

Mapping Multi-Host TB Risk: The Central Role of Wild Boar and Red Deer in Environmentally Mediated Transmission

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INTRODUCTION

- Animal tuberculosis (TB) persists in multi-host communities
- Transmission occurs via shared contaminated environments
- Integration of host ecology and environmental data is crucial

OBJECTIVES

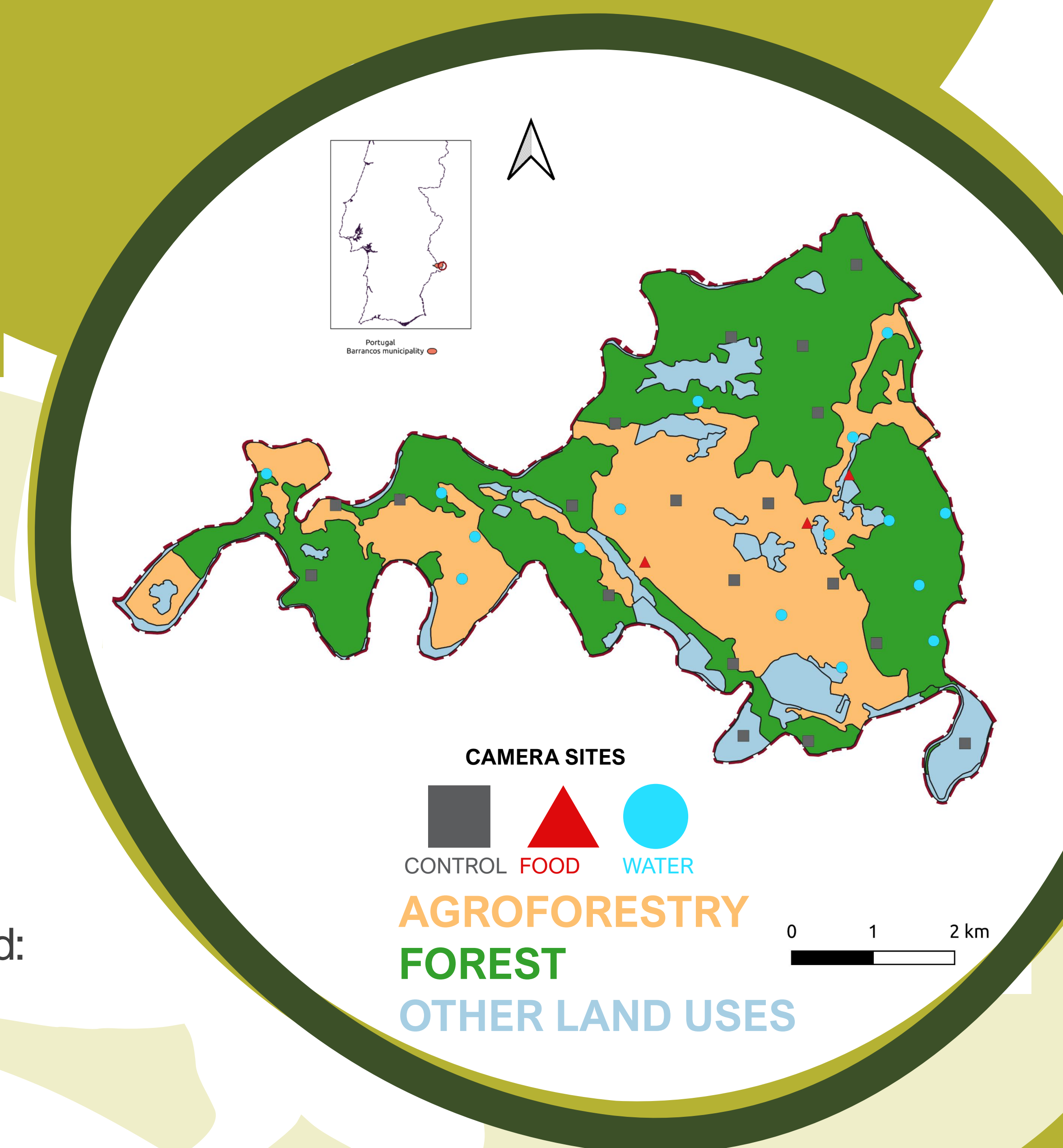
1. Characterise interspecies interactions
2. Detect MTBC DNA in environmental samples
3. Map spatial risk zones for TB transmission

RESULTS

- Indirect interactions more frequent → **wet season**
- Natural resource availability increased wildlife-cattle interactions.
 - **49%** environmental samples **positive** for MTBC DNA.
 - Main contamination predictor: terrain slope
 - **26.5%** area = high transmission risk (mostly forest)

METHODS

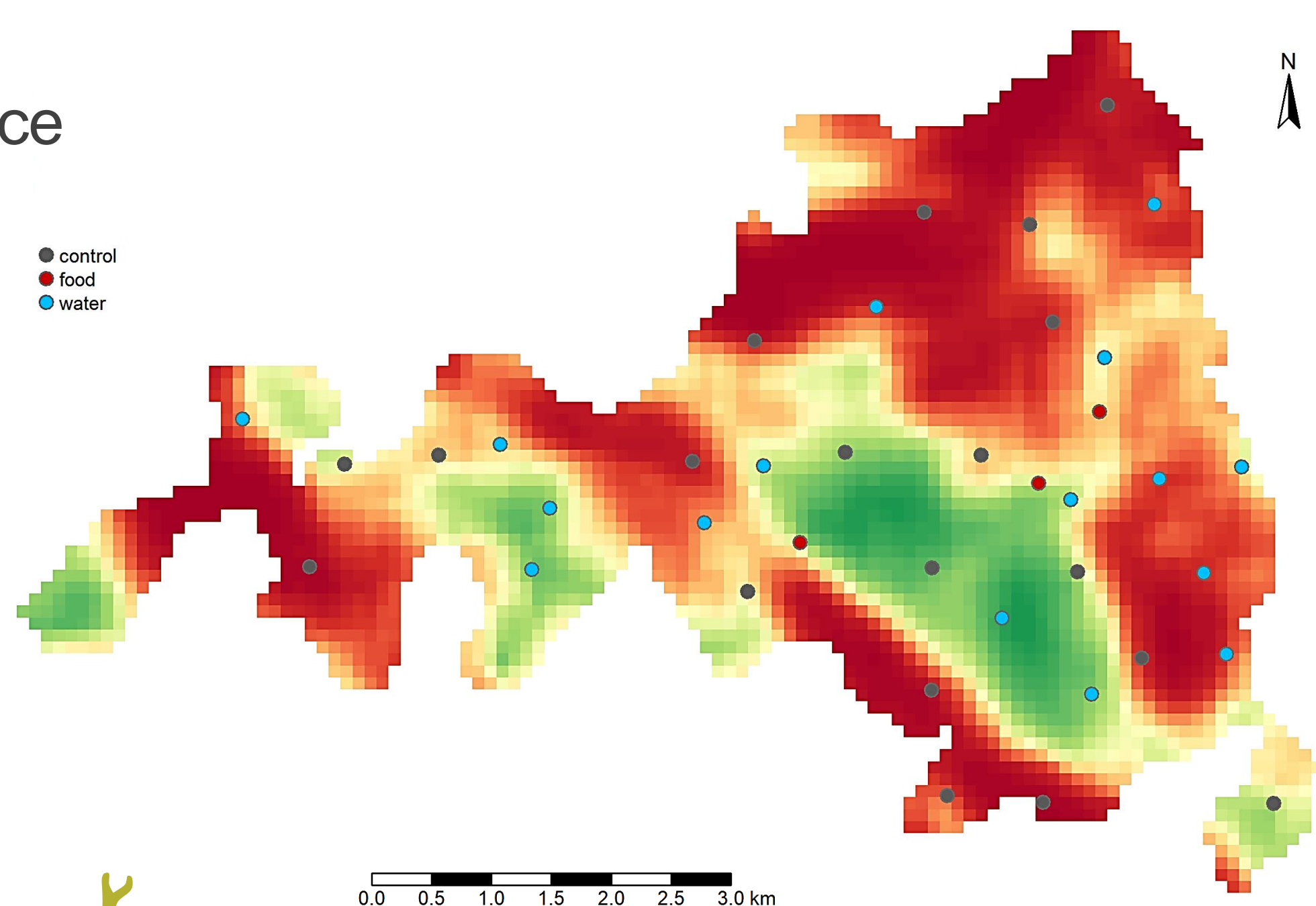
- Study area: **Barrancos, Portugal**
Mediterranean Montado system
- 38 sampling sites:
water, food, and control
- 89 environmental samples:
water, soil, mud
- Camera trapping (2021–2022)
→ host space-use maps
- qPCR detection of MTBC
(IS6110 target)
- GLM models
- Five **ecological hypotheses** tested:
(H1–H5: human, landscape, topography, weather, natural resources)



ENVIRONMENTAL CONTAMINATION



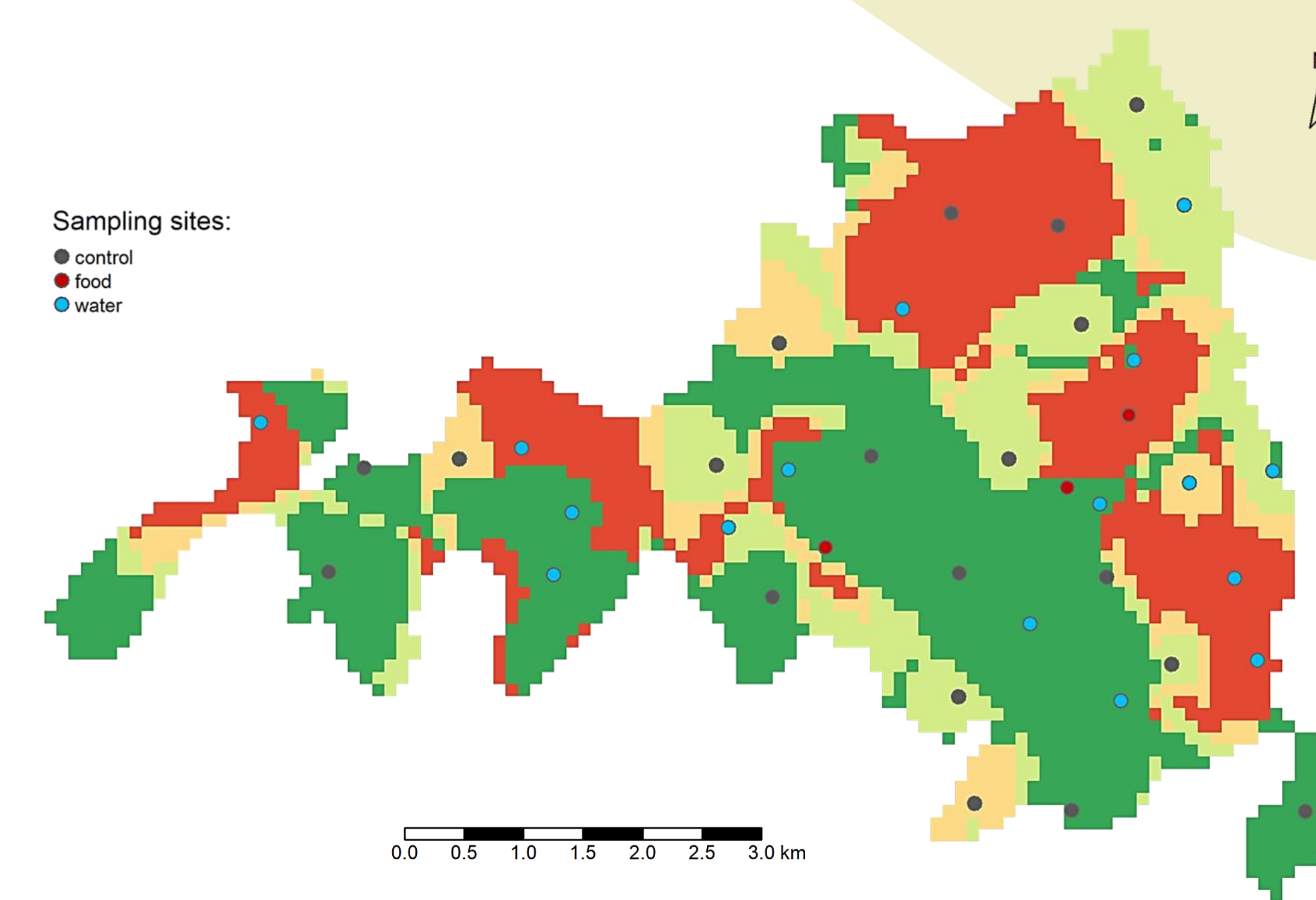
Probability of
MTBC occurrence



TRANSMISSION RISK: A MULTI-HOST SCENARIO



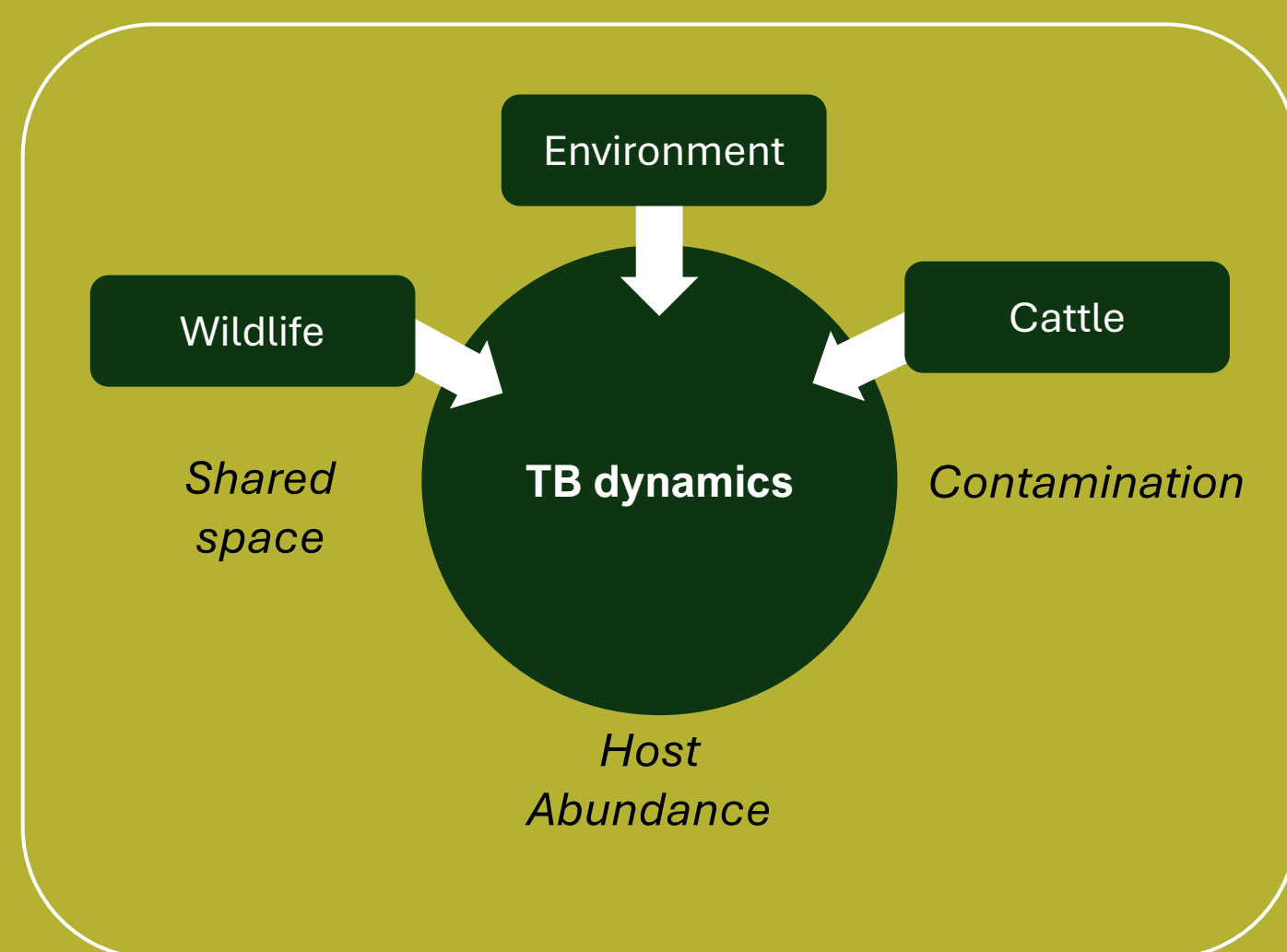
High-risk areas:
transmission



CONCLUSIONS & IMPLICATIONS

- Indirect interactions: key drivers of pathogen transmission
- Linking ecological and contamination data improves spatial risk prediction
- Red deer and wild boar act as environmental amplifiers
- High-priority areas can be identified for targeted TB control

Management | Biosecurity | TB control



HIGH-RISK areas
Gradient of hosts

