

**Lactic acid treatment and P levels in the diet impact microbial dynamics in lactating dairy cows**

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Recent in vitro data indicates that there are beneficial effects of treating grain with lactic acid (LA) on specific ruminal microbes, fermentation profiles and fiber degradation in low phosphorus (P) diets. This study used lactating dairy cows (n=18) to assess the impact of LA treated diet with either non-supplemented (low) or supplemented (high) inorganic P content on fecal microbial populations compared to an LA untreated control diet. Extracted fecal microbial DNA was sequenced using the Illumina MiSeq platform. Sequenced DNA was then stitched, cleaned, analyzed using QIIME software. Significant OTUs were blasted using the NCBI database. A total of 2,268 OTUs were identified as representing a minimum of 1% of the total population. The treatment of diet with LA significantly impacted 10 OTUs whereas the variation in P significantly impacted only three OTUs from the fecal microbiota. Of the OTUs impacted by the LA treatment, 6 OTUs had an increased abundance in the control diet. From those 6 OTUs, two showed an additional significant effect of P. These two OTUs were classified as being members of the RC4-4 genus and the Ruminococcaceae family respectively. Comparison of these OTUs to the NCBI database gave identification as *Peptococcus niger* and *Defluviitalea saccharophila* with 89 and 88% respective similarity. A total of 15 of the 18 OTUs impacted by LA treatment or P level belong to one of the following *Clostridium* clusters: i, iii, iv, xi, or xv. These results show a large representation of fecal bacteria from the Ruminococcaceae family. Additional qPCR analysis, performed using *Ruminococcus* genus primers, showed no significant differences based on LA treatment or P levels in the diet. The lack of qPCR response and the low percent identification provided by curated databases indicates that there are many members from the ruminococci group which remain unknown. By increasing organic P availability from feedstuffs and decreasing supplemented inorganic P without adversely impacting the rumen microbial community, it may be possible to reduce the amount of P excretion in commercial dairy production.

## Session 72

## Theatre 3

**Recording of feed efficiency under on-farm conditions**F. Steininger<sup>1</sup>, M. Ledinek<sup>2</sup>, L. Gruber<sup>3</sup>, B. Fuerst-Waltl<sup>2</sup>, K. Zottl<sup>4</sup> and C. Egger-Danner<sup>1</sup>*<sup>1</sup>ZuchtData EDV-Dienstleistungen GmbH, Dresdner Str. 89/19, 1200 Vienna, Austria, <sup>2</sup>University of Natural Resources and Life Sciences, Department of Sustainable Agricultural Systems, Division of Livestock Sciences, Gregor-Mendel-Str. 33, 1180 Vienna, Austria, <sup>3</sup>Agricultural Research and Education Centre Raumberg-Gumpenstein, Raumberg 38, 8952 Irdning, Austria, <sup>4</sup>LKV Austria Qualitätsmanagement GmbH, Dresdner Str. 89/19, 1200 Vienna, Austria; steininger@zuchtdata.at*

During recent years discussions about greenhouse gas emissions, higher costs for concentrates and decreasing producer milk prices resulted in increased interest in feed efficiency in dairy production. Calculation of measures for feed efficiency is challenging as it is influenced by several factors. Several possibilities to use feed efficiency data for a genetic evaluation exist: (1) to record the feed intake precisely for a small group of animals on station; (2) to estimate feed intake of many animals on farm based on animal and diet information with impact on the feed intake or (3) to work with further auxiliary traits like mid-infrared-spectra. Within the Austrian project 'Efficient Cow' composition of diets, feed analyses and amounts of concentrates based on automatic transponder feeders were recorded for approximately 5,400 cows, i.e. 3,100 Fleckvieh (FL – dual purpose Simmental), 1,300 Brown Swiss (BS), 1,000 Holstein (HF), kept on 167 farms. Based on parameters breed, live weight, milk yield, number of lactation, days in milk, proportion of concentrates and net energy content of forage the dry matter intake (DMI) for every single cow was estimated using the model of Gruber et al. To make the results comparable between animals a standardisation for the 100<sup>th</sup> day in milk and without pregnancy was done. The means for standardized DMI were 20.0 (FL), 19.4 (BS), and 21.3 (HF) kg dry matter with a standard deviation of 2.9 (FL), 2.9 (BS), 3.1 (HF). On average, the cows produced 0.23 (FL), 0.22 (BS), and 0.24 (HF) kg milk per MJ NEL intake on their 100<sup>th</sup> day in milk. The proportion of milk produced out of forage (grass, hay, silage or maize silage) was in the range of 20 to nearly 100% with a mean of 60.1% (FL), 63.6% (BS), and 59.9% (HF).