**METHODS**

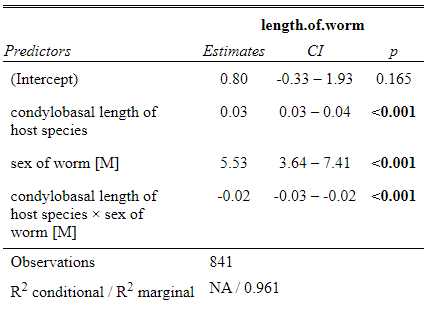
Statistical analyses were performed in program R v.4.2.0 (R Core Team 2022), and all the generalised linear mixed effects models (GLMMs) were created with the glmmTMB package (Brooks et al. 2017). We systematically calculated the variation inflation factors (VIFs) with the full GLMMs without interactions to check for multicollinearity. We considered that there was no substantial correlation when VIF values were <5 (James et al. 2013). We only included two-way interactions to avoid convergence and fitting issues, and to ease interpretation. We considered the identity of each host individual as random effects (random intercepts) to account for inter-individual stochasticity. We evaluated whether the inclusion of random effects improved the model by comparing the Akaike information criteria (AIC) of models with zero, one, or both random effects, fit with restricted maximum likelihood (Zuur et al. 2009).

To calculate AIC for all potential models fit with non-restricted maximum likelihood, we used the dredge() function in the MuMInv.1.46.0 R package (Bartoń 2022). We then selected the models which AIC values were within 2 of that of the model with the lowest AIC. We selected the most parsimonious model (lowest number of degrees of freedom) within that subset of models. Finally, we conducted model averaging using the model.avg() function of the MuMIn package. Model averaging helped us evaluate the importance of each predictor when multiple models were of similar performance according to AIC. In addition to model averaging, we counted how many times each predictor was present in models within the subset. Because condylobasal length of host and host species were highly correlated, we ran our procedure excluding one and then the other.

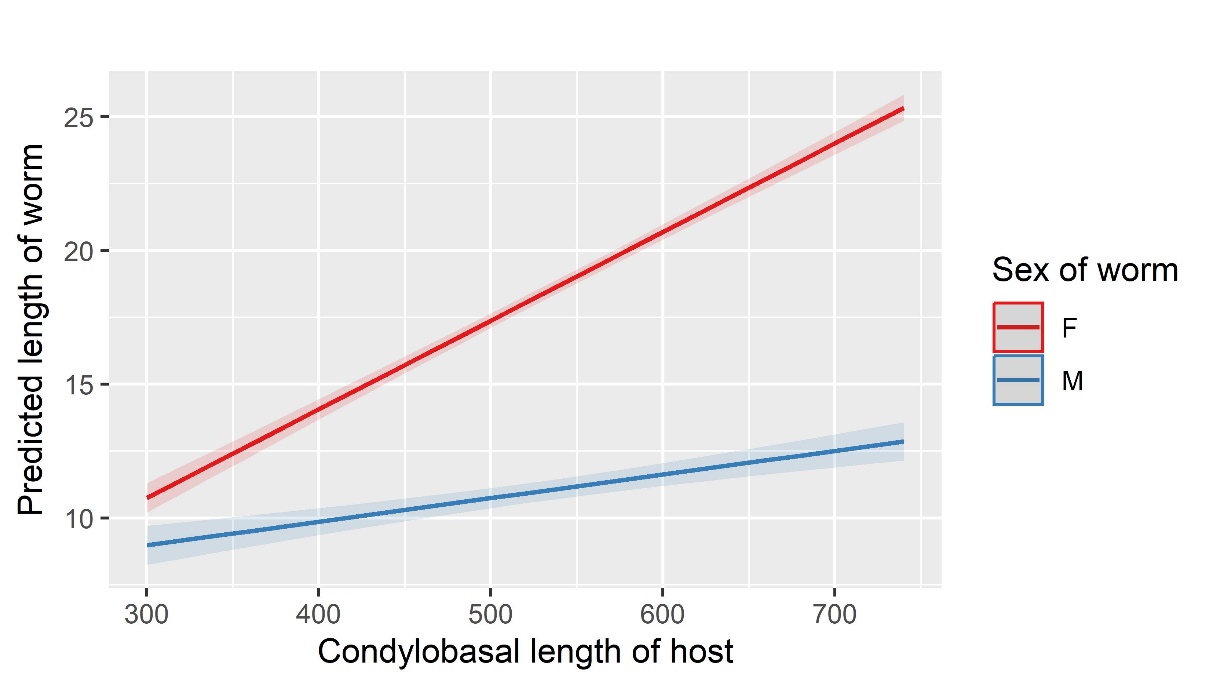
We first sought to identify the most important predictors to explain the length of worms. They included the numbers of worms (to test for a potential density-dependent effect of size), the sex of the worm (to characterize sexual dimorphism), the sex of host (to evaluate sex-dependent disease dynamics), which side of the skull (. We tested for overdispersion in the Poisson models (Gelman and Hill 2006).

**RESULTS**

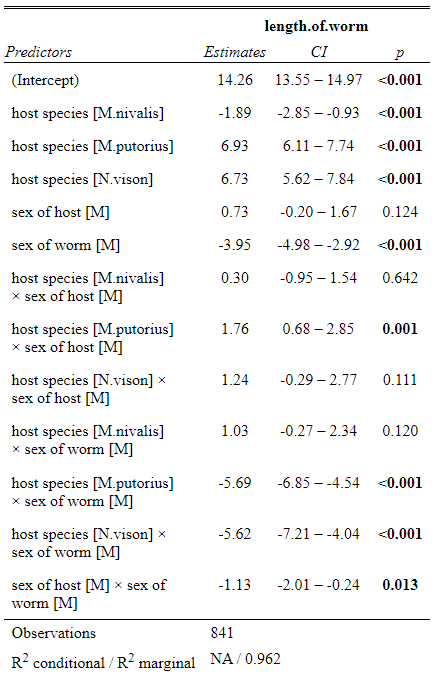
**Table 1:** Summary of the most parsimonious model of the length of worms using condylobasal length



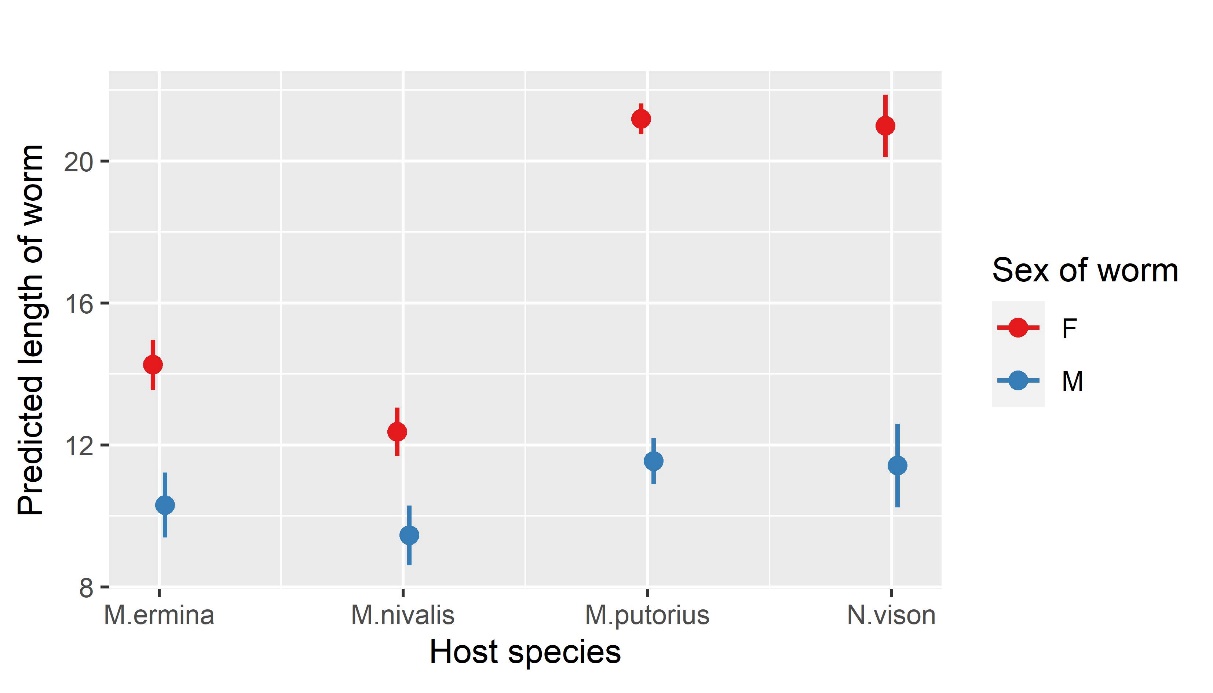
**Figure 1:** Prediction of the length of worm using condylobasal length and sex of worm.



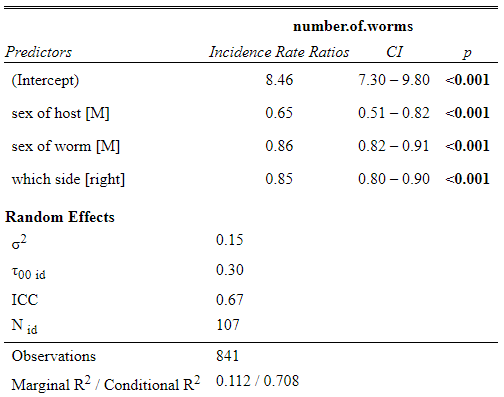
**Table 2:** Summary of the most parsimonious model of the length of worms using host species



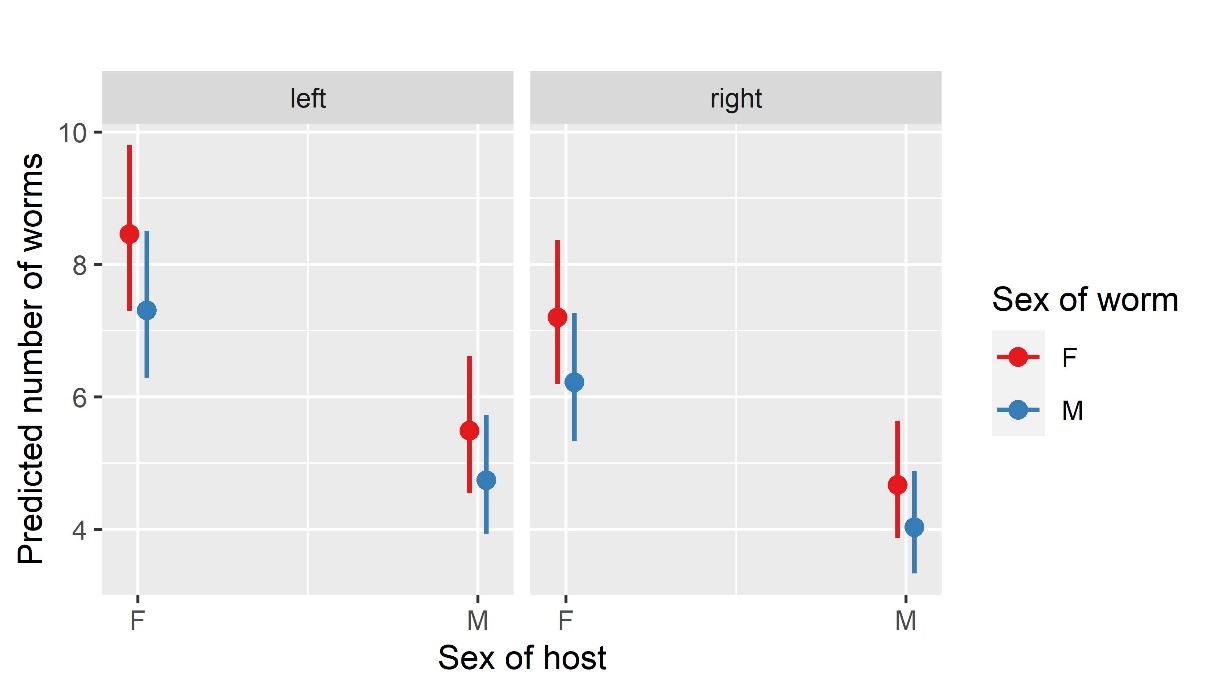
**Figure 2:** Prediction of the length of worm using host species and sex of worm.

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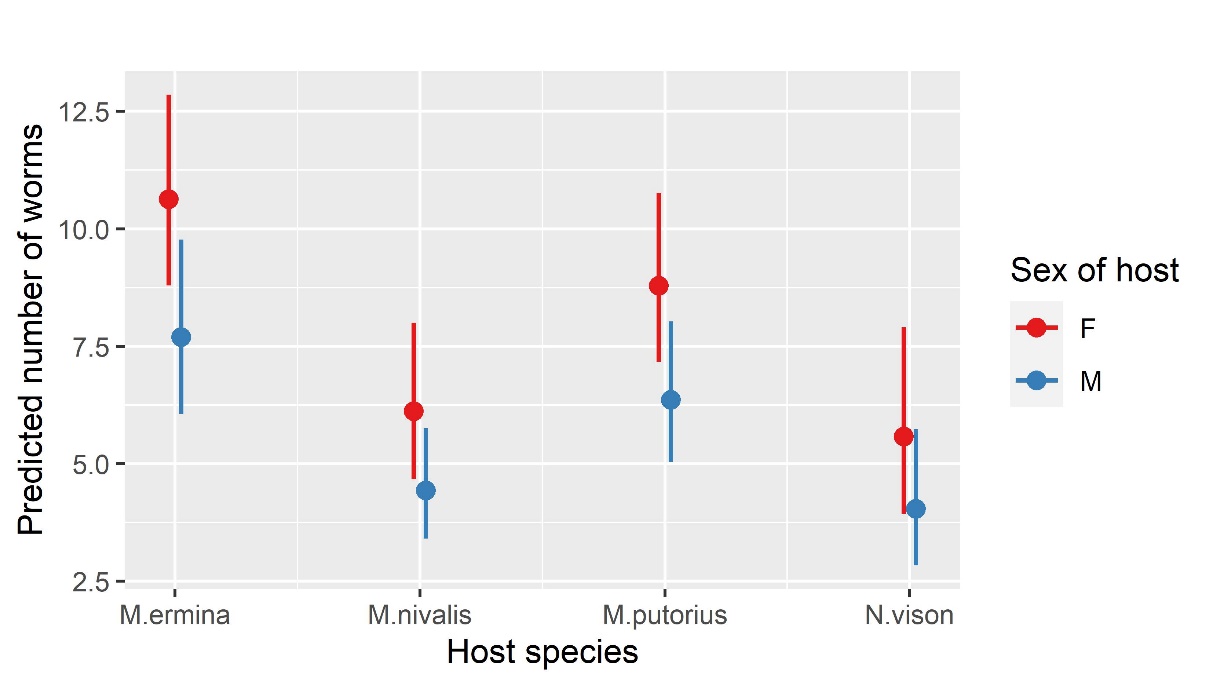
**Table 3:** Summary of the most parsimonious model of the number of worms using condylobasal length



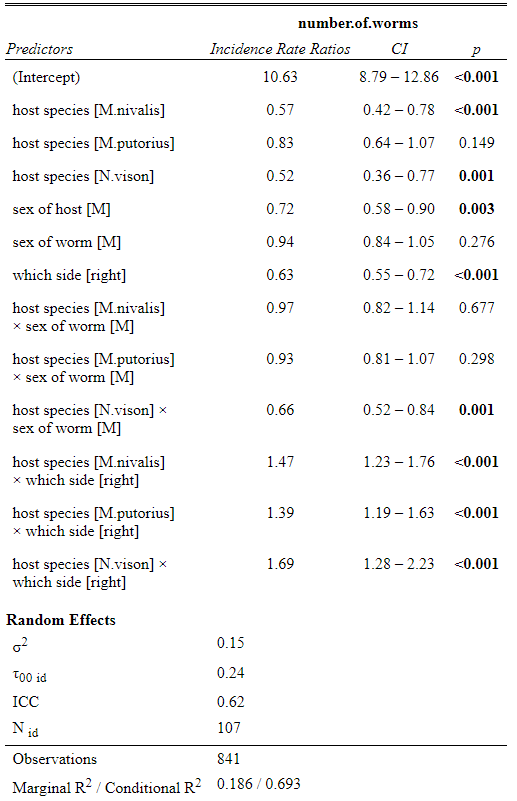
**Figure 3:** Prediction of the number of worms using skull side, sex of host, and sex of worm.

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**Figure 4:** Predictionof the number of worms using host species and sex of host.

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**Table 4:** Summary of the most parsimonious model of the number of worms using host species



**DISCUSSION**

The side of the skull in which worms were collected had an effect on their number. This could hint at a larger size of the left part of the skull providing more space for more worms to grow. Left-right asymmetry exists in many species (Compagnucci et al. 2014). For example, humans skull are often larger on the left (Sarac - Hadzihalilovic and Dilberovic 2004) and leftward skull asymmetry has also been noted in the fish *Astyanax mexicanus* (Powers et al. 2017). Measuring this asymmetry in mustelids was beyond the scope of this paper. The origin of a left-side asymmetry in worm numbers could also be due to another factor: asymmetric infection by the worms. This phenomenon has been described in other taxa; parasite infection has been shown to be significantly biased towards one side in 26 species (Johnson et al. 2014). For example, the nematode *Dioctophyma renale* infects mink (*Neogale vison*)(Our study adds to this continually growing pile of evidence about asymmetric infections. Finally, we did not detect this effect of skull side on the average length of the worms and we need more data to uncover the complex interplay between the demography and size distribution of parasites.

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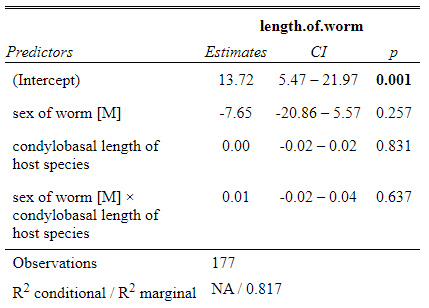
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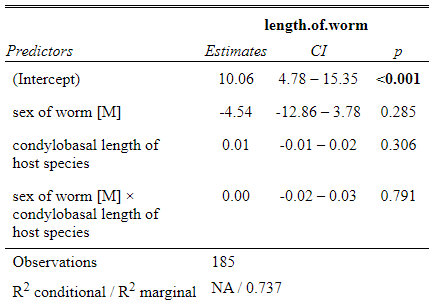
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**SUPPLEMENTARY MATERIAL**

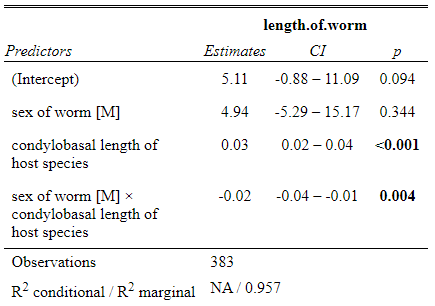
**Sup. Mat. 1** M. ermina modelling results with best model formula based on full dataset



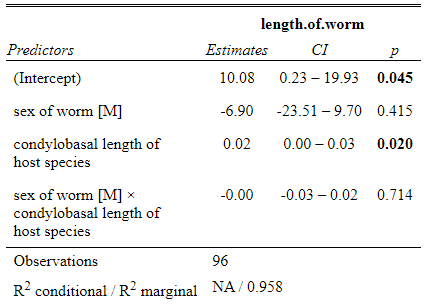
**Sup. Mat. 2** M. nivalis modelling results with best model formula based on full dataset



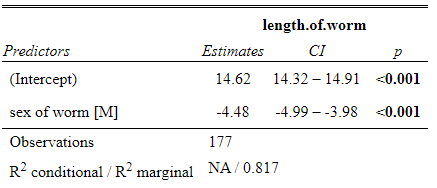
**Sup. Mat. 3** M. putorius modelling results with best model formula based on full dataset



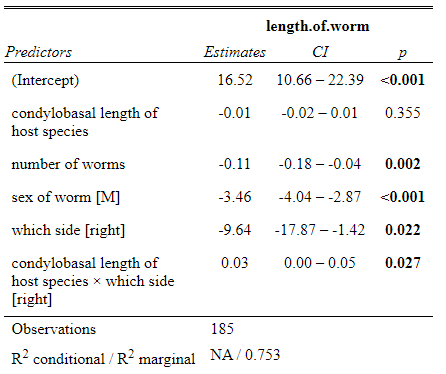
**Sup. Mat. 4** N. visonmodelling results with best model formula based on full dataset

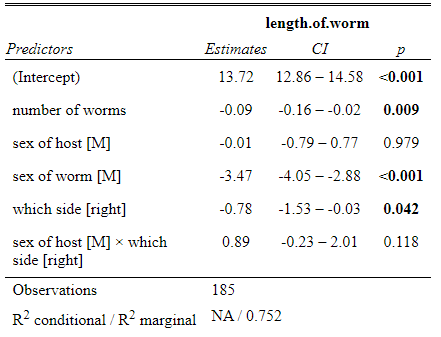


**Sup. Mat. 5** M. ermina modelling results based on subset reanalysis

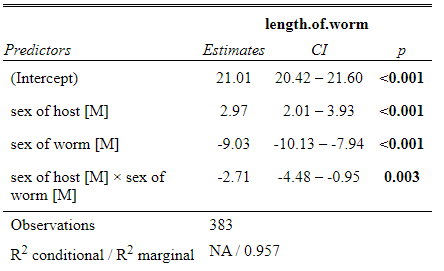


**Sup. Mat. 6** M. nivalis modelling results based on subset reanalysis. Two models are presented because they had the same number of degrees of freedom





**Sup. Mat. 7** M. putorius modelling results based on subset reanalysis



**Sup. Mat. 8** N. vison modelling results based on subset reanalysis

