

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

Alice Balard^{1,2}, Victor Jarquin^{1,2}, Francisca Böhning¹, Thi Phuong Li¹, Stuart J.E. Baird³, Jaroslav Piàlek³, D.T?⁴, and Emanuel Heitlinger^{1,2}

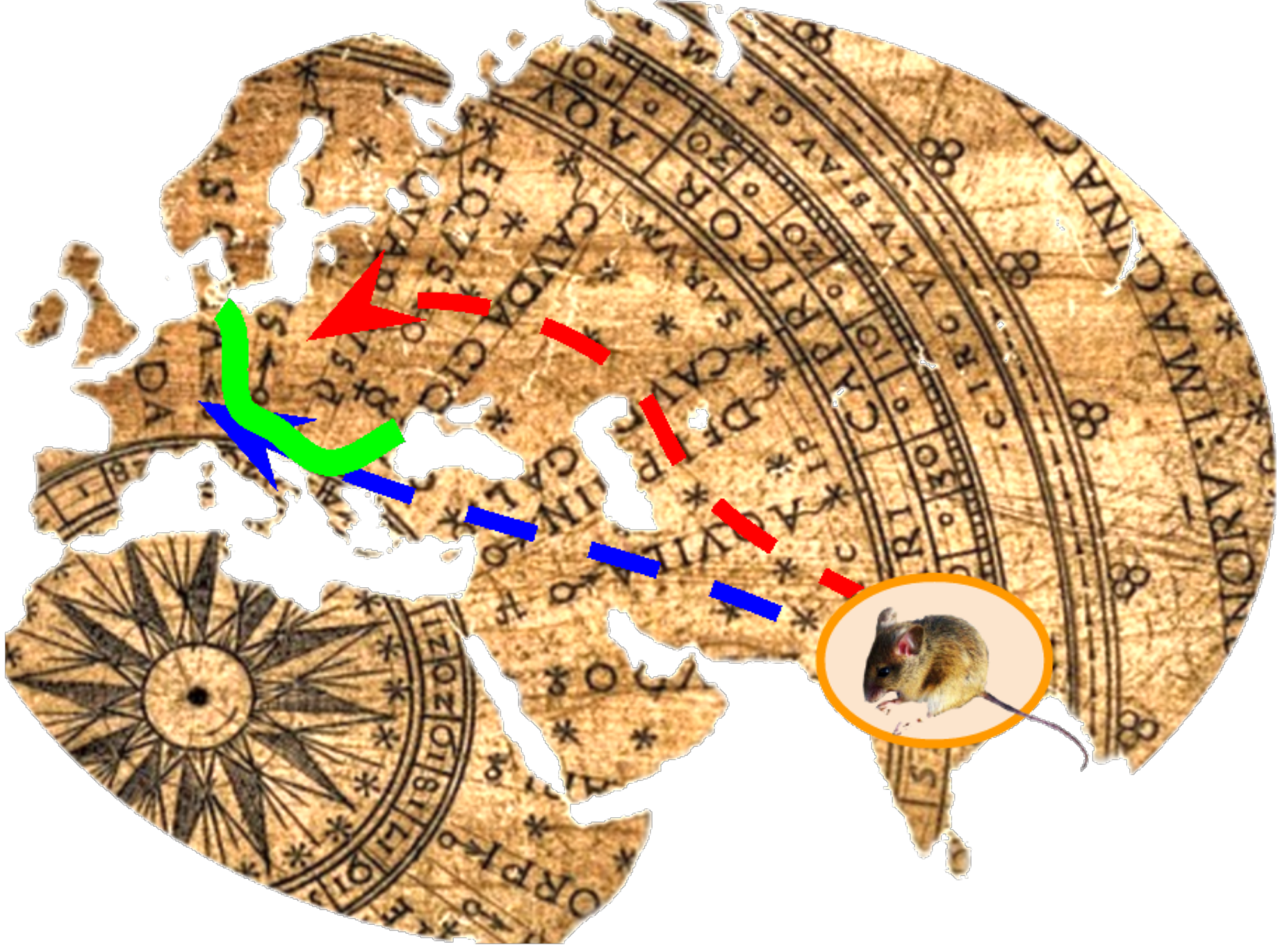
¹Ecology and Evolution of molecular Parasite-Host Interactions (HU/IZW), Leibniz Institute for Zoo and Wildlife Research (IZW) in the Forschungsverbund Berlin e.V. Alfred-Kowalke-Strasse 17, 10315 Berlin, Germany

²Department of Molecular Parasitology, Humboldt University, Philippstrasse 13, 10115 Berlin, Germany

³Department of Population Biology, Institute of Vertebrate Biology, ASCR, Brno and Studenec, Czech Republic

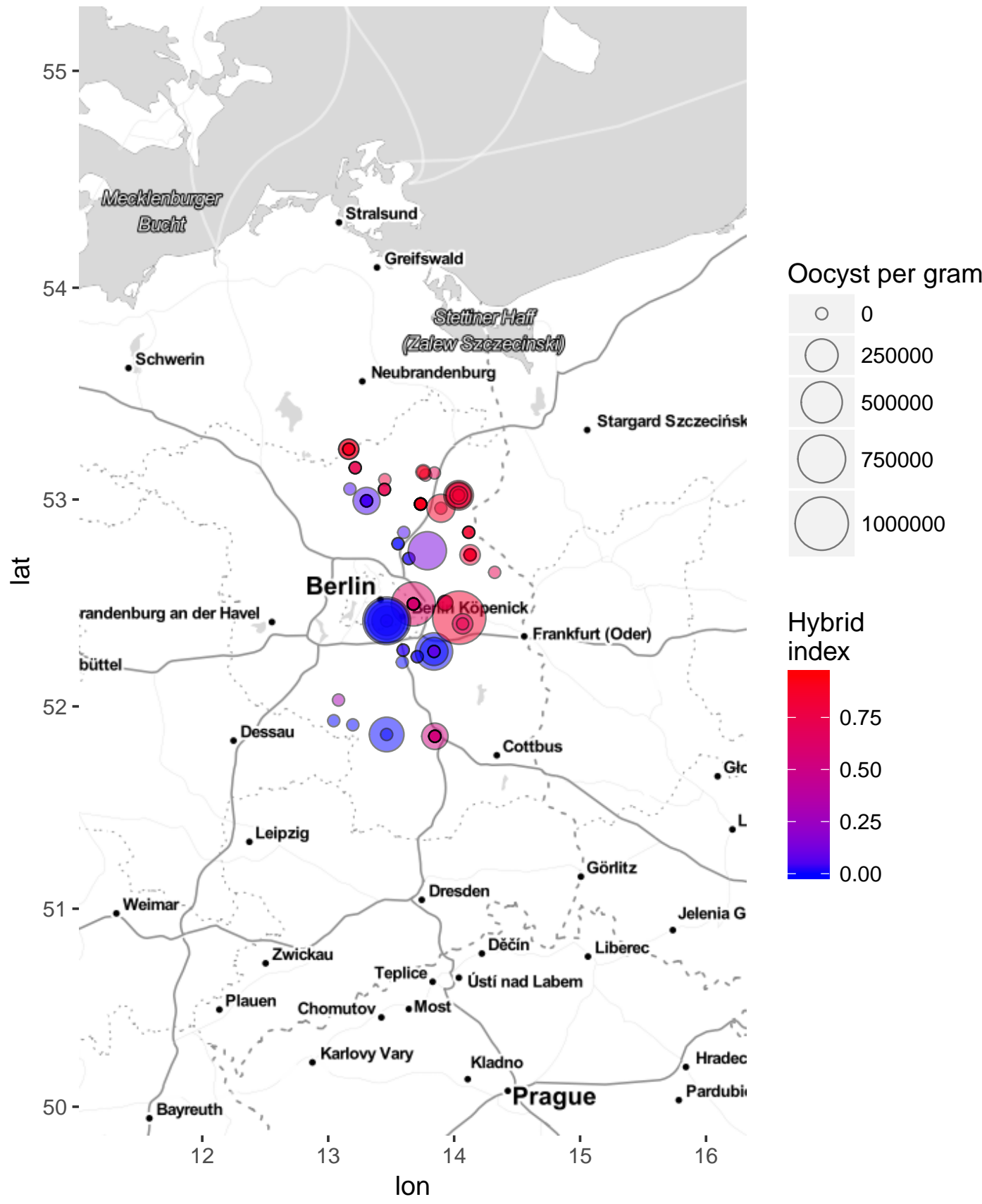
Context

- 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)

Preliminary results : exploring hybrid vigor/resistance in the wild



- Prevalence :
19% infected farms in 2015
2016 : pending analysis...
2017 : upcoming sampling

- Hybrid index assigned to all mice
0 = *Mus musculus domesticus*
1 = *Mus musculus musculus*
in between = hybrids

Goal : using our glm.hybrid model to assess the existence of hybrid vigor/resistance, taking into account the parasite strains

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

Material & Methods : Field study

- Annual sampling every September
104 mice in 2015 from 48 localities
103 mice in 2016 from 34 localities
upcoming sampling in 2017
Brandenburg area (Germany)
- Oocyst counted in mice feces
All parasite strains genotyped using 3 markers, then assigned to an haplotype
- 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

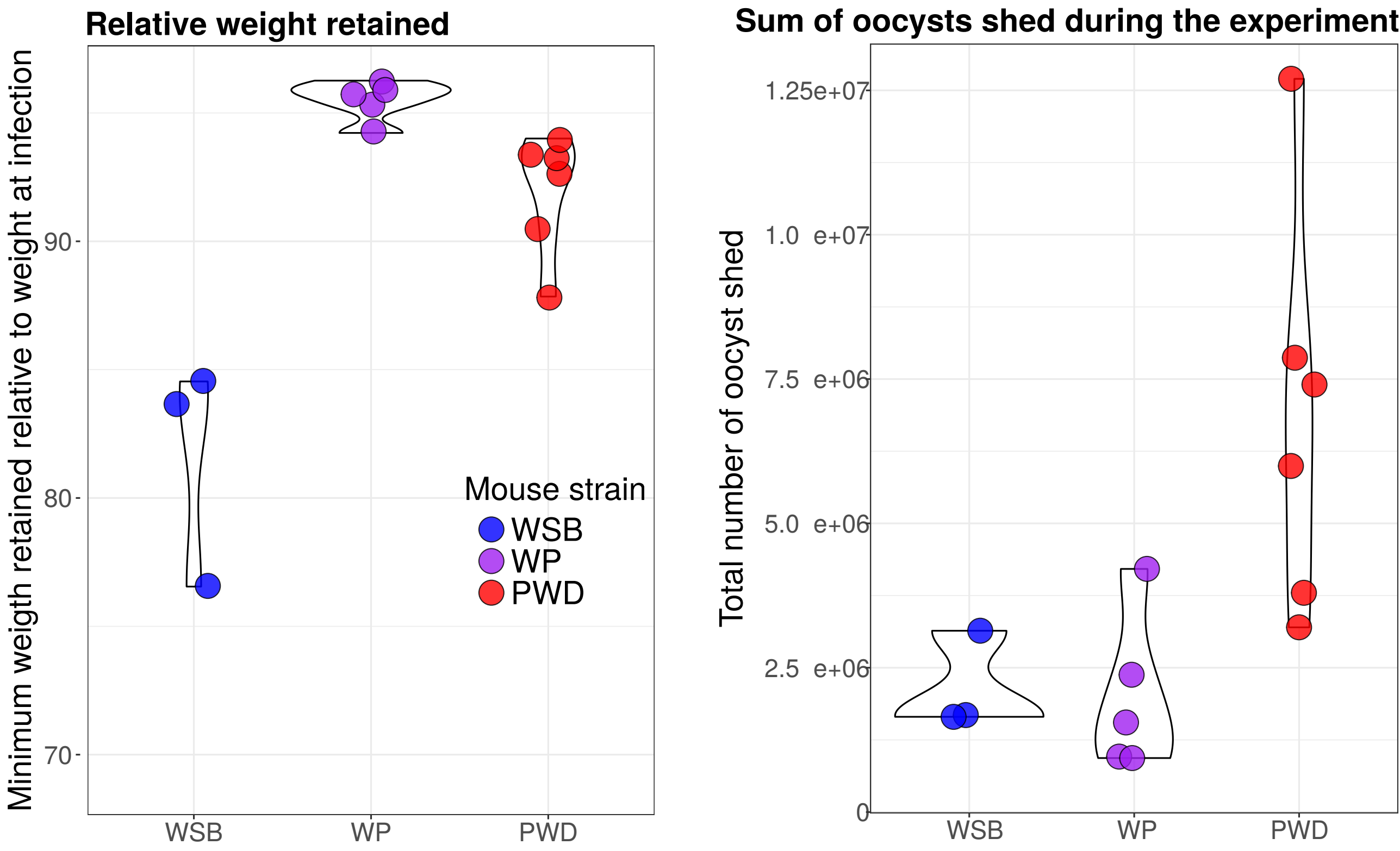
$$\text{Parasite load} \sim \text{mouse heterozygosity level} * \text{parasite strain}$$

- R package under development : https://github.com/alicebalard/Parasite_Load

Evidence of local adaptation

Results of the infection experiment :

- Eimeria* strain haplotype B has **lowest parasite shedding** in mice strains WSB compared to PWD, for a **highest relative weight loss** : indication of **local adaptation**
- Mice hybrids lost less weight and were less infected than the pure strains
Possible hybrid vigor (limitation : unknow effect of general heterosis)



some stats here! OUR MODEL? +lm

Material & Methods : Cross infection

Pilote experiment

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

Perspective

- Next cross infection experiment : verify our hypotheses (hybrid vigor, local adaptation), measure the effect of heterosis (within subspecies heterosis vs between subspecies)
- Assess local adaptation in other parasite strains
- 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
Macholán *et al.* (2012) Evolution of the House Mouse *Cambridge University Press*

Funding : This research has received funding from the DFG, and is part of a IZW/HU project
A. Balard is part of the Dahlem Research School
Contact : alice.balard@fu-berlin.de



Leibniz-Institut für
Zoo- und Wildtierforschung
IM FORSCHUNGSVERBUND BERLIN E.V.



DAHLEM
RESEARCH
SCHOOL
DFG
Deutsche
Forschungsgemeinschaft