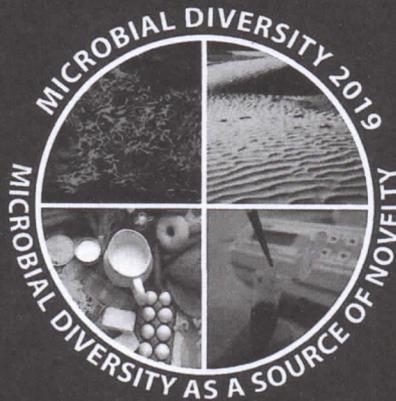


# MICROBIAL DIVERSITY 2019

MICROBIAL DIVERSITY AS A SOURCE OF NOVELTY:  
FUNCTION, ADAPTATION AND EXPLOITATION



**MD 2019**

## Composition and evolution of ruminal fluid microbiota changes when cattle are moved from a permanent valley-farm to a temporary highland farm

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**Introduction:** Ruminal microbiota consists in an extremely biodiverse environment, which includes bacteria, archaea, fungi and protozoa. Microbial populations contribute to the health and productivity of ruminants, and shifts when dairy cow changes diet. To this end, we investigated shifts in the ruminal bacterial and fungal communities in two groups of cows, one remaining in the permanent valley farm and the other moving to a summer highland farm.

**Materials and methods:** Twelve healthy Brown-Swiss cows were selected from a permanent valley-farm located in Trentino (Northern East Italy). In summer 2017, 6 of the 12 cows were moved to the temporary summer farm (1,860 m altitude) for three months. The remaining cows stayed in the permanent farm over the entire duration of the study. A total of 60 ruminal fluid samples were collected monthly by using an esophageal probe, processed for microbiological analysis, extracted for genomic DNA, amplified using archaeal and fungal specific primers, sequenced on a MiSeq Illumina platform and analyzed using QIIME 2.0.

**Results:** Ruminal fluid from cows moved to the temporary alpine farm showed increased microbial counts compared to samples collected from the permanent farm over the summer. Illumina data also showed significant changes of microbial and fungal relative abundance in alpine samples: *Fibrobacter*, *Lachnospiraceae*, *Veillonellaceae* and *Tenericutes* significantly changed among bacteria;

*Neocallimastigaceae*, *Didymosphaeriaceae*, *Dothideomycetes*, *Podospora*, *Filobasidium*, *Vishniacozyma*, *Basidiomycota*, *Aspergillus* and *Wallemia* significantly changed among fungi. Both microbiological counts and metagenomics data at the end of summer (after transhumance) regressed to values registered at the beginning of summer (before transhumance), confirming the hypothesis that alpine pasture strongly influences the microbiota composition of ruminal liquid.

**Conclusions:** This is the first study aiming to analyze the microbial evolution of ruminal fluid before, during, and after summer transhumance, and in particular to compare the microbiota of two groups of cows maintained over summer in the permanent farm or in a temporary highland farm, respectively. This research provides a broad picture of microbial populations residing the ruminal fluid of dairy cows bred in the permanent farm or in a temporary alpine farm, demonstrating the influence of diet, in particular of alpine pasture, on the microbial composition.