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Impact of host genetics and abiotic stresses on caecal microbiota composition in four different laying hen lines?

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In the context of climate change and feed-food resources competition, the description of the gut microbiota of different chicken lines with distinct levels of feed efficiency and heat sensitivity, is a first step in determining its functional role in feed efficiency and environmental adaptation.



EXPERIMENTAL DESIGN

Four experimental chicken lines submitted to 3 rearing environments:

- standard temperature and optimal diet, CTR; j)
- chronic heat stress (4 weeks at 32°C), Heat; ii)
- chronic feed stress (from 17 to 31 weeks of iii) age fed with a lower energy diet), LE.



Heat resistance



Anova p-values < 0,001 for line, condition and interaction

The gut microbiota of 146 laying hens (from 11 to 20 samples per line and condition) were sequenced by 16S metabarcoding.

The alpha diversity measures showed large differences among lines and conditions with the particular case of the non efficient line (R+) in **CTR condition** having an extremely low richness in comparison with all other groups.

Beta diversity analysis confirmed the **line effect** was significant mainly under CTR conditions, while it was largely reduced under heat and feed stress conditions. Moreover, a significant impact of feeding or temperature conditions on microbiota richness and diversity was observed in all lines.

Permanova p-values < 0,001 for line, and condition.

MICROBIOTA LINKS WITH FEED EFFICIENCY AND FEEDING CONDITIONS

Differential abundance (DA) analysis confirmed that lines differed almost exclusively under optimal feeding (CTR) and that the efficient line (R-) was much less impacted by the feed stress than the inefficient line (R+). Moreover, the DA OTUs followed an interesting pattern: the more abundant OTUs in the R-line under CTR feed were often more abundant under LE diet in the R+ line. This suggests that the microbiota of the R+ line feed with the LE diet, moved closer to the natural microbiota of the R-line, which is more diverse and probably underlines a better capacity to adapt to the diet change.

Among the taxonomies associated with these DA OTUs, 2 families were predominant: Lachnospiraceae and Ruminococcaceae with diverse genera such as Faecalibacterium, Subdoligranulum known to be short-chain fatty acid producers. However, based on their richness we cannot associate these genera to any of the conditions analysed. Among the other DA OTUs identified, those of the Oscillospiraceae family were preferentially more abundant in R-line and/or in LE diet, and on the contrary, the *Bifidobacteriaceae* and *Lactobacillaceae* families were more abundant in R+ line and/or in CTR diet.



At the functional level, we found same pattern of differences between lines under the CTR feed or between diets in the R+ line. The R+ under CTR feed were characterised by differential functions involved in fatty acid biosynthesis, starch and sucrose, amino sugar and nucleotide sugar metabolisms. In the **R- and the LE diet**, we found differential **functions involved in a** variety of metabolic pathways, including **carbohydrate metabolism** (in particular pyruvate, and glycolysis), fatty acid biosynthesis and degradation, and protein metabolism with various amino acid metabolisms.



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CTR A Heat LE