



Faecal microbiota and their association with heat stress in *Bos taurus*

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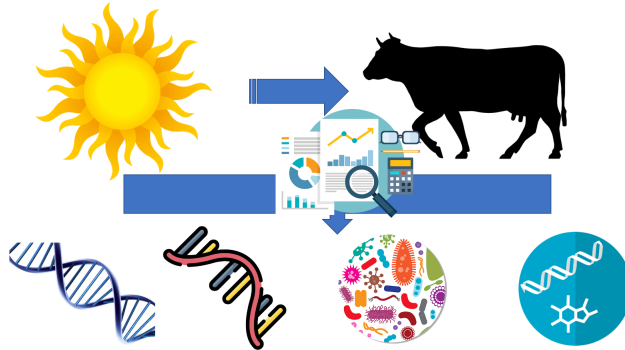
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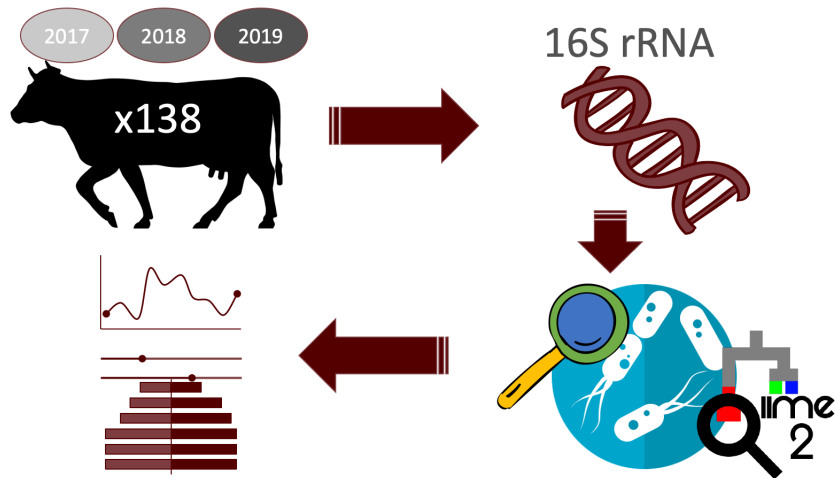
Introduction

- heat stress \Rightarrow microbiota
- qualitative vs. quantitative condition?

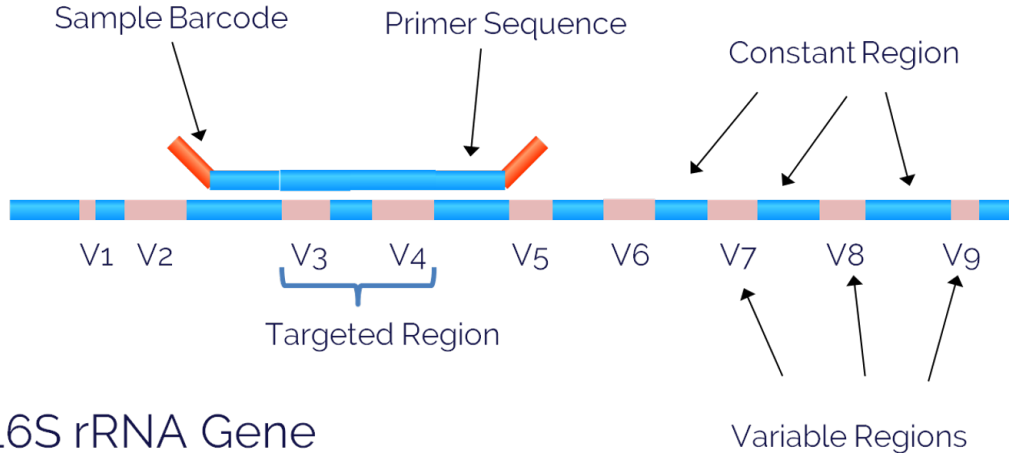
Objective: The identification of bacteria associated with heat stress



Material and methods (1)



Material and methods (2)



16S rRNA Gene

Material and methods (3)



Taxonomic level	Number of unique features	Percent of classified reads
Domain	2	100.00
Phylum	29	97.94
Class	72	97.81
Order	114	97.50
Family	156	70.16
Genus	235	20.93
Species	152	2.35

Material and methods (4)

EBVs:

- rectal temperature
- drooling score
- respiratory score

MME:

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

where: y – phenotype (RT, DS, RS);

\mathbf{X} – design matrix of fixed effects; \mathbf{Z} , \mathbf{W} – design matrices of random effects;

\mathbf{B} – matrix of fixed effects (farm-year, parity, lactation stage, milking stage, testing time, temperature-humidity index);

a – vector of animal additive genetic effects;

p – vector of permanent environmental effects; e – vector of residual errors



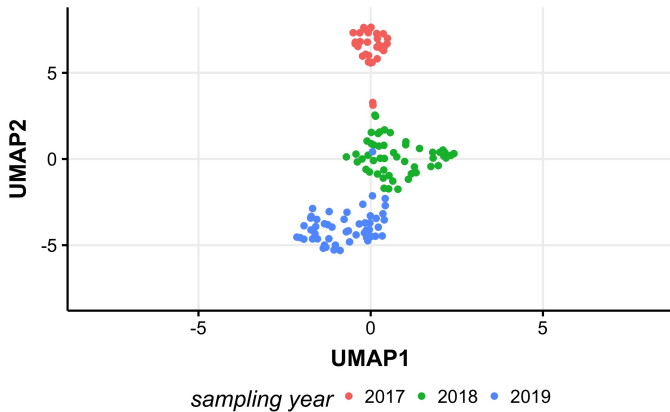
Material and methods (5)

Statistical analysis

- dimension reduction: **Uniform Manifold Approximation and Projection (UMAP)**
- alpha diversity: **Simpson's evenness and Shannon diversity**
- association of microbes composition with heat stress: **aGLMM-MiRKAT test**
- differential abundance analysis: **negative binomial regression**

Results (1)

UMAP





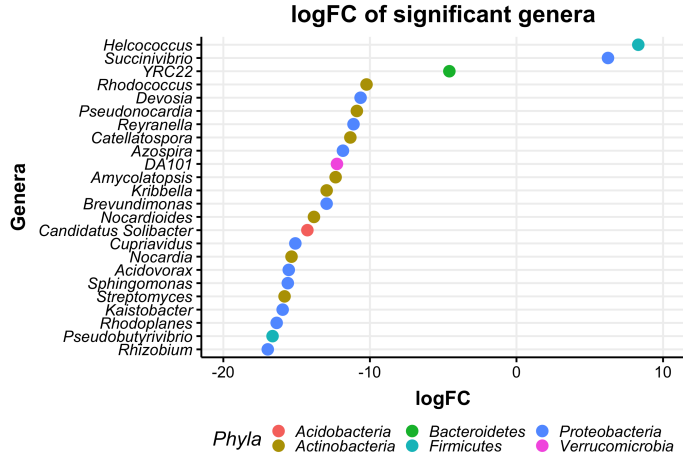
Results (2)

Alpha diversity correlation analysis

Table: Pearson correlation coefficients between EBVs and alpha diversity measures expressed by Simpson's evenness and Shannon diversity.

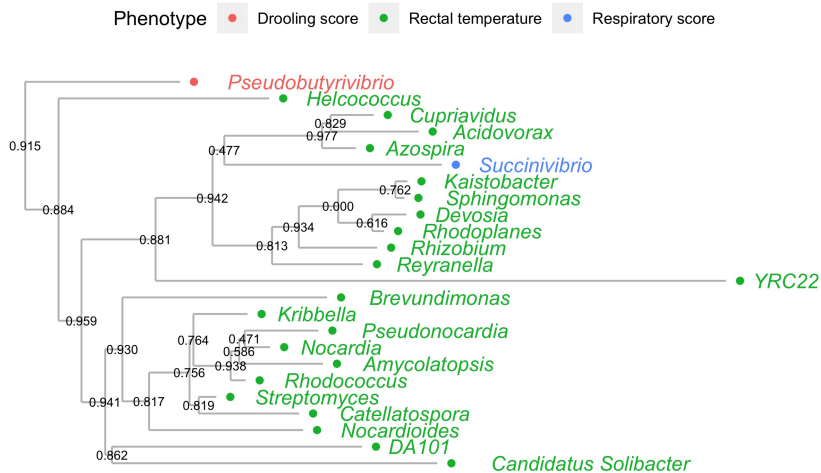
	EBV	Simpson's evenness	Shannon diversity
Rectal temperature		0.25	-0.04
Drooling score		0.13	0.23
Respiratory score		0.27	0.11

Results (3)





Results (4)





Conclusions

- the overall composition of microbiota was not altered by heat stress
- most of the genera were significantly associated with rectal temperature
- heat stress favors the inhibition of growth of some microbial populations
- differences in microbial abundance may occur due to adapting to climate change



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