

Relationship between ruminal and cecal microbial signatures and feed efficiency in growing cattle

Sarah Jade Meale, Milka Popova, Gonzalo Cantalapiedra-Hijar, Diego Morgavi

▶ To cite this version:

Sarah Jade Meale, Milka Popova, Gonzalo Cantalapiedra-Hijar, Diego Morgavi. Relationship between ruminal and cecal microbial signatures and feed efficiency in growing cattle. 10. Joint Symposium Inra Rowett, Jun 2016, Clermont-Ferrand, France. 2016. hal-02739540

HAL Id: hal-02739540 https://hal.inrae.fr/hal-02739540v1

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.

Relationship between ruminal and cecal microbial signatures and feed efficiency in growing cattle

Sarah J. MEALE¹, Milka POPOVA¹, Gonzalo CANTALAPIEDRA-HIJAR¹ and Diego P. MORGAVI¹

¹UMR Herbivores, INRA, Vetagro Sup, 63122, Saint-Genès-Champanelle, France

Evaluating feed efficiency of ruminants fed non-competitive feed resources is an important avenue to increase the profitability and sustainability of ruminant farming systems. As digestion is considered an important physiological driver of variation of ruminant feed efficiency our objective was to correlate rumen and cecal microbial community signatures to efficiency phenotypes. Twenty-four Charolais bulls fed forage and grain (67:33) were enrolled for 16 weeks in a residual feed intake (RFI) test at 11-12 months of age, during which feed conversion efficiency (FCE) was also determined. Animals with extreme (±0.5 SD from the mean) efficiency indices comprising the groups: High-FCE (n=9), Low-FCE (n=8), High-RFI (n=6) and Low-RFI (n=6), were examined. Following slaughter at ~700 kg LW whole ruminal and cecal contents were collected. DNA was extracted and subjected to Illumina MiSeq sequencing. Output reads were analyzed using QIIME and aligned to the Greengenes database. Differences in β -diversity were determined using PermANOVA and differences in α -diversity and taxa abundance were determined using a paired t-test. Alpha-diversity of bacteria and archaea was similar across RFI (p>0.05), whereas, Shannon and Chao1 indices varied with FCE in both ruminal and cecal bacteria (p≤0.03). Beta-diversity tended (p≤0.10) to differ in cecal bacteria and ruminal archaea of bulls with divergent FCE and RFI, respectively. Within Archaea, the relative abundance of Methanobrevibacter was higher (p=0.01) in the rumen of low-RFI compared to high-RFI bulls. Relative abundance of bacterial Paraprevotellaceae was higher (p<0.01) in the rumen of low-FCE and cecum of high-FCE bulls, compared to the rumen of high-FCE and cecum of low-FCE, respectively. Conversely, Rikenellaceae genus? was greater or more adundant? (p<0.01) in the cecum of low-RFI, compared to high-RFI bulls. Our results suggest that oonly a small number of differences were observed between ruminal and cecal microbiota of bulls with divergent feed efficiencies, which this may be due to the limited number of animals examined.