



between groups. Conversely, piglets on the FFP diet showed a better FCR ( $p < .05$ ). The gut microbiota did not show differences in microbial taxa composition, while further investigations are necessary to clarify the effects of FFPs on gut bacterial abundance and biodiversity.

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## O037

### Administration of green tea and pomegranate extract in drinking water on broiler growth performance, total blood antioxidant activity and gut microbiota

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The plant-derived products as green tea extracts have been extensively used in poultry nutrition due to their antioxidant, anti-viral and anticoccidial properties. Furthermore, they have the capacity to lower cholesterol and reduce lipid peroxide level in plasma and meat, and improve the growth performance and meat quality of broiler. The pomegranate peel extract has also been showed pharmacological, anti-inflammatory, antioxidant and anticoccidial properties. The combination of green tea and pomegranate extract might be able to modulate intestinal microflora. The aim of this study was to evaluate the influence of the combination of natural extract of pomegranate and green tea extract on growth performances, blood antioxidant status and gut microbiota in broiler chicks. A completely randomised block design with two experimental treatments (CTR and plant extracts, PE) was carried out. Each treatment group included 240 male birds allotted in 12 pens (replicates). PE were supplemented through drinking water at the dosages of 0.2 mL/L at days 0–4, 10–11, 20–21 and 45–46. During the trial, birds weight and pen feed intake were measured. At slaughtering (day 50), blood samples and caeca content were collected from one broiler per pen. Moreover, carcass and breast percentage were also evaluated. Blood total antioxidant activity was measured by KRL test. 16S amplicon sequencing for microbial community profiling was performed on caeca content. Feed conversion ratio was significantly affected by PE treatment from 21 to 50 days ( $p = .029$ ). No other growth and slaughter parameters were affected. Total antioxidant activity on blood ( $p = .009$ ) and red blood cells ( $p = .02$ ) were higher in PE group. Microbial profiling analysis showed no difference in richness and diversity of caeca

bacterial composition between groups. Microbiome analysis indicates a slight increase in treated group of beneficial bacteria such as *Rikenellaceae*, *Ruminococcaceae*, *Lactobacillaceae* that represent the most abundant families found in the gut environment and have been associated with the maintenance of gut health. The obtained results indicate that administration of pomegranate and green tea extracts through drinking water is able to ameliorate the total blood antioxidant activity and modulate gut intestinal health.

## ANIMAL BREEDING AND GENOMICS – GENETIC DIVERSITY

## O038

### Genome-wide association study and functional analysis of carcass and meat quality traits in double-muscling Piemontese cattle

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Meat quality traits are important drivers of consumer acceptance and purchase intention. Recently, Piemontese meat was awarded the EU Protected Geographical Indication (PGI) status 'Vitelloni Piemontesi della coscia' which has increased the interest in improving the meat quality attributes for this breed. Therefore, aim of this study was to investigate the genomic regions and biological pathways controlling the variation in carcass and meat quality traits in double-muscling Piemontese cattle breed. We carried out genome-wide associations (GWAS) and pathway enrichment analyses for carcass traits (age at slaughtering [AS], carcass weight [CW], carcass daily gain [CDG], conformation score [EUS] and ribeye muscle area [REMA]) and meat quality traits (pH, Warner-Bratzler shear force [WBSF], purge loss [PL], cooking loss [CL] and colour parameters [lightness, L\*; redness, a\*; yellowness, b\*; chroma, C\*; hue, H\*]) in a cohort of 1166 Piemontese young bulls. Animals were slaughtered at 539 days on average. Genotype data from the 'GeneSeek Genomic Profiler Bovine LD' array was used. A single marker regression model was applied for GWAS using the GenABEL R package and the GRAMMAR-GC approach. The functional enrichment analysis was conducted using the Cytoscape plugin ClueGo to identify significantly overrepresented pathways and ontologies (right-sided hypergeometric test with false discovery rate correction). In total,

we identified 37 significant single nucleotide polymorphisms (SNPs), which were associated with 12 traits ( $p < 5 \times 10^{-5}$ ). Notably, 14 SNPs associated with CW, CDG and AS were detected in the region at ~38.57–38.94 Mb on *Bos taurus* autosome (BTA) 6 and mapped within four genes, i.e. Leucine Aminopeptidase 3 (*LAP3*), Family with Sequence Similarity 184 Member B (*FAM184B*), Non-SMC Condensin I Complex Subunit G (*NCAPG*) and Ligand-Dependent Nuclear Receptor Corepressor-Like (*LCORL*). Significantly enriched GO terms and KEGG pathways were found for four meat quality parameters, i.e. a\*, b\*, C\* and CL, and for two carcass traits, i.e. CW and EUS. In particular, pathways related to transmembrane transport (i.e. oxygen, calcium, ion and cation) were overrepresented for meat colour parameters. The information acquired might be useful for genomic selection programmes aimed at improving beef production and meat quality in the Piemontese breed.

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## O039

### Genomic adaptation of local cattle breeds in the alpine massif

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Understanding adaptive ability of livestock is a key factor in the context of global climate change and become a crucial focus in conservation and management for a sustainable farming in a changing environment. One way to better understand adaptation abilities is to identify genes underlying adaptation phenotypes. This goal can be achieved by genetically characterising livestock species and detecting footprints of selection in the animal genome. The recent availability of genome-wide SNP panels allows providing background information concerning genome structure in domestic animals, opening new perspectives to livestock genetics.

In order to investigate the genetic regions with a potential adaptive role, we investigate 24 cattle breeds, (high productive specialised breeds and several autochthonous populations) reared in six different neighbouring nations from East to West Alpine Massif. Several analyses have been performed to detect footprints of selection and genomic regions associated with climate variables. More precisely, using breed GPS coordinates, 4 climatic variables (annual mean temperature, annual precipitation, annual mean radiation, and annual mean moisture index) were extracted from the Climond database. In order to identify footprints of selection, a whole genome scan for adaptive differentiation were performed using Bovine 50K SNP chip genotyping data with the XtX model implemented in the BAYPASS software. In addition, across-population whole genome scans for association with the population-specific climatic variables were performed using the AUX model. Footprints of selection were detected on BTA6 and BTA18 pointing out several candidate genes (i.e. *LCORL*, *PDGFRA*, *KDR* and *SPG7*); moreover different genomic regions (on BTA 6, 10, 19 and 20) were associated with annual mean radiation. Ongoing analyses will specify candidate regions and genes involved in local adaptation in the Alpine massif.

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## O040

### The Italian cattle breeds in a worldwide context for a genome-wide diversity study

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The availability of genome-wide single nucleotide polymorphism (SNP) data has made it possible to provide a detailed assessment of the genetic relationship among different cattle populations across the world. These comprehensive studies, however, did not include several European populations, such as the Italian breeds. With a total of 3283 individuals, representing 205 different domesticated bovid breeds, we have now assembled the largest and most divergent dataset to place the Italian breeds into a global context and to perform a worldwide study on cattle using genome-wide SNPs. To understand these aspects, in this preliminary step,