



Introduction/Background Information

- Host populations harboring macroparasites, which include parasitic helminths and arthropods, typically display skewed infection burdens, with consequences for transmission and host fitness.
- Knowledge across host-parasite systems on the extent of variation in infection burdens, and reasons for it, are incomplete. To address this, we developed the first meta-database of macroparasite burdens among diverse host species with an emphasis on sources of heterogeneities in host-parasite systems.
- Macroparasite distribution patterns can give rise to rise to **superspreading**, when the majority of individuals in the population are infected with very few parasites while a few individuals are infected with many parasites.
 - Research Question: Do certain ecological characteristics of the individual host, the parasite, or their environment influence superspreading patterns?**
- Additionally, individual hosts are commonly concurrently infected by multiple parasitic species, known as **co-infection**, influencing parasite fitness and transmission.
 - Research Question: Does parasite relatedness predict the strength of competition between co-infecting parasite species within hosts?**



Objective 1: Assess whether there are host traits that give rise to superspreading of one or more parasites in specific individuals

Objective 2: Identify significant relationships between co-infecting parasite pairs and assess whether parasite taxonomy affects such relationships

Summary of Data

- Individual level data was pooled across 12 datasets, each containing the following information for each individual host: host species, host characteristics (sex, body size, etc.), abundance of each parasite species observed.
- Total host species: 69 fish species, 2 crab species, 1 eel species, 1 amphipod species, 2 polychaeta species
- Total number of macroparasite species: 94
- Total number of coinfecting macroparasite pairs: 4,267

Methods

Objective 1:

- Defined ‘Superspreader’: Individual hosts whose abundance of a macroparasite species is above the 80th percentile for the population.
- Estimated the probability of an individual host superspreading for one or more parasite species, based on their body length and weight: Conducted using logistic regression analysis.

Objective 2:

- Determined if macroparasite pairs influence each other’s abundance in a host: For each co-infecting macroparasite pair, we calculated Spearman’s correlation coefficient and associated p-value.
- Evaluated if parasite relatedness influences correlation in abundance: Conducted an ANOVA test to compare the correlation coefficients of co-infecting parasite pairs with different levels of highest shared taxonomic rank.

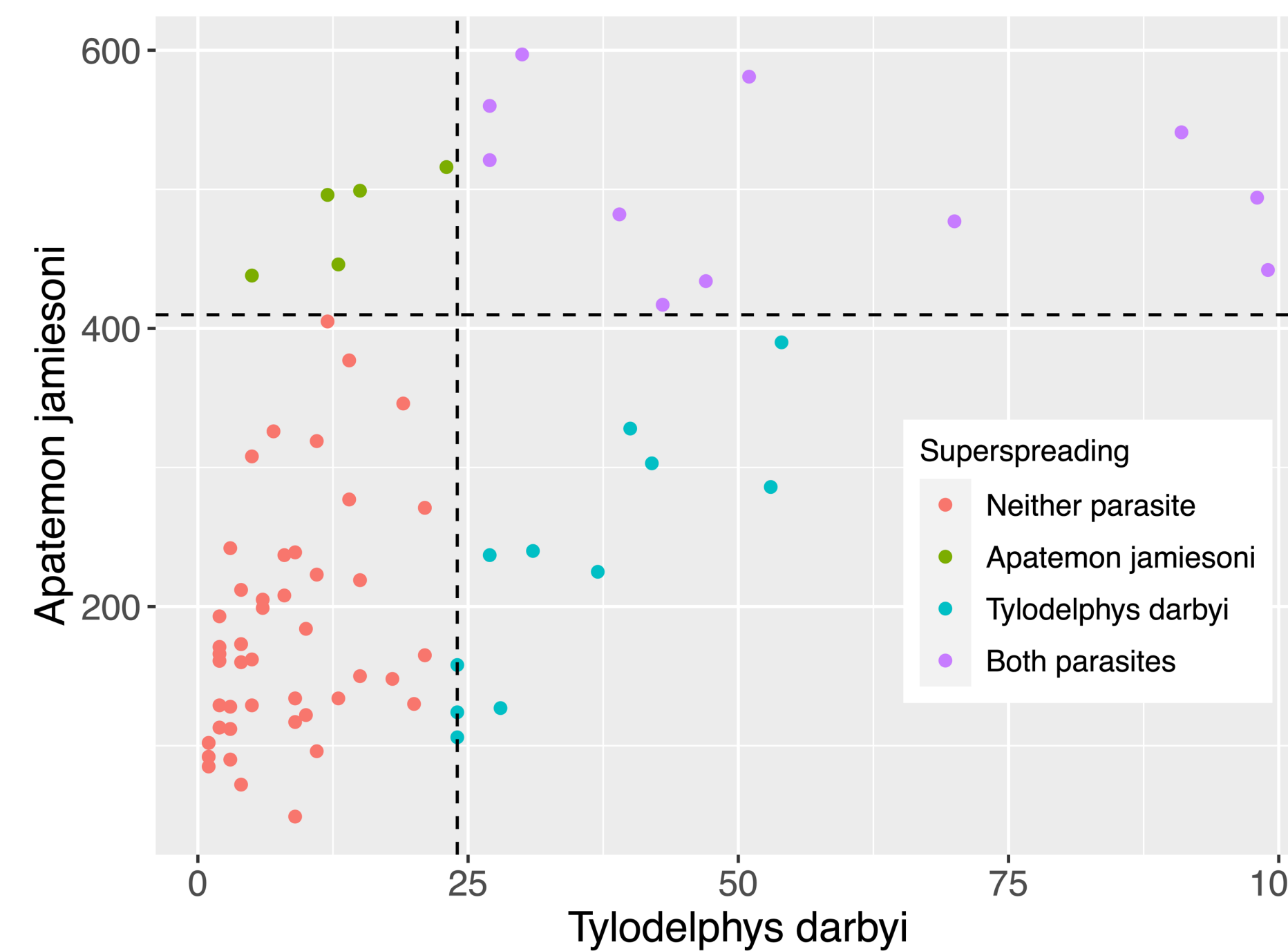
Results

Number of Parasite Species the Individual is ‘Superspreading’	Proportion of Individuals
0	0.713
1	0.201
2	0.053
3	0.020
4 or more	0.013

Proportion of individuals in the dataset who are classified as a ‘superspreader’ for one or more parasite species

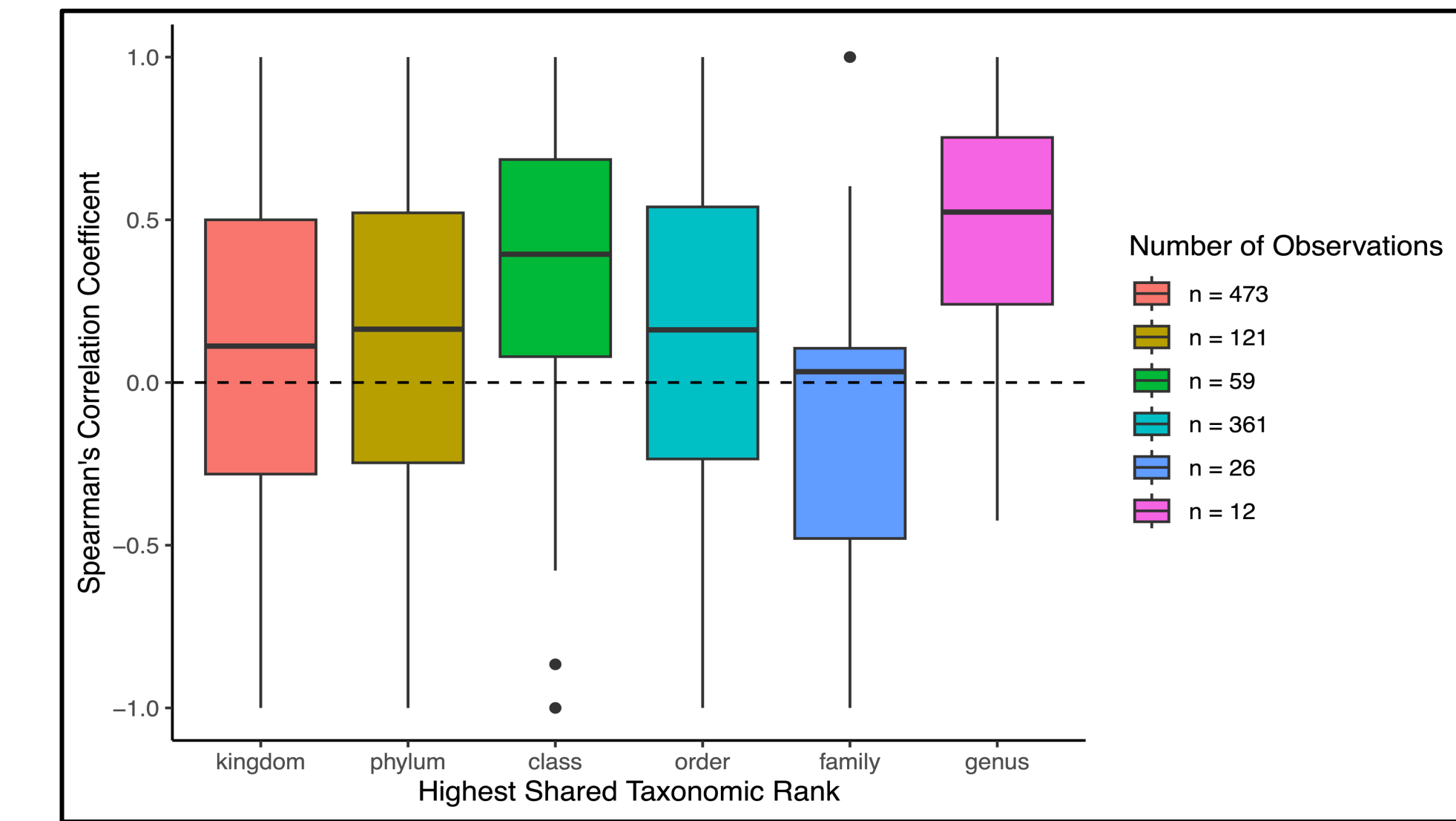
Response Variable	Predictor Variable	Estimate	P-Value
Superspreading for 1+ parasite species? (Y/N)	Length (cm)	4.9904×10^{-3}	0.259
	Weight (g)	2.435×10^{-4}	0.407
Superspreading for 1 or multiple parasite species? (1/1+)	Length (cm)	-2.3914×10^{-3}	0.725
	Weight (g)	2.196×10^{-4}	0.643

Logistic regression with ‘superspreading’ response variables explained by predictor variables Length (cm) and Weight (g)



An example of ‘superspreading’ pattern quadrants in a host population co-infected by a macroparasite pair

Results (continued)



Comparison of correlations coefficients for highest shared taxonomic rank between co-infecting macroparasite pairs

Independent Variable	Degrees of Freedom	F-Value	P-Value
Highest Shared Taxonomic Rank	5	3.413	4.59×10^{-3}
Shared genus, Shared family, or Shared higher rank	2	2.615	7.36×10^{-2}

ANOVA of correlation coefficients for levels of Shared Taxonomic Rank

Objective 1 findings:

- Neither host body length nor weight were significant predictors for the capacity to ‘superspread’ or the strength of ‘superspreading’ (p-value > 0.05).

Objective 2 findings:

- There is a significant difference between the mean correlation coefficient of each Shared Taxonomic Rank level (p-value < 0.05).

Conclusions and Future Directions

- Body length and weight, which typically increase with age, do not appear to drive ‘superspreading’.
- Shared taxonomic rank (i.e., relatedness) of coinfecting macroparasites impacts their correlation in abundance (potentially their competitive effects on each other), which improves our understanding of the fate of co-infecting parasites in host populations.
 - Relatively unrelated co-infecting parasites exhibit all possible correlations in abundance
 - Within families, many parasite pairs are negatively correlated
 - Within genus, parasite pairs are positively correlated
- Future work may focus on macroparasite niches, such as host resource use and infection site, to better understand why genus, family, and higher relatedness show different levels of antagonistic interactions between coinfecting species.

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References

* Images created in biorender
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