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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

Maria Bernard, Alexandre Lecoecur, Jean-Luc Coville, Nicolas Bruneau, Deborah Jardet, S. Lagarrigue, Annabelle Troegeler-Meynadier, Fanny Calenge, Géraldine Pascal, Tatiana Zerjal

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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

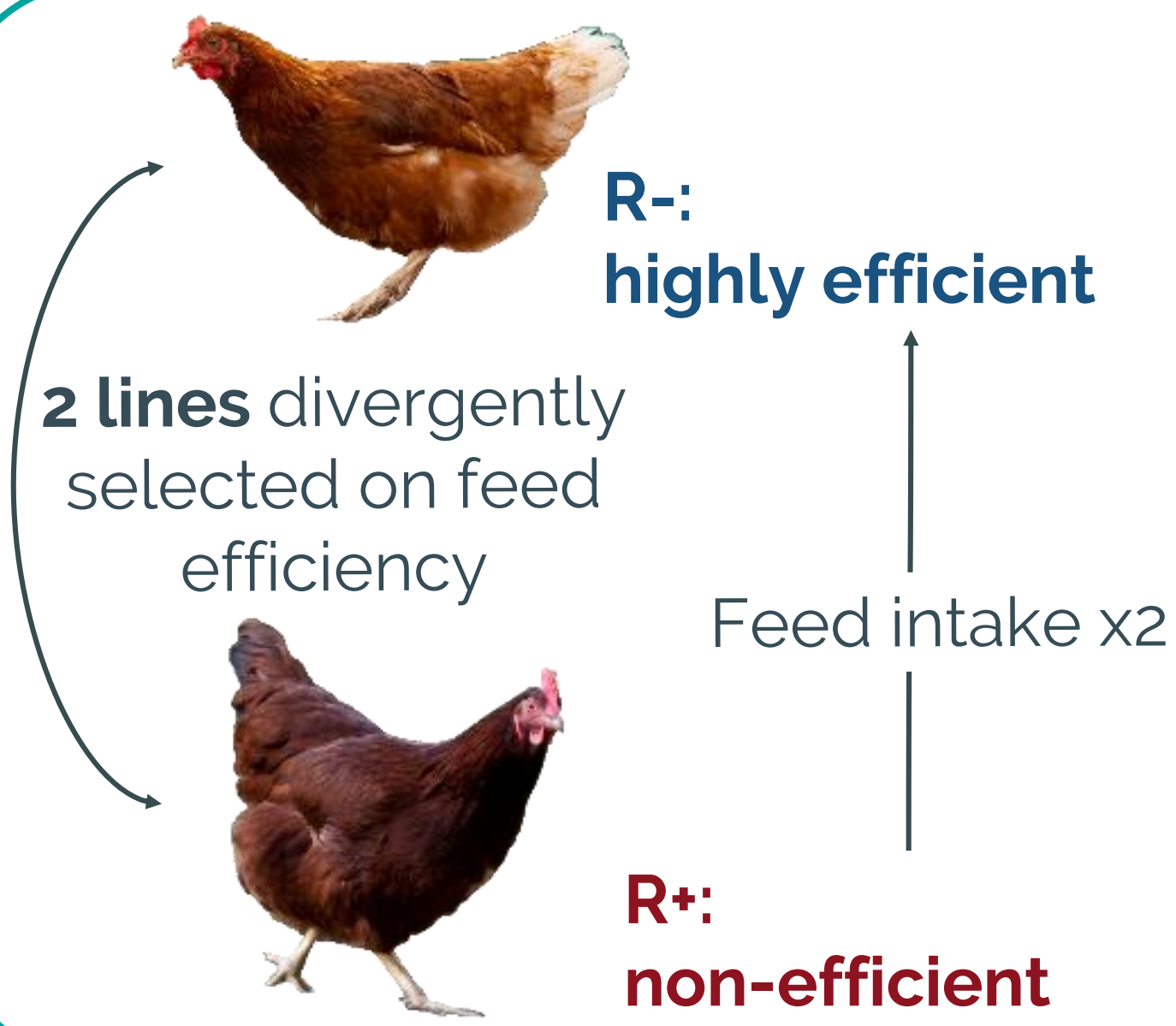
Bernard M.^{1,2}, Lecoœur A.¹, Coville J-L.¹, Bruneau N.¹, Jarret D.¹, Lagarrigue S.³, Meynadier A.⁴, Calenge F.¹, Pascal G.⁴, Zerjal T.¹

1: Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350, Jouy-en-Josas, France, 2: INRAE, SIGENAE, 78350, Jouy-en-Josas, France,

3: INRAE, INSTITUT AGRO, PEGASE UMR 1348, Saint-Gilles, France, 4: GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326, Castanet Tolosan, France

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



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

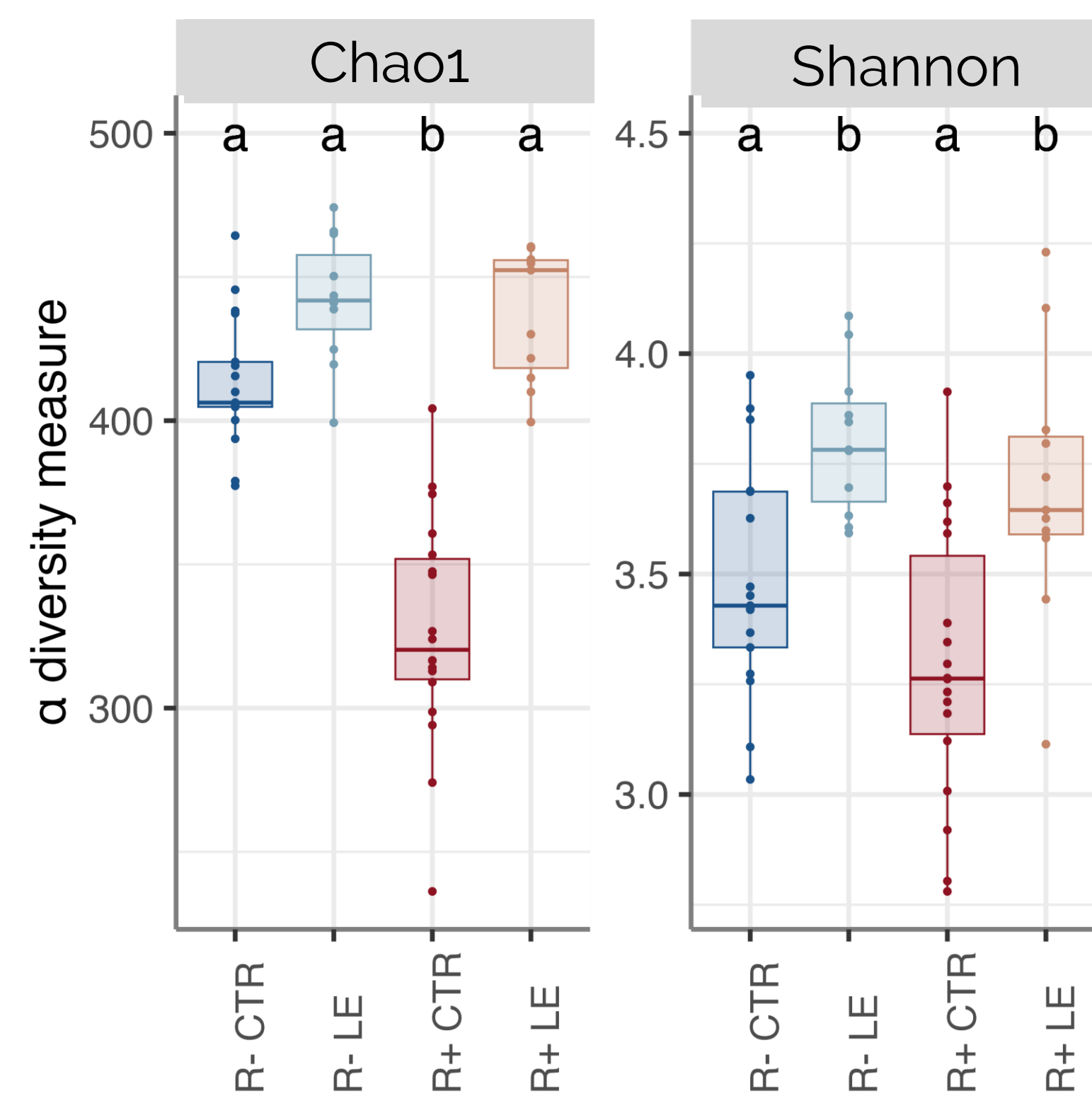
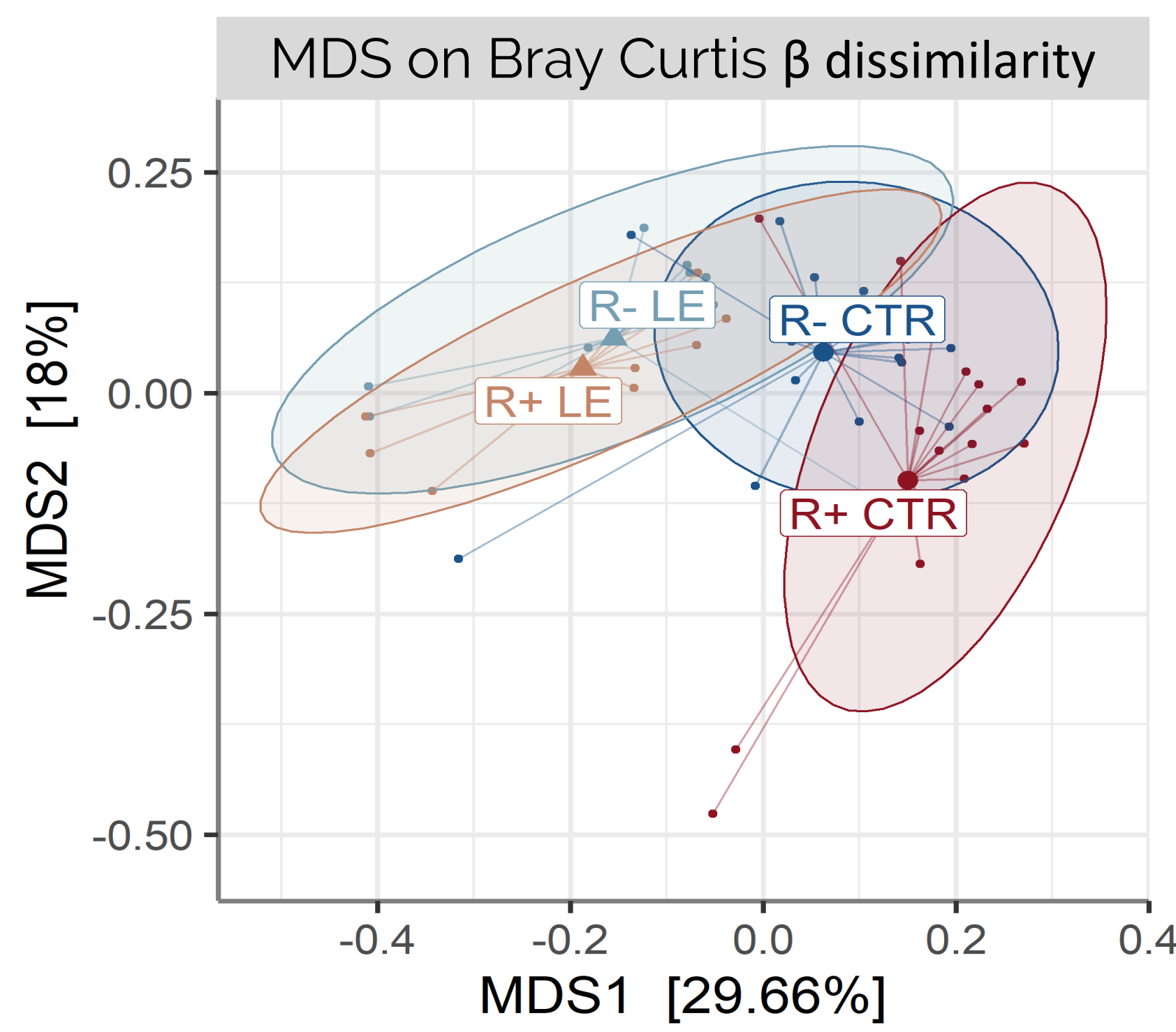
Tools: FROGS¹, Phyloseq², DESeq³, PICRUST⁴

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

[1] Escudié, F. et al., Bioinformatics 2018;

[3] Love, M. I. et al., Genome Biology 2014;

[2] McMurdie, P. J. & Holmes, S., PLOS One 2013; [4] Douglas, G. M. et al., bioRxiv 2019



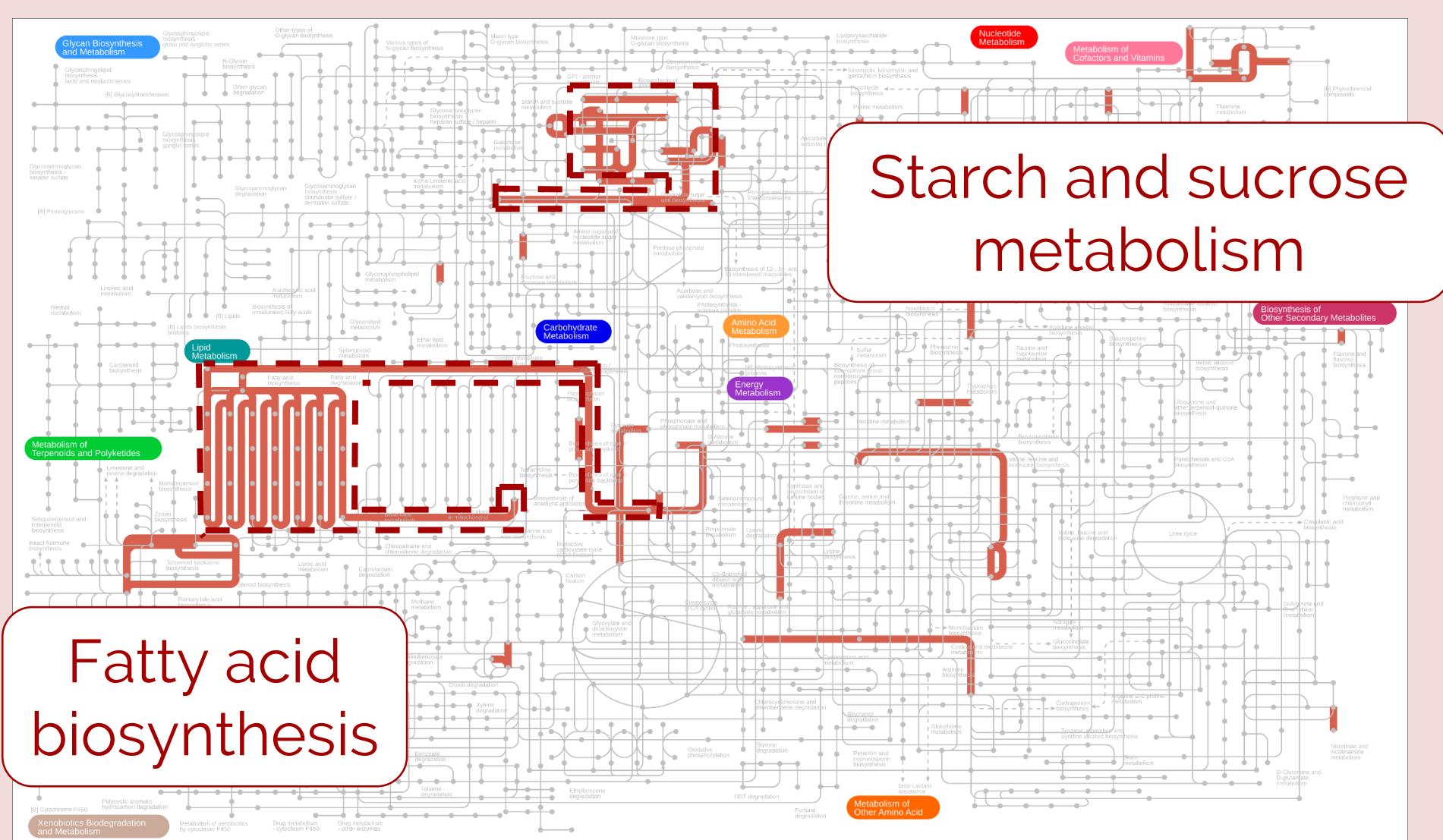
Alpha and beta diversity analyses, as well as differential ASV abundance analysis revealed :

- > 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.



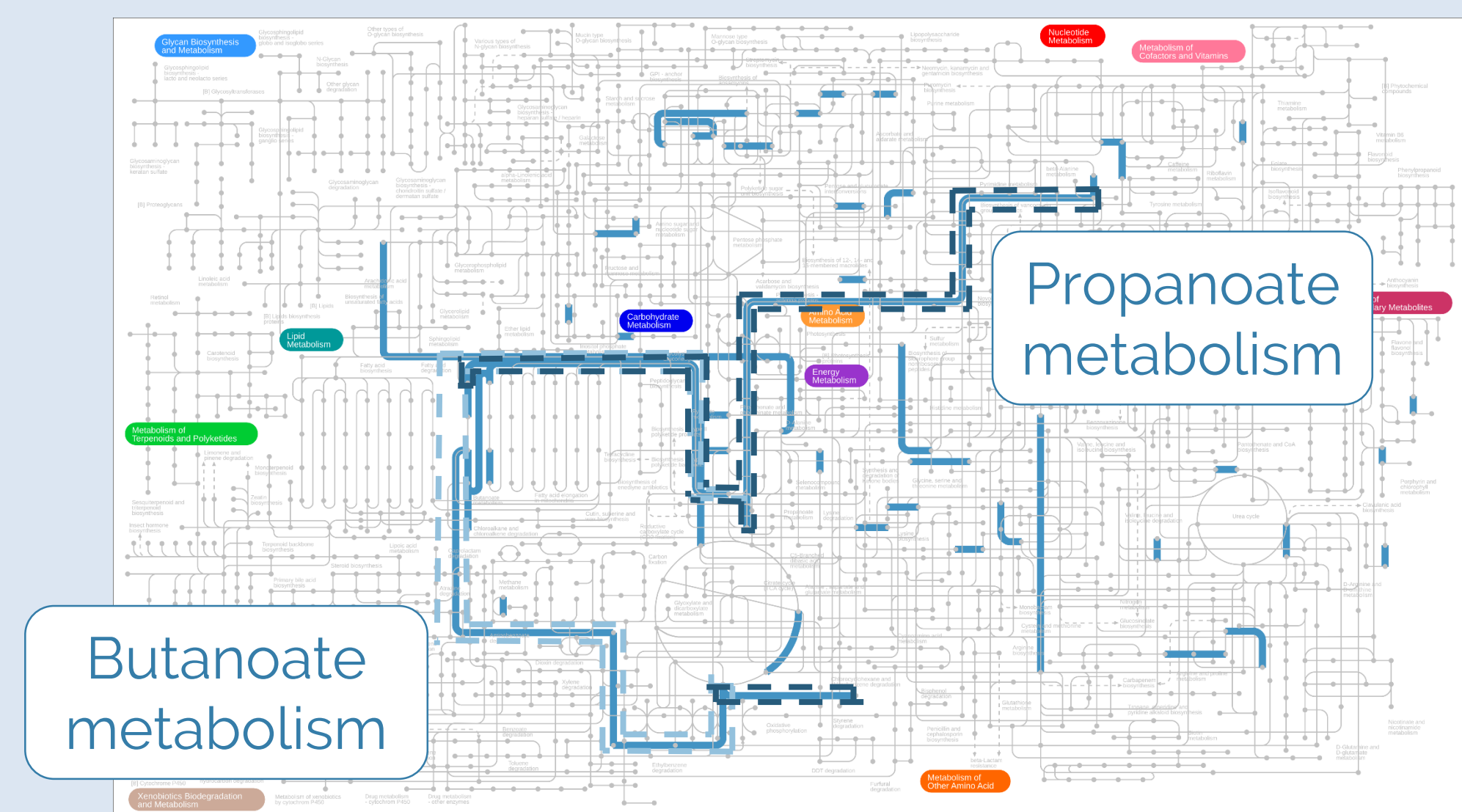
- > a greater abundance of *Actinobacteriota*, with in particular more abundant *Bifidobacterium* and *Olsenella* ASVs, which **degrade several nature of carbohydrates, in particular starch**.



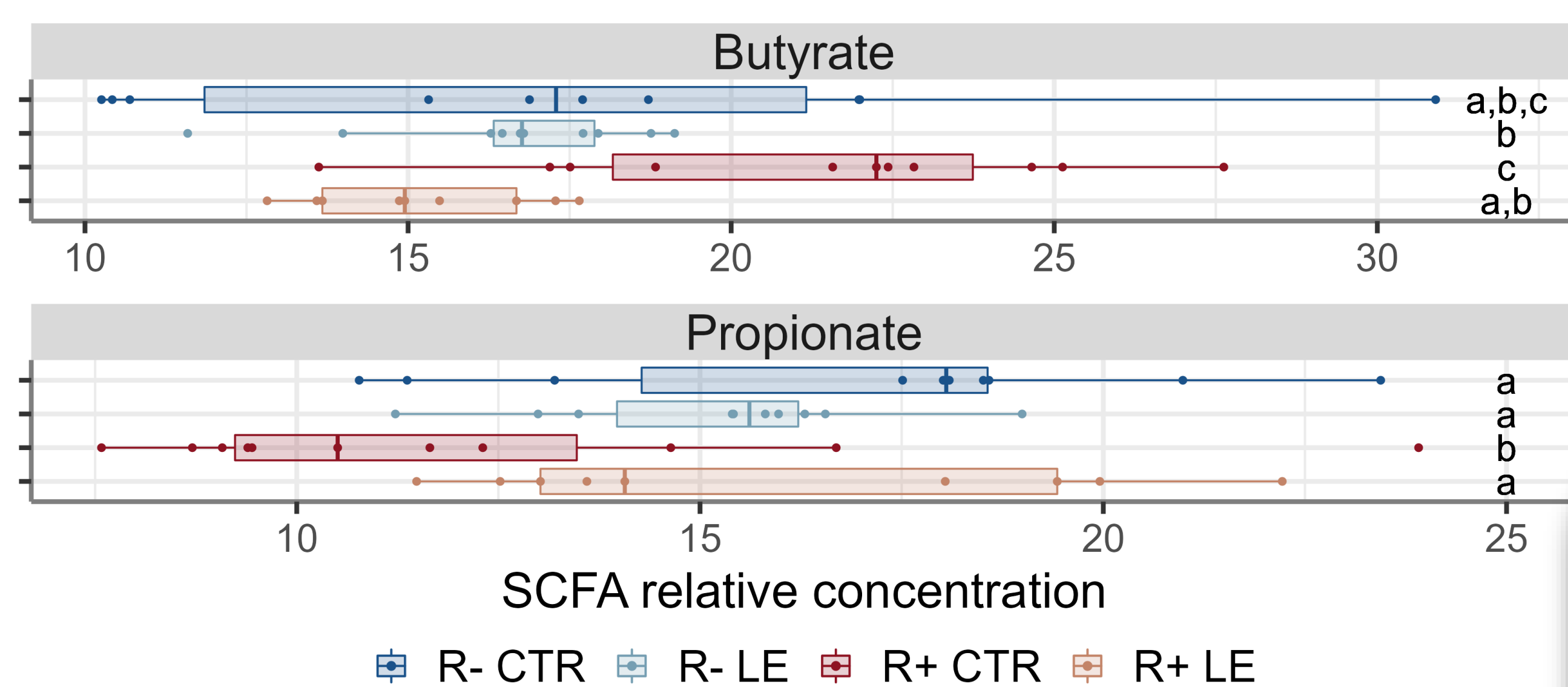
Hypothesis : The lower richness observed could illustrate an opportunistic state linked to the high amount starch reaching the caecum.



- > a greater abundance of *Bacteroidota*, with in particular more abundant *Alistipes*, *Anaerosporebacter* or *Bacteroides* ASVs, **known to degrade various complex polysaccharides**.



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.