

THE EFFECT OF WHEY SUPPLEMENTATION ON FAECAL MICROBIOME COMPOSITION IN PIGS

Anna Maria Sutera (1), Viviana Floridia (1), Valentina Riggio (2), Giuseppe Tardiolo (1), Alessandro Zumbo (1), Enrico D'Alessandro (1)

(1) Università degli Studi di Messina, Dipartimento di Scienze Veterinarie. (2) University of Edinburgh, The Roslin Institute and R(D)SVS.

Corresponding author: A.M. Sutera (asutera@unime.it)

The gut microbiota plays a pivotal role in different physiological processes. The composition of the microbial community can be influenced by several factors, including nutrition [1-3]. Liquid whey (LW) represents a highly nutritious byproduct of the dairy industry. Its administration can affect body weight gain, feed efficiency, protein and fat digestibility, as well as mineral absorption and retention [4]. This study explored the effects of LW integration on faecal microbiota in 20 crossbred pigs (Landrace x Large White). The animals were homogeneous for body weight, age, and breeding management, and were divided in two groups (i.e., 10 individuals each), with the control group (CTRLg) fed with a pellet complete feed and the treatment group (LWg) receiving the same diet supplemented with LW, *ad libitum*. The trial lasted for a total of 60 days, from post-weaning (30 days old) until growing (90 days old), including an adaptation period of 15 days. Stool samples were collected at 30 (T0), 60 (T1), and 90 (T2) days of age. The environmental parameters, as well as the physiological condition of the animals, were daily monitored. The V3-V4 hypervariable regions of the bacterial 16S rRNA gene were sequenced in two MiSeq (Illumina) runs with 2 × 300-base paired-end reads. Raw sequences were processed using a pipeline combining QIIME2 and DADA2. High-quality reads were clustered into high-resolution Operational Taxonomic Units (OTUs). Using taxonomic assignment, OTU tables were collapsed from phylum to genus level. At the phylum level, *Firmicutes* and *Bacteroidetes* were the most abundant phyla at all times regardless of treatment. At genus level, the most prevalent genus was *Prevotella* regardless of the diet, whereas *Lactobacillus* showed differences between the two groups, being the predominant genus ($p = 0.002$) in LWg. Chao1 and ACE indices and Shannon, Simpson, and Fisher's alpha were used to calculate within sample microbial richness and diversity, respectively. Beta diversity was estimated by computing Bay-Curtis distances into Principal Coordinates Analysis (PCoA). Significant differences in alpha or beta diversity were assessed by a Kruskal-Wallis and Wilcoxon test, with significant differences observed between CTRLg and LWg ($p < 0.001$) and at T2 ($p < 0.002$). Alpha and Beta diversity analyses indicate that LW addition shifted the gut microbial community structure. In conclusion this study has shown that LW supplementation to the diet can have an effect on the bacterial community in the pigs' gut and should be further investigated.

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