



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

Maria Bernard, Jean-Luc Coville, Nicolas Bruneau, Deborah Jarret, Sandrine Lagarrigue, Fanny Calenge, Géraldine Pascal, Tatiana Zerjal

► To cite this version:

Maria Bernard, Jean-Luc Coville, Nicolas Bruneau, Deborah Jarret, Sandrine Lagarrigue, et al.. Impact of host genetics and abiotic stresses on caecal microbiota composition in four different laying hen lines?. Journées Scientifiques du Département de Génétique Animale, Sep 2022, Bordeaux, France. hal-03930049

HAL Id: hal-03930049

<https://hal.inrae.fr/hal-03930049>

Submitted on 9 Jan 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

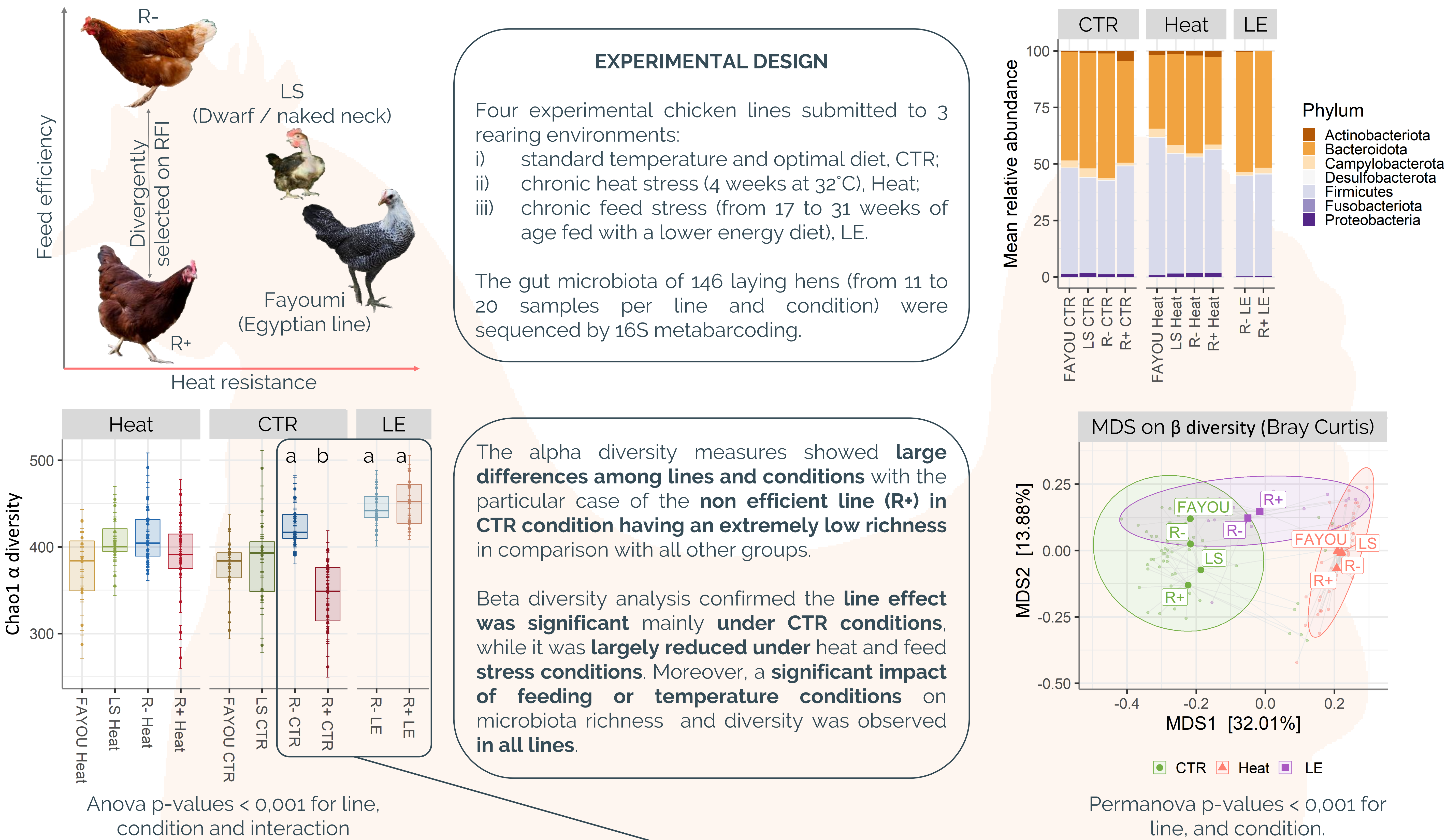
L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Bernard M.¹, Coville J-L.¹, Bruneau N.¹, Jarret D.¹, Lagarrigue S.², Calenge F.¹, Pascal G.³, Zerjal T.¹

1 : Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France; 2 : 1INRAE, INSTITUT AGRO, PEGASE, 35590 Saint-Gilles; 3 : GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326 Castanet Tolosan, France

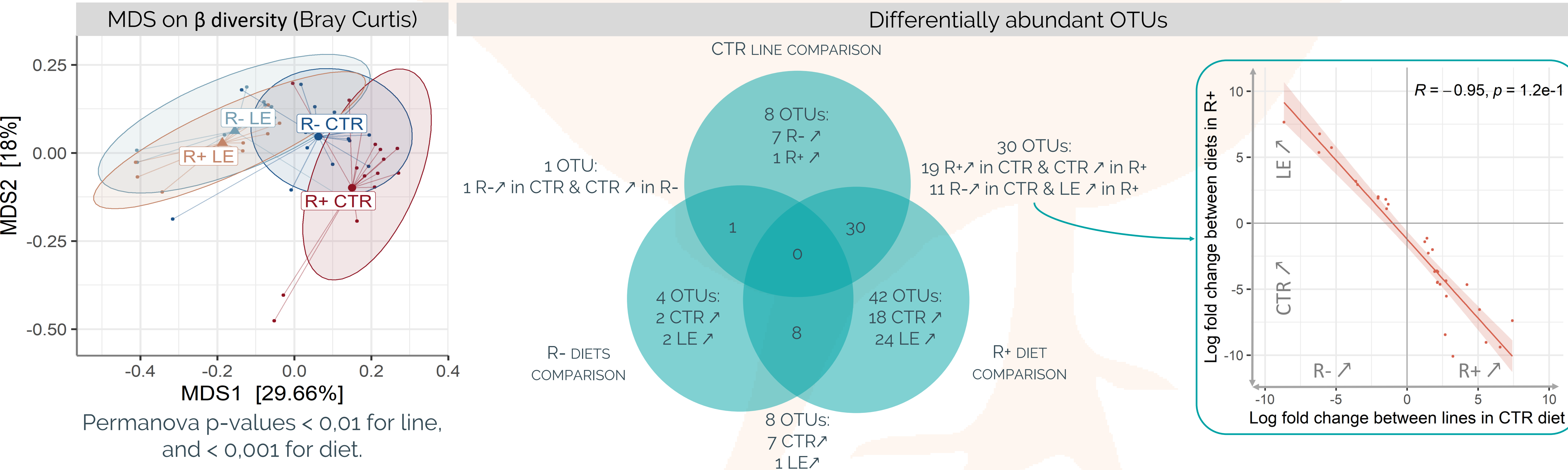
In the context of climate change and feed-food resources competition, the description of the gut microbiota of different chicken lines with distinct levels of feed efficiency and heat sensitivity, is a first step in determining its functional role in feed efficiency and environmental adaptation.



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**.