Transcriptominc divergence of a parasite-populations: two common garden experients in two hosts

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Abstract

Background:

Results:

Conclusions: Yeh!

Background
Results

The populations differ

We sampled worms The gene expression does too

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tGO_sex_MF_classic_10_all  --- no of nodes:  24

tGO_sex_BP_classic_10_all  --- no of nodes:  58

tGO_sex_CC_classic_10_all  --- no of nodes:  24

tGO_eel_MF_classic_10_all  --- no of nodes:  22

tGO_eel_BP_classic_10_all  --- no of nodes:  14
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label	sex	host	population	intensity	worms in prep	conc in prep
AA/T20F	female	AA	T	1	1	5.60
AA/T12F	female	AA	T	14	1	6.80
AA/T45F	female	AA	T	5	1	8.00
AA/T24M	male	AA	T	6	3	4.80
AA/T42M	male	AA	T	11	1	5.60
AA/T3M	male	AA	T	5	4	4.88
AA/R18F	female	AA	R	4	1	4.80
AA/R28F	female	AA	R	10	1	5.20
AA/R8F	female	AA	R	27	1	5.20
AA/R16M	male	AA	R	10	4	5.20
AA/R11M	male	AA	R	25	14	6.40
AA/R2M	male	AA	R	10	4	6.60
AJ/T8F	female	AJ	T	10	1	5.91
AJ/T5F	female	AJ	T	2	1	4.80
AJ/T26F	female	AJ	T	2	1	2.40
AJ/T25M	male	AJ	T	24	5	4.05
AJ/T19M	male	AJ	T	24	7	3.50
AJ/T20M	male	AJ	T	20	8	3.80
AJ/R1F	female	AJ	R	3	1	5.92
AJ/R3F	female	AJ	R	3	1	6.90
AJ/R5F	female	AJ	R	10	1	4.04
AJ/R1M	male	AJ	R	3	1	2.50
AJ/R3M	male	AJ	R	3	2	2.60
AJ/R5M	male	AJ	R	10	1	2.23

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tGO_eel_CC_classic_10_all  --- no of nodes:  48

tGO_pop_MF_classic_10_all  --- no of nodes:  33

tGO_pop_BP_classic_10_all  --- no of nodes:  44

tGO_pop_CC_classic_10_all  --- no of nodes:  30


tGO_sex_ortho_MF_classic_10_all  --- no of nodes:  20

tGO_sex_ortho_BP_classic_10_all  --- no of nodes:  64

tGO_sex_ortho_CC_classic_10_all  --- no of nodes:  25

tGO_eel_ortho_MF_classic_10_all  --- no of nodes:  23

tGO_eel_ortho_BP_classic_10_all  --- no of nodes:  28

tGO_eel_ortho_CC_classic_10_all  --- no of nodes:  50

tGO_pop_ortho_MF_classic_10_all  --- no of nodes:  19

tGO_pop_ortho_BP_classic_10_all  --- no of nodes:  53

tGO_pop_ortho_CC_classic_10_all  --- no of nodes:  30


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library	raw.reads	raw.mapped	tax.mapped	screened
AA_R11M	11986442	8628520	7869248	6889908
AA_R16M	10810349	6858585	6219909	5277418
AA_R18F	9227615	6552527	5933941	5201576
AA_R28F	10135670	6665381	6007900	5173988
AA_R2M	12469746	7628428	6930848	5907261
AA_R8F	15270570	11527867	10758715	9453617
AA_T12F	11299438	7842479	7197313	6333734
AA_T20F	11740839	7744179	7114509	6323566
AA_T24M	8552723	5254194	4662363	3969533
AA_T3M	11031751	6460836	5800115	4993790
AA_T42M	11573501	7567845	6787449	5694864
AA_T45F	10646847	7714472	7174696	6284382
AJ_R1F	9855005	6400558	5892964	5169577
AJ_R1M	10211903	5851063	5314793	4507265
AJ_R3F	9897937	6425201	5950371	5125838
AJ_R3M	8775211	4562324	4075888	3424353
AJ_R5F	11949105	8442537	7830725	6882456
AJ_R5M	11231532	7504494	6772805	5913268
AJ_T19M	9195576	4798404	4294094	3636579
AJ_T20M	10862591	6880937	6253215	5281736
AJ_T25M	11195315	7162880	6480780	5645562
AJ_T26F	11195335	7439917	6648897	6036513
AJ_T5F	10357569	7413685	6795948	6009106
AJ_T8F	14196382	10275074	9497028	8364914

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Discussion

mitochondrial ATP synthetase subunits 6 and 8 (atp6 and atp8), cytochrome c oxidase subunits I–III (cox1–cox3), apocytochrome b (cob), and NADH dehydrogenase subunits 1–6 and 4L (nad1–6 and nad4L),

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 TEXcode in a single file. All intermediate data files needed to compile the present manuscript from data-sources are provided upon request. For visualistaion we used the R-packages lattice [4] and ggplot2 [5].

Competing interests

The authors declare no competing interests.

Authors contributions
Acknowledgments

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Figures
Figure 1 -
Figure 2 -
Figure 3 -
Figure 4 -
Figure 5 -

Tables

Table 1 -

Table 7 -

Additional Files