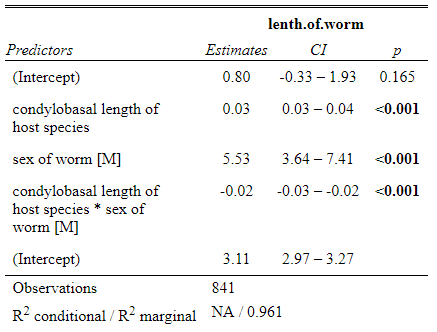
**METHODS**

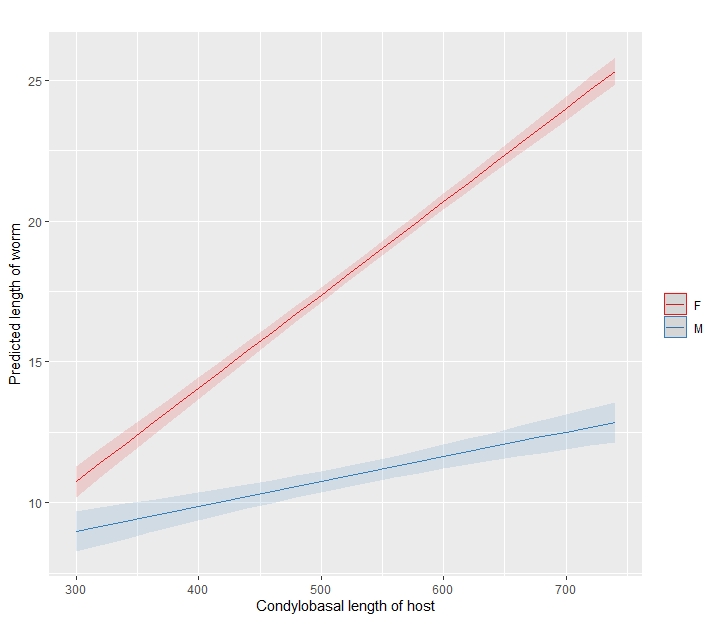
Statistical analyses were performed in program R v.4.2.0 (R Core Team 2022), and all the generalised linear mixed effects models (GLMMs) were created with the glmmTMB package (Brooks et al. 2017). We systematically calculated the variation inflation factors (VIFs) with the full GLMMs without interactions 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).

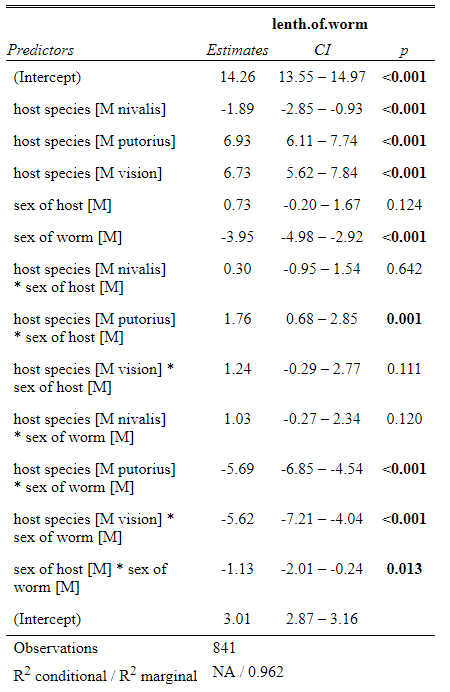
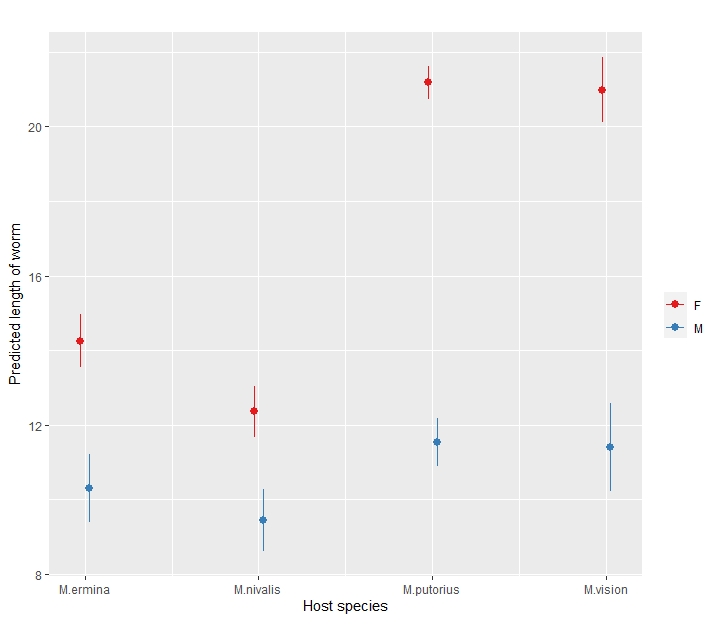
To calculate AIC for all potential models fit with non-restricted maximum likelihood, we used the dredge() function in the MuMInv.1.46.0 R package (Bartoń 2022). We then selected the models which AIC values were within 2 of that of the model with the lowest AIC. We selected the most parsimonious model (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.

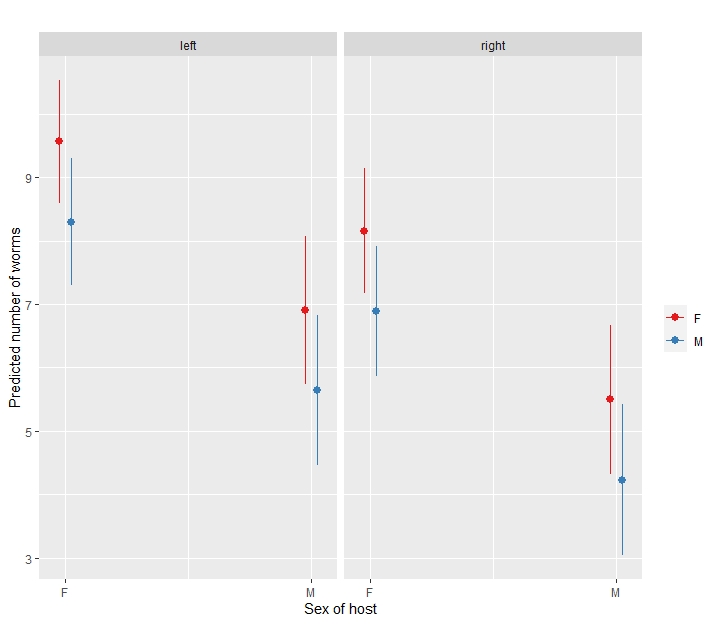
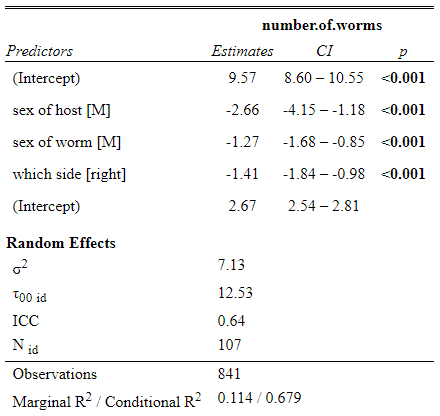
We first sought to identify the most important predictors to explain the length of worms. They included the numbers of worms (to test for a potential density-dependent effect of size), the sex of the worm (to characterize sexual dimorphism), the sex of host (to evaluate sex-dependent disease dynamics),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

**RESULTS**

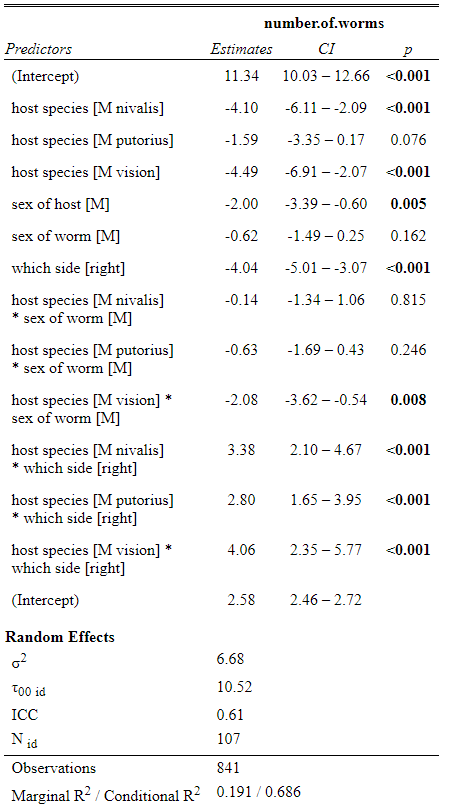
****Avec condylobasal length :

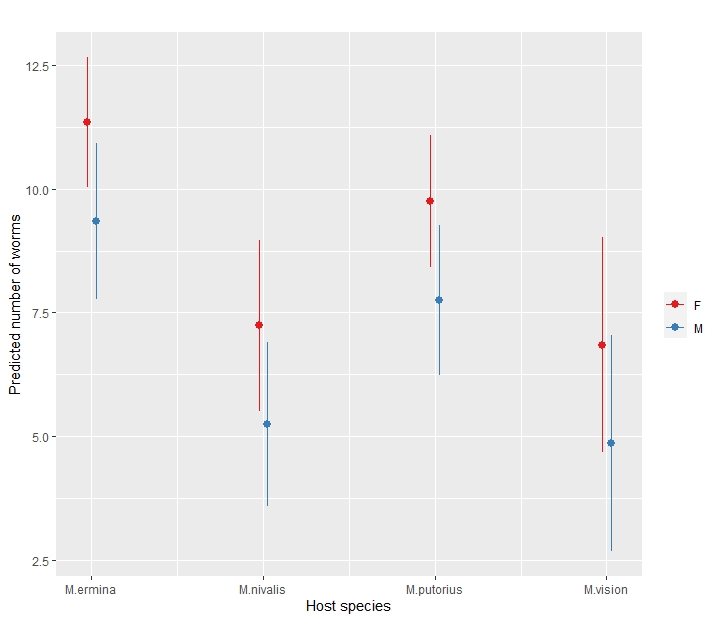


Avec host species:

Pareil pour le nombre de vers, avec condylobasal length :

Avec host species :





**DISCUSSION**

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).