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Composition and fermentative efficiency of dairy goat rumen microbiota: study of their resilience after a disruption of their rumen ecosystem

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Promoting a sustainable ruminant production requires understanding of the structure and functions relationships of rumen microbiota. In 10 rumen-cannulated lactating goats fed a mixed diet, whole rumen contents were collected, anaerobically pooled and the mixed contents reintroduced in rumens (day d0). The rumen microbiota composition and *in vitro* fermentations were investigated before (d-8 and d-5) and after (d+2, d+6, d+16, d+71, d+78, d+139 and d+148) disruption. The amounts of hexoses fermented (HF), short chain fatty acids (SCFA) and gases specific productions (mol/100 mol of HF) were measured in 24h incubations of a cellulose/starch/casein mixture. The 16S rRNA genes region V4-V5 was amplified from rumen metagenomic DNA. Using Illumina MiSeq platform and FROGS pipeline, 5037729 sequences were clustered into 1716 OTUs assigned using 138 SILVA 16S database. PCoA at OTU level revealed along the two first principal coordinates a distinct clustering according to day, the microbiota compositions being greatly modified shortly after disruption (d+2, d+6 and d+16) and restored in the long term (d+139/d+148). While fermentation variables were similar before disruption and from d+71, the butyrate and CH₄ specific productions decreased 33% and 25% respectively after disruption to the benefit of propionate which increased 119% and H₂ 268% on d+2, and, of H₂S on d+2, d+6 and d+16 which increased 170%, 111% and 112% indicating a shift in reducing equivalent disposal from methanogenesis. The PCA plot (Fig. 1) illustrates the correlations of the 15 most abundant genera with specific productions of gases and SCFA. Despite the quick changes in microbial communities and in H₂ removal pathways following disruption, the microbiota composition and fermentative efficiency returned close to initial within weeks, illustrating a high resilience of individual ruminal microbiota.

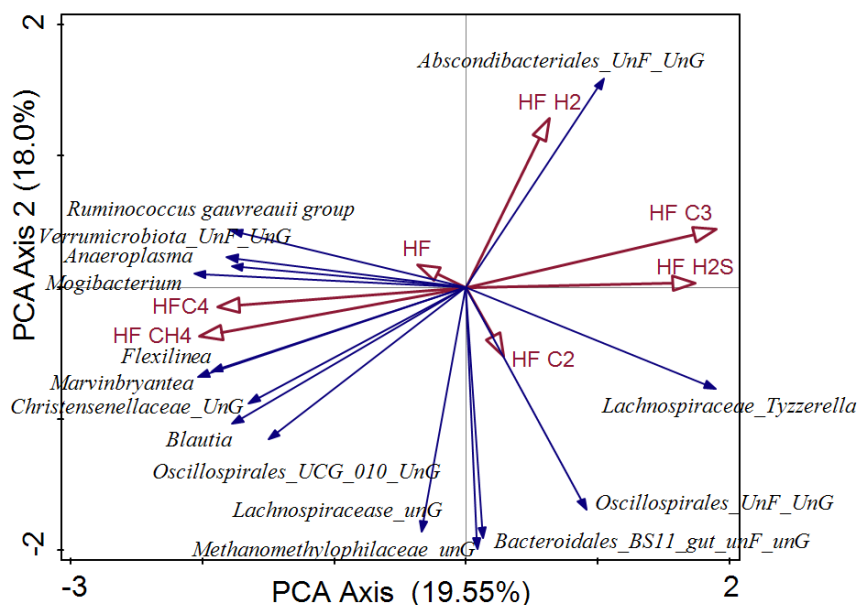


Figure 1 PCA on log transformed microbiota counts at genus level with HF, and gas and SCFA specific productions as supplementary variables