



uate the archaeal community of the horse digestive tract and to compare the methanogens between caecum and rectum. The total DNA was extracted from lyophilised samples of horse caecal and rectal content. The archaeal communities were analyzed by the amplification and sequencing of 16S rRNA gene, using a clone library approach. The phylogenetic analysis was carried out by MEGA 5.2 software program, using the maximum likelihood method. The analysis of the methanogens residing in the horse digestive tract revealed differences between the caecal and rectal samples. In the caecum 64% of the methanogen sequences have a low similarity (96%) with the uncultured archaeon and the cultivable *Methanocorpusculum*, 2 clones have a good similarity (99%) with the uncultured archaeon obtained from equidae faeces and 35% of the sequences represent a cluster of the unknown archaea. In the rectum 90% of the sequences have 96-99% similarity with the uncultured archaeons found in the equidae faeces and rumen content. 50% of the rectal methanogen sequences are phylogenetically related to the cultivable species *Methanomicrococcus*, *Methanocorpusculum* and *Methanobrevibacter*, the other 50% represent a cluster of unknown archaea. The horse methanogenic archaea profile differs between caecum and rectum. Most of the sequences (85%) are related to the unknown uncultured archaeons, which makes very difficult the evaluation of our results. The methanogenic archaea of the horse digestive tract represent new microorganisms, showing that this ecosystem is still rather unexplored. The research was carried with the contribution of the following programmes: Erasmus+; Visiting Professor and Master and Back 2012/2013 Regione Autonoma Sardegna.

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The effect of the genetic type and handling immediately prior to stunning on pro- and macro- glycogen in two porcine muscles

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The muscular glycogen plays an important role on the extent of the pH decline after slaughter. Two glycogen fractions are described, pro- and macro-, which are metabolized with different priority during physical efforts. The aim of the present study was to evaluate the contents of pro-, macro-, total glycogen, lactate and pH in two muscles of pigs belonging to three genetic types submitted to a rough or gentle pre-slaughter handling. Twenty-eight pigs from Large White (LW), Duroc (DU) and Pietrain halothane-gene-free (P) breeds were

slaughtered with the average final weight of 114.0, 123.0 and 115.2 kg. Half of each group, being 5LW, 5DU and 4P, was subjected to one of pre-slaughter handling. Measures of pH and samples were collected from *Longissimus thoracis* and *Semimembranosus* at 1 h post mortem. In the rough pre-slaughter handling group (RPH) the animals were submitted before stunning to a fast driving supported by the use of electric prods, accordingly to the EU regulations. In the gentle pre-slaughter handling group (GPH) the animals were driven slowly without electric prods. The data were processed by a model including the fixed effects of handling, genetic type and their interaction. In *Longissimus thoracis*, the effects of handling, genetic type or interaction in the contents of pro-, macro and total glycogen were not observed. The content of macroglycogen was lower in animals of the RPH group ($P < 0.001$) in *Semimembranosus*: 9.7 vs. 16.7 $\mu\text{mol/g}$. The only interaction was observed between handling and genetic type in total glycogen of *Semimembranosus* ($P < 0.05$), showing that LW pigs of GPH have higher levels than DU of RPH (106.3 vs. 54.4 $\mu\text{mol/g}$). The total glycogen of these two groups was similar to the others. The lactate content in *Longissimus thoracis* was higher in RPH than GPH ($P < 0.01$) (50.9 vs. 37.0 $\mu\text{mol/g}$, respectively) while the genetic type did not show any effect. In *Semimembranosus*, the effect of both handling and genetic type or their interaction on the lactate contents was not observed. The pH in animals submitted to RPH was lower in both muscles ($P < 0.05$) while the genetic type or the interaction between handling and genetic type did not show any effect. We conclude that the effects of handling and genetic type on the levels of pro-, macro- and total glycogen varies according to the measured muscle, being more evident in *Semimembranosus* and these contents tend to be lower in animals submitted to a rough pre-slaughter handling.

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Effect of dietary inclusion of Spirulina on nutrient apparent digestibility in chinchillas

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Spirulina (*Arthrospira platensis*) is a blue-green microalgae characterized by a high level of protein as well as potential anti-obesity, antioxidant and hypolipidemic effects. The objective of the study was to evaluate the nutrient apparent digestibility of two isoprotein (15.7% crude protein), isoenergy (16.8 MJ/kg) and isofiber (17.8% crude fiber) pelleted diets for chinchillas, with or without *Spirulina* supplementation. With this aim, 20 growing chinchillas (*Chinchilla lanigera*) of both sexes, with an average body weight (BW) of 268 g, were fed either a control diet (diet C) or an experimental diet with *Spirulina* at 2% inclusion level (diet S). The animals were individually allocated in



digestibility cages for an adaptation period of 7 days followed by a 5 day-digestibility trial. During the digestibility trial, for each subject feed intake was calculated and faeces were collected and weighed. Diets and faeces were analysed for dry matter, organic matter, crude protein, ether extract, ash, starch, crude fiber, and fiber fractions content. The effect of the diet was tested by ANOVA using the results from the animals that completed the trial: 5 on diet C and 8 on diet S. The treatment showed no difference on feed intake (0.10 g DM/kg BW for C and S diets). The energy digestibility of the experimental diets (C: 41.3 vs. S: 49.1%), as well as the digestibility of dry matter (C: 38.0 vs. S: 44.9%) and organic matter (C: 40.7 vs. S: 47.3%) were similar although generally low. Contrarily to what was observed in rabbits and guinea pigs, enriching the diet of chinchillas with *Spirulina* resulted in higher crude protein (C: 50.0 vs. S: 59.8%; $P < 0.05$) and ether extract (C: 70.2 vs. S: 80.3%; $P < 0.05$) digestibility as well as in a higher starch (C: 98.7 vs. S: 99.0%; $P = 0.05$) digestibility. In chinchillas, the dietary inclusion of *Spirulina* has the potential of improving the nutritional value of the diet.

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Influence of early microbial association and dietary medium chain triglycerides on development of gastric function in pig

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Several environmental factors shape the gut microbiota in the early life, but it is not clear if early microbial colonization affects the gut functional development. The priming effect of oral association with microbiota of different complexity and of dietary medium chain fatty acids (MCT) was tested on the gastric transcriptome profile, in 24 pigs obtained by caesarean delivery (day 0), housed in two separate rooms, that received 45 mL pasteurized sow colostrum at 1 and 5 h after birth, and 2 mL of a starter microbiota (10^7 CFU of each *Lactobacillus amylovorus*, *Clostridium glycolicum*, and *Parabacteroides* spp.) on d 1, 2 and 3 of life. In addition, the pigs received either a complex microbiota in 2 mL of either a placebo inoculant (simple association, SA) or an inoculant consisting of diluted feces of an adult sow (complex association, CA) on d 3 and 4. Piglets were fed *ad libitum* a milk replacer diet till d 4 and then till d 21 a diet with either 7%

coconut oil (MCT) or soybean oil (CTRL). Samples of oxyntic tissue were obtained of all pigs euthanized on d 21. Total RNA expression was analyzed by Affymetrix Porcine Gene 1.1ST array strips. Exploratory functional analysis of gene expression values was done by Gene Set Enrichment Analysis. SA phenotype enriched 292 gene sets compared to CA. Most of them were related to mitosis and cell cycle phases, and DNA and RNA replication. CA phenotype enriched 125 gene sets compared to SA. Provision of the MCT diet enriched 184 gene sets, compared with CTRL, including sets related to response to virus, chemokine activity and binding, response to stimuli, and neurite development. Provision of the CTRL diet enriched only 14 gene sets, compared with feeding the MCT, related to energy and lipid metabolism. Several nodes of genes related to anion channel activity were up-regulated in CA-associated pigs fed MCT, compared to SA-associated pigs, fed the same diet. The results suggest that a. early association of newborn pigs with a complex microbiota favorably prevents the activation of pathways related to cell division in the gastric mucosa, compared to the association with a simple microbiota, presumably in relationship with previous observations that a short encounter of gastric tissue with a complex microbiota can be sufficient to influence the intestinal microbiota in the subsequent period and b. provision of an MCT diet has an effect on gastric transcriptome similar to the early association with a simple microbiota.

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Microscopic differential cell counting and viability evaluation of milk somatic cells during lactation in goat

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Milk contains different cell populations commonly known as somatic cells, changing their distribution under the influence of several factors as physiological status and stage of lactation, and useful to assess the transcriptional activity of the mammary gland in livestock. The aim of this study was to compare the differential somatic cells counting (DCCs) and cell viability in goat milk samples collected at morning milking (MM) and 2 hours later (2H), in order to verify if some difference occurred between the two sampling times. This investigation was carried out within a project addressed to optimize studies on gene expression in goats mammary gland. In 11 pluriparous Alpine goats lactations were studied for 21 wks. Individual