Supplementary Material for "Morph-dependent effect of nematode infection on host movement in the land snail *Cepaea nemoralis* (Mollusca, Gastropoda)"

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S1 - detailed math description of both models

Size model

Multivariate model of parasites abundance and snail behaviours

S2 - descriptive stats about parasites

We present here information about each parasite prevalence (% of potential hosts infected) and infection intensity (number of parasites per *actually infected host*). For trematode and nematode data, the provided 95% intervals are the Highest Density intervals based on binomial GLMs (prevalence) and negative binomial GLMs (intensity) with morph, population and morph *population fixed effects. The intensity models are fitted on intensity - 1, to account for the zero exclusion. Priors are as in S1, with the addition of a halfnormal(0-1) prior on the inverse of the negative binomial shape parameter, per REF. Note that we do not provide 95% intervals for Acari, given rarity of infection. and also not for encapsulated parasites, for reasons presented at the end of the main text methods. The individual that died is excluded from all tables below and harboured 102 live nematodes, 0 live trematodes, 0 live mites, had encapsulated 14 nematodes and 0 mites.

(morph and population specific prevalence, as well as min/mean/median/max CI abundance and/or intensities)

table x nematode

shell morph	n	prevalence	95% interval
Open habitat			
0 bands	29	0.90	[0.73; 0.95]
3 bands	30	0.67	[0.49; 0.8]
5 bands	30	0.40	[0.26; 0.57]
Shaded habitat			
0 bands	30	0.00	–
3 bands	30	0.00	–
5 bands	30	0.00	–

table x trematode

shell morph	n	prevalence	95% interval
Open habitat			
0 bands	29	0.14	[0.07; 0.29]
3 bands	30	0.23	[0.13; 0.39]
5 bands	30	0.10	[0.05; 0.23]
Shaded habitat			
0 bands	30	0.13	[0.05; 0.26]
3 bands	30	0.23	[0.1; 0.38]
5 bands	30	0.03	[0.01; 0.14]

Table x acari

shell morph	n	prevalence
Open habitat		
0 bands	29	0.00
3 bands	30	0.00
5 bands	30	0.00
Shaded habitat		
0 bands	30	0.03
3 bands	30	0.00
5 bands	30	0.00

table x nematode

shell morph	n(infected)	mean intensity	95% interval	min	max
Open habitat					
0 bands	26	4.27	[4.81; 10.63]	1	11
3 bands	20	5.3	[3.18; 7.39]	1	12
5 bands	12	4.33	[2.27; 6.38]	1	24
Shaded habitat					
0 bands	0	–	–	–	–
3 bands	0	–	–	–	–
5 bands	0	–	–	–	–

table x trematode

shell morph	n(infected)	mean intensity	95% interval	min	max
Open habitat					
0 bands	4	1.75	[1.29; 5.33]	1	4
3 bands	7	5.71	[2.52; 9.6]	1	14
5 bands	3	4.33	[1.51; 6.97]	1	9
Shaded habitat					
0 bands	4	7.25	[2.1; 13.04]	1	18
3 bands	7	7.14	[2.94; 14.6]	1	28
5 bands	1	4.00	[1.13; 14.16]	4	4

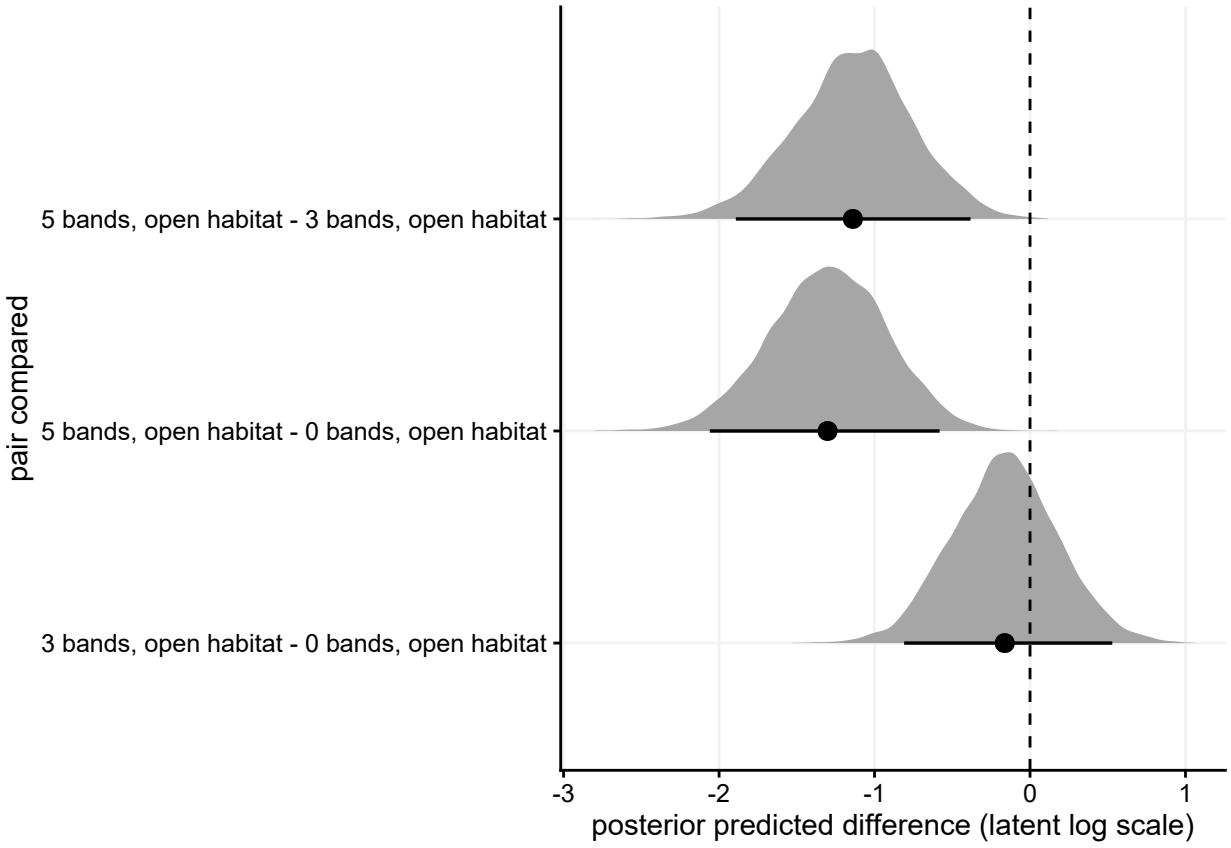
Table x acari

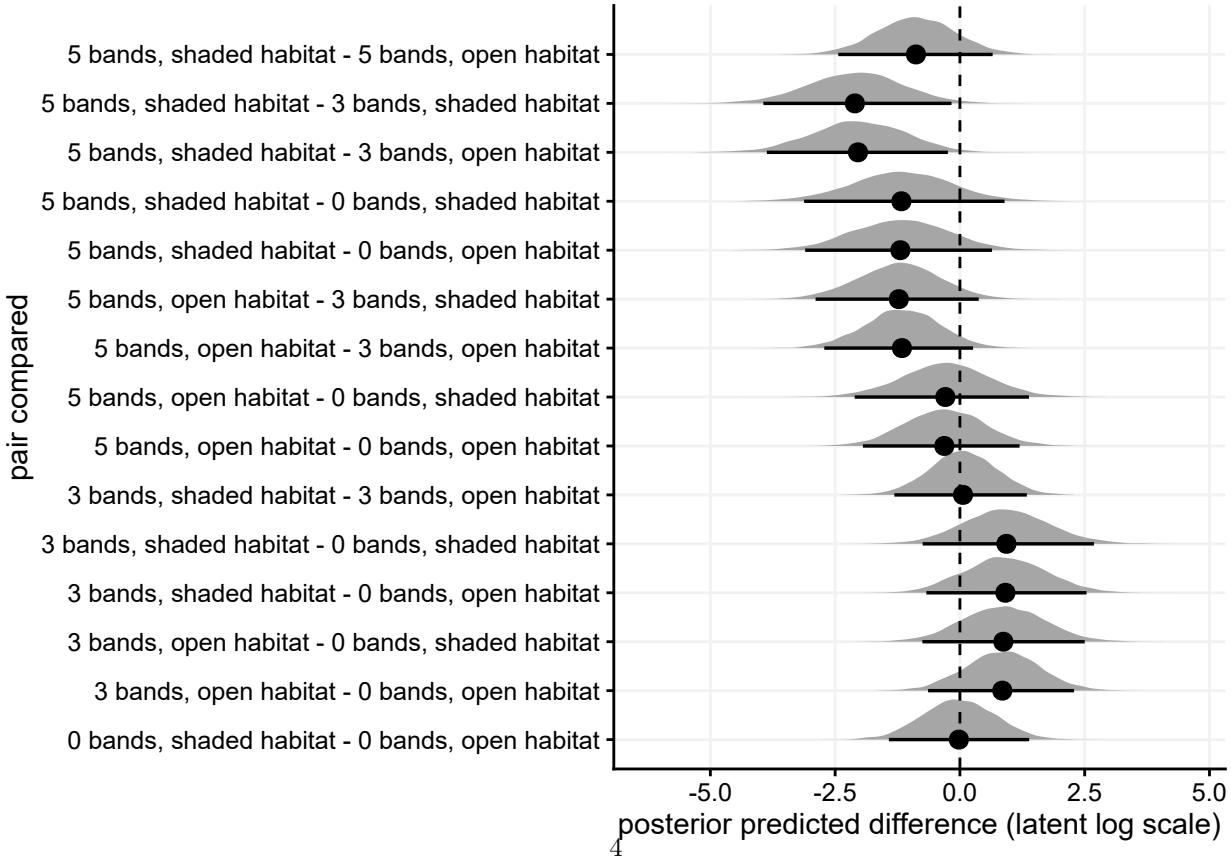
shell morph	n(infected)	mean intensity	min	max
Open habitat				
0 bands	0	–	–	–
3 bands	0	–	–	–
5 bands	0	–	–	–
Shaded habitat				
0 bands	1	93	93	93
3 bands	0	–	–	–
5 bands	0	–	–	–

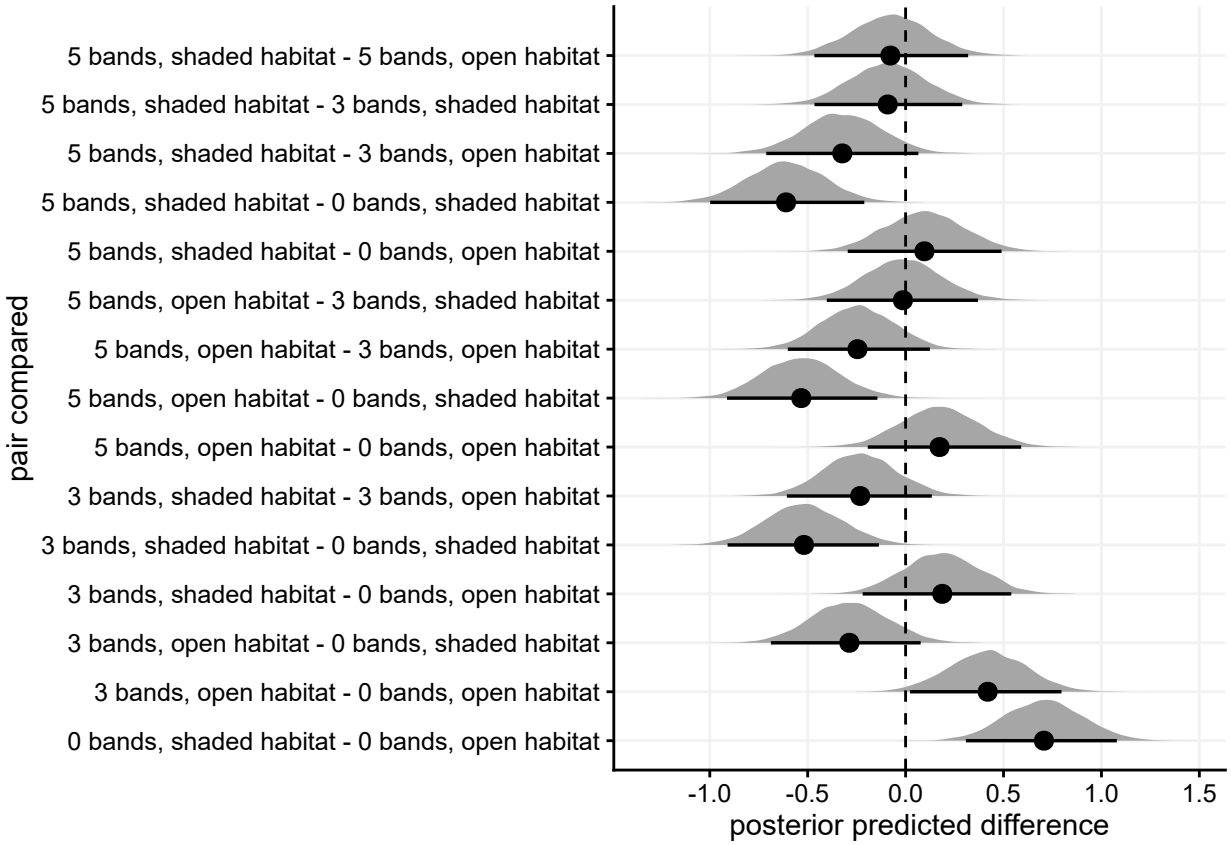
Table x encaps

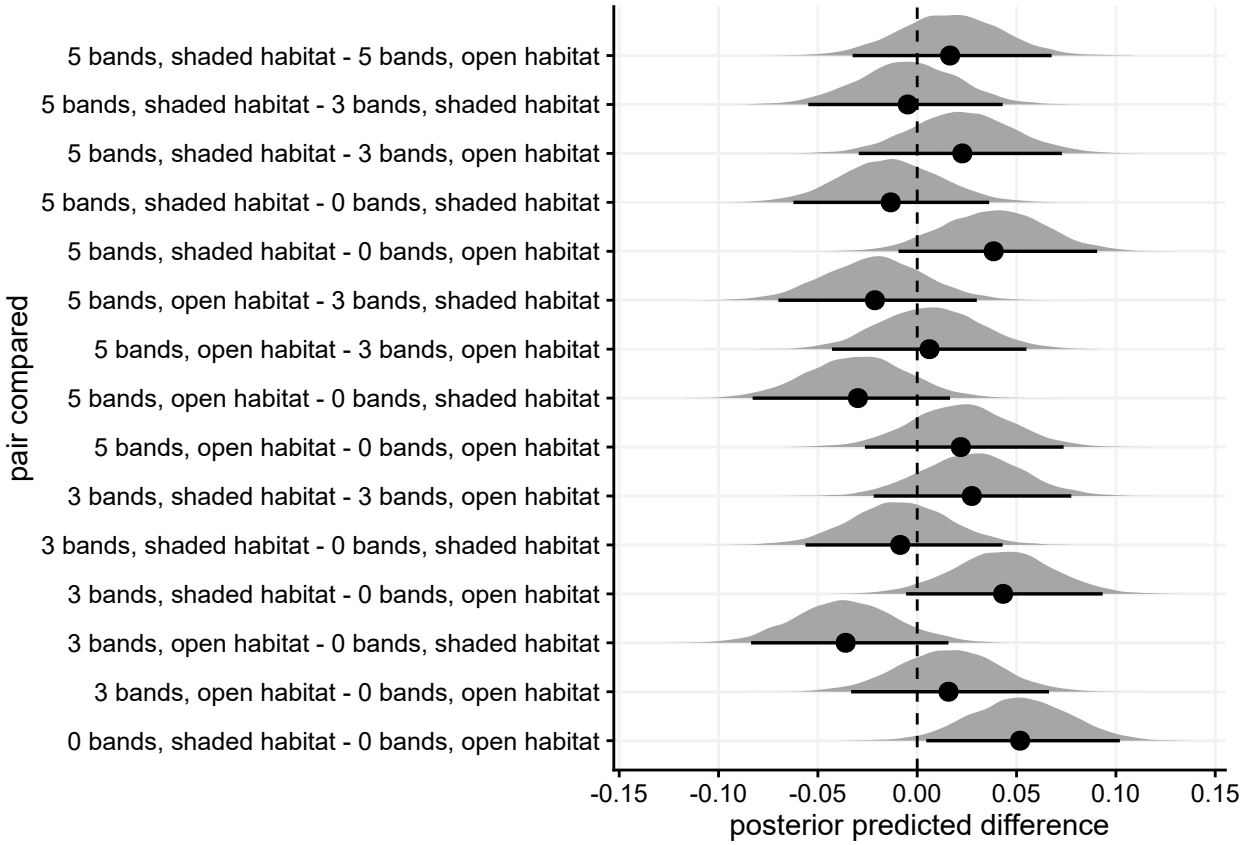
shell morph	n	proportion with encapsulated nematodes	proportion with encapsulated mites
Open habitat			
0 bands	29	0.72	0.0
3 bands	30	0.83	0.0
5 bands	30	0.70	0.0
Shaded habitat			
0 bands	30	0.57	0.0
3 bands	30	0.93	0.0
5 bands	30	0.83	0.1

S3 - pairwise posterior comparisons for each trait



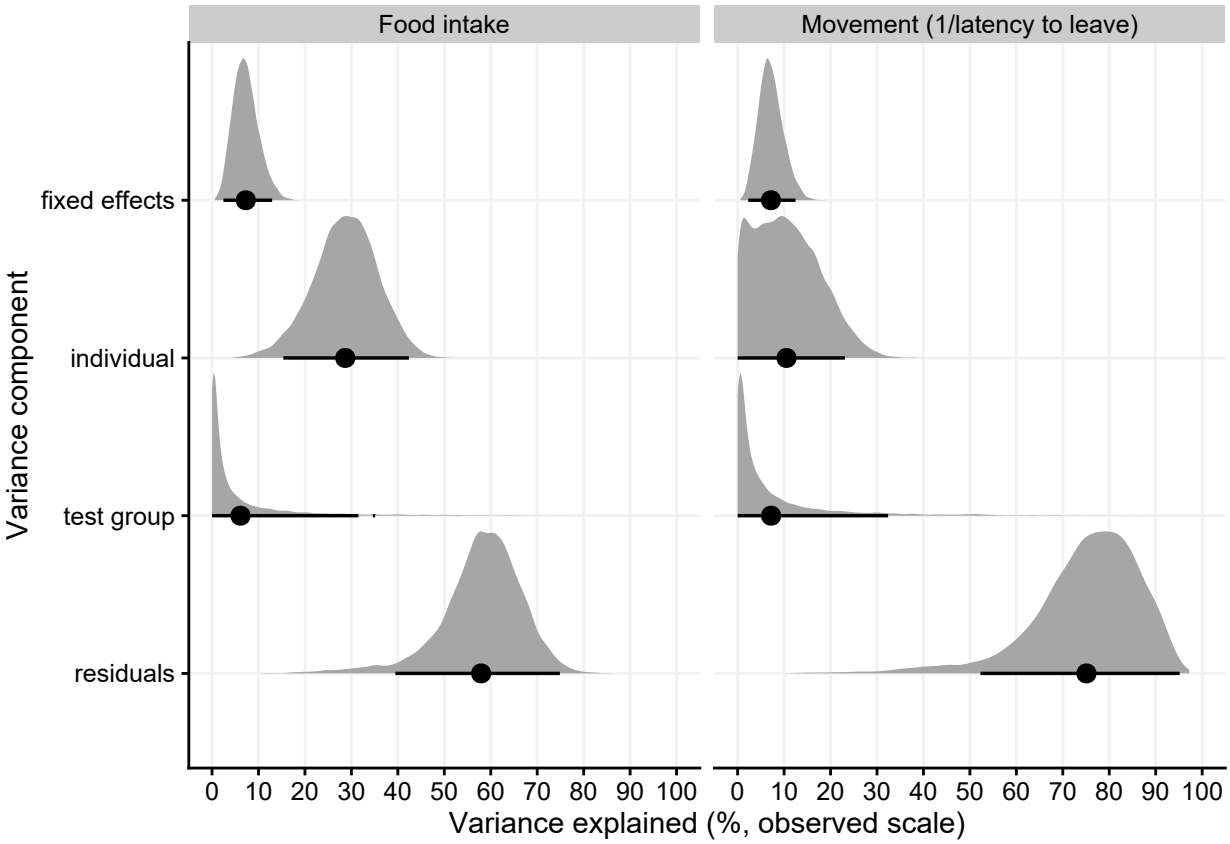



5 bands, shaded habitat - 5 bands, open habitat
5 bands, shaded habitat - 3 bands, shaded habitat
5 bands, shaded habitat - 3 bands, open habitat
5 bands, shaded habitat - 0 bands, shaded habitat
5 bands, shaded habitat - 0 bands, open habitat
5 bands, open habitat - 3 bands, shaded habitat
5 bands, open habitat - 3 bands, open habitat
5 bands, open habitat - 0 bands, shaded habitat
5 bands, open habitat - 0 bands, open habitat
3 bands, shaded habitat - 3 bands, open habitat
3 bands, shaded habitat - 0 bands, shaded habitat
3 bands, shaded habitat - 0 bands, open habitat
3 bands, open habitat - 0 bands, shaded habitat
3 bands, open habitat - 0 bands, open habitat
0 bands, shaded habitat - 0 bands, open habitat
pair compared
-1.0
-0.5
0.0
0.5
1.0
1.5
posterior predicted difference



S4 - Posterior proportion of total variance associated with fixed effects vs. random effects in movement and food intake

Both movement behaviour and food intake were observed twice, which allows us to partition variance into among-individual and within-individual components. We show that although in both cases, within-individual/"residual" variation is the dominant component, there is a non-negligible among-individual variance component: both traits are repeatable (**Supporting Information Figure SX**).



Supporting Information Figure SX. Mean (points) and posteriors for the proportion of variance explained by the different variance components. See **Methods** and **Supporting Information S1** for a description of the model underlying these estimates.

References