Hybrid resistance to pathogenic coccidia *Eimeria* spp. in the European House Mouse Hybrid Zone

Target journal: Evolution. Limit of 7500 words.

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Keywords: *#parasites #hybridisation #resistance #eimeria*

# Abstract

Parasite infections have been suggested to modulate the fitness of hybrid hosts, either limiting or facilitating hybridisation. To test hybrid susceptibility vs. hybrid vigour, we assess intracellular infections by \_Eimeria\_, a parasite with high pathogenicity, and test its intensity in hybrids and pure \_Mus musculus\_ subspecies in a novel transect of the European House Mouse Hybrid Zone.

We find lower abundance of \_Eimeria\_ in hybrid hosts. Additionally we show that parasite intensities in infected hybrid hosts are lower than in pure genotypes largely excluding ecological epidemiological factors. We thus show hybrid vigour against this parasite. Using the same approaches in our new transect we additionally reproduce findings of hybrid vigour against pinworm infections.

Lower impact of parasites on hybrid hosts health could offset reductions in fertility in house mouse hybrids. Improved health could counterbalance reductions in other fitness components and thereby reduce the “net strength” of isolating speciation barriers.

# Introduction

The prevalence of hybridisation and gene introgression between species might be underestimated by biologists using the -otherwise often immensely helpful- biological species concept of reproductively isolated populations (@Mayr\_1942). Mallet, however, suggested that hybridisation occurs in more than 10% of animal species and 25% of plant species (@mallet\_hybridization\_2005) and own species hybridised recently (@green\_draft\_2010).

Hybrid zones, areas where individuals of different species meet and hybridise, can be studied over decades and allow to infer the impact of the different endogenous and exogenous forces at play in this process. The European House Mouse Hybrid Zone (HMHZ) is a tension zone characterized by selection against hybrids replaced by immigrating less admixed mice (@barton\_analysis\_1985). The two house mouse sub-species \_Mus musculus domesticus\_ and \_Mus musculus musculus\_ (hereafter Mmd and Mmm) have entered into this secondary contact around 5000 years ago as a result of their colonization of Europe during the Iron age following the spread of human agriculture (@boursot\_evolution\_1993, @macholan\_evolution\_2012). After 500 000 years of allopatric divergence house mice can be found nowadays separated by the 20 km-wide and 2500 km-long HMHZ, stretching from Scandinavia in the North, to the Black Sea in the South (@macholan\_genetic\_2007, @jones\_norwegian\_2010). The HMHZ is barrier with limited permeability to gene flow between mouse taxa (@macholan\_assessing\_2011). The main selective forces acting against hybrids are thought to be endogenous rather than ecological (@macholan\_genetic\_2007), mainly acting on sperm-related traits (@albrechtova\_sperm-related\_2012)

The HMHZ was one of the first animal hybrid zones studied for the role of parasitism on species barriers (@sage\_wormy\_1986). Parasites by definition decrease their hosts’ fitness (@poulin\_evolutionary\_2006). One can thus suppose that parasitism has an influence on the hybridisation process, if resistance to parasites differs between hybrid and pure hosts (@fritz\_resistance\_1999).

Nevertheless the intensity of a particular parasite infection is not necessarily correlated with a fitness decrees. Indeed, animals tolerant for lowly pathogenic parasites might not see their fitness decrease with higher parasitemia. This could be the case if the parasite is beneficial for the host in interactions with other parasites (@heitlinger\_intestinal\_2017) or if immune reactions against it are costly in relation the harm it causes. Besides, as a foundation of the “Old Friend” (or “Hygiene”) hypothesis, the constant presence of helminths in (not only human) populations has lead to the evolution of a background basal release of regulatory cytokines (@rook\_review\_2009) which might in turn impact the outcome of more pathogenic infections. Having considered these cases, one can still wonder if parasitic infections are positively or negatively influencing the spread of hybrid genotypes. This question was studied for decades in the HMHZ as host model, initially considering helminths as parasite model.

Parasite infections were originally thought to prevent hybridisation in house mice, as hybrid susceptibility to helminths was believed to be observed in field and experimental studies (@sage\_wormy\_1986, @moulia\_wormy\_1991, @moulia\_experimental\_1993). Infection experiments using the protozoan \_Sarcocystis muris\_ lead to similar conclusion (@derothe\_susceptibility\_2001) of hybrid susceptibility. This phenomenon was explained by the perturbation of co-adapted host immune gene complexes in recombinant hybrids. These findings came to be questioned when laboratory experiments showed either no hybrid effect on helminth load, or even reduced load in hybrids compared to pure strains (@moulia\_hybrid\_1995, @derothe\_recombination\_2004). Moreover, in 2012, Baird et al. Provided evidence of hybrid vigour in the HMHZ in response to helminths infection (especially the pinworms Aspiculuris tetraptera and \_Syphacia obvelata\_ and the whipworm \_Trichuris muris\_ (@baird\_where\_2012)). In species other than helminths, laboratory infections with the protozoan \_Trypanosoma musculi\_ did not show significant difference of parasite load between hybrid mice and pure Mmd or Mmm (@derothe\_experimental\_1999).

Several factors could explain these discrepancies. In 1999, Derothe et al. proposed the “parasite constraint” hypothesis (@derothe\_experimental\_1999). It states that a parasite should exert sufficient selective pressure on the host to lead to host hybrid susceptibility, as co-adapted complexes would be selected in hosts on this basis.

In addition design of the studies preceding Baird et al. 2012 was limited in terms of statistical, experimental and sampling procedures. Low sample size and long maintenance of mice in laboratory before assessment of parasite burden (@baird\_where\_2012) might have introduced bias. Finally, the definition of hybrids status can be considered problematic: house mouse hybrids are thoroughly admixed (“late-generation”) (@macholan\_genetic\_2007) and therefore should not be considered in categories, but rather on a continuous scale.

Pinworms (oxyurids) have been shown to be the most prevalent helminths infecting house mice in the HMHZ (@baird\_where\_2012). They are broadly distributed, can reinfect their host all along their lives and can be considered close to non-pathogenic (@taffs\_pinworm\_1976). Following Derothe’s reasoning it is arguable whether pinworms would apply strong enough selection pressure on their hosts to induce hybrid susceptibility according to the parasite constraint hypothesis. Therefore it is questionable whether pinworms should be the only parasite to test the parasite constraint hypothesis in natural systems.

In an attempt to address the inconsistencies we selected a parasite model that is likely to exert selective pressure on its host, the intracellular coccidia from genus \_Eimeria\_. Different \_Eimeria\_ spp. infect the intestinal epithelial cells of several vertebrates and provoke symptoms such as weight loss and diarrhoea in mice. Infection experiment in laboratory (NMRI) mice showed a weight loss up to 20% following infection with oocysts isolated from mice captured in the HMHZ (\hl{Al-Khalifeh et al. unpublished}). Eimeria are often considered host-specific, with several thousand species parasitising different vertebrates (@haberkorn\_entwicklung\_1970, @chapman\_selective\_2013). In the European HMHZ, three \_Eimeria\_ species have been identified so far in mice: \_E. ferrisi\_, \_E. falciformis\_ and \_E. vermiformis\_. The three species have a distribution throughout the HMHZ with a prevalence of 20 to 30% \hl{(Jarquin et al. unpublished)}. In populations of bank voles, \_Eimeria\_ spp. has been shown to reduce breeding success (@hakkarainen\_eimeria-parasites\_2007) and overwinter survival of deer mice (@fuller\_effects\_1996) is affected. Moreover, \_Eimeria\_ spp. intensity was found positively correlated with bank vole’s age, indicating re-infection throughout life (@winternitz\_parasite\_2012). For all these reasons, we consider \_Eimeria\_ a good candidate to question the parasite constraint hypothesis.

We assessed \_Eimeria\_ infection in a novel transect of the HMHZ just outside of Berlin in the North-East of Germany. We test the impact of hybridization on both abundance and intensities of this parasite.

# Material & Methods

## Sampling

House mice (\_Mus musculus\_) were trapped every year in Brandenburg (Germany) in September from 2014 to 2017, using individual plastic live traps placed into farms or houses. The considered transect ranges from 51.68 to 53.29 degrees of latitude (200 km) and from 12.52 to 14.32 degrees of longitude (140 km). At this period of the year it is possible to catch a high number of mice along the hybrid zone, and sampling at the same season every year reduces potential seasonal variability (@haukisalmi\_population\_1988, @abu-madi\_seasonal\_2000). Sampling was planned to maximize capture of the full range of mice genotypes. Mice individually isolated in cages were euthanized by isoflurane inhalation followed by cervical dislocation and dissected within 24 hours after capture (capture permit No. 2347/35/2014). Mouse tissue samples (muscle and spleen) were collected in liquid nitrogen then stored at -80°C for host genotyping. Digestive tracts were dissected and ileum, cecum and colon tissues stored separately in liquid nitrogen followed by conservation at -80°C.

## Host genotyping

The strength of hybridization was estimated for each mouse as a value of hybrid index (HI). HI is calculated as proportion of Mmm alleles within a set of fourteen biallelic diagnostic markers fixed as either Mmd or Mmm. This set consists in one mitochondrial marker (mtBamH, restriction site in mitochondrial Nd1 gene which discriminates between mice subspecies (@munclinger\_genetic\_2002, @bozikova\_mitochondrial\_2005, @dureje\_mouse\_2012)), one Y-linked marker (presences/absence of insertion in Zfy2 gene (@nagamine\_musculus-type\_1992, @boissinot\_discordant\_1997, @dureje\_mouse\_2012)), six X-linked marker (three short interspersed nuclear elements, namely Btk, Tsx (@munclinger\_b1\_2003) and Syap1 (@macholan\_genetic\_2007), and three SNPs, namely X332, X347 and X65 (@payseur\_differential\_2004, @dufkova\_inference\_2011, @dureje\_mouse\_2012)), and six autosomal markers (Es1, Gpd1, Idh1, Mpi, Np, Sod1) (@bonhomme\_biochemical\_1984, @munclinger\_genetic\_2002, @macholan\_genetic\_2007, @dureje\_mouse\_2012). HIs range from 0 to 1, HI of 0 indicating a pure Mmd and HI of 1 a pure Mmm (@wang\_measures\_2011, @baird\_where\_2012).

A map delimiting the probabilistic separation between both sub-species was computed using the program Geneland with some graphical modifications using the six autosomal markers (Es1, Gpd1, Idh1, Mpi, Np, Sod1). Geneland uses a Markov chain Monte Carlo (MCMC) approach to combine both geographical and genetic information (@guillot\_geneland:\_2005). Number of clusters was set to 2, 10000 MCMC iterations were performed and saved every 100 iterations (100 iterations saved). First five iterations were discarded as burn-in, and the resolution of the map was set to 100 pixels for both x and y axes.

## Parasite loads estimation

Mice digestive tracts were dissected and inspected for helminths presence with a binocular microscope. Helminths were counted and stored in 70% ethanol for later identification by molecular analysis and in 3.5% formalin for later morphological comparison with species descriptions. In this study we considered only the more prevalent helminths, the oxyurids \_Syphacia obvelata\_ and \_Aspiculuris tetraptera\_.

DNA was extracted from ileum and cecum tissues and quantitative PCR (qPCR) were completed to estimate \_Eimeria\_ spp. load. DNA extraction was performed using the innuPREP DNA Mini Kit (Analytik Jena AG, Jena, Germany) following the instructions of the manufacturer with additional mechanical tissue disruption with liquid nitrogen in a mortar. Both quality and quantity of isolated DNA were measured by spectrophotometry in a NanoDrop 2000c (Thermo Scientific, Waltham, USA). \_Eimeria\_ spp. presence was tested by qPCR to detect intracellular stages of the parasite as well as house mouse nuclear genome as internal reference. Primers used for \_Eimeria\_ spp. detection targeted a short mitochondrial COI region (Eim\_COI\_qX-F: TGTCTATTCACTTGGGCTATTGT; Eim\_COI\_qX-R: GGATCACCGTTAAATGAGGCA), while \_Mus musculus\_ primers targeted the CDC42 nuclear gene (Ms\_gDNA\_CDC42\_F: CTCTCCTCCCCTCTGTCTTG; Ms\_gDNA\_CDC42\_R: TCCTTTTGGGTTGAGTTTCC). Reactions were performed using 1X iTaqTM Universal SYBRⓇ Green Supermix (Bio-Rad Laboratories GmbH, München, Germany), 400 nM of each primer and 50 ng of DNA template in 20 µL final volume. Cycling amplification were carried out in a MastercyclerⓇ RealPlex 2 (Eppendorf, Hamburg, Germany) according to the following amplification program: 95°C initial denaturation (2 min) followed by 40 cycles of 95°C denaturation (15 s), 55°C annealing (15 s) and 68°C extension (20 s). Melting curve analyses were performed in order to detect primer dimer formation and unspecific amplification. ΔCt was calculated as difference of threshold cycle (Ct) between mouse and \_Eimeria\_ spp. values. Samples with a ΔCt higher than -5 for at least one of the two intestinal tissue were considered positive (\hl{Jarquin et al., unpublished}), and in case of a detection in both tissues, the higher value was taken as a proxy of individual parasite load. This parasite load of intestinal tissue stage is expressed in “ΔCt Eimeria-host” throughout this paper. For statistical modelling 5 was added to “ΔCt Eimeria-host” values so that negative samples present a load of zero and positive samples a load > 0.

## General parasite assessment

For each parasite and detection method, abundance (mean parasite load of all hosts) and intensity (mean parasite load of infected hosts) were estimated (@rozsa\_quantifying\_2000). Bias-corrected and accelerated bootstrap confidence intervals as proposed by Efron and Tibshirani (@efron\_introduction\_1993) were computed with 1000 bootstrap to account for skewness of the distribution of parasite loads. Prevalence (number of infected individuals amongst all tested individuals) was calculated and confidence intervals obtained with Sterne's exact method (@sterne\_remarks\_1954, @reiczigel\_exact\_2010). Calculations were performed using the software R (@r\_development\_core\_team\_r:\_2008) and the epiR package (@nunes\_epir:\_2018).

## Statistical test of hybridisation effect

Following the approach of Baird et al., we tested if hybrid mice had higher or lower parasite load than expected in case of load intermediate between that of pure hybridizing taxa (“additivity”, @baird\_where\_2012). The hybridization effect on each individual is modelled by the degree at which new gene combinations are brought together compared to the pure sub-species. Following Barton's approach (@szymura\_genetic\_1986, @macholan\_assessing\_2011) this was estimated from the hybrid index using the function for expected heterozygosity: He = 2 HI (1-HI). ~~An individual with a pure mouse subspecies genotype would have a heterozygosity of 0, while a perfect mix of both parental genotypes would have the maximal level of heterozygosity, 0.5.~~

We considered four nested hypotheses increasing in complexity, and compared them with a G-test (likelihood ratio test) to consider a more complex hypothesis only when justified by a significant increase in likelihood. Expected parasite load is fixed to be identical for both subspecies and both host sexes in hypothesis H0. The more complex H1 introduces load differences for the host sexes. H2 allows loads to be different between subspecies at the extremes of the hybrid index. H3, finally, combines differences between pure subspecies and host sexes.

The covariates considered were subspecies and sex, both known to potentially interfere with parasite load (@wilson\_heterogeneities\_2002).

We developed an R-package (@balard\_parasite\_2018 \hl{to put on platform}) to provide a statistical model assessing the influence of a hybrid index on parasite load. The package allows different distributions of errors when estimating parasite load. We used the package to fit models by maximum likelihood (using R package mle2 (@bolker\_bbmle:\_2017)). The parasite load was estimated including a hybridization effect parameter or not, and we compared these two models using a G-test (maximum likelihood statistical significance test). Adequate distributions of errors for each parasite and detection method considered were selected using log likelihood and AIC criteria and by comparing goodness-of-fits plots (density, CDF, Q-Q, P-P) (R packages MASS (@venables\_modern\_2002) and fitdistrplus (@delignette-muller\_fitdistrplus:\_2015)).

Negative binomial distribution should perform well for macroparasite counts (@crofton\_quantitative\_1971, @shaw\_patterns\_1995), which was confirmed for helminths. Values of (Δct Eimeria-host +5) were found be well described by a Weibull distribution.

All graphics were produced using R package ggplot2 (@wickham\_ggplot2:\_2016), R package ggmap (@kahle\_ggmap:\_2013), and compiled using the free software inkscape.

# Results

## Host genotyping and characterisation of the HMHZ in a novel transect

A total of 660 mice were caught and genotyped during four sampling seasons (2014: N=87; 2015: N=163; 2016: N=167; 2017: N=243) in 157 farms and houses in the North-East of Germany. Overall, 4.2 mice were caught on average per locality (95% CI: [3.8-4.6]). To estimate the amount of hybridization in each individual we estimated a hybrid index as the proportion of Mmm alleles all (six to 21) genotyped alleles. A table containing hybrid indices, georeference and parasite load for each individual is available in supplementary material (table S1). To locate the centre of the HMHZ we constructed a probabilistic map of the hybrid zone centre in this transect using six autosomal markers genotyped in all mice (Es1, Gpd1, Idh1, Mpi, Np, Sod1). Describing the HMHZ centre in detail from South to North, it first makes a small bent to go in the East around the city of Berlin. Further North it turns back take a more North-Westward direction running towards the “Müritz” area through large forests with few small villages in between (figure 1).

## Parasite prevalence and inteslity

To investigate \_Eimera\_ infections we assessed 384 mice sampled in 2016 and 2017 for the presence and intensity of tissue stages. The parasite had a prevalence of 18.2% (70/384) (Sterne’s Exact method CI 95%: [14.5-22.5]). To quantify the intensity of infection we determined the amount of \_Eimeria\_ mitochondrial DNA per host nuclear DNA. We use ΔCt, the difference in “threshold cycle” (the cycle at which quantitative PCR reaches fluorescence threshold) to express \_Eimeria\_ intensity. ΔCt corresponds to a log2 ratio between parasite and host DNA.

~~After these transformations we obtain an average \_Eimeria\_ abundance of 0.6 (95%CI: [0.4–0.8]) and a mean intensity of 3.2 (95%CI: [2.7-3.9]).~~

~~For statistical modelling we add 5 to these values to set our detection threshold of -5 to zero.~~

Between 2014 and 2017, 585 mice were investigated for helminths. Prevalence of pinworms in the transect was 52.5% (307/585) (Sterne’s Exact method CI 95%: [48.4–56.5]) with an average abundance of 18.7 (95%CI: [15.5–23.3]) pinworms per mouse and intensity of 35.7 (95%CI: [29.6-44.2]) pinworms per infected mouse (maximum number of pinworms in one host: 489).

## Resistance against \_Eimeria\_ spp. is elevated in hybrid mice compared to pure strains

\_Eimeria\_ spp. tissue stage intensity was modelled with a Weibull distribution of errors, along the hybrid index. Our most basic model (H0) containing no load differences between Mmd and Mmm pure subspecies and between hots sexes was found to fit our observations significantly better than more complex models including those factors (table 2). The fit integrating a hybridisation effect showed significantly higher likelihood than a model without hybridization effect (G-test; p-value < 0.001). Hybrids have significantly lower load of \_Eimeria\_ spp. tissue stages (a hybridisation effect parameter of 0.86) than expected if load was linear along the hybrid index (Fig. 2a, values of parameters of the fitted model given in table 1).

A reduced abundance (strength of infection in both infected and uninfected hosts) of \_Eimeria\_ spp. (and of any parasite) could be explained by either ecological and epidemiological factors or by host-intrinsic factors: resistance. To test more specifically the resistance of hybrids compared to pure mice, we considered only individuals infected by \_Eimeria\_ spp. tissue stages (N = 70). Again the model containing no differences between Mmd and Mmm taxa and between host sexes was also found to fit significantly better our observations than more complex models (table 2). The fit integrating a hybridisation effect showed significantly higher likelihood than the model without it (G-test; p-value = 0.026). Infected hybrids have significantly lower load of \_Eimeria\_ spp. tissue stages than expected if the load was linear along hybrid index, with a hybridisation effect parameter alpha of 0.88 (Fig. 2b, values of parameters of the fitted model given in table 1).

## Hybrid vigour against pinworms and comparisons of it’s strength with previous reports

We modelled pinworm abundance with a negative binomial distribution of errors along the hybrid index. The most complex model tested (H3) including a load difference between Mmd and Mmm pure subspecies and between host sexes was found to fit our observations significantly better than the less complex models (table 2) in this case. For both sexes, the model including a hybridisation effect showed significantly higher likelihood than the model without (G-test; p-value < 0.01 for both males and females). Hybrids have significantly lower pinworms load than expected if the load was linear along the hybrid index, with a hybridisation effect parameter alpha of 1.11 (females) and 1.33 (males) (Fig. 3a, values of parameters of the fitted model given in table 1).

To compare the strength of hybridisation effect between our Brandenburg transect and the Czech-Bavarian transect investigated by Baird et al., we compared the model fitted to our data for H1 (considering no sex differences) (table 1) to a model fitted on the same data, optimized with a fixed hybridisation parameter of 1.39 (corresponding to the alpha parameter of Baird et al. 2012 for pinworms abundance). Comparison between the models with freely varying alpha and restricted alpha did not show any significant differences in likelihood (G-test; p-value = 0.25). Therefore we conclude that the strength and direction of hybrid vigour are coherent with results in the previously studied Czech–Bavarian transect of the HMHZ.

## Resistance against pinworms is elevated in hybrid mice compared to pure strains

To exclude ecological and epidemiological explanation also for pinworms we again tested the resistance of hybrids compared to pure mice in our Brandenburg transect, we considered only individuals infected by pinworms (N = 307). Model H3 integrating a difference between taxons and sexes was found to fit our observations significantly better than lower models of lower (table 2). For both sexes, the fit including a hybridisation effect showed significantly higher likelihood than the model without it (G-test; p-value = 0.04 for females, p-value < 0.01 for males). Infected hybrids have significantly lower pinworms load than expected if the load was linear along hybrid index, with a hybridisation effect parameter alpha of 0.89 (females) and 1.43 (males) (Fig. 3b, values of parameters of the fitted model given in table 1).

# Discussion

We tested hybrid vigour vs. susceptibility analysing infections of house mice with the intracellular parasites \_Eimeria\_ spp. in a novel transect of the HMHZ. We found a positive effect of hybridisation (that is, hybrid vigour) both when considering all host (parasite abundance) or infected hosts only (parasite intensity).

To our knowledge no previous study tested an effect of hybridization in mice on other than helminth infections using field sampling in the HMHZ. To quantify the intensity of \_Eimeria\_ infections, we used as a quantitative PCR as proxy for parasite load. Such qPCR data of intestinal reflects the intensity of infection more accurately than traditional coprological (flotation) techniques (E. tenella ref, ref Jarquin et al, ref Al-Khlifeh et al.), we additionally argue that the intensity of tissue stages is a better proxy for host health than the intensity of reproductive stages of the parasite detected in faeces.

We adapted the statistical analysis of Baird et al. (@baird\_where\_2012) and explicitly model the effect of hybridisation on parasite load by approximating the amount of recombined alleles using expected heterozygosity. We use this to derive non-linear predictions for hybridisation effect based on the observed hybrid index. To increase reproducibility we make our analysis available in an R package (ref Balard on Zenodo).

Different measures of response to parasites can be chosen (@fritz\_resistance\_1999), including two different measures of load: in this work we consider both parasite abundance (parasite load amongst all potential hosts) and parasite intensity (parasite load amongst infected hosts). Practically this means in- or excluding non-infected hosts from the analysis. The latter might not only reduce problems in statistical inference caused by false negative measurements (so called zero-inflation) but we also address two different hypotheses: (i) are hybrid hosts differentially likely to be infected strongly by parasites than more pure subspecies host? and (ii): do infected host present a different parasite intensity when they are hybrids? We argue here that ii) isolates hybrid resistance from potential ecological and epidemiological determinants. Host density and \_Eimeria\_ spp. prevalence are, for example, negatively correlated in bank voles (Winternitz et al. 2012). Considering that hybrid populations might be less dense (e.g. because of selection against hybrids or the HMHZ falling into areas of low population density due ecological factors (ref Macholan)) it could be problematic that abundance is logically correlated with prevalence (ref Morand). Therefore we propose to consider only infected individuals for load estimations, arguing that parasite intensity relates more closely to intrinsic resistance of individual hosts.

We replicated the result of Baird et al 2012 (@baird\_where\_2012), confirming hybrid vigour in response to pinworm infection. We additionally show that not only pinworm abundance in our novel transect suggests hybrid vigour but also resistance of infected hosts (pinworm intensity excluding uninfected hosts). Following the same logic we apply to \_Eimeria\_ infections this argues for hybrid vigour to be an effect intrinsic to host individuals.

We found that our own results were very similar to the results of Baird et al., both in the direction and strength of the hybridisation effect. In this context it is noteworthy that prevalence and abundance were both lower in our Brandenburg transect (respectively 52.5% and 18.7) than in the previously studied Czech-Bavarian transect (70.9% and 39.19) (@baird\_where\_2012). Other differences compared to the Baird et al. 2017 study include a significant sex difference for pinworm load in our transect. Ecological differences may apply in different parts of the hybrid zone, as well as over time. The similar strength of hybridisation effect in the presence of these epidemiological differences in replicate transects reinforces our confidence hybrid resistance being a host-intrinsic effect instead of by-product of altered epidemiology in the HMHZ.

When results contradictory to the hypothesis of hybrid susceptibility were first found in laboratory experiments (@derothe\_recombination\_2004), Derothe formulated the parasite constraint hypothesis. It states that parasites need to exert high enough selective pressure on their hosts to lead to the evolution of co-adapted gene complexes. Hybridisation would then lead to the errosion of these complexes ant to Bateson-Dobzhansky-Muller incompatibilities (@orr\_dobzhansky\_1996) in recombinants. In contrast to pinworms, \_Eimeria\_ spp. are both pathogenic and prevalent and can thus be expected to exert a high selective pressure. Hybrid vigour observed in response to this infections with this parasite hereby disqualifies the parasite constraint hypothesis.

Hybrid mice of the HMHZ likely have higher fitness when confronted to parasite infections than hosts of pure subspecies faced with the same infections. Parasitism can therefore be expected to have direct consequences for the strength of the species barrier and the dispersal of hybrids. In the HMHZ male hybrid mice have reduced fertility compared to more pure individuals (@albrechtova\_sperm-related\_2012) and it is therefore important to stress that hybridisation can have different effects on different components of Darwinian fitness: while reproductive fitness can lower in hybrids, e.g. health upon infection and (potentially resulting) survival to adulthood could be higher. While some physiological systems (e.g. reproductive) are more dependent on “co-adapted complexes”, others benefit from diversity, in particular resistance to parasite. In the HMHZ context, parasitism is likely to increase the “net-fitness” of hybrids and thereby reduce the “net-strength” of isolating barriers.

This phenomenon is not trivial to study in hybrid mice, as different genes (two genes of the house major histocompatibility complex (MHC)) showed different levels of polymorphism as well as population structure (@cizkova\_genetic\_2011). It has been shown in other systems that a higher MHC diversity could lead to hybrid resistance to parasites (@nadachowska-brzyska\_interspecific\_2012, @grossen\_introgression\_2014) but could also be found even in presence of hybrid susceptibility (@sommer\_maintaining\_2014). To shed some light on this question, further work is ongoing to examine in parallel hosts and \_Eimeria\_ genes associations in the HMHZ.

Introgression of alleles that confer parasite resistance might occur.

The positive effects of genotypic diversity can be explained by either hybrids presenting overall a better immune system, or by parasites being more adapted to a common host genotype successful, this second case implying long term host-parasite association. Nevertheless, hybrid resistance was shown in both cases of intimate or generalist parasites. The genetic structure of the pinworm \_Syphacia obvelata\_ matches that of its host and hybrid parasites are found associated geographically with the host zone centre (@bellocq\_holobiont\_2018). On the opposite, \_Eimeria\_ spp. did not show any genetic structure in the HMHZ when three markers, one from each genome (nuclear, mitochondrial and apicoplast) were considered (Jarquin et al., unpublished), and the same was true for the helminth \_Trichuris muris\_ using one mitochondrial, one ribosomal DNA and ten microsatellites markers (@baird\_where\_2012, @wasimuddin\_testing\_2016).

A recent review (@theodosopoulos\_parasites\_2018) reported the impact of parasitism of diverse animal hybrid zones in 44 studies. Parasitism seems to be a factor of species isolation in 40% of them, while selection seems to favour hybrids in regard to parasitism in 40% of the cases, and no advantage or disadvantage of being a hybrid in respect to parasitism has been found in 20% of the cases.

This question has number of implication in various fields, especially in biomedical research where the need of increasing the variability of mice models have been recently reviewed (@ehret\_translational\_2017). In the case of parasite infection studies and associated immune reactions, one strategy is to collect "dirty mice" from the wild, namely exposed to a variety of pathogens (@maizels\_into\_2013). We therefore want to emphasize the need of studying further the impact of genomic admixture on immunological functions.

# Acknowledgement

Collection of data would not have been possible without the collaboration of farmers and house owners where mice were trapped. We also thank the students of bachelor of Biology of the Humboldt University of Berlin for their contribution. This work was supported by the German Foundation of Scientific Research (DFG) [\hl{grant number}].

# Tables

\*\*Table 1. Parametrisation of the fitted models\*\*

Parameters estimated by maximum likelihood for each dataset.

\*\*Table 2. Comparison and G-test significance of the four nested hypotheses\*\*

H0: same expected load for the subspecies and between sexes; H1: same expected load across sexes, but can differ across subspecies; H2: same expected load across subspecies, but can differ between the sexes; H3: expected load can differ both across subspecies and between sexes.

\*\*Table S1. Hybrid indexes, georeference and parasite load for each individual\*\*

\hl{Full table}

# Figures

\*\*Figure 1. Map of the probabilistic spatial range of both house mice parental populations in the European House Mouse Hybrid Zone\*\*.

The spatial organisation was calculated using six autosomal markers (Es1, Gpd1, Idh1, Mpi, Np, Sod1). Mmd is found in the West of the hybrid zone (blue), Mmm on the East (red). Numbers in the map indicate posterior probabilities of population membership for each mouse sub-species.

\*\*Figure 2. Abundance and intensity of \_Eimeria\_ spp. tissue stages infection\*\*

Hybrid index is represented as a gradient ranging from 0 (pure Mmd, in blue) to 1 (pure Mmm, in red). Map of all individuals tested for detection and quantification of \_Eimeria\_ spp. tissue stages and corresponding fitted model (a), and map of positive individuals tested for detection and quantification of \_Eimeria\_ spp. tissue stages and corresponding fitted model (b). The optimised fit is represented by a solid line; 95%CI of the fit is plotted as a grey ribbon, where all parameters are allowed to vary in their 95%CI and likelihood is maximized (upper bound) or minimized (lower bound); 95%CI of the hybridization parameter alpha is plotted as dashed lines, where all parameters are fixed to their fitted value while alpha is allowed to vary in its 95%CI and likelihood is maximized (upper bound) or minimized (lower bound).

\*\*Figure 3. Abundance and intensity of pinworms count in feces\*\*

Hybrid index is represented as a gradient ranging from 0 (pure Mmd, in blue) to 1 (pure Mmm, in red). Map of all individuals tested for detection and quantification of pinworms count and corresponding fitted model (a), and map of positive individuals tested for detection and quantification of fecal pinworms count and corresponding fitted model (b). Pinworm load given on a log transformed y-axis. Females individual loads and fit are represented in orange, males ones in green. The optimised fit is represented by a solid line; 95%CI of the fit is plotted as a grey ribbon, where all parameters are allowed to vary in their 95%CI and likelihood is maximized (upper bound) or minimized (lower bound); 95%CI of the hybridization parameter alpha is plotted as dashed lines, where all parameters are fixed to their fitted value while alpha is allowed to vary in its 95%CI and likelihood is maximized (upper bound) or minimized (lower bound).

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