

## EFFECTS OF SUPPLEMENTARY FEEDING USING A DAIRY BY-PRODUCT ON FAECAL MICROBIOTA COMPOSITION IN NERO SICILIANO PIG

Anna Maria Sutura, Viviana Floridia, Laura De Maria, Giuseppe Tardiolo, Alessandro Zumbo, Enrico D'Alessandro

Università degli Studi di Messina, Dipartimento di Scienze Veterinarie.

Corresponding author: A.M. Sutura (asutura@unime.it)

Pigs' gut harbours thousands of different bacteria, whose composition and relative proportions vary depending on the breed, age, nutritional and environmental factors. In particular, genetic background is strongly associated with the host's gut microbial taxa and characteristics [1]. The Nero Siciliano is an autochthonous breed of a domestic black pig reared in Sicily (Italy) [2]. Recently, the faecal microbiome of the Nero Siciliano pig was explored [3] by using whole-metagenome shotgun sequencing approach, to increase the knowledge regarding the taxonomic and functional profiles of microbes associated with this rare and endangered-maintained pig breed. The present study evaluated the effects of supplementing the diet with liquid whey (W), a highly nutritious dairy by-product on faecal microbiota in 12 Nero Siciliano pigs. Six individuals were assigned to a control group (Cg) fed with a pelleted complete feed and the remaining six to a treated group (Wg) that received the same diet supplemented with W, *ad libitum*. The animals were homogeneous for body weight, breeding condition and age. The trial lasted 60 days (including ten days of adaptation to the diet). Faecal samples were collected from the rectal ampoule of each animal at different time points (T0, T1 and T2). The interval between T1 and T2 collection was of twenty-five days. The procedure of samples collection, storage, DNA extraction and sequencing, bioinformatic and statistical analysis followed a defined pipeline. The extracted DNA was prepared for the sequencing of the V3 and V4 regions of the 16 rRNA gene with a MiSeq (illumina, San Diego, CA, USA) in a 2×300 paired-end mode. Raw sequences were processed using the bioinformatics program QIIME 2 and Phyloseq packages of R. The alpha-diversity was similar between the groups and a tendency to a higher evenness was observed in the Wg. The classes *Clostridia*, *Bacteroidia*, *Bacilli* and *Spirochaetia* accounted for more than 90% of the community (~40, ~39, ~8, and ~7%, respectively), regardless of the diet. Concerning beta-diversity, the gut microbiome clearly changed between treatments and time-points (p-value=0.04). Despite the small sample size, these preliminary results show that W supplementation can have an effect on gut microbiome of the the Nero Siciliano pig. Further studies are therefore required, using bigger sample sizes.

[1] Lu et al. Bacterial communities in manures of piglets and adult pigs bred with different feeds revealed by 16S rDNA 454 pyrosequencing, *Appl Microbiol Biotechnol*, 98:2657-65, 2014.

[2] D'Alessandro et al. Whole genome SNPs discovery in

Nero Siciliano pig, *Genet Mol Biol*, 42:594-60, 2019.

[3] Giuffrè et al. Whole-metagenome shotgun sequencing of pig faecal microbiome. *Italian Journal Ital J Anim Sci*, 1: 1147-55, 2021.