The richer the better: 16S metabarcoding analysis of gut microbiota of laying hens in relation to feed efficiency and adaptation to diet change

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The richer the better: 16S metabarcoding analysis of gut microbiota of laying hens in relation to feed efficiency and adaptation to diet change

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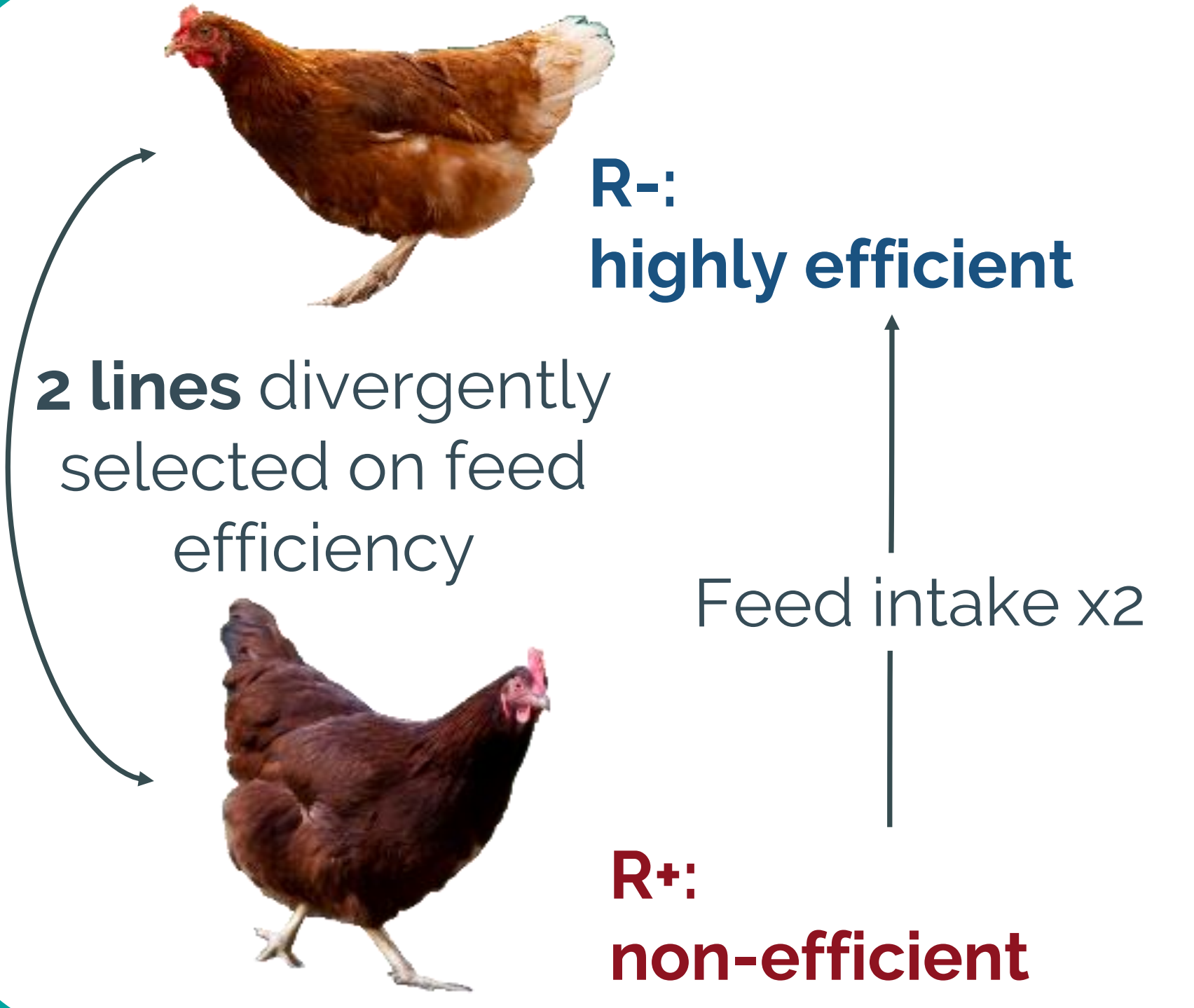
The gut microbiota is known to play an important role in energy harvest and is likely to affect feed efficiency. In the context of feed-food competition and where feed cost represents 70% of eggs production cost, studying the gut microbiota of laying hens allow to determine its role in feed efficiency and its sensitivity to the diet composition.

SCIENTIFIC QUESTIONS & EXPERIMENTAL DESIGN



R-:
highly efficient

2 lines divergently selected on feed efficiency

Feed intake x2

R+:
non-efficient

How can microbiota influence the feed efficiency of laying hens ?

How are bacterial populations impacted by the diet composition ?

2 diets:
commercial diet, CTR (soybean + wheat based)
low-energy, LE (corn + sunflower based):
- -15% metabolisable energy and
- 2.4 times more raw cellulose
- -30% starch

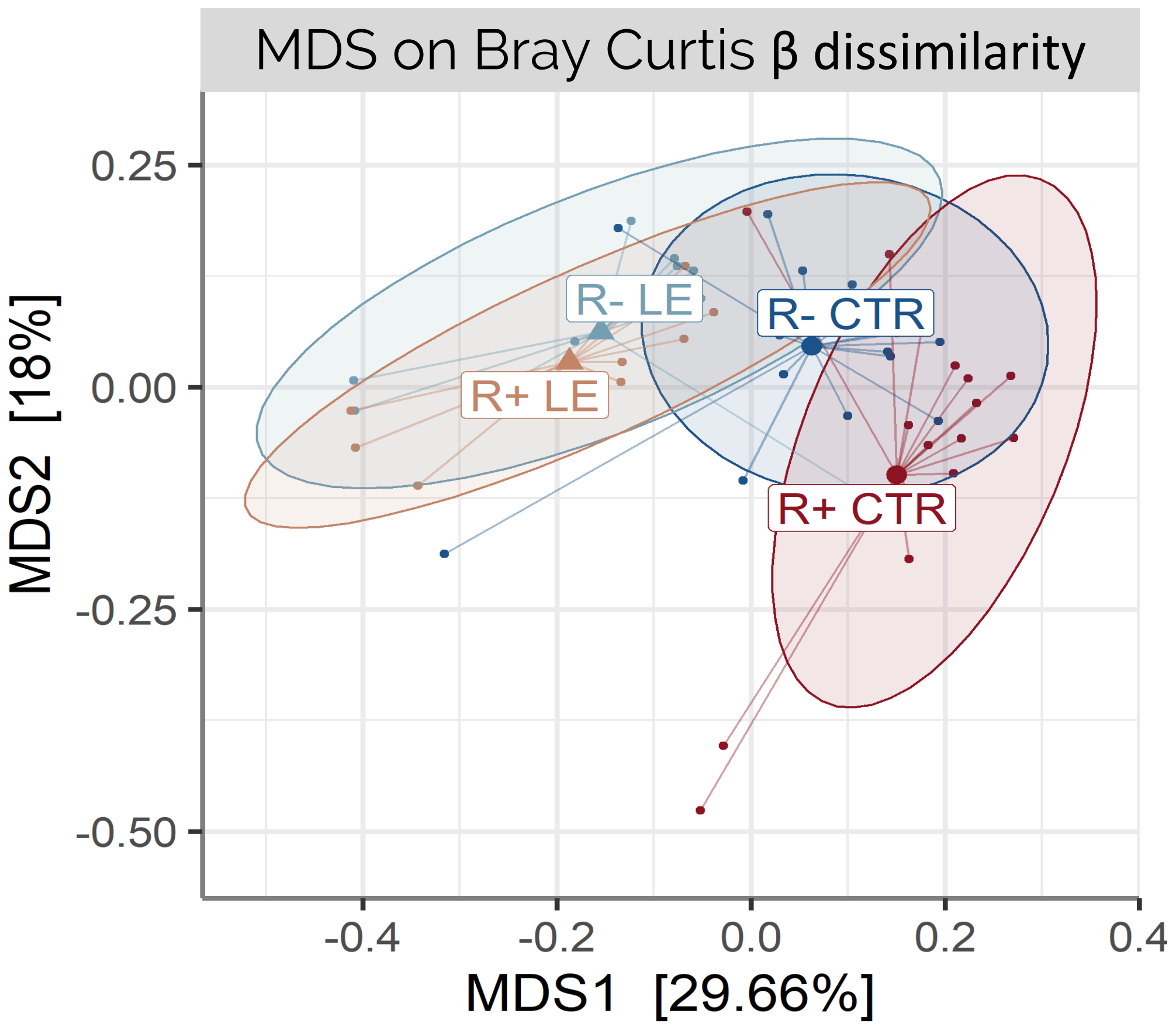
Material: 57 laying hens, 16Sv3V4 metabarcoding reads

Tools: FROGS[1], Phyloseq[2], DESeq2[3], PICRUSt2[4]

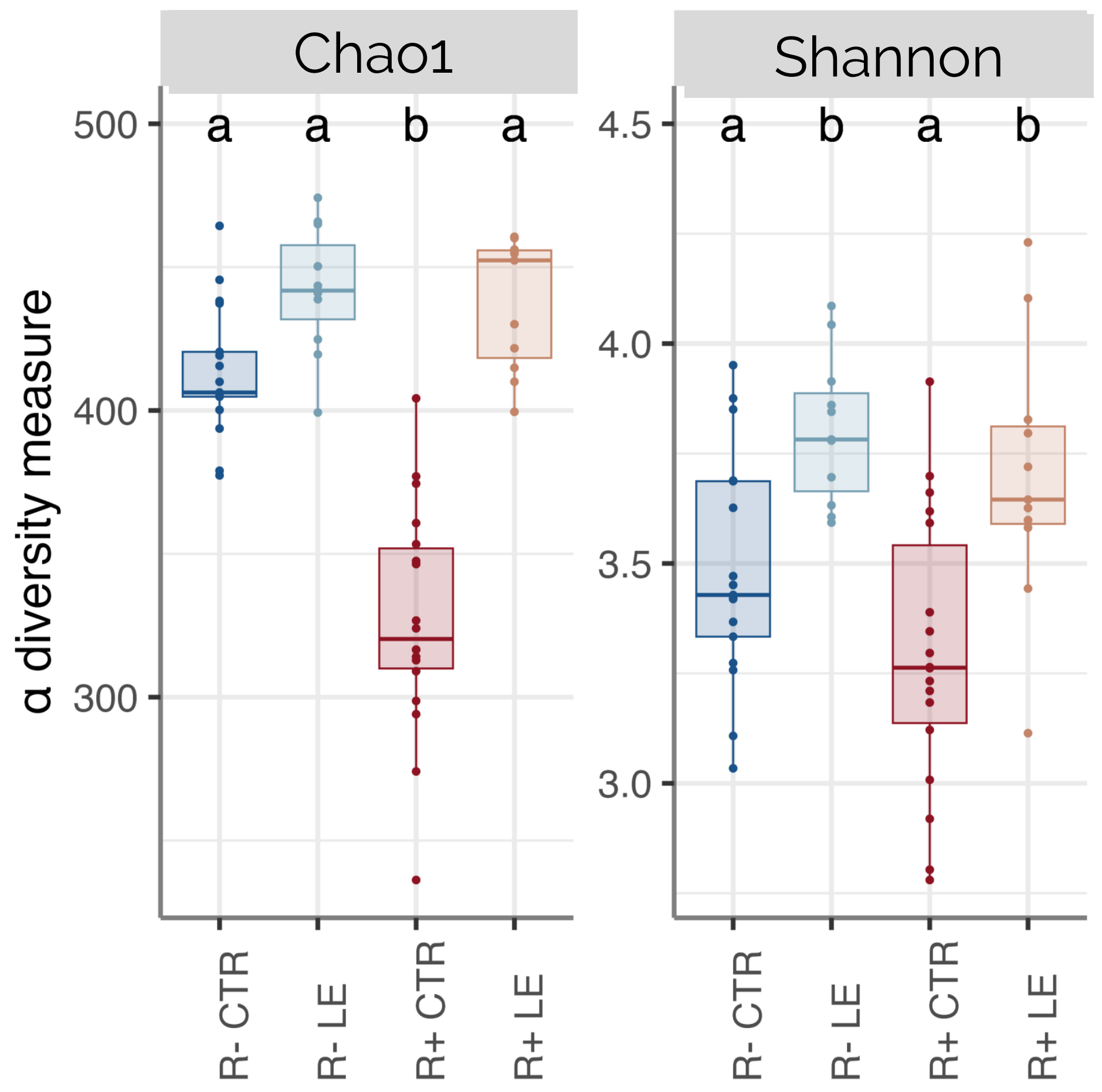
Bioinformatic output : Amplicon Sequence Variant (ASV) abundance table with taxonomic affiliation.

[1] Escudié, F. et al., Bioinformatics 2018;
[2] McMurdie, P. J. & Holmes, S., PLOS One 2013;
[3] Love, M. I. et al., Genome Biology 2014;
[4] Douglas, G. M. et al., bioRxiv 2019

RESULTS



Permanova p-values < 0.01 for line, and < 0.001 for diet.



Anova p-values < 0.03 for the line, = 0 for the diet, and for the line x diet in Chao1.

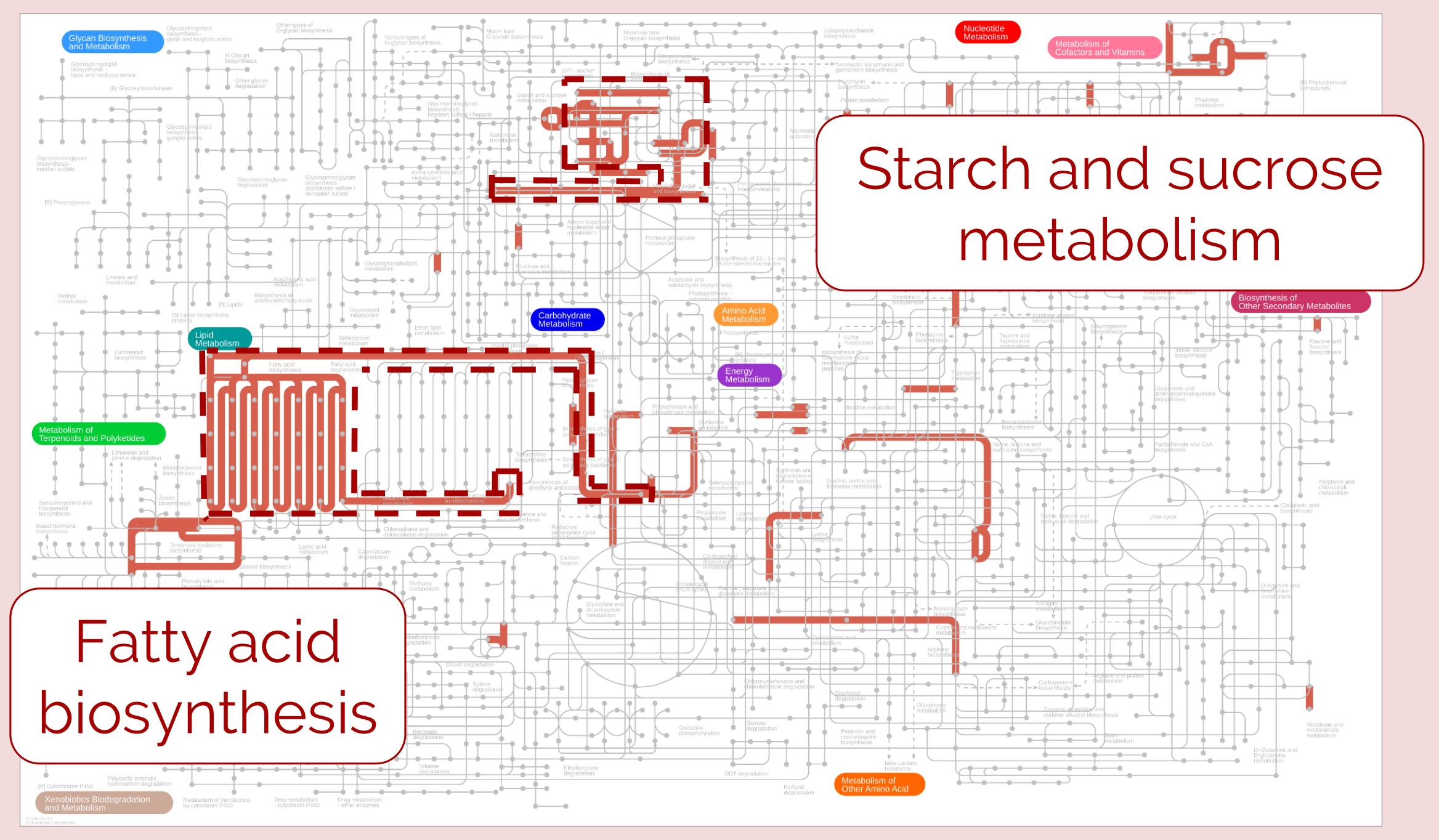
Alpha and beta diversity analyses, as well as differential ASV abundance analysis revealed :

- a **line effect** mostly observed **in the CTR diet:** difference in richness and structure between lines.
- a **diet effect** on the microbiota composition and structure is observed **in both lines** with an increase of diversity but with a **minor effect on the efficient line** R-.

Interestingly, taxonomies associated with **differentially abundant ASV and inferred functions** were shared between the R- efficient line fed the CTR diet and the LE diet groups. This **suggests** that **common** microbiota **mechanisms between feed efficiency and adaptation to non-traditional diet** exist.

R+ & CTR

- a greater abundance of *Actinobacteriota*, with in particular more abundant ***Bifidobacterium*** and ***Olsenella*** *ASVs, which* ***degrade sereval nature of carbohydrates, in particular starch.***



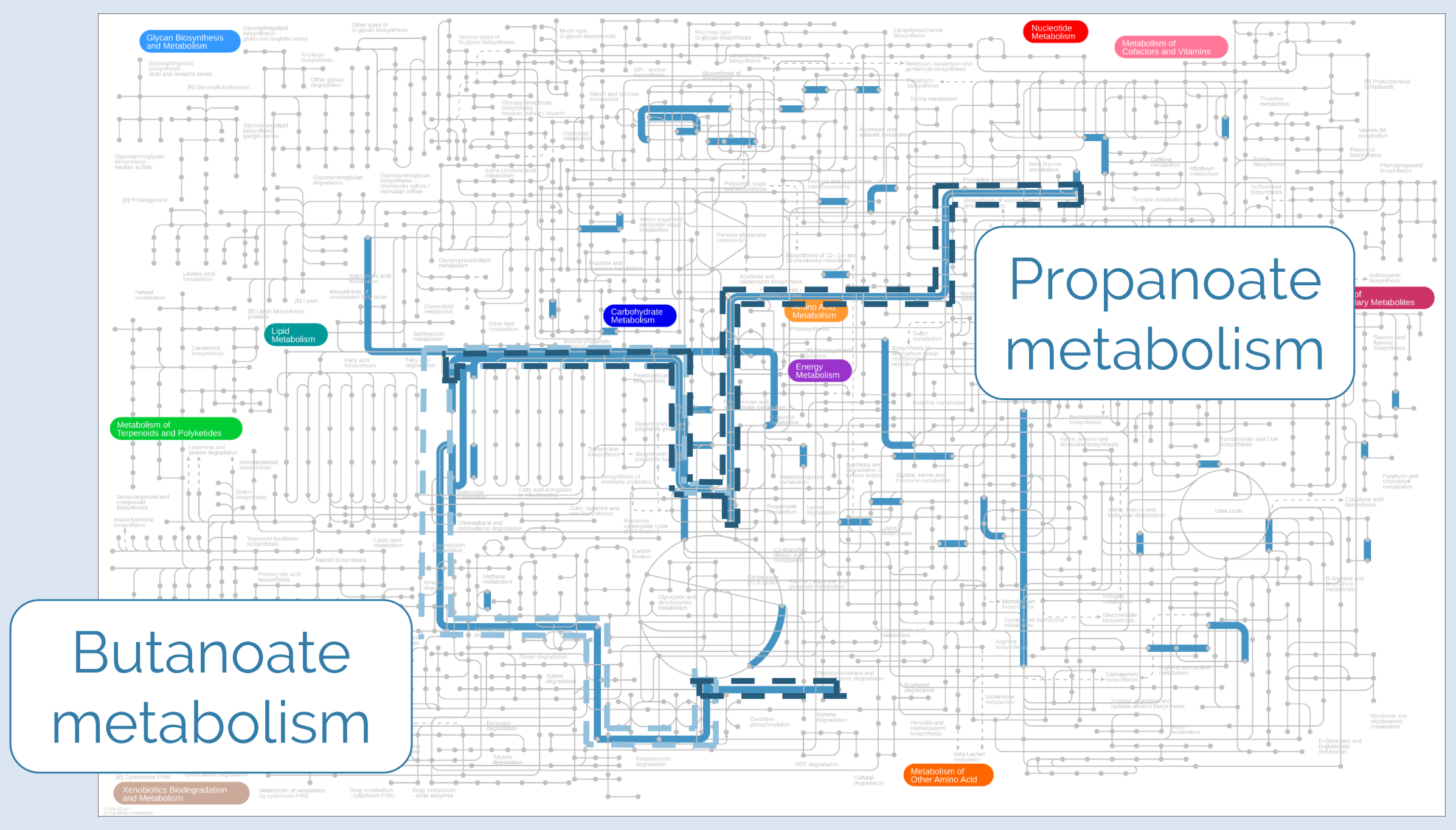
Starch and sucrose metabolism

Fatty acid biosynthesis

Hypothesis : The lower richness observed could illustrate an opportunistic state linked to the high amount starch reaching the caecum.

R- / LE

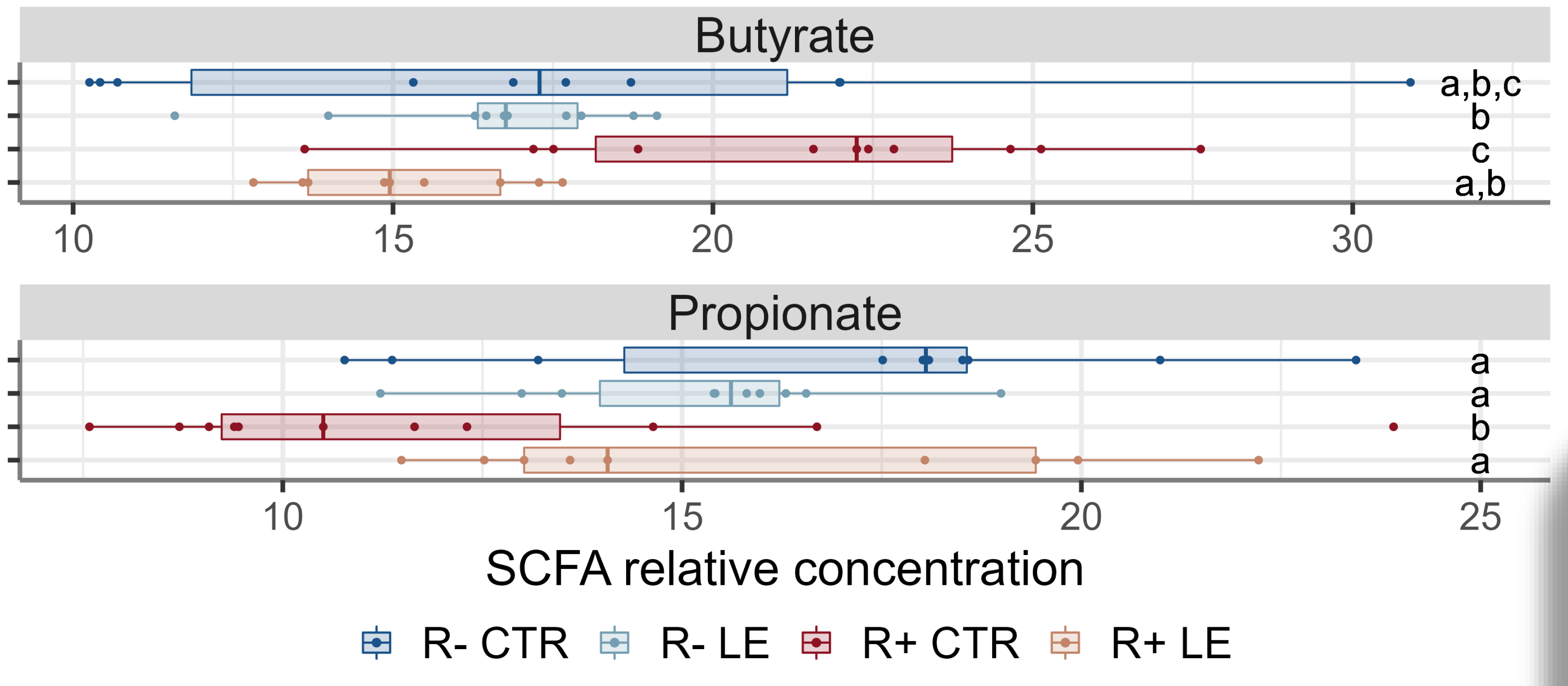
- a greater abundance of *Bacteroidota*, with in particular more abundant ***Alistipes***, ***Anaerosporobacter*** **or Bacteroides** ASVs, **known to degrade various complexe polysacharrides.**



Propanoate metabolism

Butanoate metabolism

Hypothesis : The higher and more diverse type of substrats, as undigested fibres, in the caecum is expected to increase the microbiota richness.



- The **greater** concentration of the **butyrate** in the **R+** line fed the **CTR** diet compared to the LE diet, **could be explained by more abundant** ***Firmicutes*** bacteria such as *Feacalibacterium* or *Subdoligranulum*.
- The **greater** concentration of the **propionate in the efficient** R- line or the LE diet, **corroborates** the functional inference and **the observed increase of glucose metabolism in the liver** of this line.

CONCLUSION

Our results are consistent with the idea that a **richer and more diverse microbiota** contributes to **improve animal feed efficiency** but this association is highly feed dependent. In optimal context, we hypothesise that efficient birds **optimise nutrients absorption**, through fibre degradation by fibrolytic bacteria that produce **propionate** and influence the host metabolism.

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