Host transcriptome and microbiome data integration in Chinese Holstein cattle under heat stress

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Introduction

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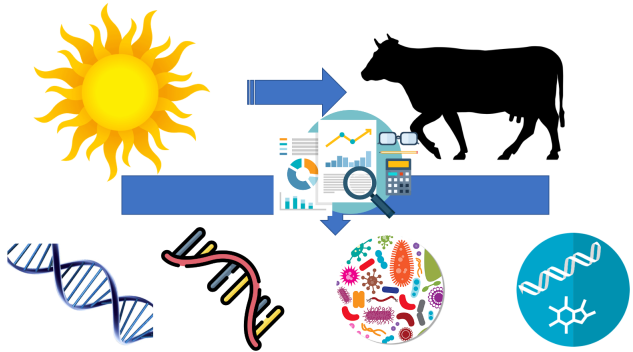
- heat stress $\Rightarrow$ mRNA and microbiota
- heat stress $\Rightarrow$ complex trait
- complex trait modeled as quantitative trait

Objective: The identification of mRNA, bacteria and their association with heat stress



Material and methods – phenotype

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EBVs:

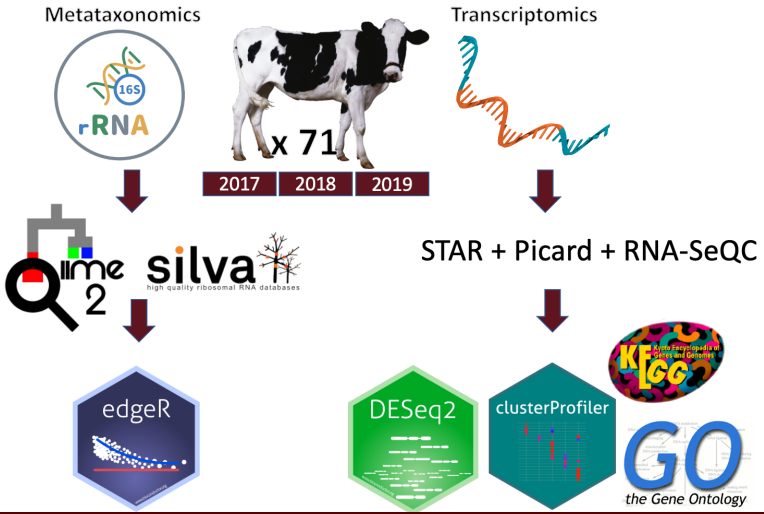
- rectal temperature
- drooling score
- respiratory score

MME:

$$y = \mathbf{XB} + \mathbf{Z}a + \mathbf{W}p + e$$

where: y – phenotype (RT, DS, RS);
B – fixed effects (farm-year, parity, lactation stage, milking stage, testing time, temperature-humidity index);
a – animal additive genetic effects;
p – permanent environmental effects; e – residual errors

Material and methods – workflow



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Material and methods – integration analysis

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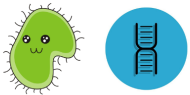
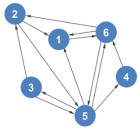
1. Correlation analysis

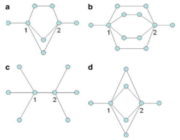


2. Adjacency matrix

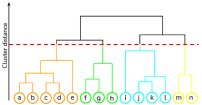


$$a_{mn} = |c_{mn}|^{\beta}$$

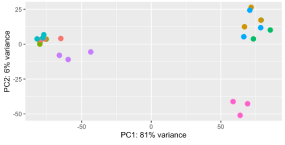
3. Topological overlap matrix (TOM)



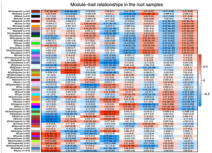
4. Hierarchical clustering (dynamic tree)



5. Eigengenes calculation for each module



6. Correlation analysis of eigengenes with phenotypes



Results – 16S rRNA

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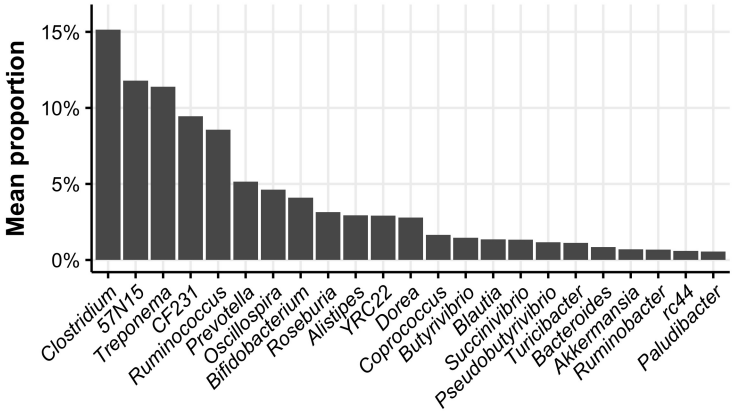
232 unique genera



Results – mRNA

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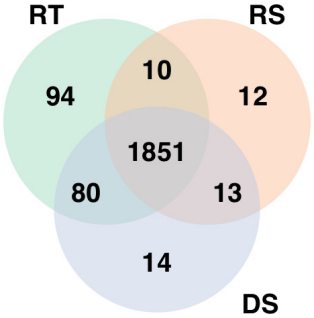
- 2,035 differentially expressed genes for rectal temperature
- 1,886 for drooling score
- 1,958 for respiratory score
- expression of around 80% diferentially expressed genes was down-regulated



Results – GSEA (KEGG)

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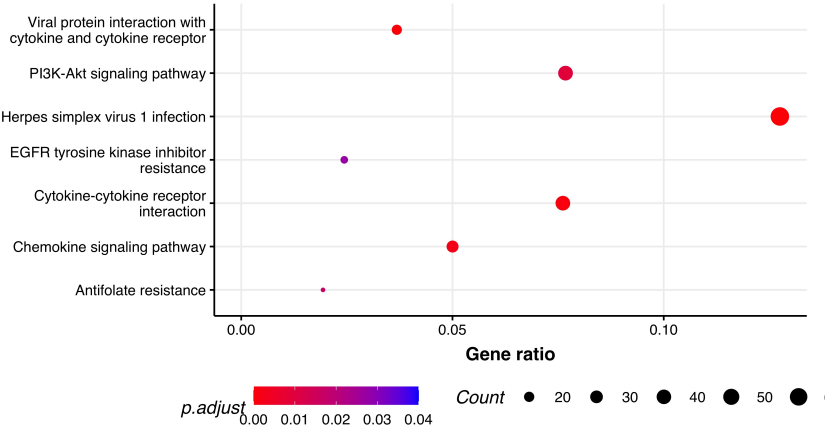

Results – GSEA (GO)

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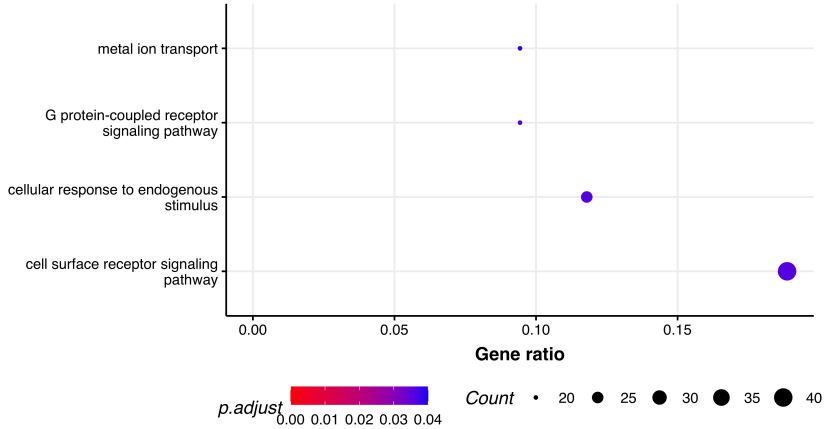

Results – WGCNA (hierarchical clustering)

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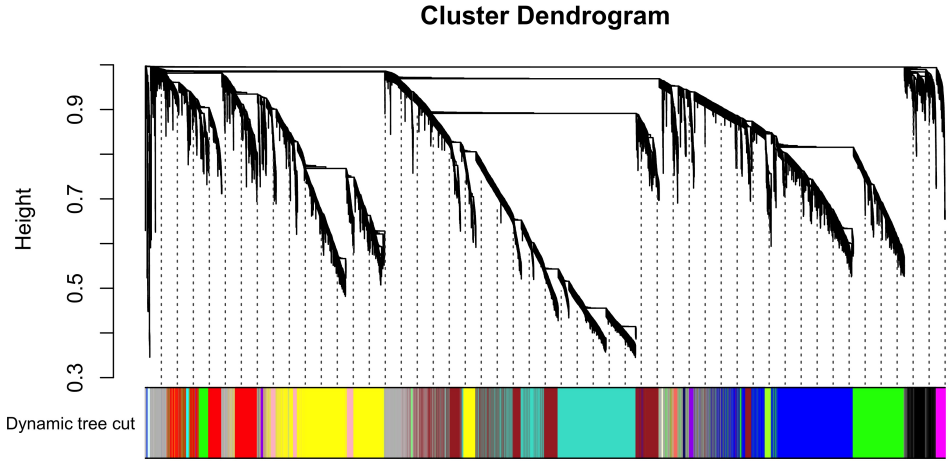
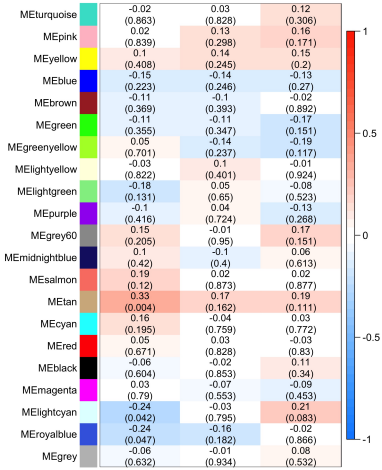


Results – WGCNA (module-trait association)



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Conclusions

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- most of the genera were significantly associated with rectal temperature
- heat stress causes the inhibition of growth of some microbial populations
- heat stress causes down-regulation of gene expression
- significantly associated microbiome-host transcriptome interaction
- hub genes/bacteria of significantly associated modules (*CSF3R*, *Lactococcus* and *Rhizobium*) showed the importance of multiomics integration in the analysis of complex traits

Acknowledgement

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THANK YOU FOR YOUR ATTENTION!

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