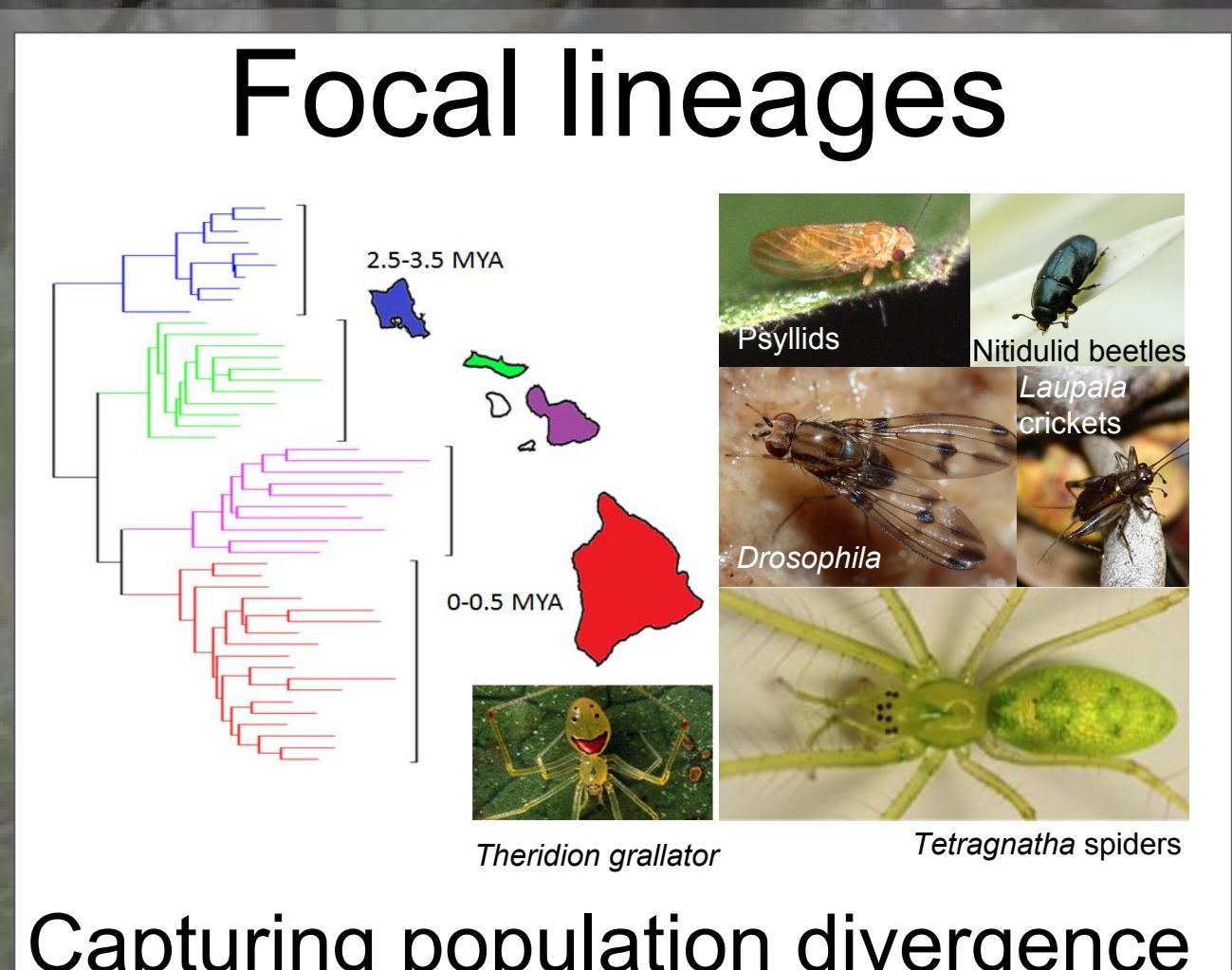


Patterns in degree distributions of herbivorous hemipterans across sites show that networks deviate most from maximum entropy predictions on youngest and oldest sites. The trade-off between early immigration and later co-diversification is consistent with the maximum entropy analysis showing that the middle-aged site is in equilibrium.

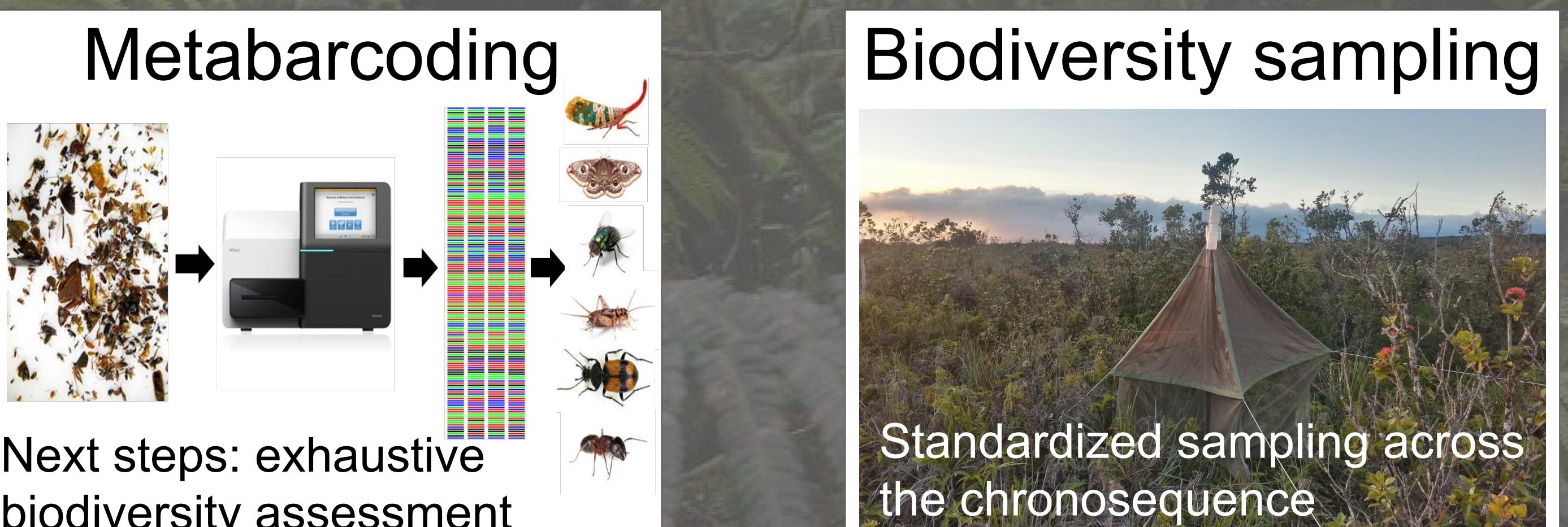
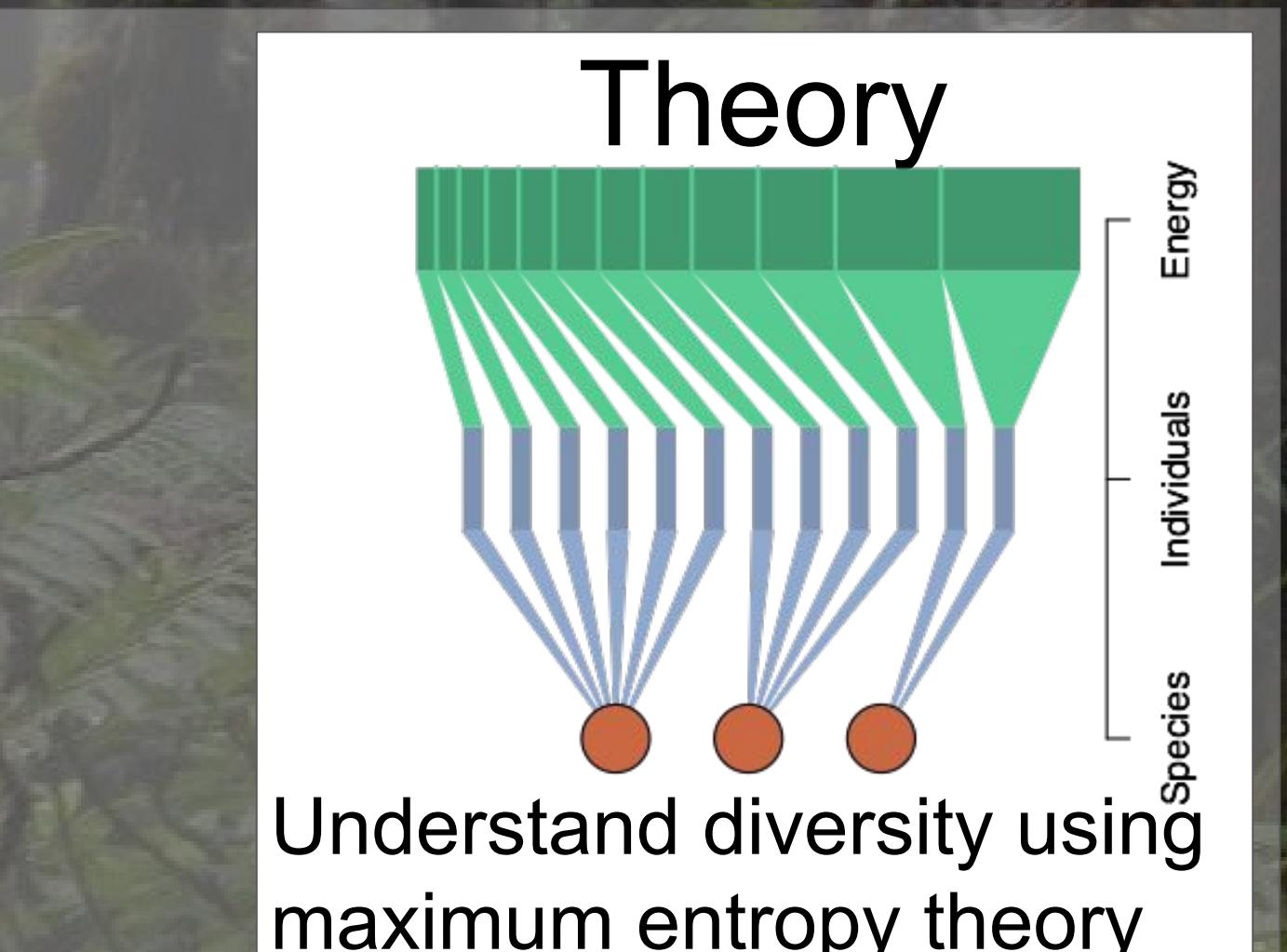
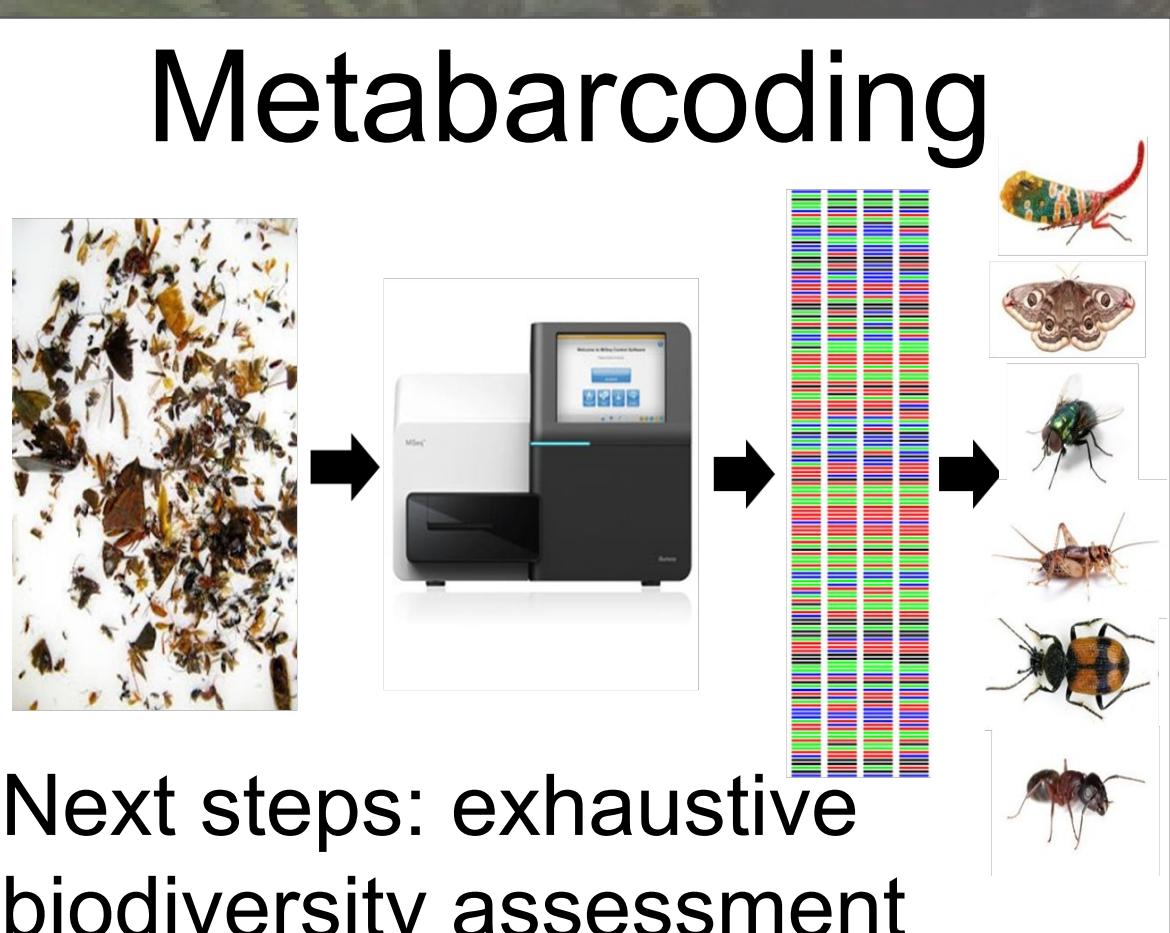
Population Genomics



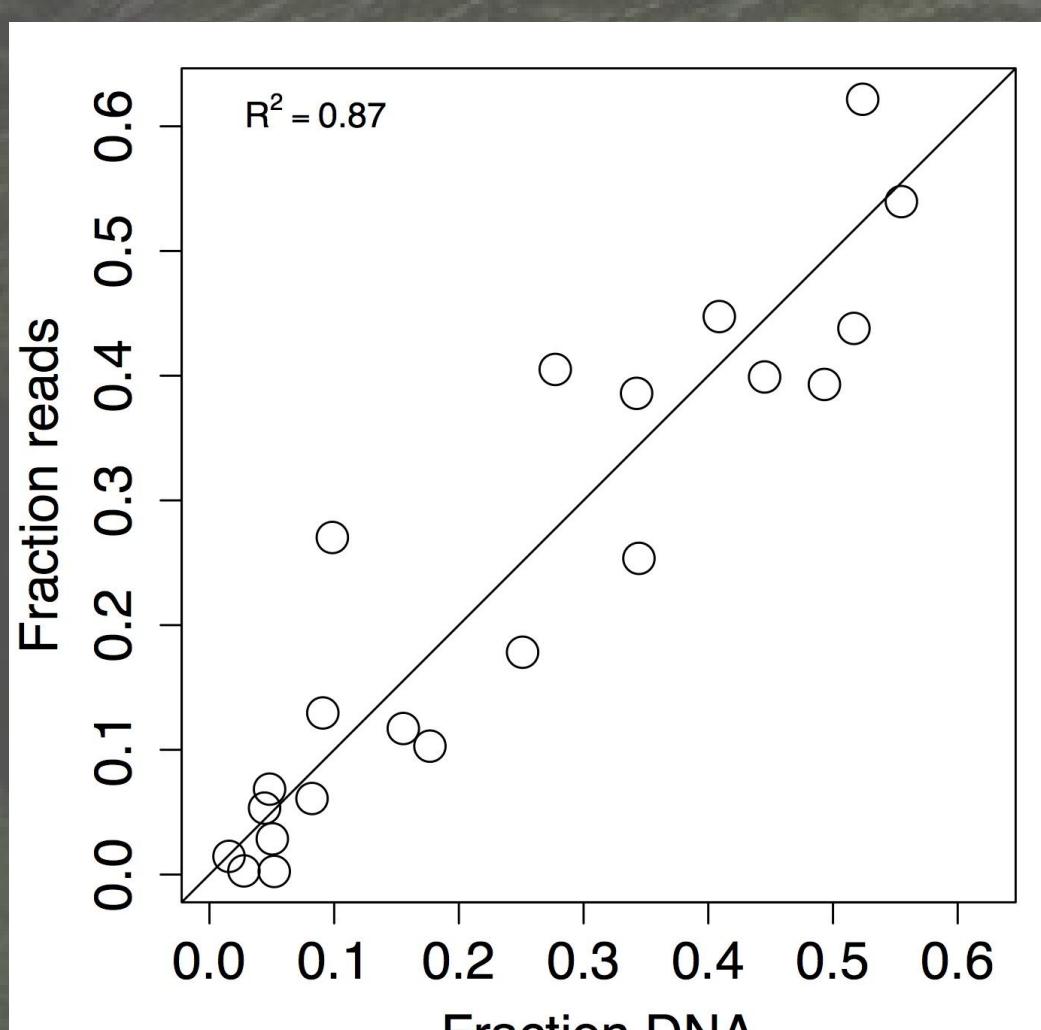
Splits trees, estimated from exon capture and RAD data, showing population divergence based on geography and ecological interactions.



How does the evolutionary history of biotas influence their contemporary ecological equilibrium?



High throughput ecology



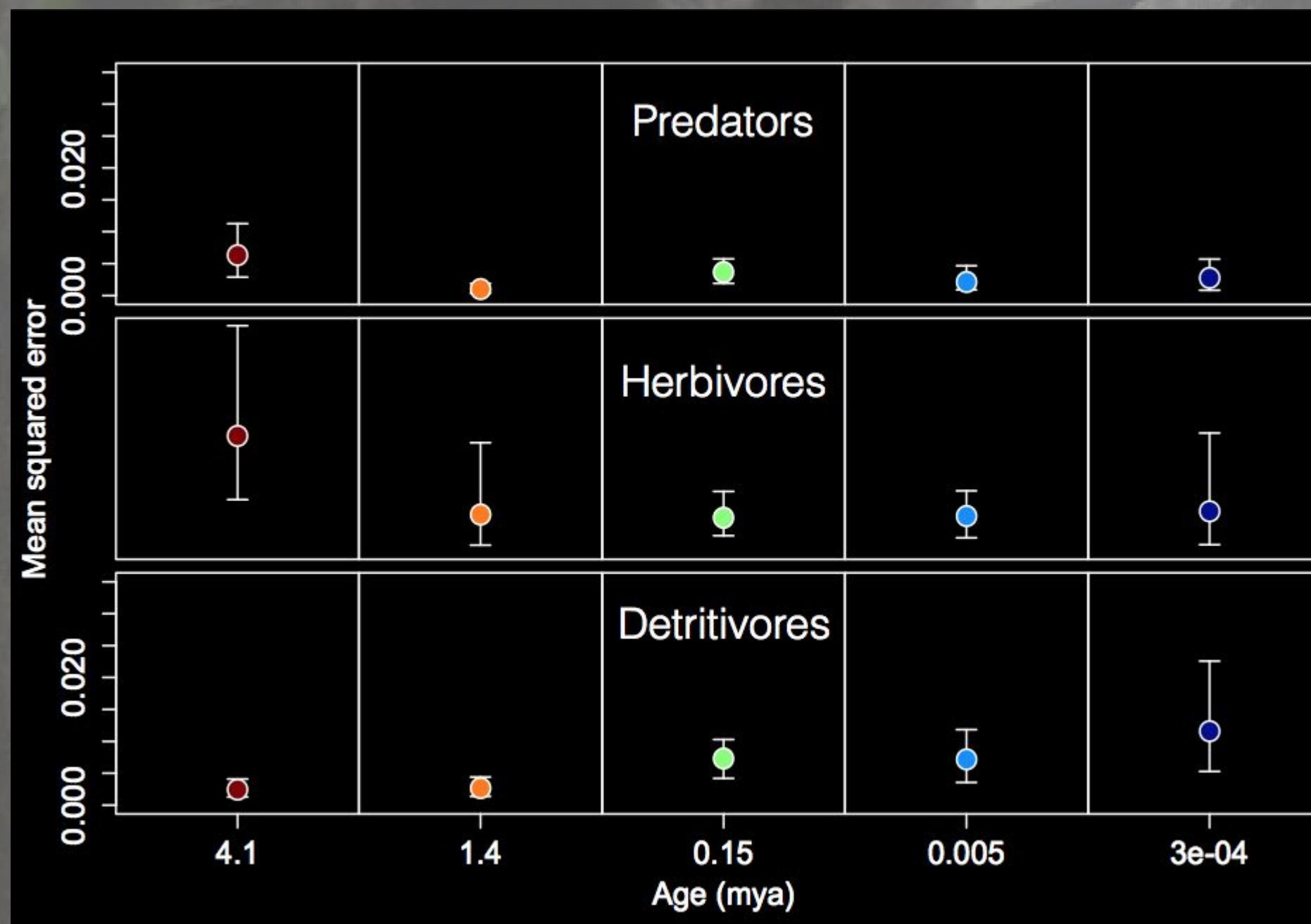
Experiment to evaluate recovery of abundance from sequence data

Next generation sequencing based taxonomy, species abundance estimates and gut content analysis of consumers

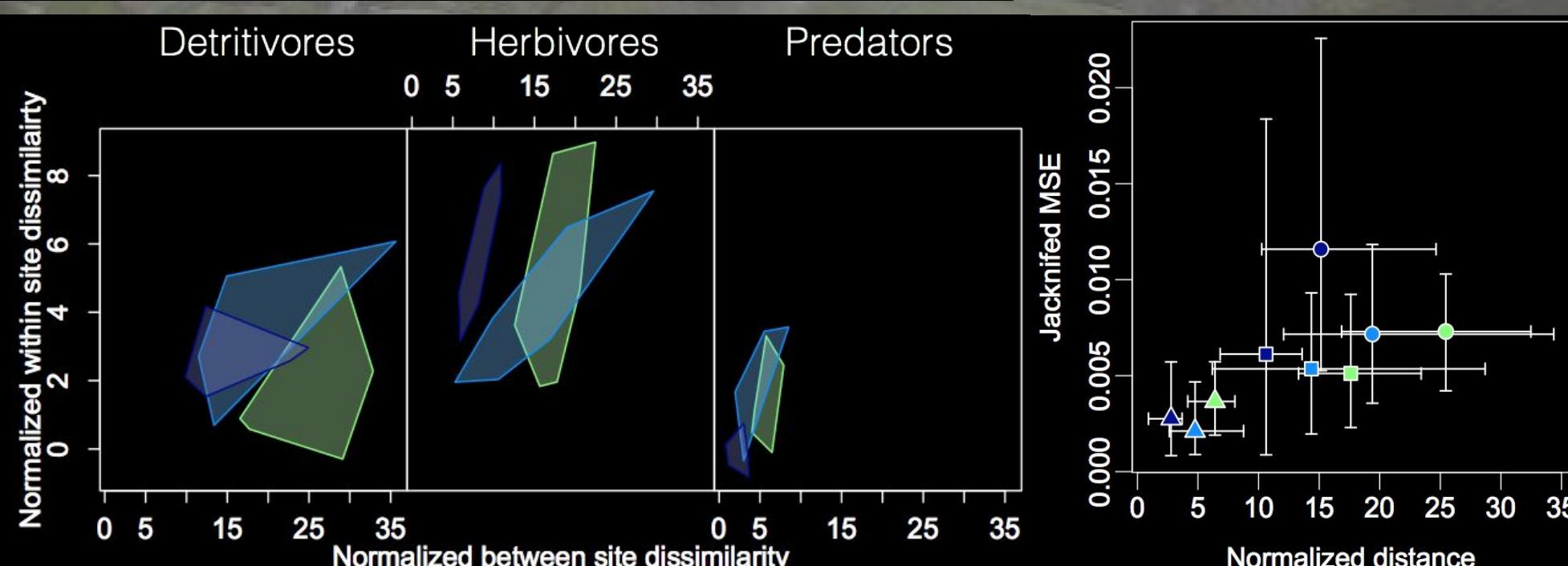
With these approaches we can evaluate the phylogenetic structure of all ecological patterns

Community Structure

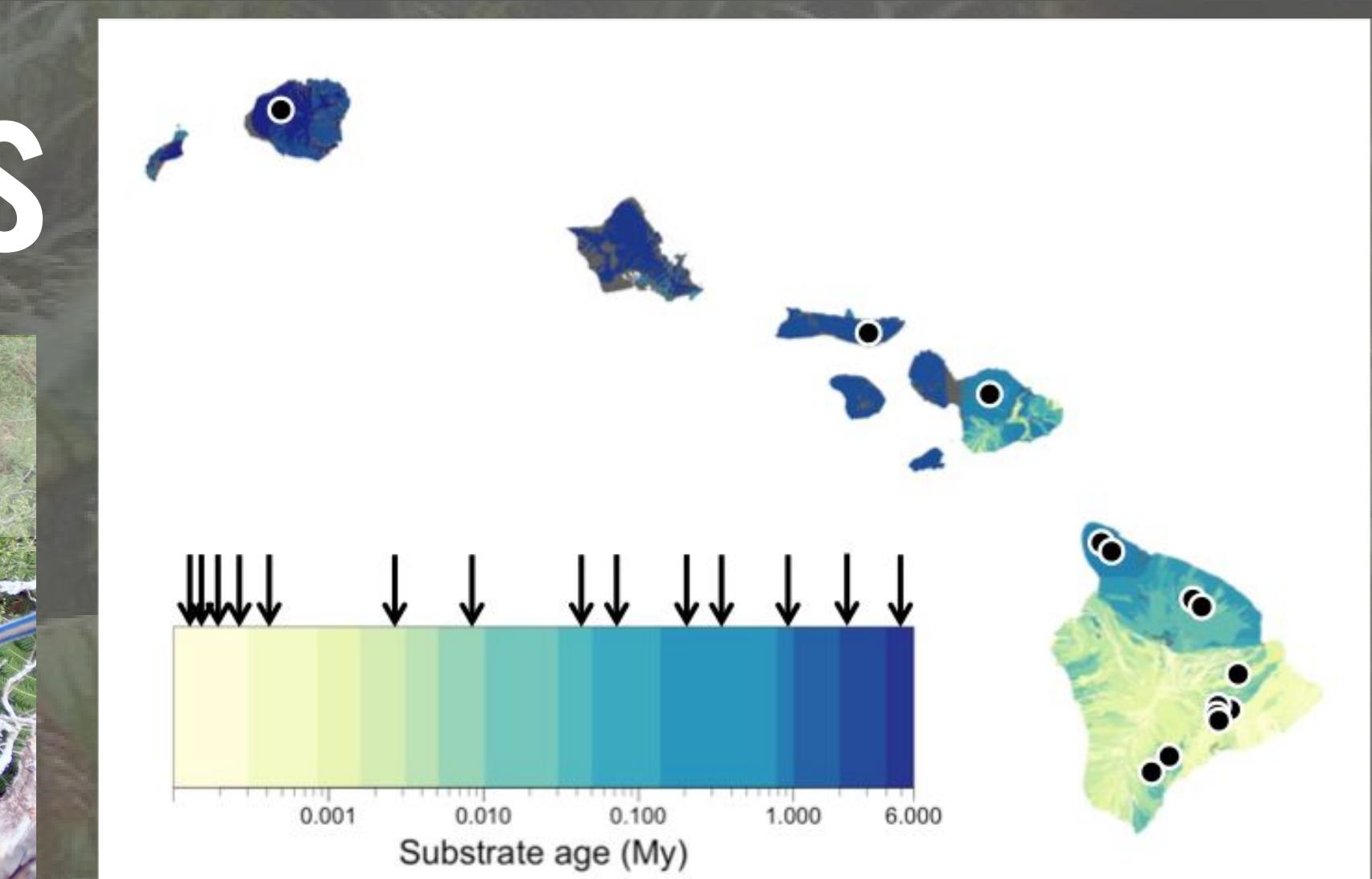
Different trophic groups show different patterns of deviation from maximum entropy theory with respect to substrate age.



With data from PI Gruner's study (2007 *Biol. J. Linn. Soc.*), we see that herbivores deviate from theory most at young and old sites, consistent with foodweb analyses.



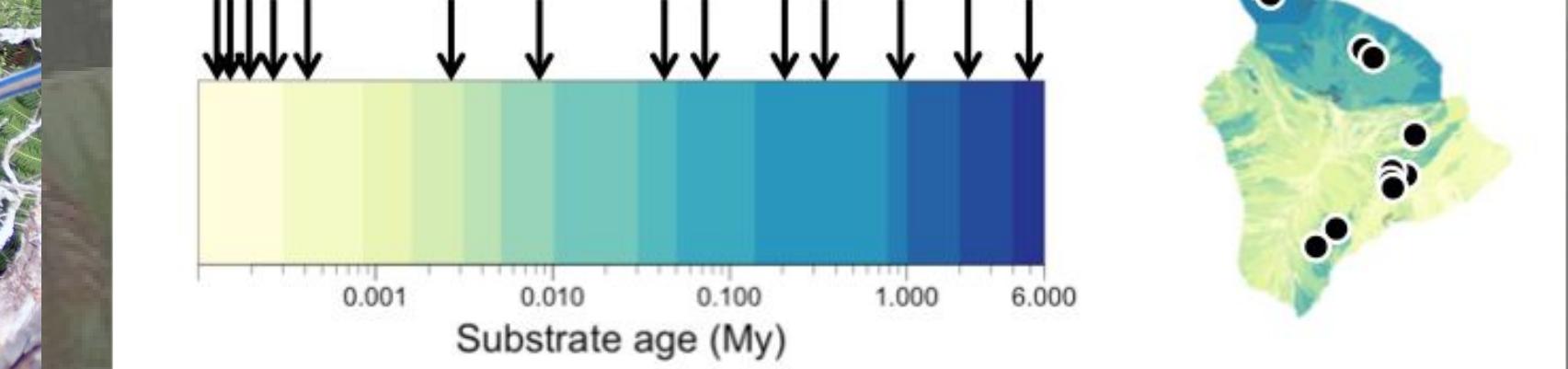
In the youngest sites beta-diversity is correlated with deviation from theory



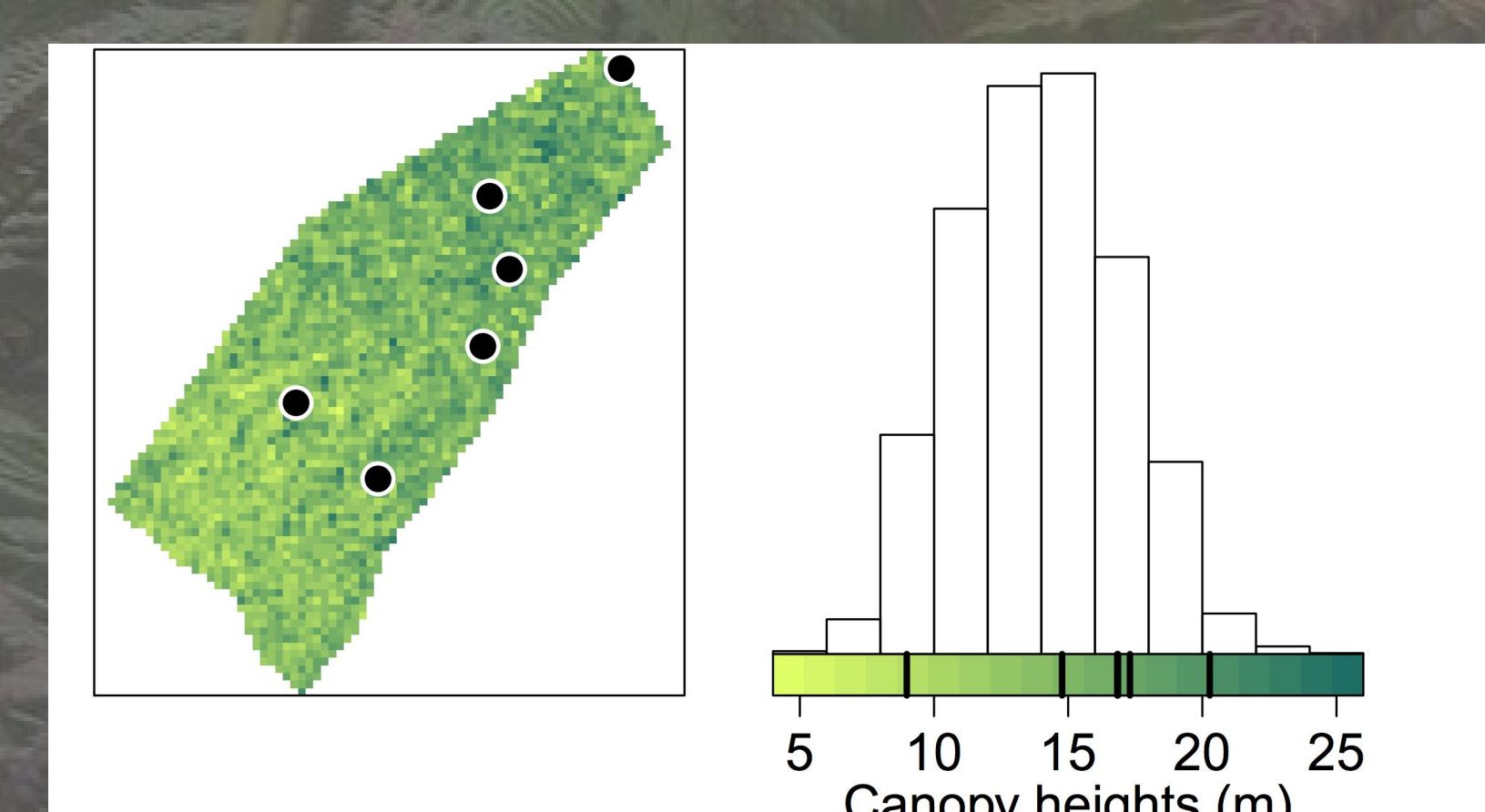
Field sites



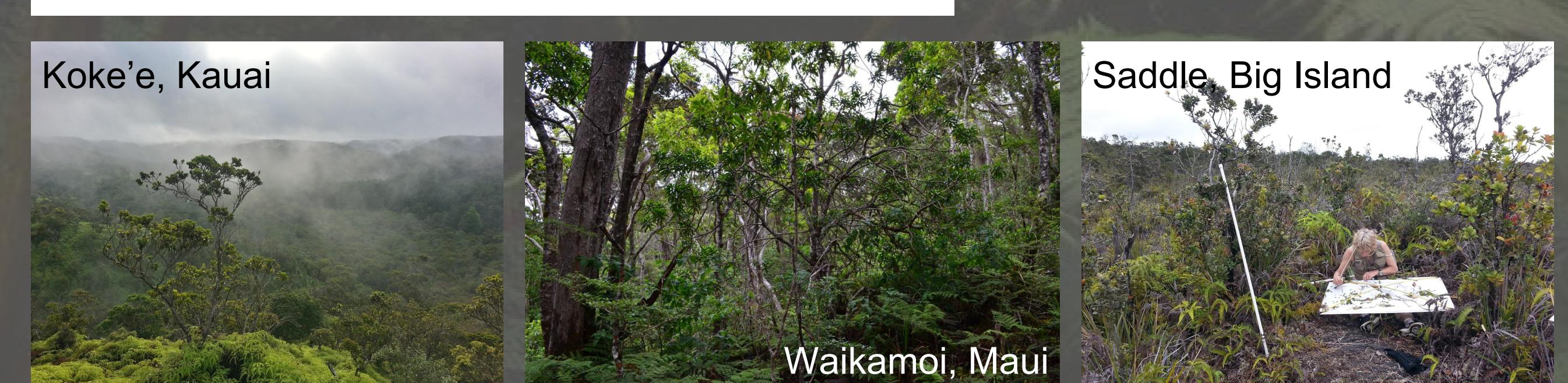
Arthropod sampling in the canopy



Sites were selected to represent the chronosequence, but constrained to similar elevation and precipitation.



Within sites, we used Carnegie Airborne Observatory data to select six random replicate plots, stratified with respect to canopy heights



We would like to thank the National Science Foundation for making this work possible, as well as the dedicated land managers in Hawaii.