Drivers of diversity differ between specialist and generalist avian malaria parasites

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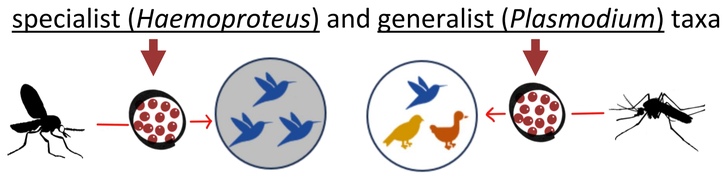
Introduction

- Parasites are **symbionts** that depend on another **living organism** – the host – for their survival and reproduction
- The effects of parasites on their hosts at **individual- and population-scales** have long been appreciated[1]
- However, parasites also **shape community and ecosystem structure** via myriad mechanisms such as apparent competition and altered food-web connectivity[1]
- Critically, increasingly parasites are also being recognized as a taxa of **special conservation concern** because they comprise over **40%** of all known species[2]
- In free-living species, it has been demonstrated that diversity patterns are shaped by niche breadth (e.g., differential effects of disturbance on specialists vs. generalists)[3]
- Like free-living species, parasites can also be classified into **generalists** and **specialists** based on niche breadth (i.e., the taxonomic diversity of hosts they can infect)[4]
- In this study we use **avian haemosporidian parasites** as a model system to identify factors affecting parasite α- and β-diversity patterns and test if these patterns differ between specialist (*Haemoproteus*) and generalist (*Plasmodium*) taxa



Methods

Study area

The study sites were located at *Shola* sky-islands distributed across the southern 600 km of the Western Ghats, Southern India (Fig. 1)[4]

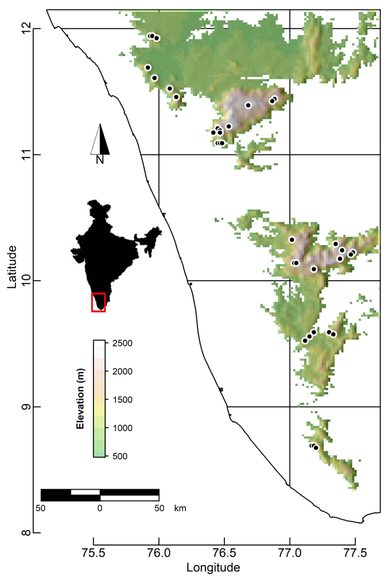


Figure 1: The study area

Study system

Avian haemosporidian, infect many bird species (Fig. 2a) and include 2 main genera:
(i) Haemoproteus (2b), vectored by biting midges (2c), which tend to be specialists[4];
(ii) Plasmodium (2d), vectored by mosquitoes (2c), which tend to be generalists[4]

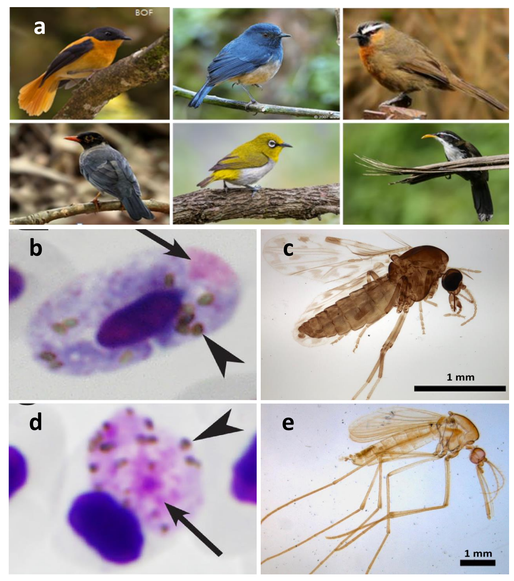
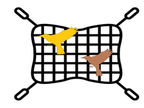


Figure 2: The study system

Field and laboratory methods

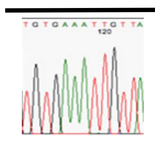


Mist netting of birds:
- Birds were captured using standard mist-netting protocols[5]
- Birds were trapped at 42 sites across the study area (Fig. 1)

Bird handling and identification:
- A total of 1177 birds were captured
- Birds were sampled from 28 species (including 14 species endemic to the Western Ghats)

Blood collection:
- We collected blood from the bird's ulnar vein
- Blood was stored in Queen's lysis buffer, as described earlier[5]

Genomic DNA extraction:
- Genomic DNA was extracted using Qiagen blood and tissue extraction kit (Qiagen, Hilden, Germany)[5]

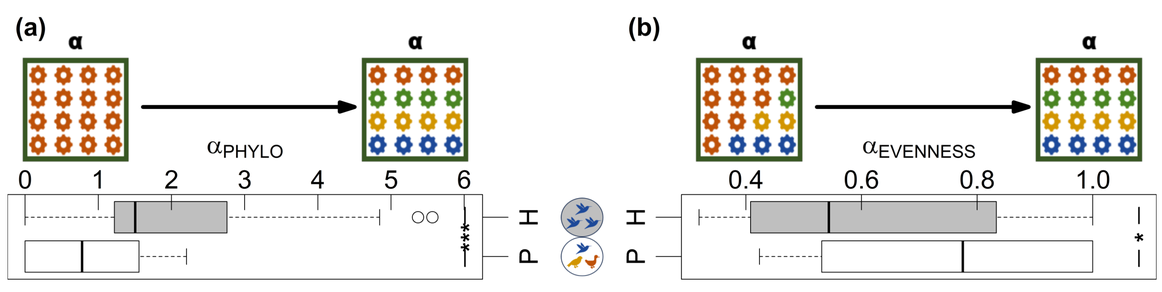


PCR and sequencing:
- We tested for infection by PCR amplifying and sequencing 478 bp mitochondrial cytochrome b gene (cyt-b) of avian haemosporidians[4]

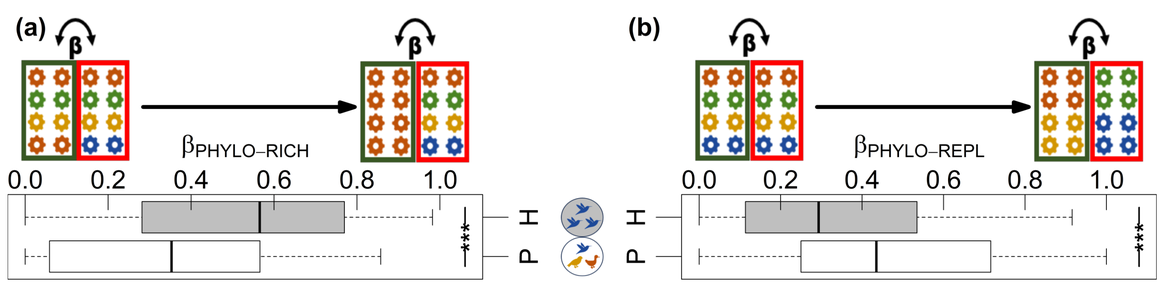
Data analyses

- *Spatial data*: Environmental data (i.e., climate, land-cover and terrain) were from publicly available datasets (see details as reported earlier[5]) and processed using R packages SP and RASTER
- *α-diversity*: Phylogenetic α-diversity for each site was calculated with R package BAT, and spatial analyses were carried out using random forest models as implemented in the R package RANGER
- *β-diversity*: Phylogenetic β-diversity for all site pairs was calculated with BAT, and spatial analyses were carried out using generalized dissimilarity modeling as implemented in the R package GDM

Results: Alpha Diversity



Results: Beta Diversity



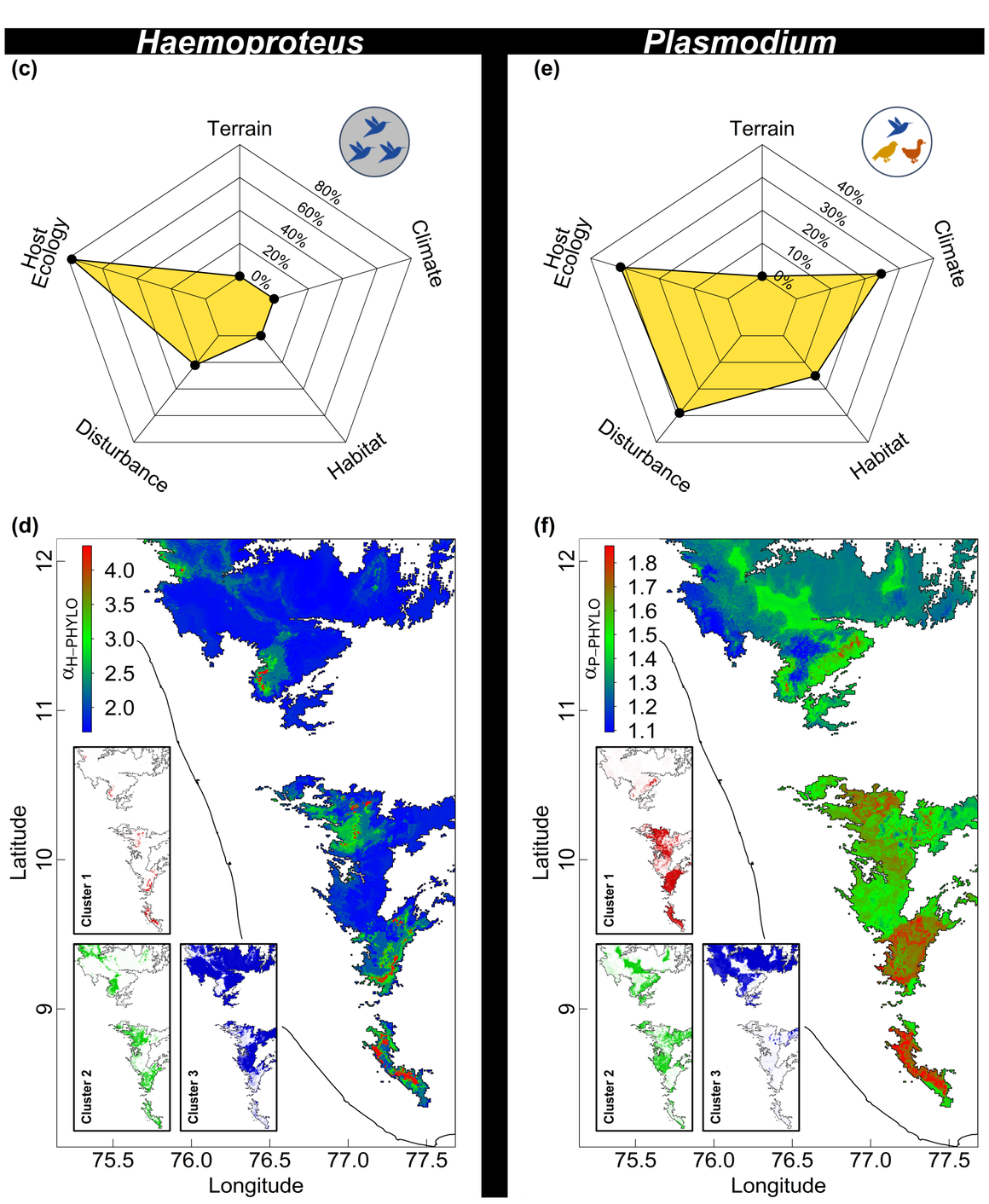


Figure 3: Spatial patterns of α-diversity in specialist (*Haemoproteus*) vs. generalist (*Plasmodium*) parasites

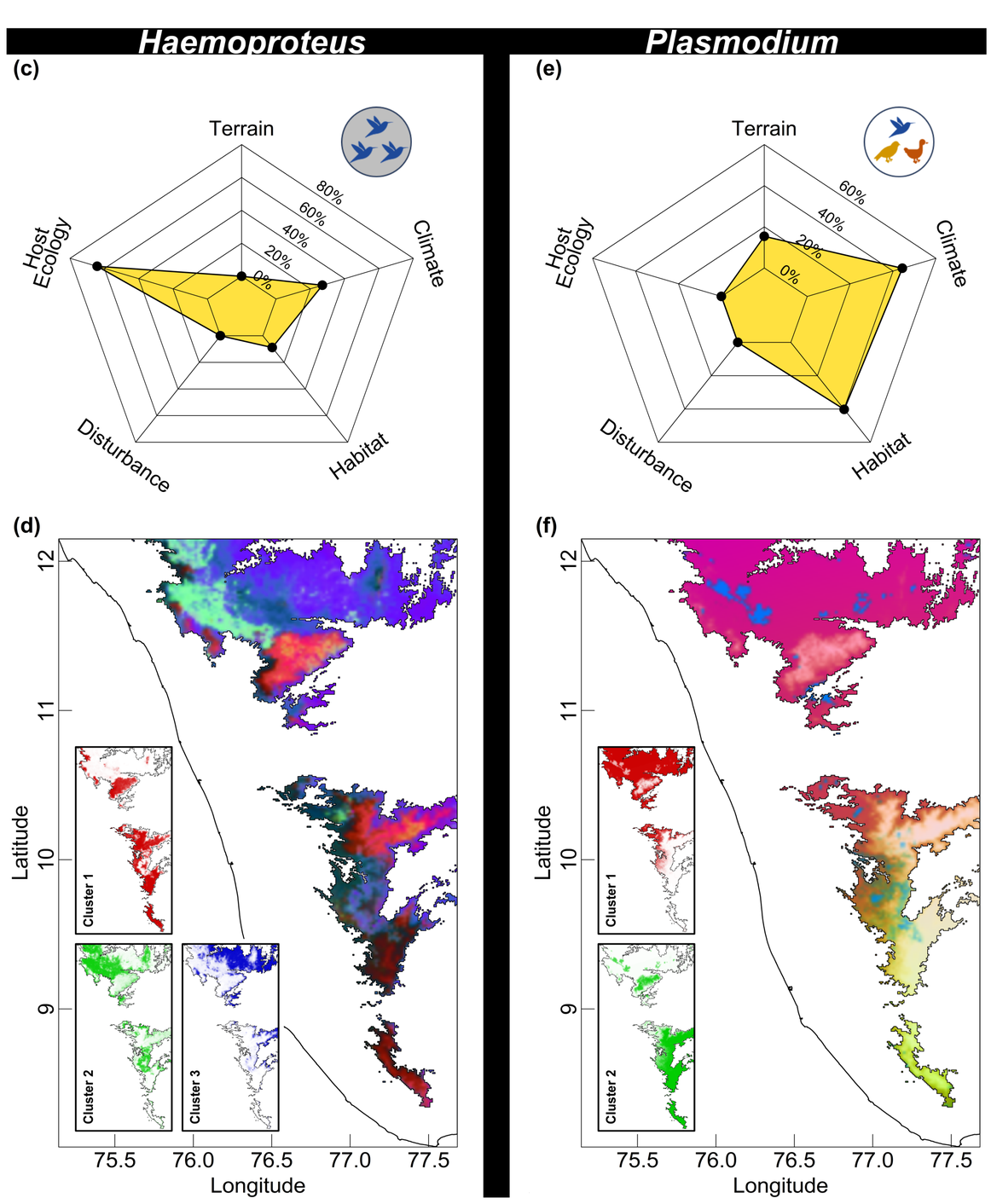


Figure 4: Spatial patterns of β-diversity in specialist (*Haemoproteus*) vs. generalist (*Plasmodium*) parasites

Discussion

- As predicted by theory, we find that specialist vs. generalist parasites show:
  - Higher α-diversity (α_{PHYLO}; Fig. 3a) and lower α-evenness ($\alpha_{EVENNESS}$; Fig. 3b)
  - Higher β-diversity due to changes in richness ($\beta_{PHYLO\text{-}RICH}$; Fig. 4a) and lower β-diversity due to taxon replacement ($\beta_{PHYLO\text{-}REPL}$; Fig. 4b)
  - Stronger effects of host- vs. environment-related variables on patterns of α-diversity (Fig. 3c vs. 3e) and β-diversity (Fig. 4c vs. 4e)
- In the case of parasites, specialist are particularly important from a ecosystem health perspective, while generalists are associated with many Emerging Infectious Diseases (EIDs; e.g., avian malaria, amphibian chytridiomycosis and bat white-nose syndrome)
- Thus, our results have broad implications for understanding parasites as indicators of ecosystem health, as well the rising incidence of EIDs in natural populations globally

Acknowledgements

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Photographs courtesy of Prasenjeet Yadav and V. V. Robin

All analyses were carried out using R ver. 4.3.1 (The R Foundation for Statistical Computing 2019)

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