Unraveling the effects of the gut microbiota composition and function on horse endurance physiology

Sandra Plancade, Allison Clark, Catherine Philippe, Jean-Christophe Helbling, Marie-Pierre Moisan, Diane Esquerré, L. Le Moyec, Céline Robert, Eric Barrey, Núria Mach

▶ To cite this version:

> Sandra Plancade, Allison Clark, Catherine Philippe, Jean-Christophe Helbling, Marie-Pierre Moisan, et al.. Unraveling the effects of the gut microbiota composition and function on horse endurance physiology. 37. International Society for Animal Genetics, Jul 2019, Lleida, Spain. 208 p. hal-02734533

HAL Id: hal-02734533
https://hal.inrae.fr/hal-02734533v1

Submitted on 2 Jun 2020

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.

Kooverjee[1], and F. Muchadeyi[2], [1]*Agricultural Research Council, Animal Production, Irene, Pretoria, South Africa,* [2]*Agricultural Research Council, Biotechnology Platform, Onderstepoort, Pretoria, South Africa.*

Dohne Merino sheep of South Africa are bred and selected for high fertility, rapid lamb growth and wool production. The gastrointestinal tract (GIT) of sheep contains complex microbes that influence its health and development. Molecular approaches for microbial analysis of gut samples have become a widely accepted method to characterize microbial communities. The introduction of third generation sequencing platforms such as Oxford Nanopore Technologies (ONT) MinIon platform, has resulted in long sequencing reads that can be used to study human health, disease and antimicrobial resistance. Abomasum contents from 7 sheep naturally infected with *Haemonchus contortus* were collected and microbial DNA extracted using QIAamp DNA Microbiome Kit. Each DNA sample was barcoded and sequenced using the MinIon system. The bacterial composition of the abomasum was investigated at phylum, class, order, family, genus, and species levels using R packages. A total of 24 phyla were detected, where 16 were present in all samples. *Firmicutes* (78.35%) and *Bacteriodetes* (13.03%) were the most abundant phyla present in the GIT. Furthermore, *Cyanobacteria* (0.23%), *Patescibacteria* (0.19%), *Spirochaetes* (0.18%), *Epsilonbacteraeota* (0.14%), *Synergistetes* (0.13%), *Fibrobacteres* (0.10%) and *Elusimicrobia* (0.07%) were the least abundant phyla. A total of 39 genera (n = 7) with operational taxonomic units (OTU) abundance greater than 1% were identified across all samples. *Christensenellaceace R-7* group (9.93%), *Christensenellaceace R-7* group (rumen) (7.08%) and *Rikenellaceace RC9* gut group (5.18%) represents the top 3 core genera. A total of 3404 species were detected in all samples, however, they were dominated by uncultured bacterium of specific genera. Results indicate that several genera contribute to the differences in community composition between individuals. This is the first study to characterize the abomasum contents of South African Dohne merino sheep by use of ONT MinIon technology, expanding our knowledge of sheep microbiota. This information may allow the possible use of symbiotic bacteria as biocontrol of *H. contortus*.

Key Words: microbiomics, small ruminants, biodiversity, nematodes

OP205 Correlated responses to selection for intramuscular fat in the metagenomic profile on three gut sites in rabbits.

M. Martínez-Álvaro, A. Zubiri-Gaitán*, A. Blasco, and P. Hernández, *Instituto de Ciencia y Tecnología Animal, Universitat Politècnica de València, Valencia, Spain.*

This study reveals the effect of divergent selection for intramuscular fat (IMF) on the rabbit's metagenomic profile. The novelty of this work lies on the study of the observed correlated response in the microbial genes abundances after a selection procedure, which implies a link between the genes of the individuals and the genes of their microbes. We considered 3 different gut sites, ileum, cecum and feces, to additionally discover whether selection has had a stronger effect in any of these sites. Samples were taken from 16 and 17 rabbits divergently selected for high (H) and low (L) IMF during 10 generations. The selection procedure showed a mean response of 0.5 standard deviations per generation. Counts of microbial genes in a sample are compositional variables, constrained by the sequencing depth of the instrument. This restriction creates dependencies between the microbial genes, since an increase in the abundance of one gene requires a decrease for some other genes. For this reason, we analyzed our data with specific compositional data statistic tools. We used *Selbal* algorithm to find the linear combination of the log-transformed microbial genes that better fits to the response variable, H or L line, in each gut site. We will reference this solution as the selected balance. Preliminary results showed that balances selected on each of the gut sites showed a similar high classification ability between H and L, showing R^2 ranging from 0.90 to 0.97 when being tested in a log regression model. Selected balances were composed by a low number of microbial genes in all sites, from 2 to 6. For instance, in cecum, glucose 1-dehydrogenase (K00034) with other 2 microbial genes from unknown pathways (K03439 and K03969) comprised the numerator of the selected balance, and malate-CoA ligase subunit β (K14067) comprised the denominator. H animals were associated with lower balance values; that is, larger relative abundances of K00034, K03439 and K03969 referred to K14067, in comparison to L animals. This preliminary analysis shows that selection for IMF led to a correlated response in the ileum, cecum and feces metagenomic profiles.

Key Words: metagenomics, selection, fat/lipid, compositional data, rabbits

OP206 Unraveling the effects of the gut microbiota composition and function on horse endurance physiology.

S. Plancade[1], A. Clark[2], C. Philippe[3], J.-C. Helbling[4], M.-P. Moisan[4], D. Esquerre[5], L. Le Moyec[6], C. Robert[7,8], E. Barrey[7], and N. Mach*[7], [1]*MaIAGE, INRA, Université Paris-Saclay, Jouy en Josas, France,* [2]*Gastroenterology Department, Vall d'Hebron Institut de Reserca, Barcelona, Spain,* [3]*UMR 1319, INRA, AgroParisTech, Université Paris-Saclay, Jouy en Josas, France,* [4]*UMR 1286, INRA, Université Bordeaux, Nutrition et neurobiologie intégrée, Bordeaux, France,* [5]*UMR 444, INRA, Plateforme GET, Castanet-Tolosan, France,* [6]*Unité de Biologie Intégrative et Adaptation à l'Exercise, UBIAE, EA7362, Université d'Evry, Evry, France,* [7]*UMR 1313, INRA, AgroParisTech, Université Paris-Saclay, Jouy en Josas, France,* [8]*Ecole Nationale Vétérinaire d'Alfort, Maisons-Alfort, France.*

An integrated analysis of gut microbiota, blood biochemical and metabolome profiles in 52 endurance horses was performed. Clustering by gut microbiota composition revealed the existence of 2 communities that varied in taxa and functional composition. Community type 1 presented a low abundance of fibrolytic and cellulolytic bacteria as well as anaerobic fungal loads, but a higher abundance of pathobionts and the predicted lipopolysaccharide biosynthesis pathway. Moreover, its microbial diversity was higher than community type 2, meaning these individuals likely had a greater ability to respond to abiotic and biotic stressors in the gut. Presumably, the 2 communities were mainly driven by diet as host properties showed little effect.Community type 1 was associated with lower estimated daily forage and energy intakes, but higher proportion of acetate in feces and predicted pathways involved in lipid metabolism. Conversely,community type 2 was related to higher proportions of propionate and butyrate in feces together with predicted pathways related to carbohydrate metabolism, but also inflammation and fatigue, evoking an adaptation of gut microbiota to mitigate the effects of stress-induced gut dysfunction during endurance. However, the higher butyrate proportion in community type 2 was not associated with protective effects on telomere lengths. At resting time, community type 1 correlated with some blood metabolites, which may reflect compensatory mechanisms to render the gut mucosa less susceptible to endotoxin translocation during the race. Unexpectedly, the gut microbiota was neither associated with the blood biochemical markers nor metabolome during the endurance race, and did not provide a biomarker for risk of failure to finish the race or race ranking.The current data supports that the gut microbiota may exert a direct or indirect influence on physiological adaptations to endurance in horses.

Key Words: endurance, horse, microbiota, gut, systems biology

OP207 Microbiome and metabolome changes occurring in early *Salmonella* Typhimurium infection in pigs.

H. Arguello*[1], S. Zaldívar-López[1], N. Bellido[1], F. Priego-Capote[2,3], Á. Jiménez-Marín[1], L. Morera[1], and J. J. Garrido[1], [1]*Animal Breeding and Genomics Group, Department of Genetics, University of Córdoba, Córdoba, Spain,* [2]*Department of Analytical Chemistry, Annex Marie Curie Building, Campus of Rabanales, University of Córdoba, Córdoba, Spain,* [3]*Institute of Biomedical Research Maimónides (IMIBIC), Reina Sofía University Hospital, University of Córdoba, Córdoba, Spain.*

Salmonella enterica infections, in particular those caused by the serovar *S.* Typhimurium, are mainly known by their food safety relevance. From a veterinary perspective, swine salmonellosis is character-