MOLECULAR RESOLUTION FOR ISLAND RESTORATION

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Island Restoration

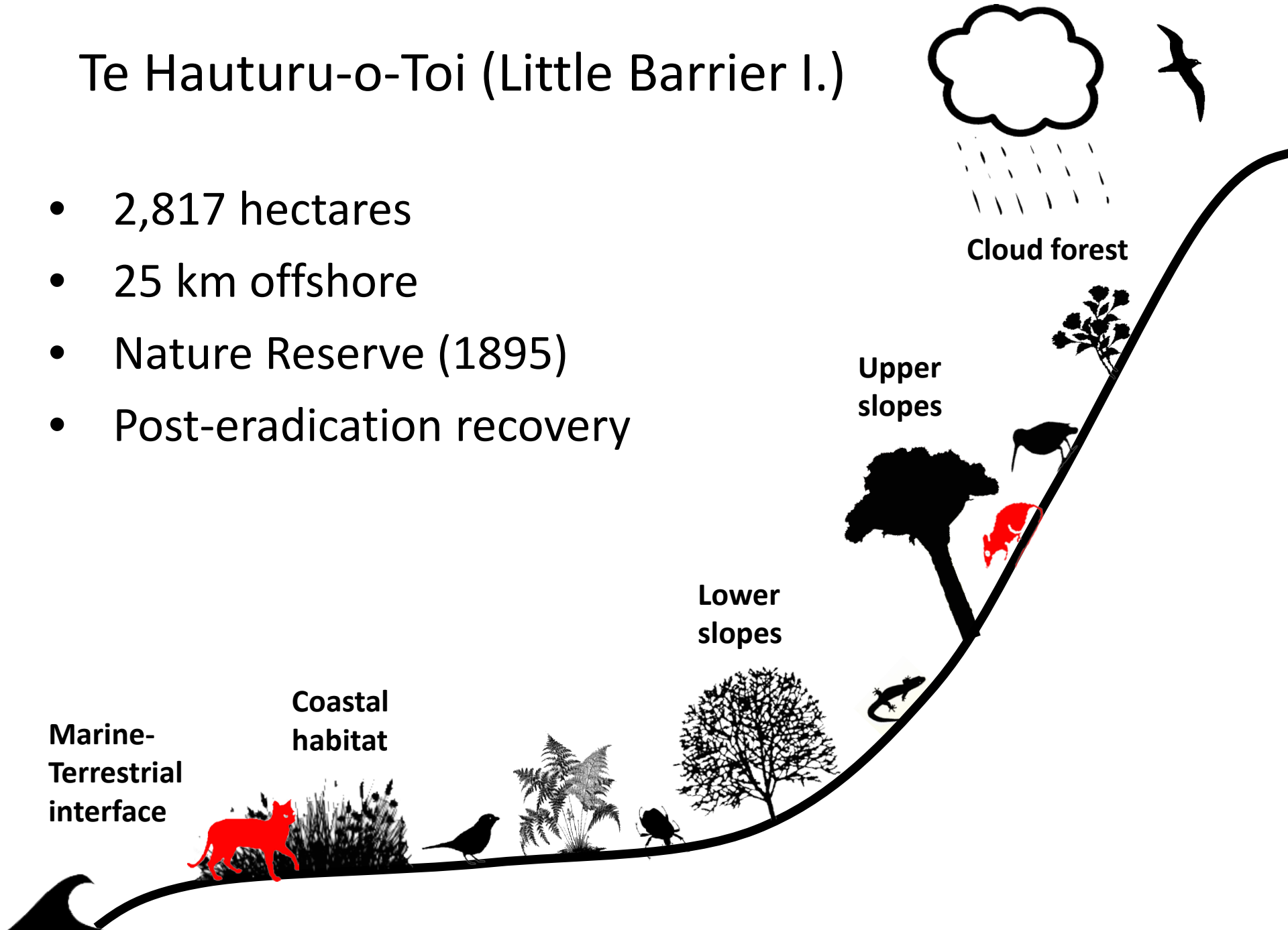
- Ecosystems are complex and most components, particularly cryptic, small and microbial, remain undiscovered
- Methods are needed for rapidly collecting data to set restoration targets and monitor whole-ecosystem recovery following conservation interventions
- Advances in molecular tools, particularly next-generation sequencing, are a powerful framework
  - characterise ecosystems by species bar-coding
  - phylogeography and species-abundance

A Model Ecosystem

- We established a **pilot** project to test the feasibility of phylogenetically and environmentally characterizing every species in a well-defined New Zealand island ecosystem using modern sequencing, informatics and biogeography **CURRENT STATUS**
- We then can investigate important ecological questions from conservation (eradication recovery, climate change) to theoretical (unified neutral theory of biogeography and biodiversity) over time and space

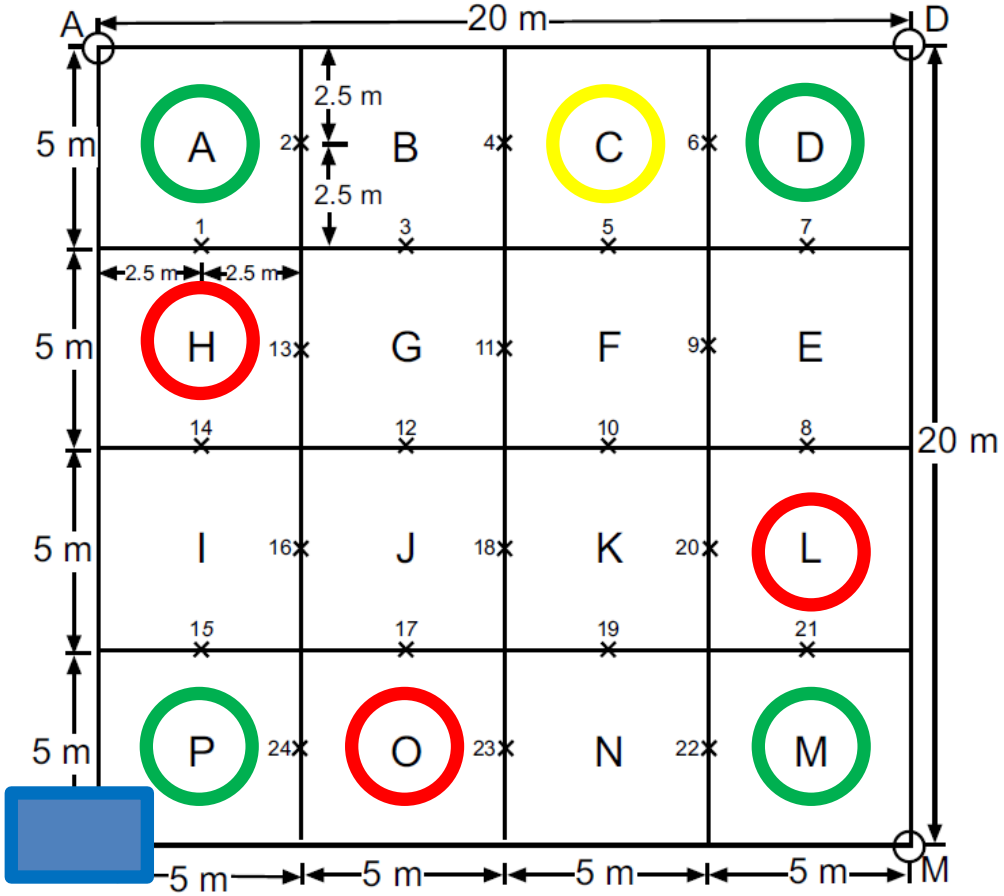
Te Hauturu-o-Toi (Little Barrier I.)

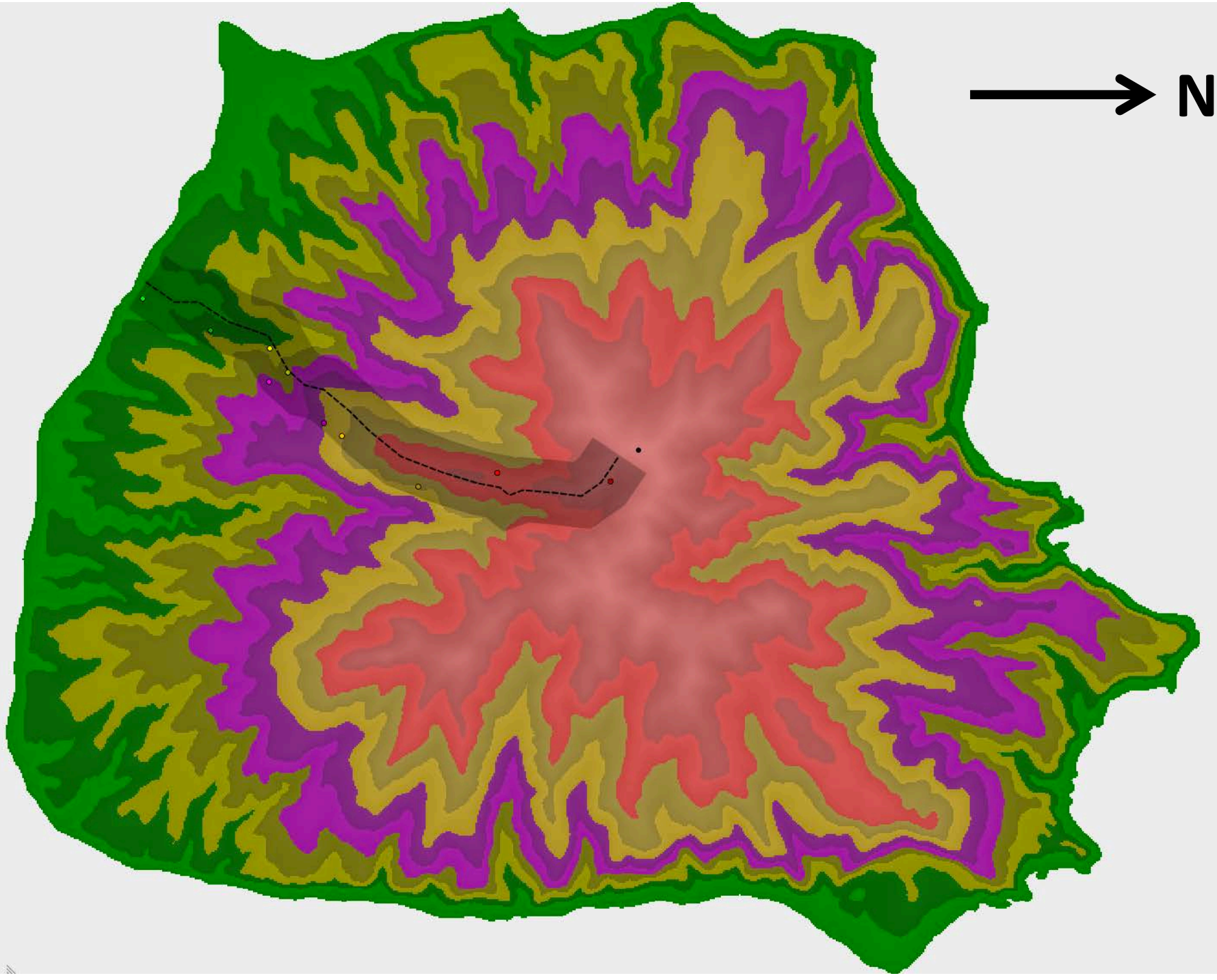
- 2,817 hectares
- 25 km offshore
- Nature Reserve (1895)
- Post-eradication recovery



Sampling Strategy

- Ten sampling sites on an elevational gradient



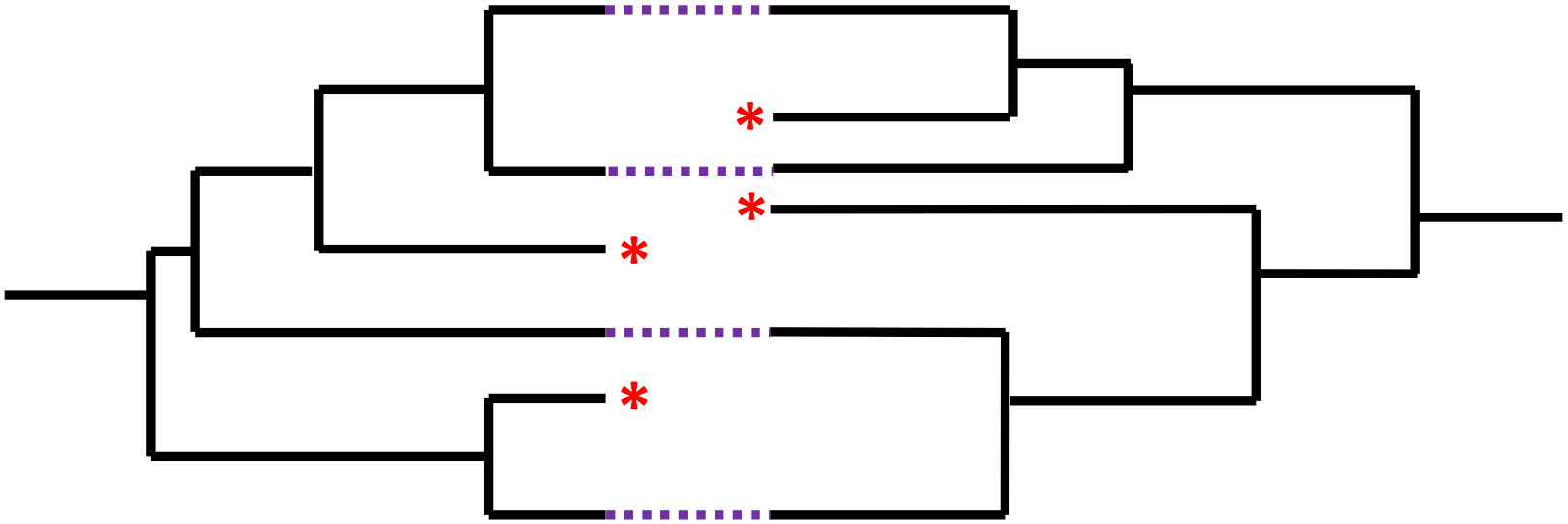

N

Molecular Tools

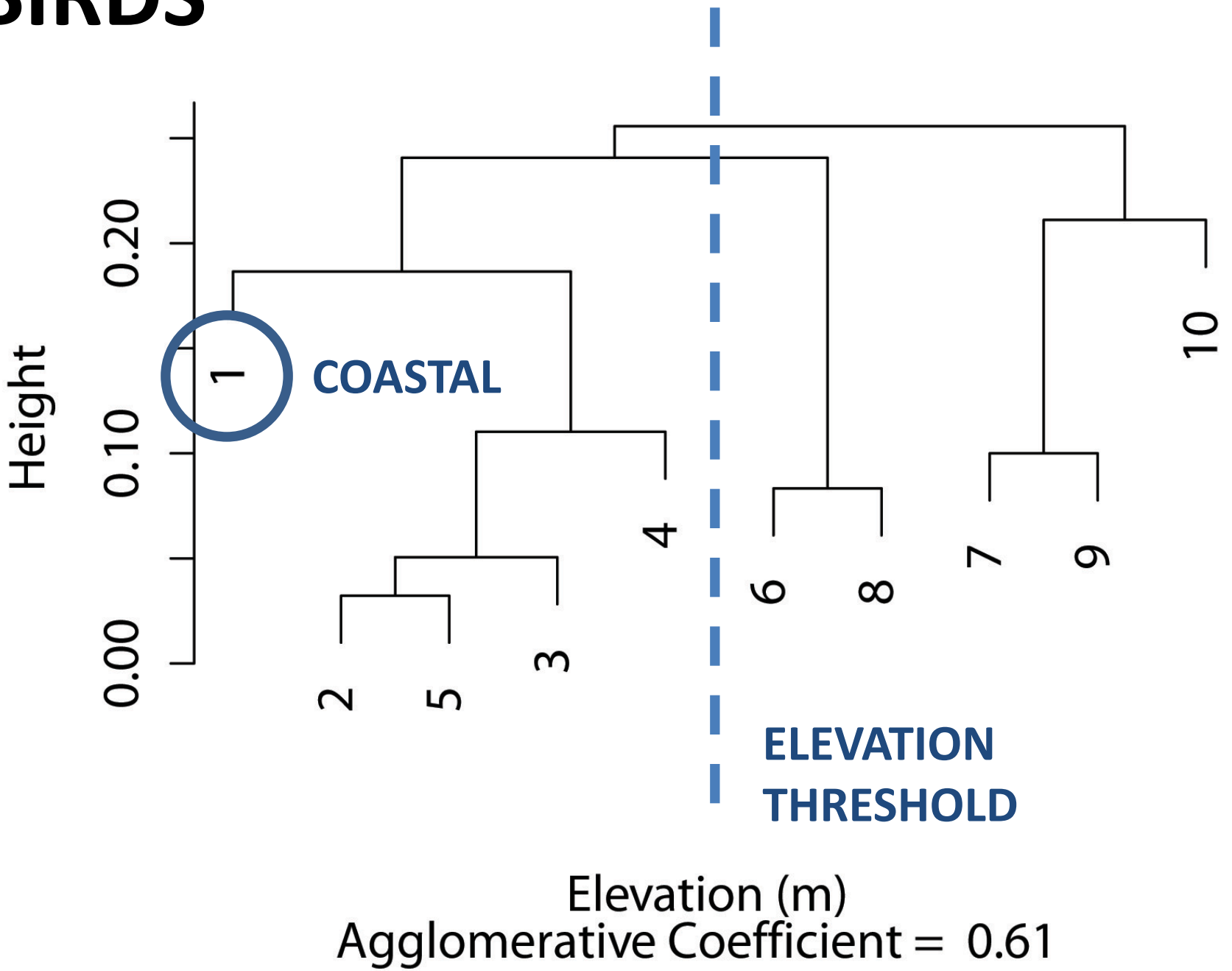
- c850 vascular plants sequenced for eight loci
  - chloroplastic: *rbc*L, *mat*K, *rpo*C1, *trn*L, *trn*L-F, *psb*A-*trn*H, nuclear ITS, and mitochondrial *nad*5
- c1200 invertebrates sequenced
  - non-destructive DNA extraction
  - cytochrome oxidase 1 (CO1)
- Avian sequences from reference database
  - cytochrome oxidase 1 (CO1)

Operational Taxonomic Units

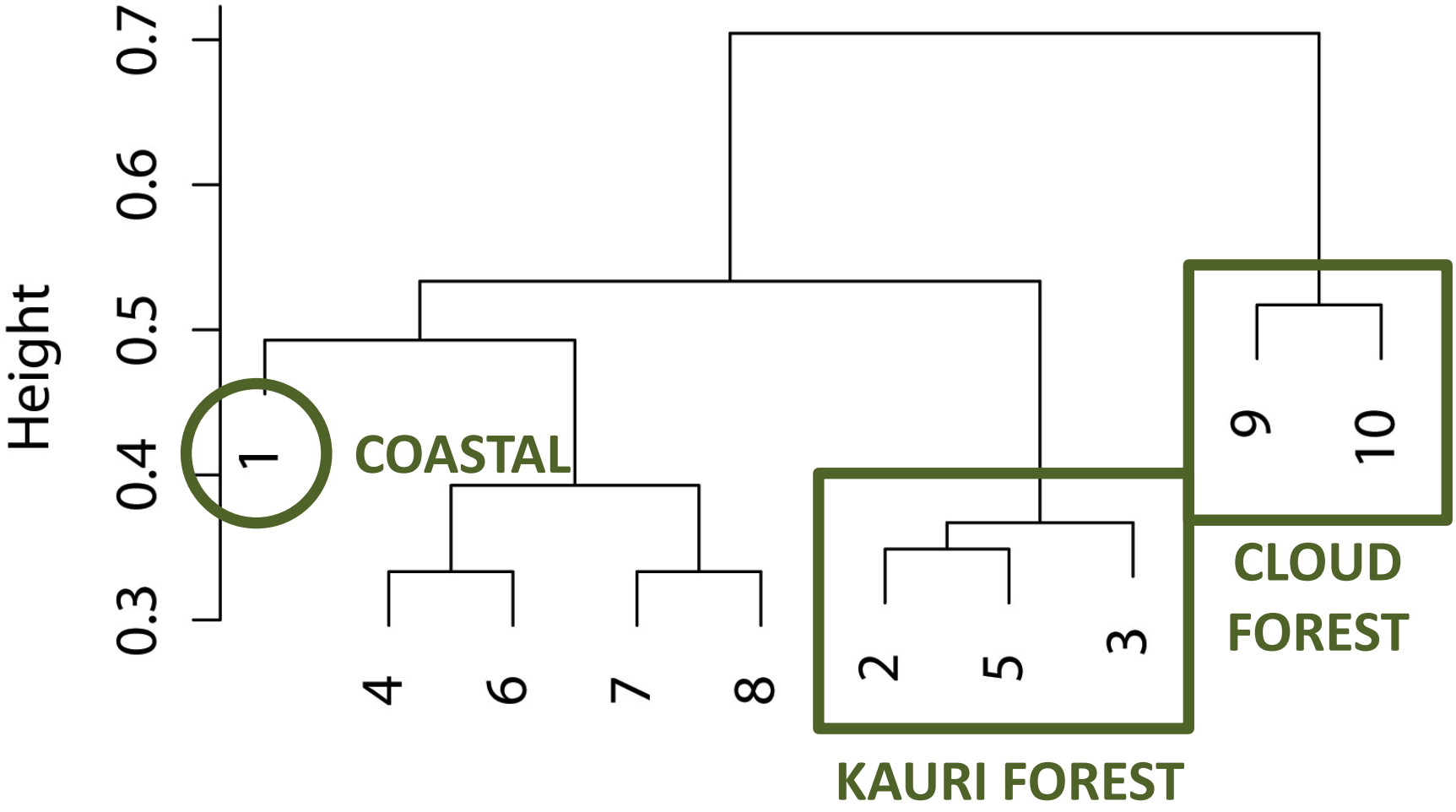
- For the pilot study we grouped operational taxonomic units (OTUs) for invertebrates
  - OTU <1% genetic divergence (529 => 212)
- Ultimately use shared phylogenetic diversity



BIRDS

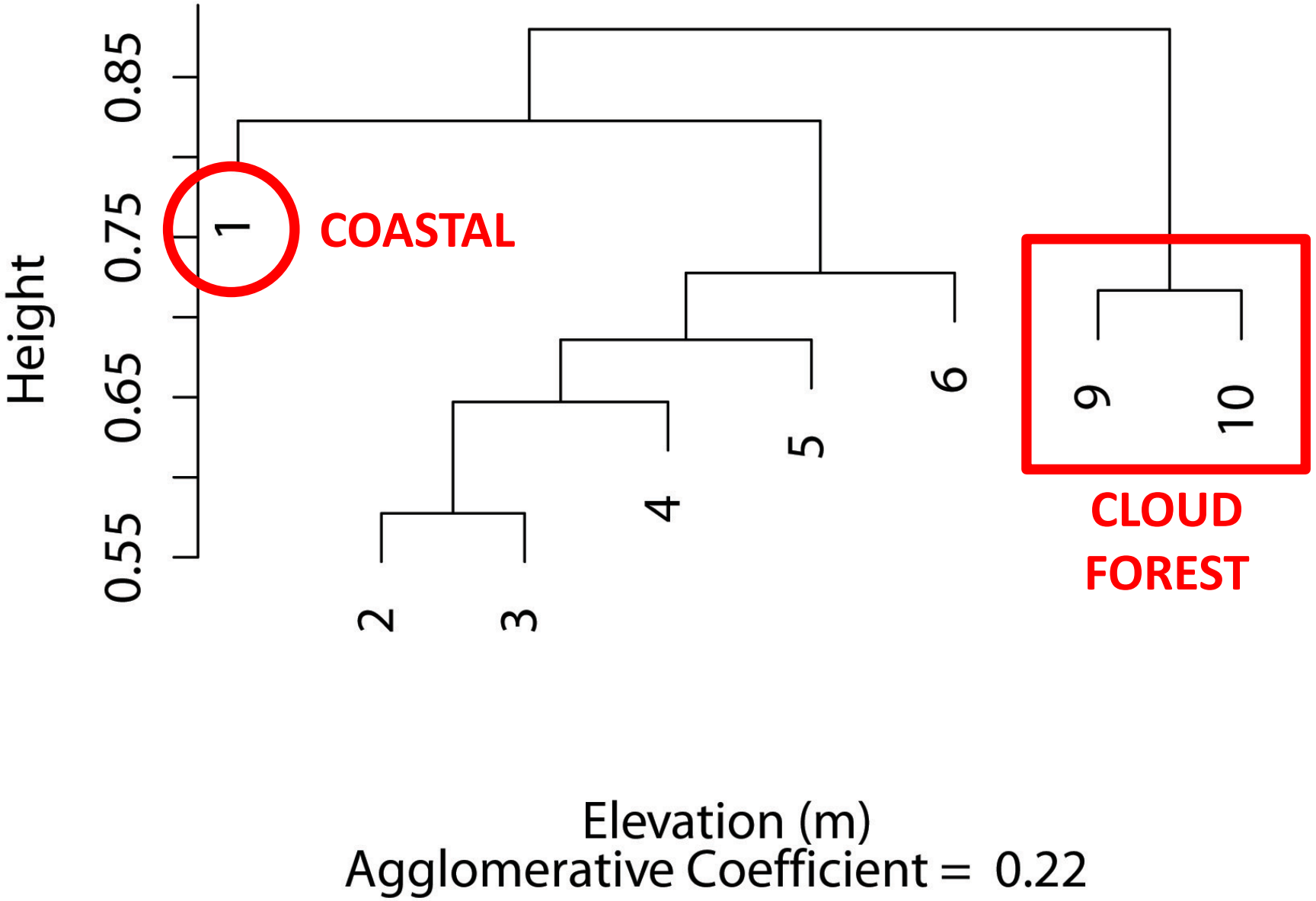

Height
0.00
0.10
0.20
1
2
5
3
4
6
8
7
9
10
COASTAL
ELEVATION
THRESHOLD
Elevation (m)
Agglomerative Coefficient = 0.61

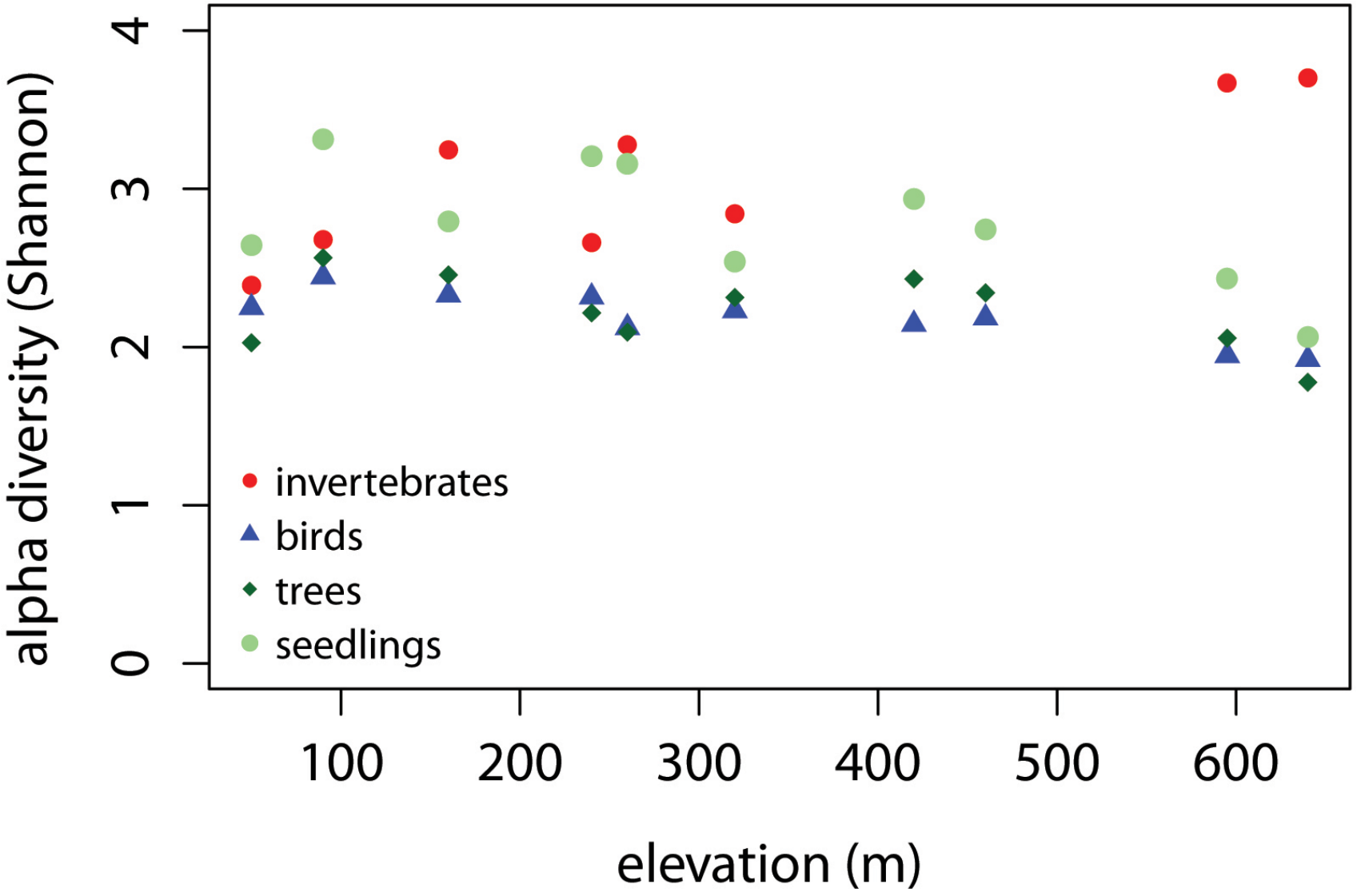
TREES

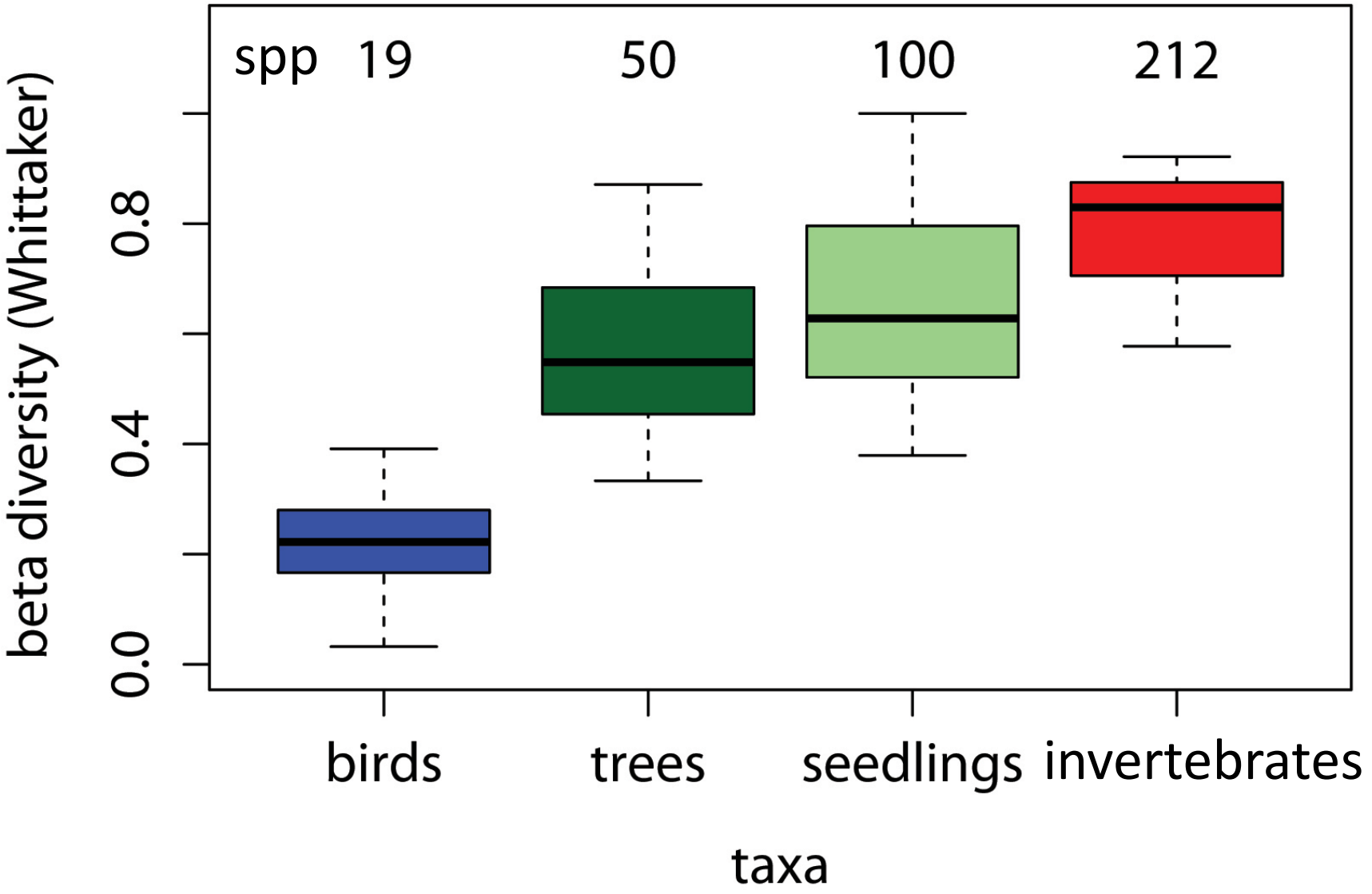


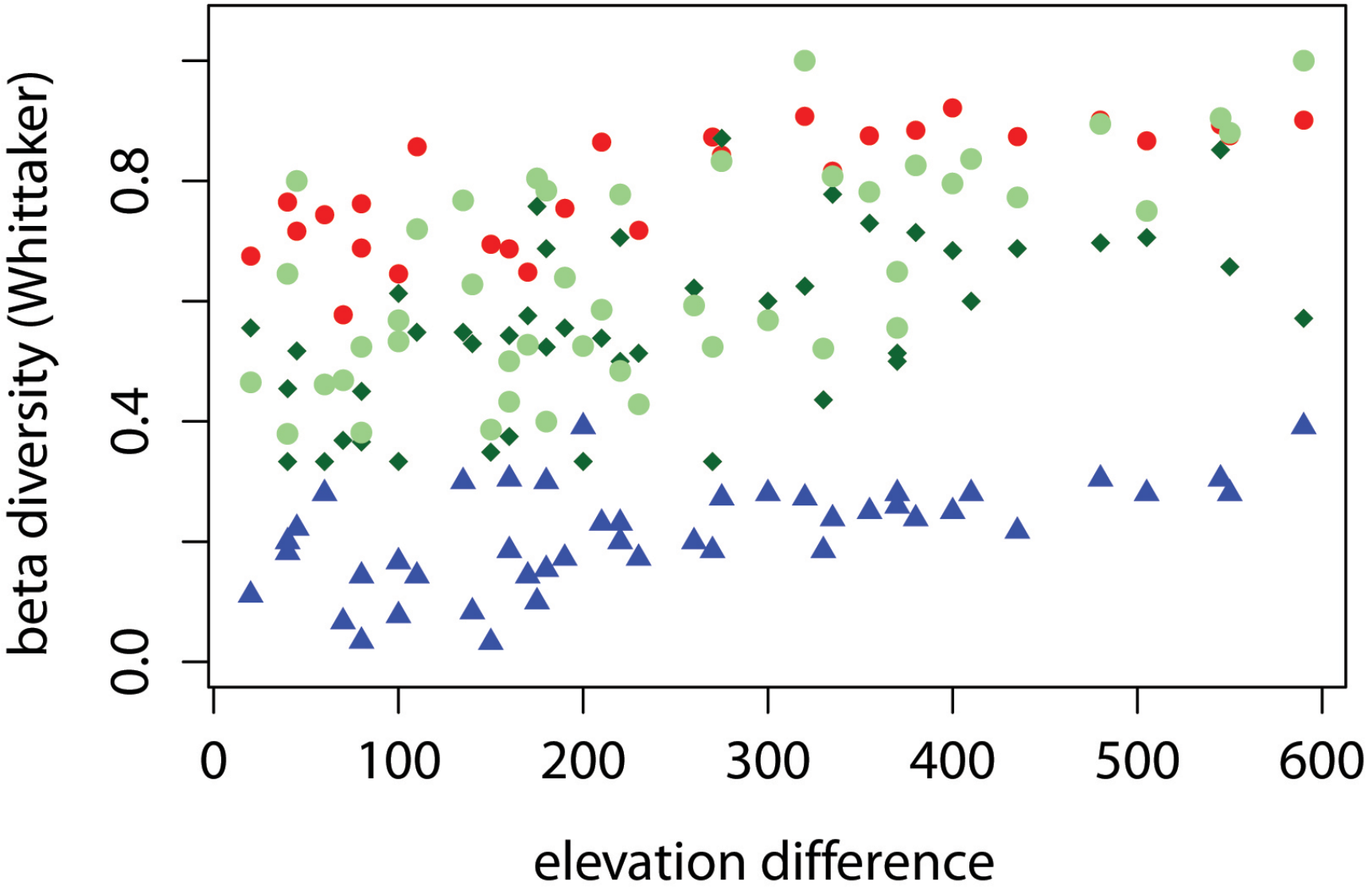
Elevation (m)
Agglomerative Coefficient = 0.44

INVERTEBRATES




alpha diversity (Shannon)
0
1
2
3
4
100
200
300
400
500
600
elevation (m)
invertebrates
birds
trees
seedlings


spp 19
50
100
212
beta diversity (Whittaker)
0.0
0.4
0.8
birds
trees
seedlings
invertebrates
taxa


beta diversity (Whittaker)
0.0
0.4
0.8
0
100
200
300
400
500
600
elevation difference

Preliminary Conclusions

- Alpha diversity relatively constant across sites
- Beta diversity differences among taxa most likely related to dispersal ability
- Beta diversity differs among sites on the elevational gradient
  - the slope of the relationship is similar for all taxa
- Additional variation in species composition explained by forest structure type

Conservation Value

- Identified that the majority of invertebrate species were unidentified
  - most Genbank hits <80% sequence similarity
- Turn-over rates of biodiversity differ by taxa but respond similarly to our underlying elevation gradient
- Taxa were additionally assorted by other mechanisms (coast, forest type)

The Future

- Refine the sequence pipeline for identifying taxonomic units
- Standardise individual-based measures of detectability across taxa
  - detectability includes sampling and sequencing
- Analyse the data within a theoretical framework such as the Unified Neutral Theory of Biodiversity and Biogeography