

Host-parasite interplay in a mammalian hybrid zone

Alice Balard^{1,2}, Victor Hugo Jarquín-Díaz^{1,2}, Jenny Jost¹, Iva Martincová³, Ľudovít Ďureje³, Jaroslav Piàlek³, Miloš Macholán⁴, Joëlle Göy de Bellocq³, Stuart J.E. Baird³, and Emanuel Heitlinger^{1,2}

¹Institute for Biology. Department of Molecular Parasitology. Humboldt University Berlin (HU). Philippstr. 13, Haus 14, 10115, Berlin, Germany

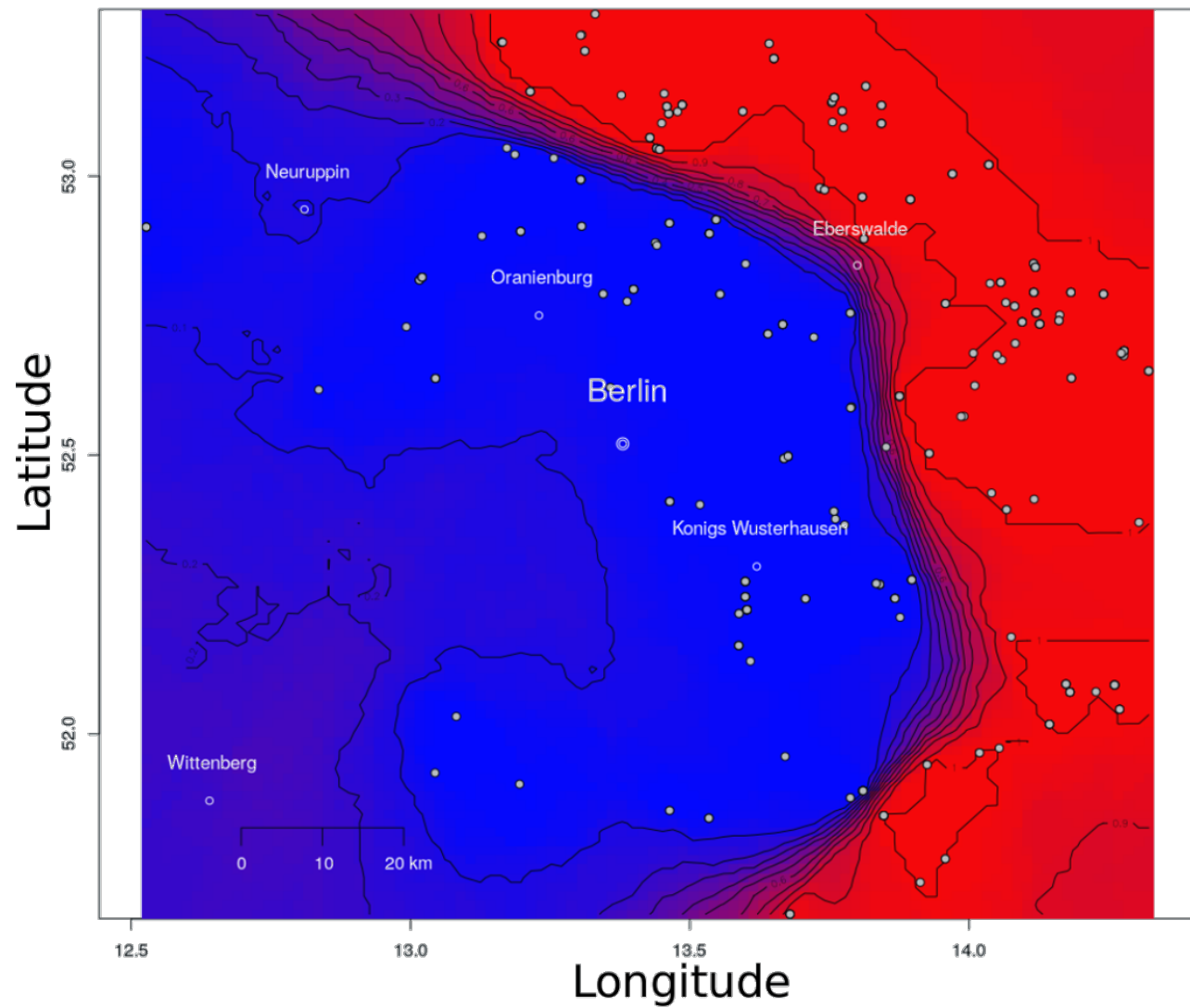
²Leibniz-Institut für Zoo- und Wildtierforschung (IZW) im Forschungsverbund Berlin e.V.. Alfred-Kowalke-Straße 17, 10315, Berlin, Germany

³Research Facility Studenec, Institute of Vertebrate Biology, Czech Academy of Sciences, Květná 8, 603 65 Brno, Czech Republic

⁴Laboratory of Mammalian Evolutionary Genetics, Institute of Animal Physiology and Genetics, Czech Academy of Sciences, Veverí 97, 60200 Brno, Czech Republic

Context

- Parasite model: *Eimeria* spp., obligate intracellular parasite (Apicomplexa: Coccidia). Three *Eimeria* spp. identified (3 markers) in the mice of the hybrid zone
- Host model: *Mus musculus domesticus*, *Mus musculus musculus*, and hybrids



Map of the spatial range of both house mouse subspecies in the European House Mouse Hybrid Zone. Spatial organization was inferred using six autosomal markers (Es1, H6pd, Idh1, Mpi, Np, Sod1). Mmd is found west of the hybrid zone (blue), Mmm east of it (red). The numbers at the level contours indicate posterior probabilities of population membership for each mouse subspecies

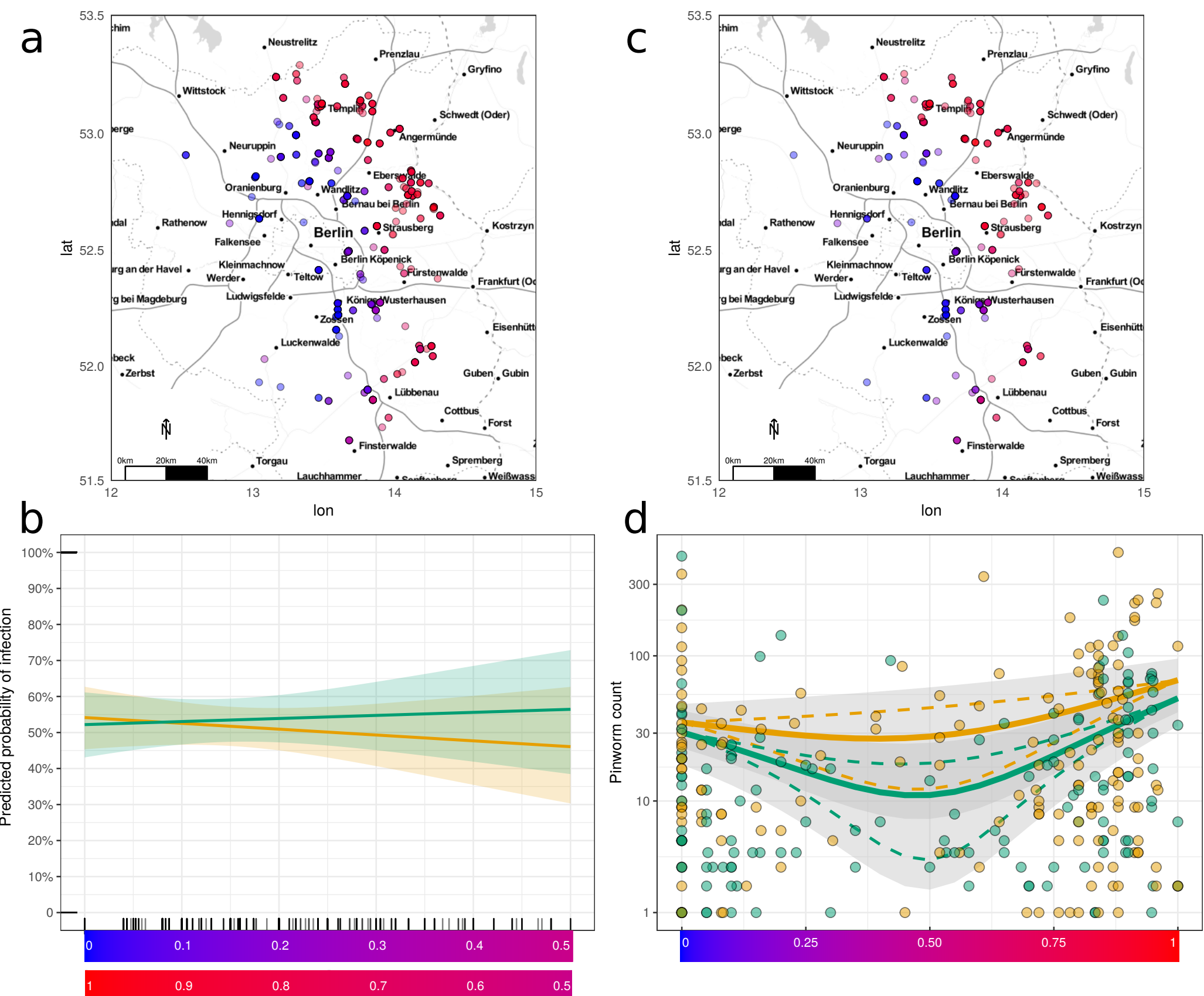
Aims of the study

- Investigate **hybrid susceptibility/resistance** of house mice to their parasite *Eimeria* spp. using prevalence and intensity data for parasite strains throughout the House Mouse Hybrid Zone
- Compare with pinworms, prevalent but less pathogenic than *Eimeria* spp

Material & Methods

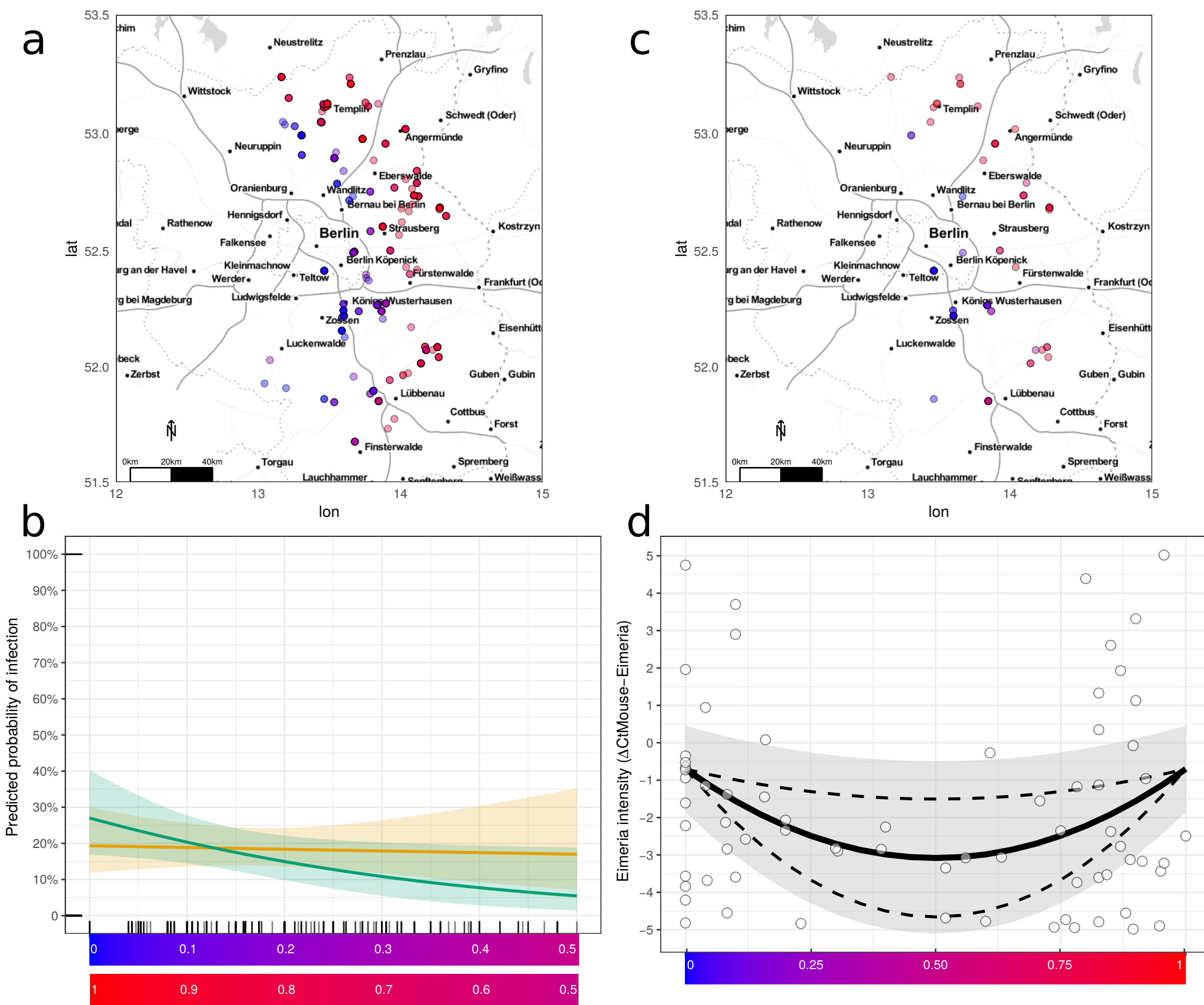
- Sampling 660 mice over 4 years; Host genotyping (4-14 diagnostic markers) on a 0 to 1 scale (50/50 hybrids = 0.5)
- Eimeria* load estimated by quantitative PCR / Pinworm load estimated by count
- Body condition estimated by residuals body length/body weight
- Statistical analyses:
 - Modellisation of parasite load along hybridization index, test hybrid effect
 - Logistic regression presence/absence of parasite in direction of the hybrid zone center

Results: Pinworm load lower in hybrids than in parental mice



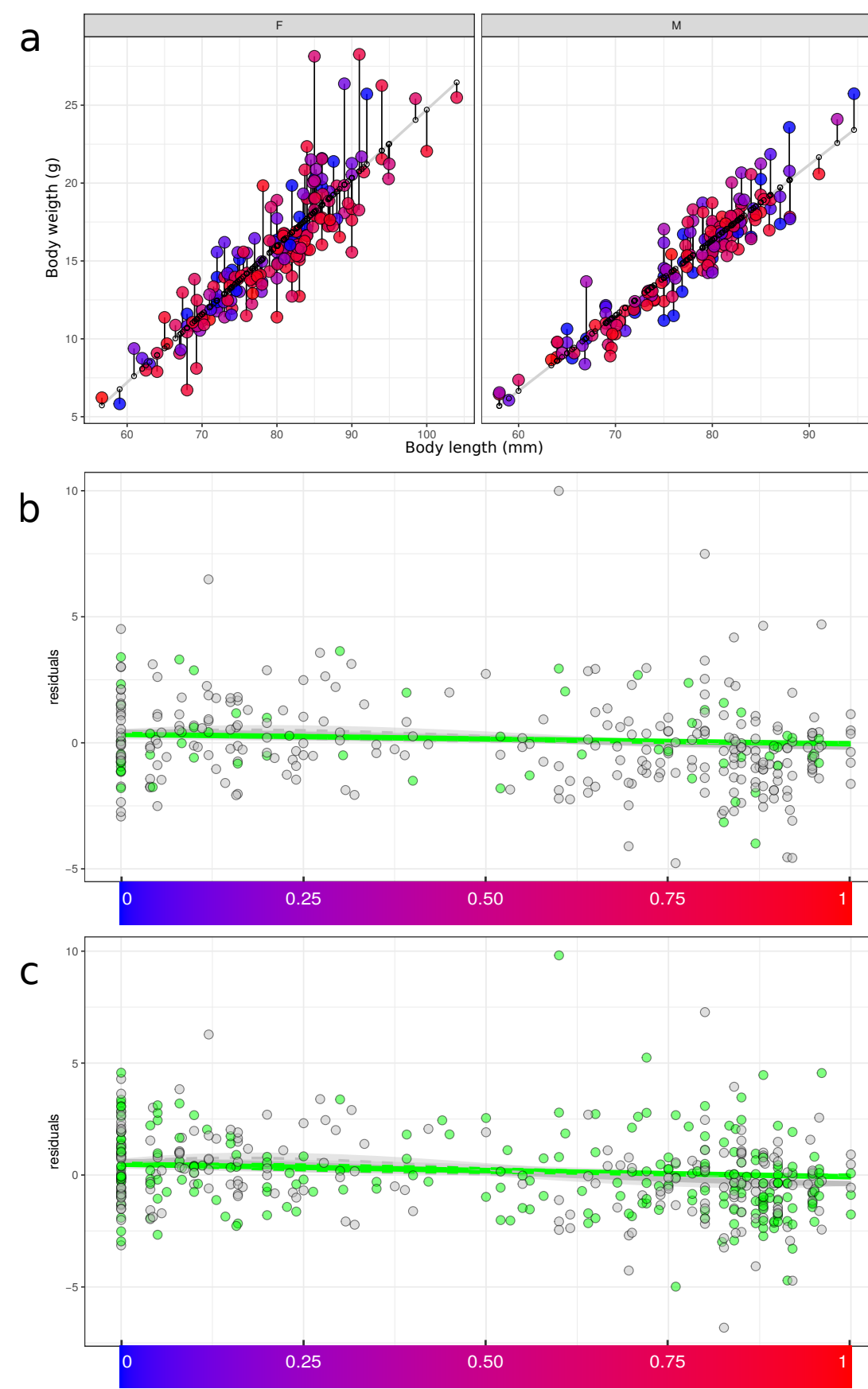
Map of all individuals (a), and predicted probability of infection when approaching the hybrid zone center (b). Map of positive individuals (c), and prediction of parasite intensity along the hybrid index (d)(males (green)/females (orange))

Results: *Eimeria* spp. load lower in hybrids than in parental mice



Map of all individuals (a), and predicted probability of infection when approaching the hybrid zone center (b). Map of positive individuals (c), and prediction of parasite intensity along the hybrid index (d)(males (green)/females (orange))

Results: no indication of differential body condition between infected/non infected



Fit of the residuals for females and males (a); prediction of residuals along the hybrid index (*Eimeria* spp. (b) and pinworms (c)) infected mice (light green) and non infected mice (grey)

Conclusion

Improving our understanding of parasite process across the HMMZ provides valuable information on the house mouse as the model species with the most thoroughly understood immune system. A transfer of knowledge from this model might help to understand the interplay between parasites and hybridizing species, our own as well as species relevant for conservation.

References

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