



Between-species transmission and host specificity of *Bartonella grahamii* strains may be context dependent

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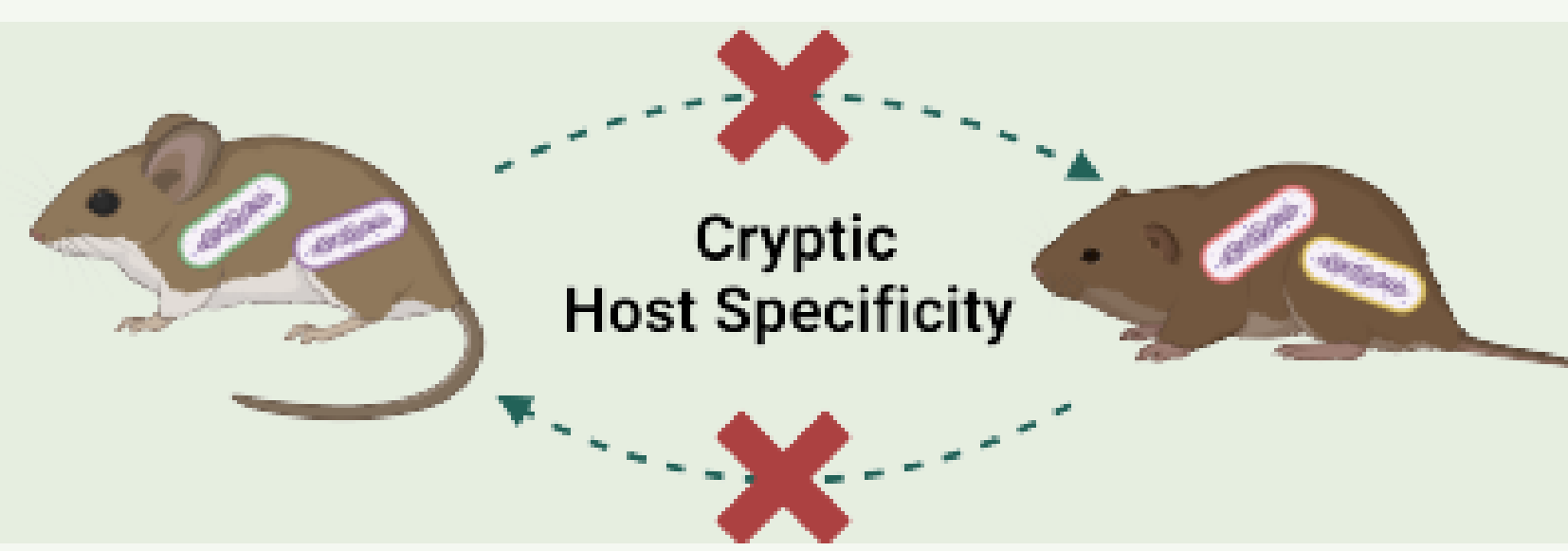
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INTRODUCTION

- **Between-species transmission** key to parasite persistence and spread ¹.
- Alternative hosts may be vital for persistence in **fragmented, unstable** host populations.



- BUT some multi-host parasites show evidence of "**cryptic host specificity**" ²⁻⁴
- Previous studies focussed on single, large host communities and phylogenetically distant hosts



AIMS

Explore between-species transmission of *B. grahamii* in two contrasting systems:

- a **highly fragmented population** of water voles and sympatric field voles, marked by small population sizes and frequent turnover
- a **large, continuous population** of field voles and bank voles

METHODS

Study Locations

Assynt Metapopulation

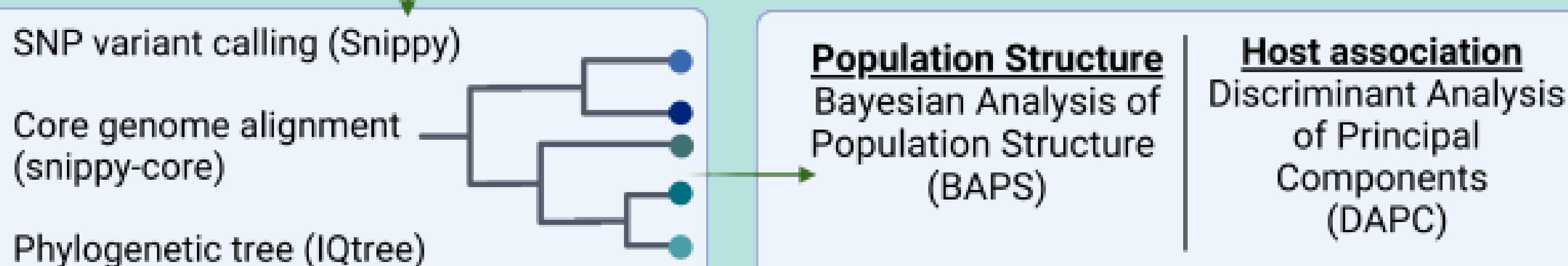
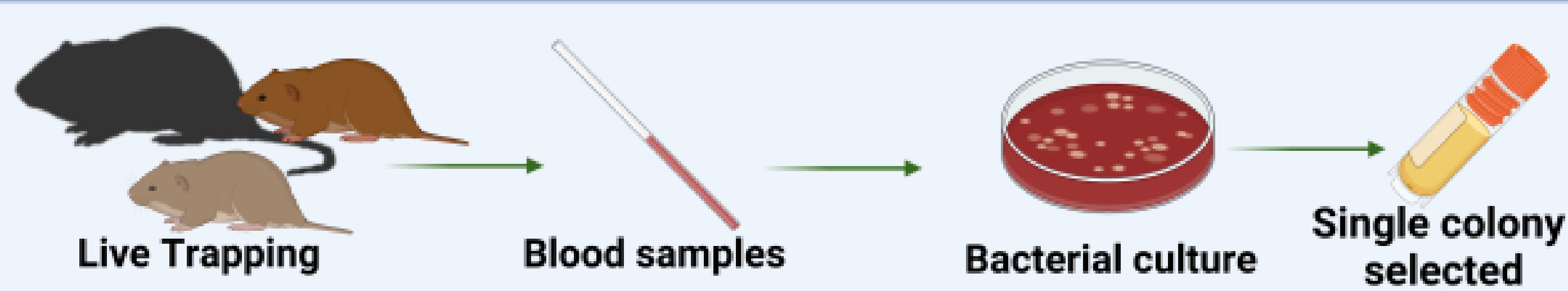
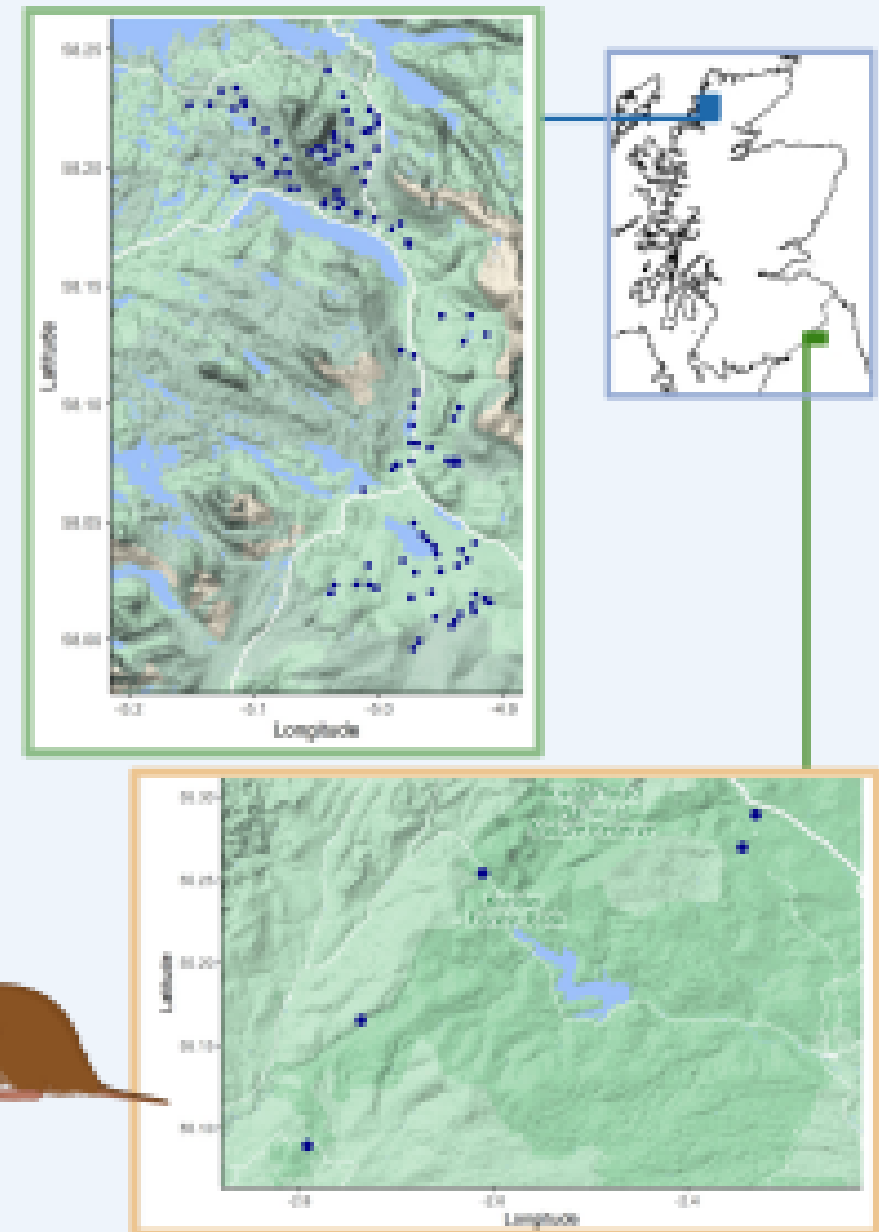
Highly fragmented - 110 habitat patches
Low densities

Field voles (*Microtus agrestis*)
& water voles (*Arvicola amphibius*)

Kielder Forest

Continuous habitat, high densities

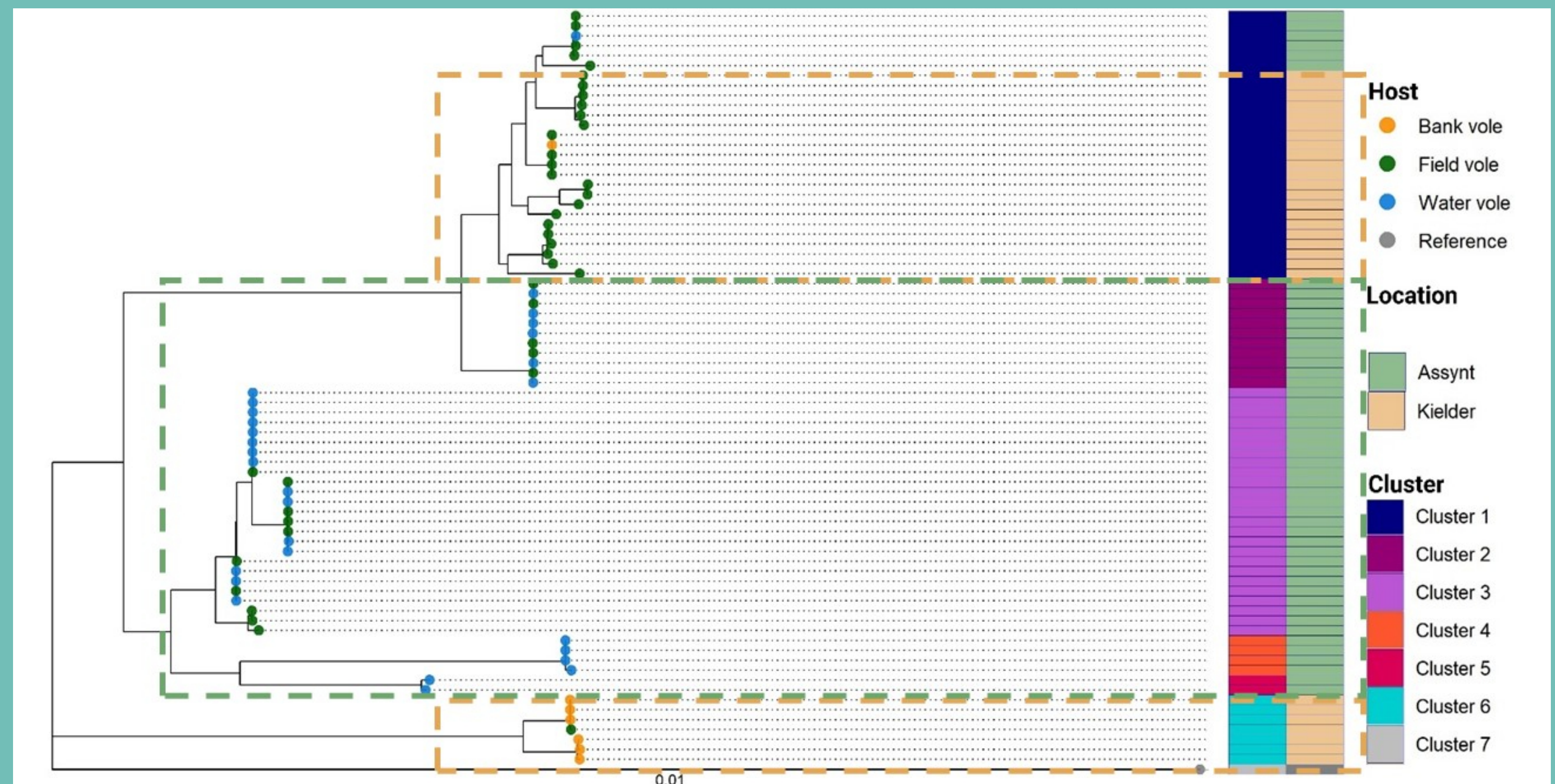
Field voles & Bank voles (*Myodes glareolus*)



RESULTS/DISCUSSION

Population structure: Do samples cluster by location and/or host species?

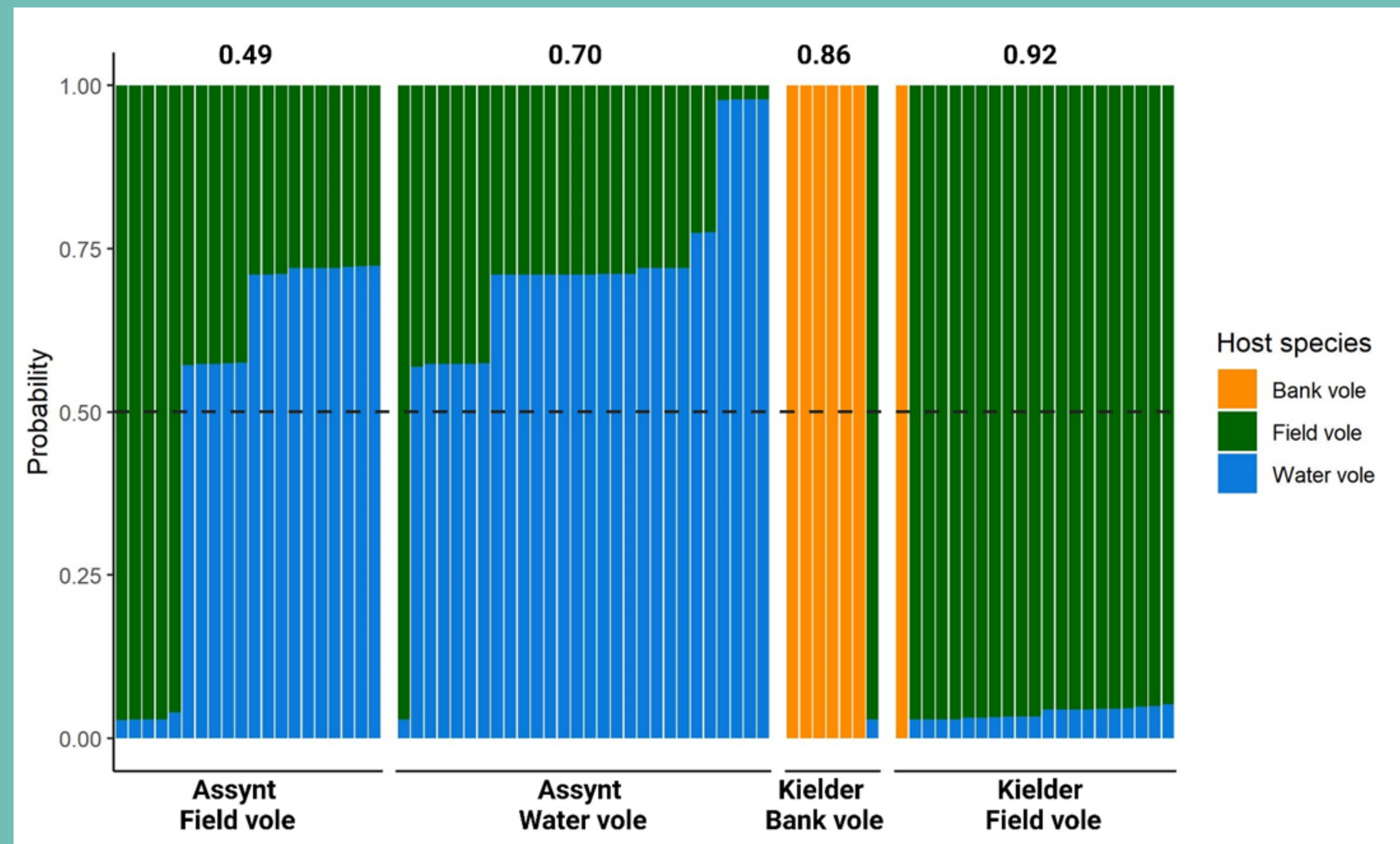
- **Kielder forest** - 2 clusters, 95% and 86% samples from one host species - **evidence of host specificity**
- **Assynt** - 5 clusters. Two most common strains found in both host species (~ 40% field voles, 60% water voles) - **host generalist**



Phylogenetic tree of *B. grahamii* samples from bank voles, field voles, water voles from Assynt and Kielder forest. *Bartonella grahamii* strain as4aup from the NCBI database was used as a reference sequence. The phylogenetic tree was constructed based on SNPs across the core genome (*snippy*) using the automated model selection algorithm.

Is there evidence of host associations?

- DAPC assigned original host species based on *B. grahamii* genotype with high certainty for strains in Kielder forest, but not for most strains in Assynt



Posterior probability of each sample being assigned to a particular host species (indicated by colour) based on Discriminant Analysis of Principal Components (DAPC). Graph split by original host and location. DAPC was carried out using the *adegenet* package, specifying the original hosts species as a prior grouping.

ACKNOWLEDGEMENTS

Evidence for **different patterns of between-species transmission of *B. grahamii* strains in two contrasting host systems** - between-species transmission can be context dependent

- Results may be related to **phylogenetic distance** of hosts.
- **Host generalists** may have evolutionary advantage in unstable, fragmented populations

IMPORTANCE AND IMPLICATIONS

Future disease modelling or management need to consider the impact of the ecological context on transmission patterns, as habitat fragmentation could alter selection pressures towards more generalist parasites.

REFERENCES

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