

Co-evolution of house mouse and an intracellular parasite, *Eimeria* spp.

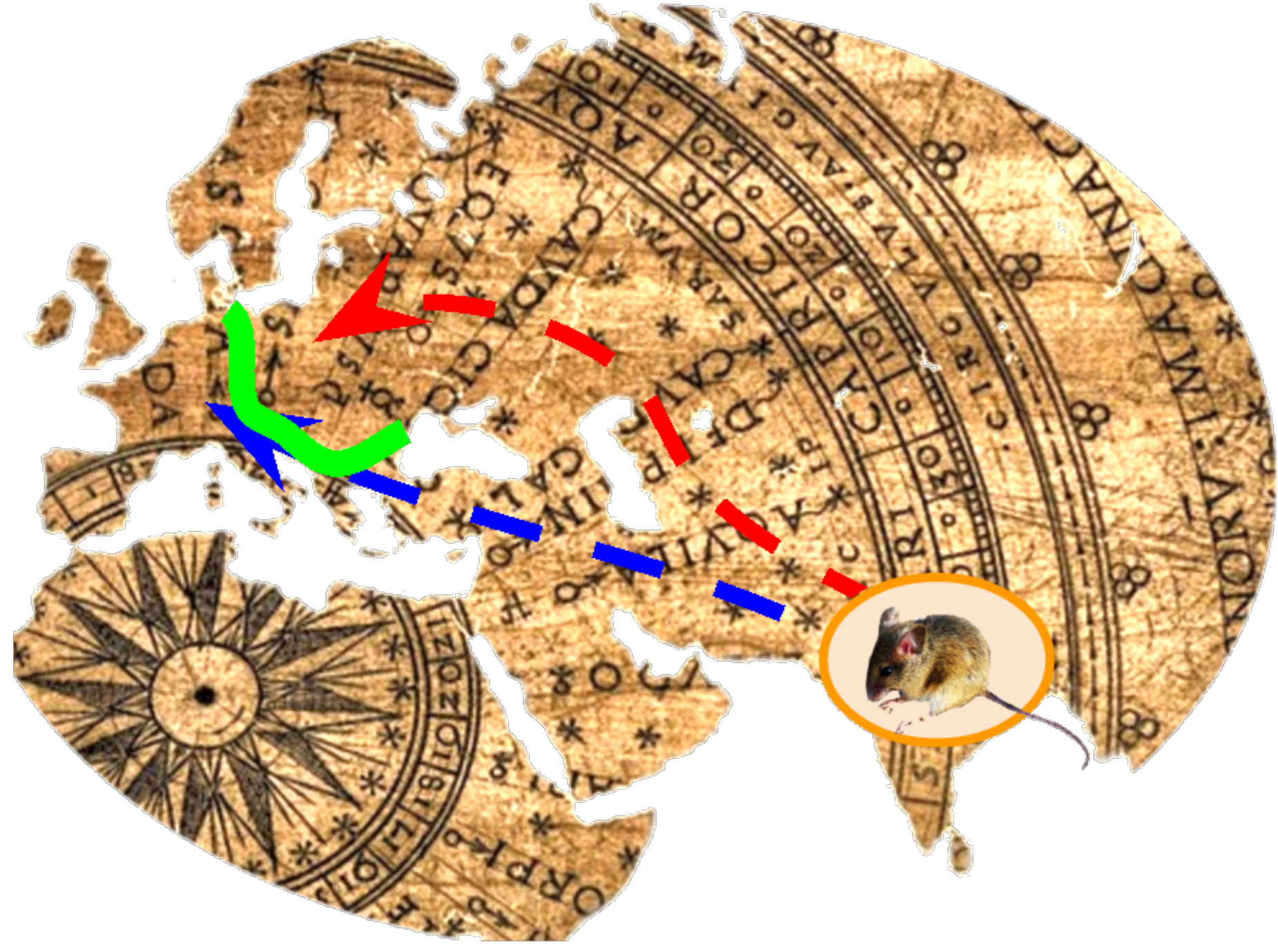
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Context

- House Mouse Hybrid Zone, 20km wide, formed by hybrids of *Mus musculus domesticus* and *Mus musculus musculus*. After 500,000 years in isolation, secondary contact 5000 years ago (Macholán et al. 2012; Boursot et al. 1993)



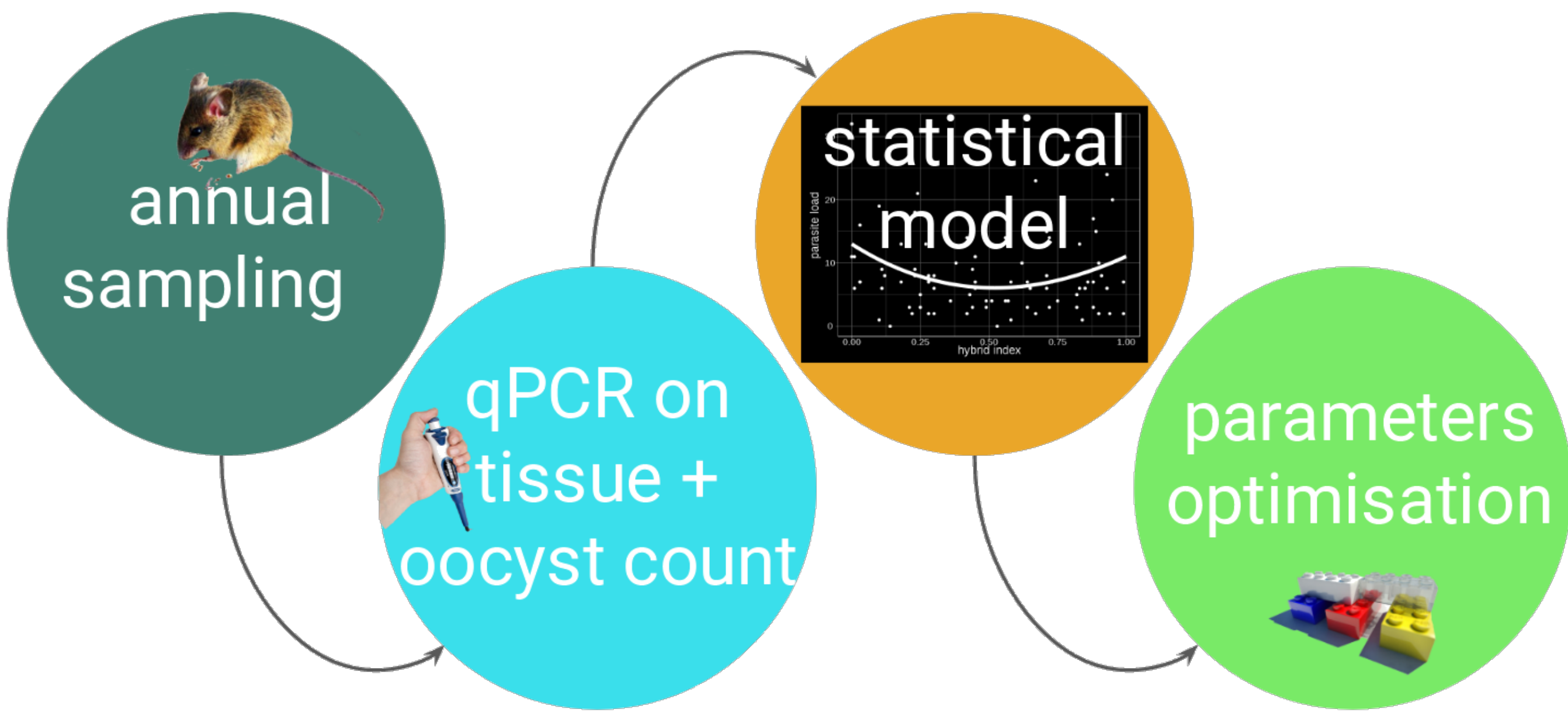
- Eimeria* spp., obligate intracellular apicomplexan parasite. **Two major clades (A & B) of *Eimeria* spp. identified (3 markers) in the mice of the hybrid zone** (Jost 2016).

Aims of the study

- Investigating the **vigor/resistance of hybrids of house mouse** to their parasite *Eimeria* spp. using prevalence and intensity data for parasite strains throughout the House Mouse Hybrid Zone.
- Looking for evidence of **local adaptation** between the murine host and its Eimerian parasite (coevolution?)

Material & Methods

- Field sampling : 110 mice, in Brandenburg area (Germany)



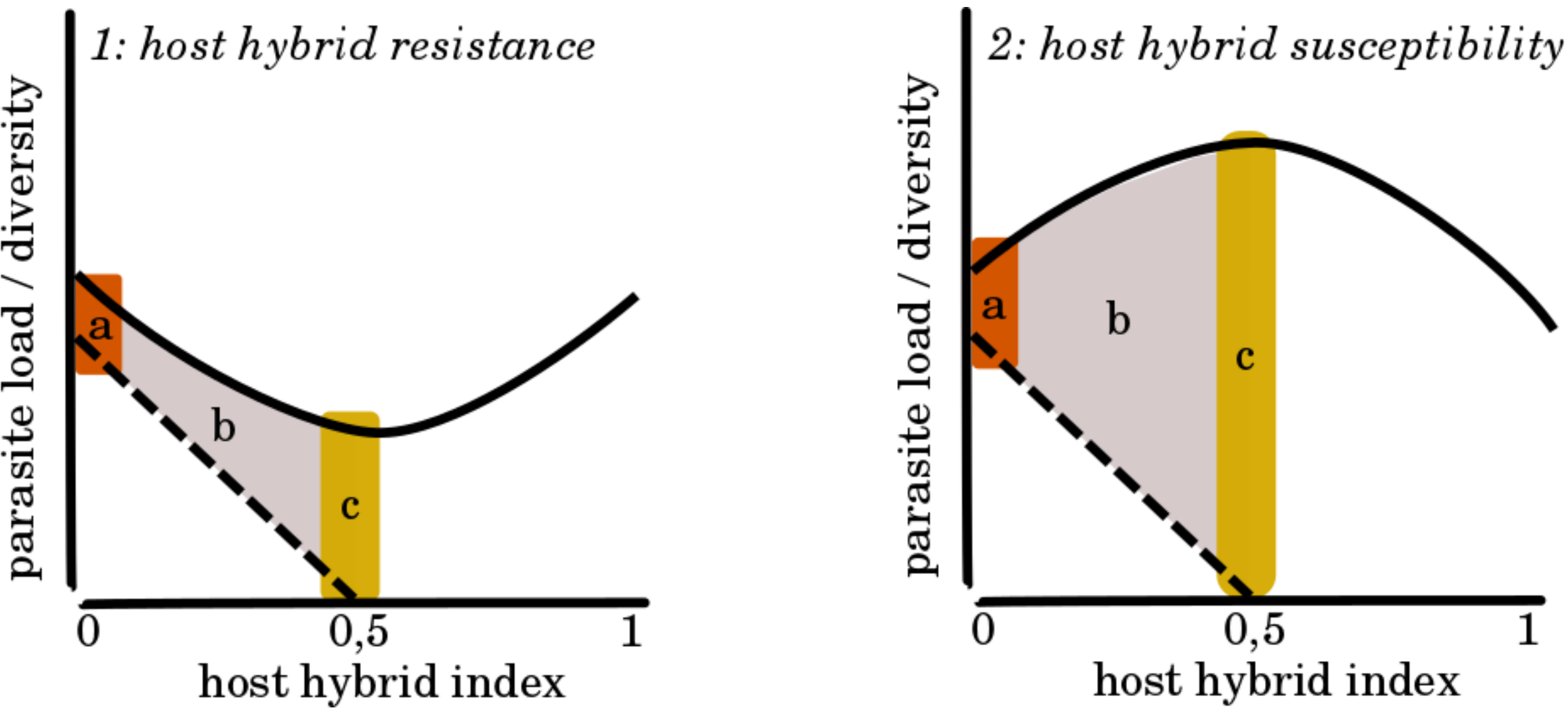
- Cross infection pilote experiment :
 - Host strains :
 - Eimeria* haplotype A** laboratory strain *Eimeria falciformis* REFFFFF
 - Eimeria* haplotype B** strain isolated in the wild
 - Parasite strains :
 - WSB** Wild-derived inbred strain. Derived from wild *Mus musculus domesticus* Region of capture : Eastern Shore, Maryland
 - PWD** Wild-derived inbred strain. Derived from wild *Mus musculus musculus* Region of capture : near Prague, Czech Republic
 - WP** Hybrids between the 2 previous commercial strains

Statistical model : glm.hybrid

$$\text{Parasite load} \sim \text{mouse heterozygosity level} * \text{parasite strain}$$

- Adaptation of the method of Stuart J.E. Baird (Baird et al. 2012) : Maximum likelihood analysis explicitly linking parasite abundance to a gradient along the hybrid index (as a proxy of host heterozygosity), generalized linear model with negative binomial distribution
- R package : https://github.com/alicebalard/Parasite_Load

Evidence (?) of hybrid vigor/resistance

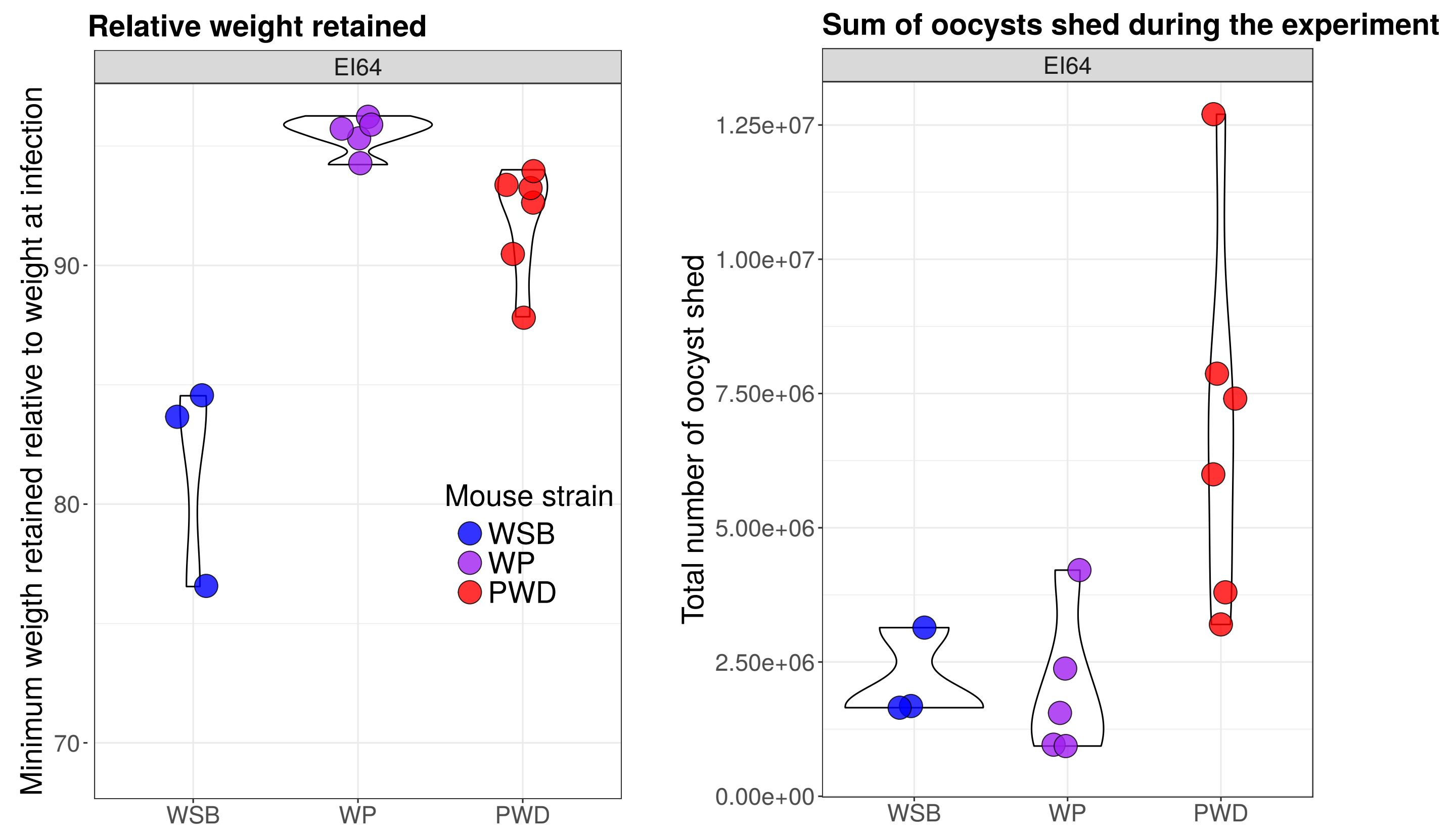


description

Evidence of local adaptation

Results of the infection experiment :

- Eimeria* strain haplotype A killed wild-derived mice at the beginning of the shedding period, regardless of mouse strain -> MORE?
- Eimeria* strain haplotype B has **lowest parasite shedding** in mice strains WSB compared to PWD, for a **highest relative weight loss** : evidence of **local adaptation**
- Mice hybrids lost less weight and were less infected than the pure strains
Possible hybrid vigor (limitation : unknow effect of heterosis)



some stats here!

Perspective

- Next cross infection experiment : verify our hypotheses (hybrid vigor, local adaptation), measure the effect of heterosis, add one parasite strains (another haplotype A, collected in the field)
- Analyse of divergence scenarios for *Eimeria* spp. based on whole genomes and comparison of models of coalescence and cospeciations with their murine hosts (beyond the house mouse).
- Investigation of loci of coevolution, identifying parasite genes under divergent selection in the two house mouse subspecies. The coevolving loci corresponding on the host side will be investigated.

References

- Baird et al. (2012) Where Are the Wormy Mice? A Reexamination of Hybrid Parasitism in the European House Mouse Hybrid Zone *Evolution* 66 (9): 2757–72.
Jost (2016) Improvement of Genetic Markers and Phylogenetics of *Eimeria* Spp. from House Mouse Edited by Emanuel Heitlinger. Humboldt University
Heitlinger et al. (2014) The genome of *Eimeria falciformis*-reduction and specialization in a single host apicomplexan parasite. *BMC genomics* 15 (1), 696
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