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

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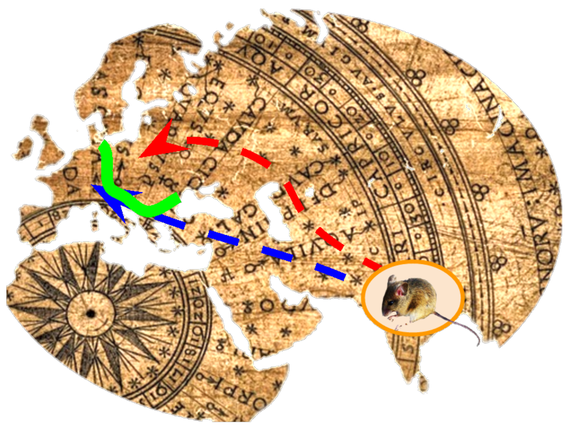
Context

- 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)



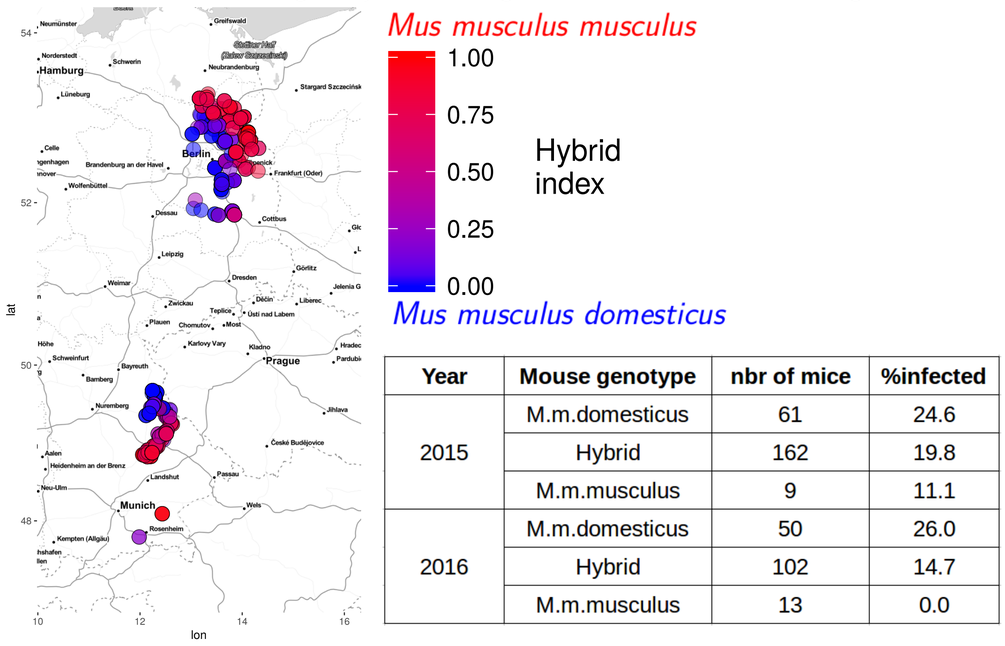
- *Eimeria* spp., obligate intracellular apicomplexan parasite. **Two major clades (A & B)** of *Eimeria* spp. identified (3 markers) in the mice of the hybrid zone (Jost 2016)

Aims of the study

1. Investigate the **hybrid vigor/resistance** of house mouse to their parasite *Eimeria* spp. using prevalence and intensity data for parasite strains throughout the House Mouse Hybrid Zone
2. Test **local adaptation** between the host and its parasite

Material & Methods : Field study

Annual sampling every September. Oocyst counted in mice feces
All parasite strains genotyped using 3 markers, then assigned to an haplotype



Year	Mouse genotype	nbr of mice	%infected
2015	M.m.domesticus	61	24.6
	Hybrid	162	19.8
	M.m.musculus	9	11.1
2016	M.m.domesticus	50	26.0
	Hybrid	102	14.7
	M.m.musculus	13	0.0

Material & Methods : Cross infection

Pilote experiment

- Parasite strains :
  1. ***Eimeria* haplotype A** laboratory strain *Eimeria falciformis* (Heitlinger *et al.* 2014)
  2. ***Eimeria* haplotype B** strain isolated in the wild
- Host strains :
  1. **WSB** Wild-derived inbred strain. Derived from wild *Mus musculus domesticus* Region of capture : Eastern Shore, Maryland
  2. **PWD** Wild-derived inbred strain. Derived from wild *Mus musculus musculus* Region of capture : near Prague, Czech Republic
  3. **WP** Hybrids between the two previous commercial strains

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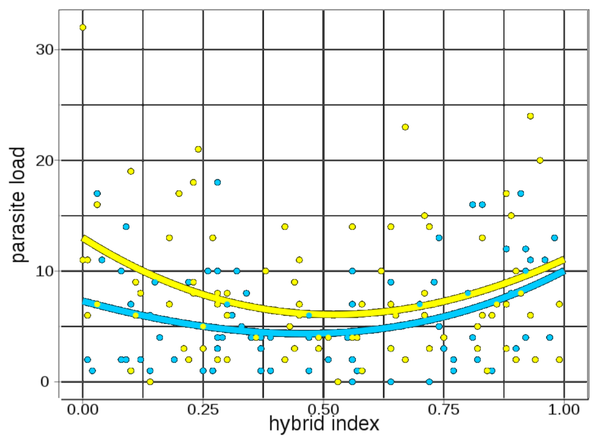
Exploring hybrid vigor/resistance in the wild

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 : **glm.hybrid**



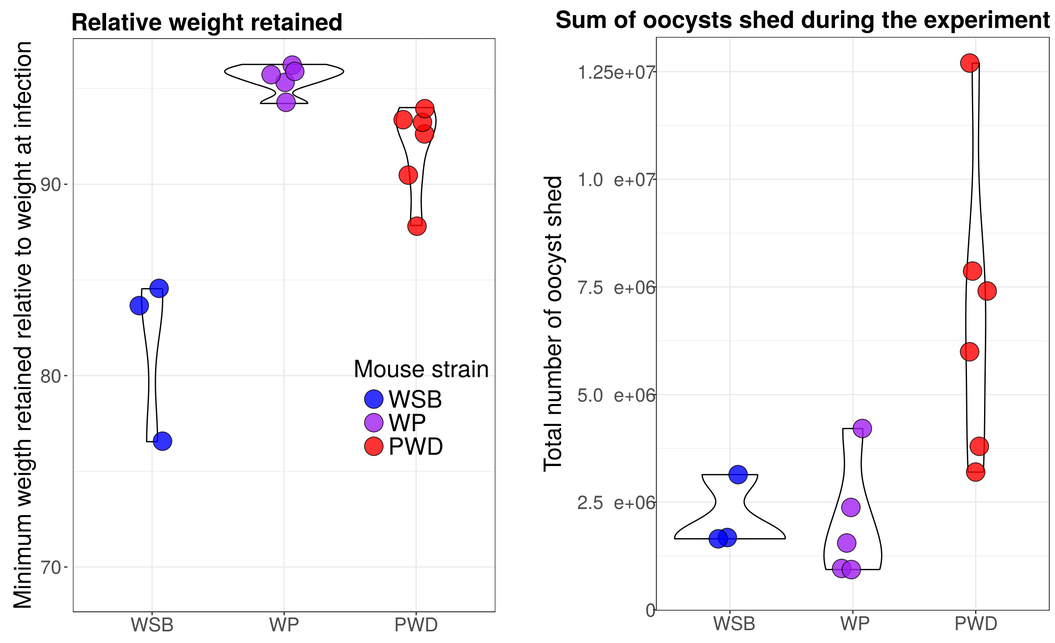
$$Parasite\ load \sim mouse\ heterozygosity\ level * parasite\ strain$$

R package under development : https://github.com/alicebalard/Parasite_Load
Goal : using our glm.hybrid model to assess the existence of hybrid vigor/resistance, taking into account the parasite strains

Evidence of local adaptation

Results of the infection experiment :

- *Eimeria* strain haplotype B has **lower parasite shedding** but are more harmed as they have a **lower relative weight retained** in mice strains WSB compared to PWD : 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)



Perspective

Next cross infection experiment :

- Test our hypotheses of hybrid vigor (within subspecies heterosis vs between subspecies)
- Assess local adaptation in other parasite strains

Field data :

- Obtain enough data (Sept. 2017) to test our hypotheses of hybrid vigor and local adaptation in the wild

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
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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