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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Worm Sex

scvPlot(cds.mf)

residualsEcdfPlot(cds.mf, "male") residualsEcdfPlot(cds.mf, "female")

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

plot(res.mf$baseMean, res.mf$log2FoldChange, log="x", pch=20, cex=.4, col = ifelse(

res.mf$padj < .01, "red", "black"), main = "Mydata")

Eel species

scvPlot(cds.eel)

residualsEcdfPlot(cds.eel, "Aa") residualsEcdfPlot(cds.eel, "Aj")

plot(res.eel$baseMean, res.eel$log2FoldChange, log="x", pch=20, cex=.4, col = ifelse(

res.eel$padj < .01, "red", "black"), main = "Mydata")

Populations

scvPlot(cds.pop)

residualsEcdfPlot(cds.pop, "EU") residualsEcdfPlot(cds.pop, "TW")

plot(res.pop$baseMean, res.pop$log2FoldChange, log="x", pch=20, cex=.4, col = ifelse(

res.pop$padj < .01, "red", "black"), main = "Differences between populations")

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library	raw.reads	raw.mapped	tax.mapped	screened
AA_R11M	11986442	8628520	7868814	6889551
AA_R16M	10810349	6858585	6217540	5276284
AA_R18F	9227615	6552527	5933235	5200958
AA_R28F	10135670	6665381	6005399	5171806
AA_R2M	12469746	7628428	6929651	5906422
AA_R8F	15270570	11527867	10758535	9453468
AA_T12F	11299438	7842479	7195621	6332396
AA_T20F	11740839	7744179	7114349	6323422
AA_T24M	8552723	5254194	4662053	3969305
AA_T3M	11031751	6460836	5800042	4993726
AA_T42M	11573501	7567845	6787375	5694801
AA_T45F	10646847	7714472	7173709	6283585
AJ_R1F	9855005	6400558	5890748	5167912
AJ_R1M	10211903	5851063	5313544	4506254
AJ_R3F	9897937	6425201	5948079	5124077
AJ_R3M	8775211	4562324	4073621	3422526
AJ_R5F	11949105	8442537	7830247	6882280
AJ_R5M	11231532	7504494	6772010	5913016
AJ_T19M	9195576	4798404	4293123	3635843
AJ_T20M	10862591	6880937	6251674	5280529
AJ_T25M	11195315	7162880	6480185	5645097
AJ_T26F	11195335	7439917	6641973	6031374
AJ_T5F	10357569	7413685	6794507	6007930
AJ_T8F	14196382	10275074	9496489	8364594

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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 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