variation in motility and progressive motility recorded among semen samples. The present data are considered preliminary results and further studies are required to confirm the different semen freezability found between and within the breed. The functional and biochemical characterisation of semen samples with extreme (highest vs. lowest) sensitivity to cryopreservation is of undeniable interest to identify biochemical markers and will be investigated.

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P063

Selective hunting plans as source of reproductive data in wild boar of the National Park of Sibillini Mountains

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The rapid increase of wild boar (*Sus scrofa*) in Italian Apennines and in many European areas is due to its generalist behaviour that has led to wide expansion causing damage to agriculture activities. Therefore, the Parks, in order to reduce density of the wild boar population, started monitoring and harvest plans, so since 1998, the Sibillini Mountains Park has implemented its wild boar management plan. Data, obtained from forms filled out by selective hunters, regarding 1821 wild boars hunted from 2015 to 2017, have been available. To evaluate the effect of year, season and age class (I and II) data on 557 wild females (their uteri were cut open to evaluate pregnancy rate and litter size) has been statistically analysed with JMP 10 software. The descriptive statistical analysis on hunted females showed: average age 26.11 ± 10.77 months, mean weight 63.11 ± 15.96 kg, mean foetus number 4.42 ± 1.25. The ANOVA considering year effect (2015, 2016, 2017) did not show significant differences for age, weight and foetus number during the three-year period. The effect of season showed significant differences ($p<.05$) for age and weight; wild females hunted in Winter were older than those hunted in Spring (27.07 vs. 23.77 months). Moreover, females hunted in Autumn reached a higher weight (68.12 kg) than the ones hunted in other seasons (Winter 62.81 kg, Spring 61.78 kg, Summer 61.68 kg). Age class II females showed heavier weight ($p<.05$) than those of class I (73.28 vs. 56.06 kg). In the three-year period, overall reproductive data on 550 wild females showed the following physiological status: 70.54% no pregnancy vs. 29.46% pregnancy. Four hundred and twenty-six out of 557 females, 22.76% were lactating vs. 77.23% no lactating. Sows hunted in Winter and Spring showed a higher ($p<.05$) pregnancy rate (62.35% and 33.33%, respectively) than those hunted in Summer and Autumn (0.62% and 3.70%, respectively). The pregnancy status was confirmed by the trend of hunted lactating females, showing a higher percentage of lactating sows in Spring (72.16%) and Summer (18.56%) than in Autumn and Winter (5.15% and 4.12%, respectively). The highest percentage of pregnant females was observed in age class II (57.41%). The analysis of data in the three-year period shows age, weight and litter size homogeneously distributed, while reproductive performance confirms the typical seasonal reproductive efficiency of wild boar with the main rutting period in Autumn-Winter seasons and lactations mainly in Spring.

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P064

In vitro digestibility protocol applied to BARF diets: pros and cons

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This study evaluated the *in vitro* dry matter and crude protein digestibility in natural pet food, also termed BARF diets. For this purpose, eight samples of dogs BARF diets and two commercial dog food, used as reference materials, were analysed and tested in the assay. The BARF diets were based on raw beef and poultry by-products, while the commercial pet food was one dry and one wet. All samples were analysed for dry matter (DM), crude protein (CP), ether extract (EE) and ash content. Furthermore, using an *in vitro* assay, simulating gastric and small intestinal digestion, both dry matter digestibility (IVD-DM) and crude protein digestibility (IVD-CP) have been measured. Briefly, after the pepsin (39 °C for 6 h) and pancreatin (39 °C for 18 h) incubation in the IVD-DM and IVD-CP test, the undigested residues were dried at 105 °C overnight. The IVD-DM was calculated from the difference between dry matter in the sample and the undigested residue. The IVD-CP was calculated from the difference between the nitrogen content in the original sample and the nitrogen content undigested residue measured by the Kjeldahl method. All BARF diets and wet pet food were characterised by high moisture content (DM: 380 g·kg^{-1}), while in the case of dry pet food DM content was 920 g·kg^{-1}. On average, BARF diets and commercial diets were characterised by the following values, on dry matter basis: CP, 368 g·kg^{-1}; EE, 442 g·kg^{-1}; ash, 52 g·kg^{-1}. All BARF samples and reference materials were characterised by high digestibility

values. Both IVD-DM and IVD-CP reached values higher than 80%. Of note, in the case of IVD-DM, a substantial variability within samples has been observed (SD: ±5.5). While in the case of IVD-CP value observed presented less variability (SD: ±1.4). In light of these results, it can be concluded that proposed IDV method has some potential in determining protein digestibility in BARF diets, while the assay seems to be limited for measuring DM digestibility, as indicated by the large SD recorded in the BARF diets. The reason for this is unclear and merit further investigations.

P065

Lactating ewes responded to a glucose tolerance test with higher glucose and insulin concentrations both in early and in mid-lactation compared to lactating goats

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In a recent study, we observed lower milk persistency and higher body fat accumulation in dairy ewes compared to dairy goats, especially during mid-lactation. Since these species might have a different regulation of glucose metabolism, in the same experiment we carried out glucose tolerance tests (GTT) to test this hypothesis.

After parturition, 30 Sarda ewes and 26 Saanen goats were fed a high-starch diet (HS: 20.4% starch; DM basis), whereas starting at 92 ± 11 days in milk (DIM) each species group was divided into two dietary subgroups, receiving HS or low starch diets (LS; 7.8% starch; DM basis). LS diet was obtained by replacing most of the corn meal and all of the barley meal of HS diet with soybean hulls, very rich in highly digestible fibre. At 50 and 148 DIM, GTT were performed in 18 ewes and 18 goats. One millilitre of a 50% glucose solution per kg of BW was injected into the jugular vein of each animal. Blood samples were collected before (−15 min (min)) and after (+5, +10, +15, +30, +45, +90 and +180 min) glucose injection. Data were analysed by the PROC MIXED procedure of SAS with repeated measurements.

The dietary starch level applied in mid-lactation did not affect any of the results. At 50 DIM, basal plasma glucose (p=.10) and insulin concentrations (p=.08) were numerically higher in ewes than in goats. After glucose infusion, glucose (206.3 vs. 177.8 mg/dL ±12.9, p=.048) and insulin (0.58 vs. 0.32 µg/L ± 0.10, p=.027) concentrations were significantly higher in ewes than in goats. At 148 DIM, basal plasma glucose (62.2 vs. 51.6 mg/dL ±3.62, p=.011) and insulin (0.34 vs. 0.13 µg/L ± 0.09, p=.036) concentration were significantly higher in ewes than in goats. After glucose infusion, glucose (p=.06) and insulin (p=.07) concentrations were numerically greatest in ewes. The area under the glucose concentration curve, fractional glucose turnover rate and half-time were not affected by species or diet, in both stages of lactation. Quantitative Insulin Sensitivity Check Index (QUICKI) and Revised QUICKI were higher in goats than in ewes in both stages of lactation, while the Homeostasis Model Assessment (HOMA) was highest in ewes. In conclusion, the highest plasma glucose, insulin and HOMA observed in ewes suggested the presence of an insulin resistance status, which was more marked in mid than early lactation and which can be the cause of greatest body fat deposition and lowest milk yield persistency observed in this species.

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Comparison among four different bacterial DNA extraction protocols for analysing milk metagenomics

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Bovine udder is colonised by a huge number of microorganisms that constitute the intramammary ecosystem, with a specific role in modulating not only the udder homeostasis and mastitis susceptibility but also the quality of the dairy products. Therefore, information on milk microbiota composition will facilitate the dairy industry in the production of safe and high-quality products. However, generating high-quality bacterial DNA could be critical.

In the present study, bacterial DNA from healthy milk samples was isolated by four different protocols to evaluate the effect of the extraction procedures on milk microbiota composition. For the characterisation of the milk microbiota by 16S deep sequencing, 500 mL of bulk tank milk samples were aseptically collected from three different farms and bacterial DNA was extracted by using an internal laboratory protocol and three commercial kits. Bacterial DNA was then amplified using the primers for the V3–V4 hypervariable regions and sequenced in one MiSeq (Illumina)