

and humidity (H) were continuously recorded and analyzed, over the lactation (July to January). Data were analyzed, by a non-parametric regression, to check for common behavior patterns and then by the following linear model: (HA, A, S, E, R) = hour + month + hour * month; which allows, for each independent variable, the reconstruction of the daily evolution as a function of the month. A strong pattern was found for each variable, with a trend to progressive variation, from the hottest to the coldest month. In July (T max >40 °C, mean 25.8 °C, 67.2 <THI <78.18), animals concentrated their activity (early morning and late afternoon). At 5 am HA was 4.27 vs. 17.34 in January and July respectively and at 5 pm 11.41 vs. 25.95 min/hour ($p < .01$). In winter range of activity was wider and trend flatter. Nevertheless, total movement (HA+A) was the same in the two opposite months (25.65 ± 0.24 vs. 25.67 ± 0.19 min/hour in January and July). This may be due to the intensity of the HA peaks. Rumination was higher ($p < .01$) in hot season (9.46 ± 0.13 min/hour in July), while eating had the same trend as moving. Probably when eating increases also high activity does, being animals involved in movement along with the manger and in competition fighting for position. In conclusion, buffalo seems sensitive to high temperature even though it is supposed more resistant than a cow, showing a modified behavioral pattern in comparison to mild (autumn) or cold periods. In particular, rumination increased and eating and movement concentrated. The cold period seems associated to more regular and distributed behavioral pattern letting suppose a certain comfort compared to hot, but we must consider that no critical temperatures were reached during observations (T min -7 °C, average 6.4 °C, in January). In mild season (data not reported) values were intermediate between the extremes.

O129

Precision livestock farming and beekeeping: development and testing of a prototypal smart hive

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With the exponential growth of the world population, there will be an increase in demand for products of animal and plant origin that will have to be met in a sustainable way due to the limited availability of land and resources. One of the solutions can be represented by the use of innovative monitoring and control approaches on production systems. The affirmation of these new technologies has given rise to precision agriculture and livestock farming, which is a way of managing agricultural activity by

monitoring and recording automatic measurements in real-time. Precision beekeeping is the monitoring of the hive to provide useful information to beekeepers such as the in-hive temperature (IHT) and humidity (IHH), hive weight (HW), and flight activity (FA). The aim of this work was the experimental validation of a prototypal precision beekeeping hive, named SMART HIVE_1.0, which allows the monitoring of all these processes already listed. The temperature and humidity control system was validated with a comparison with reference measurements by a thermo-hygrometer; a correction model was developed that allows inferring the true IHT and IHH data through equations that had an r^2 not less than 0.99. As far as the HW, some tests were carried out with increasing ballasts in the range 0.1 g–14.0 kg. It resulted that the electronic scale gave a 13% underestimated measure of the true HW, with a mean deviation of -3 kg. An HW correction model was thus obtained with r^2 equal to 0.9998. The ongoing and outgoing bee flight accuracy was assessed by using a manual bee simulator and by using manual counting of bee flight recorded through a webcam. Both methods allowed us to assess that the flight sensor was unreliable being affected by a high asymmetrical bias unevenly distributed within the range of the flight activity video recorded that make impossible to find a simple correction model to be implemented at the hive and/or server level. Further efforts are needed to get a reliable flight counter that allows for a deep evaluation of the in/out balance of foraging bees, information that can make aware the beekeepers of some possible undesired loss of honey bees during the production season.

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O130

An alternative method to identify CSD alleles of the honey bees based on NGS data

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Focus of this study is the allelic variability of the complementary sex determination (CSD) gene, which regulates sex determination in honey bees: males are hemizygous for CSD, while females are heterozygous. Diploid males develop from fertilized eggs, which are homozygous for CSD; diploid males are eaten by worker bees in the larval stage. Therefore, there is a strong advantage for heterozygotes leading to a high number of distinct *csd* alleles. A hypervariable region (HVR), located in exons 6 and 7, is responsible for *csd* allelic variability. One hundred twenty-five worker colonies were sampled within summer 2017 and summer 2018

in twelve different Italian regions: Abruzzo, Emilia Romagna, Liguria, Lombardy, Marche, Piedmont, Sicily, Trentino, Tuscany, Apulia, Umbria and Veneto. In each region, beekeepers were chosen among those belonging to the 'Associazione Italiana Allevatori Api Regine (AIAAR)' and the 'Albo Nazionale Allevatori Api Italiane' associations. Genomes of the 125 worker colonies were sequenced through Illumina NextSeq with a 150 bp paired-end module. Sequences were mapped to the HAv3.1 *Apis mellifera* genome and the HVR of the CSD gene was manually inspected with the Integrative Genomics Viewer. The nucleotide sequences of both strands of this region were successfully reconstructed for 65 samples, and each strand was translated to obtain protein sequences for each allele of the heterozygous sequenced individuals. The resulting 130 sequences include variants of the HVR region which have not been described in literature, yet, contributing to characterize CSD allelic variability in Italian honey bee colonies.

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O131

Investigating the effects of diets enriched in PUFA and antioxidants on the gene expression networks and intramuscular fatty acid composition in porcine *Longissimus thoracis et lumborum* muscle

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Western diets are rich in n-6 and deficient in n-3 polyunsaturated fatty acids (PUFAs), resulting in a high n-6/n-3 ratio. Decreasing the n-6/n-3 ratio of meat products with n-3 feeding supplementations in livestock has been suggested as a viable strategy to increase meat nutritional value, but it also rises meat susceptibility to lipid oxidation. To date, novel antioxidants are available, and some of them can be obtained from by-products discarded by other food industries, such as grape skins. This study aimed at investigating in medium-heavy pigs the effect of high linolenic acid diets supplemented with synthetic or natural antioxidants on muscle fatty acid (FA) composition, and gene expression of *Longissimus thoracis et lumborum* (LTL) muscle. For this study, 48 growing-finishing pigs, balanced for sex and weight, were

assigned to 4 isoenergetic dietary treatments (12 pigs per treatment): barley, soya bean, (control, C); C with 5% linseed (L); L supplemented with vitamin E and selenium; L supplemented with grape skin and oregano extracts rich in polyphenols (L + natural antioxidants, LNA). Total RNA was extracted from LTL muscle and analysed with RNA sequencing. After sequence alignment, 10,169 genes were found expressed in the 48 samples and submitted for Weighted Gene Co-expression Network Analysis to WGCNA package in the R environment. The samples belonging to each treatment were analysed separately and associated with the amounts of FAs found in their LTL muscle. The linseed dietary inclusion significantly reduced the n-6/n-3 ratio and increased the n-3 PUFAs in LTL ($p < .05$). These changes were also visible at the transcriptome level as the LNA diet caused great changes in the gene expression networks when compared to the gene co-expression structure identified in the LTL muscle of C pigs. In particular, the LNA supplementation stimulated the expression of genes involved in Type I interferon signaling pathway (Bonferroni $p = 4.29E-10$) and Innate immunity (Bonferroni $p = 1.17E-5$). This result agrees with the literature, which suggests that diets rich in n-3 and polyphenols may stimulate host immunity. On the other hand, the gene networks positively associated with the n-6/n-3 ratio in the C group were related to mitochondrial activity and cell energy metabolism. The obtained results support the evidence that supplementing pig diets with extruded linseed and polyphenols can positively influence the nutritional quality of meat products.

O132

Weighted Gene Co-expression Network Analysis identifies the main gene networks and biological pathways associated to chicken *Pectoralis major* myopathies

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High-throughput technologies and bioinformatics analysis represent both major tools to investigate gene expression patterns associated with pathological conditions in animal production. Growth-related myopathies affecting modern chickens (White Striping – WS; Wooden Breast – WB) have been deeply investigated in the past decade. Nevertheless, their precise etiology remains unclear. The present work aims at exploring the molecular mechanisms potentially involved in the onset of WS and WB, by identifying clusters of co-expressed genes associated with phenotypes that in our previous work resulted highly related to