

Transcriptomic divergence of a parasite-populations: two common garden experiments in two hosts

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Abstract

Background:

Results:

Conclusions: Yeh!

Background

Results

The populations differ

The gene expression does too

Foo bar

Discussion

Conclusions

Methods

General coding methods

The bulk of analysis (unless otherwise cited) presented in this paper was carried out in R [1] using custom scripts. We used a method provided in the R-packages Sweave [2] and Weaver [3] for “reproducible research” combining R and T_EXcode in a single file. All intermediate data files needed to compile the present manuscript from data-sources are provided upon request. For visualisation we used the R-packages lattice [4] and ggplot2 [5].

Competing interests

The authors declare no competing interests.

Authors contributions

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Figures

Figure 1 -

Figure 2 -

Figure 3 -

Figure 4 -

Figure 5 -

Tables

Table 1 -

Table 7 -

Additional Files