

parameters between groups, and before and after CR in OB, parametric or non-parametric tests were used as appropriate. Differences were considered significant when  $p < 0.05$ . CR resulted in WL for all OB, however none reached the IW. Median (range) BW and BCS were 6 (4.9–10.3) kg and 8/9 (7/9–9/9) at T1, and 5 (4.7–9.2;  $p < 0.01$ ) kg and 7.5/9 (6/9–9/9) at T2, respectively. Overall, an average WL of 9.2 (4.1–14.3) % of the starting BW was recorded during WL period. TRG were higher in OB vs CTRL, but within the reference range [87 (59–407) vs 57 (29–159) mg/dl, respectively;  $p < 0.01$ ]; insulin tended to be higher in OB vs CTRL [38 (17.2–110) vs 21 (4.2–68) UIU/mL, respectively;  $p = 0.060$ ]. On the contrary, SAA was lower in OB vs CTRL [2.0 (1–5) vs 8.5 (1–15)  $\mu\text{g/mL}$ , respectively;  $p < 0.05$ ], while CH, HP and IGF-1 did not differ. The TRG significantly decreased in OB after CR [T1: 87 (59–407) vs T2: 61 (38–164) mg/dl;  $p < 0.05$ ], while insulin, IGF-1, SAA, HP and CH remained unchanged. Dyslipidemia is common in obese cats, but it seems to be reversible after a few months of CR. SAA is known to be positively correlated with obesity in humans; however, in cats, it seems to have a great individual variability and it was previously reported to remain unchanged after a WL period. The present results confirm that obesity can result in higher serum insulin in cats and that a few months of CR is effective in achieving a safe and successful WL. However, metabolic and inflammatory status of obese cats needs to be further investigated.

## O12

### Effects of oral supplementation with coconut oil on fecal metabolome of healthy dogs

Carlo Pinna, Carla Giuditta Vecchiato, Costanza Delsante, Federica Sportelli, Paola Parazza, Massimo Dall'olio and Giacomo Biagi

*Dipartimento di Scienze Mediche Veterinarie, Università di Bologna, Bologna, Italy*

Based on studies on digestion and absorption of fats, medium-chain triglycerides (MCT; from C6:0 to C12:0) can be rapidly absorbed through enterocytes by passing the lymphatics. Therefore, MCT appear as an interesting energy source to improve the absorption of fats, fat-soluble vitamins, and essential fatty acids, which might be impaired in common canine gastrointestinal disorders, such as chronic enteropathies (CE). Virgin coconut oil (VCO) is the main vegetable fat rich in MCT, and it has shown antimicrobial properties when supplemented to the diet of piglets. To date, effects on intestinal microbiota induced by VCO have not been tested in healthy dogs. This study aimed to evaluate the effects of oral supplementation with VCO on fecal metabolome and fatty acids excretion in healthy dogs. Twelve healthy adult dogs, privately owned, were fed a commercial dry diet (CP 23.5%; EE 17.0%; CF 1.71%; ash 6.18%, as fed) for 30 d

and later received, for further 30 d, the same diet supplemented with VCO at 10% of ME. Fecal samples were collected at the end of each treatment and analyzed for moisture, pH, bacterial metabolites, and fatty acids. Data were tested for normality and analyzed through the Wilcoxon matched-pairs signed rank test or the paired  $t$ -test. Differences were considered statistically significant for  $p < 0.05$ .

The owners did not report food refusal problems when VCO was added, while other studies reported a worsening in palatability when MCT were added at 22–25% of ME. Supplementation with VCO led to an increase in fecal ammonia (+53%;  $p = 0.012$ ) and C12:0 (+535%;  $p = 0.009$ ) excretion, while C14:0 tended to be higher (+59%;  $p = 0.056$ ). C18:3n6 tended to decrease (–18.3%;  $p = 0.052$ ), while total medium-chain fatty acids (MCFA) were higher (+109%;  $p = 0.018$ ) in dogs receiving VCO. Fecal moisture, fecal fat content, pH, and volatile fatty acids were not affected by VCO. Coconut oil induced changes in fecal fatty acids excretion but poorly modulated the fecal bacterial metabolome. Data from this study showed that MCFA are not completely absorbed by the intestinal mucosa of healthy dogs and are in agreement with our previous study in which MCFA absorption in CE dogs was impaired. Further investigations are needed to understand the impact of oral supplementation with VCO on canine fecal microbiota and metabolome.

## O286

### Selection signatures in Italian hunting dogs

Paola Crepaldi<sup>a</sup>, Arianna Bionda<sup>a</sup>, Matteo Cortellari<sup>a</sup>, Vincenzo Lopreiato<sup>b</sup> and Luigi Liotta<sup>b</sup>

*<sup>a</sup>Dipartimento di Scienze Agrarie e Ambientali, Produzione, Territorio, Agroenergia, DISAA, University of Milan, Milano, Italy*

*<sup>b</sup>Department of Veterinary Sciences, University of Messina, Messina, Italy*

Dogs were first domesticated to assist humans in the hunt. As hunting techniques evolved, so did dogs, which became more and more specialized in different activities. Hound dogs (HD) were the first to be selectively bred to pursue the prey and bring it down, working in packs but without any human assistance. Scent hounds track the quarry using their keen sense of smell and come in a variety of sizes, according to the prey they follow and the terrain they have to deal with, whereas sighthounds mainly rely on their eyes and then chase the prey thanks to their impressive speed. Gun dogs (GD), instead, include pointing, flushing, and retrieving dogs, all of which work in partnership with hunters using rifles or shotguns.

The present study aims to investigate the genomic differences between Italian GD and HD. 60 GD (Bracco Italiano, Lagotto Romagnolo, and Spinone Italiano) and 49 HD (Segugio Italiano

a pelo forte and raso, and Cirneco dell'Etna) were genotyped with 230K SNPChip. After quality control, exclusion of relatives, and sample size reduction (max 12/breed), a total of 36 GD, 36 HD, and 120836 SNPs were retained. Multidimensional scaling (MDS) and admixture analyses were performed. GD and HD were compared using Wright's fixation index ( $F_{ST}$ ) and single-SNP cross-population extended haplotype homozygosity (XPEHH). The MDS plot showed a clear separation between the two groups and the single breeds, with the exception of the overlapping of the two Segugio Italiano. Similar results were found by the admixture analysis.

The SNPs in the top 1% of the distributions of both  $F_{ST}$  ( $>0.33$ ) and XPEHH ( $>2.79$ ) were selected and mapped on CanFam3.1, leading to the detection of 32 genes. Among these, *RSPO2* and *USH2A* are known to be responsible, respectively, for the presence of furnishing and the ticked and roan coat patterns in dogs, which are traits mainly present in GD breeds included in this study. Other 7 genes are related to dog domestication and behavioural traits, mainly aggressivity. Moreover, we also identified genes associated with hearing, vision, and sense of smell, which might have been differently selected in GD and HD for specific hunting activities.

To the best of our knowledge, this is the first study investigating the genomic differences between Italian HD and GD breeds. The genes we identified are involved in pathways related to morphological and functional phenotypes contributing to making these dogs specialized in the work for which they were selected.

## O490

### Influence of grain-free and cereal-based diets on postprandial glycaemic response

Alessandro Vastolo, Alessio Ruggiero, Serena Calabrò, Dieu Donnè Kiatti and Monica Isabella Cutrignelli<sup>a</sup>

*Department of Veterinary Medicine and Animal Production, University of Napoli Federico II, Napoli, Italy*

Recently, pet-food companies have been marketing several products such as grain-free diet to meet specific nutritional requirement. The study aimed to evaluate the administration effect of two commercial kibble diets (grain free GF vs. cereal-based CB) on postprandial glycaemic and insulin response in healthy dogs. Fifteen adult neutered healthy dogs (mean age  $5.00 \pm 1.30$  years; body weight  $21.1 \pm 5.36$  kg; and BCS  $4.20 \pm 0.86$  on 5 points scale) were homogeneously divided into two groups, alternatively fed the two diets for 5 weeks. The diets were formulated with chicken as main protein source and different carbohydrate sources. The metabolizable energy (3990 vs. 3991 kcal/kg a.f.) and protein (31.6 vs. 31.7 % a.f.) of GF and CB diets were similar. Blood samples were collected ( $\sim 10$  mL) at recruitment and at the end of each

nutritional phase. To measure dogs' post-prandial glycaemic and insulinemic responses, blood samples were collected fasting (baseline sample, time 0) and 120, 180, 240, and 360 min after the meal administration.

Regarding the biochemical profile, when the dogs fed GF diet reported higher ( $p < 0.05$ ) level of ALT than CB. On the contrary, CB diet showed higher ( $p < 0.01$ ) level of fructosamine compared to GF. Similarly, the cereal-based diet had the highest ( $p < 0.05$ ) levels of lipase. Concerning the glycaemic response, no significant effect of the diet was observed, with the exception of mean glucose concentration, which resulted higher ( $p < 0.01$ ) when dogs fed CB diet compared to GF diet (89.3 vs. 82.8 mg/dl). Otherwise, several differences were reported for insulin response. Indeed, cereal-based diet had higher ( $p < 0.01$ ) level of insulin mean concentration (11.9 vs. 9.44 mIU/l) and area under the curve (3897 vs. 3674). On the contrary, when dogs fed GF diet showed higher ( $p < 0.01$ ) insulin peak (18.1 vs. 13.1 mIU/l), which need more than 1 h to be reached compared to CB diet. Additionally, this last resulted in lower ( $p < 0.01$ ) minimum point.

The high presence of protein of animal origin and different starch sources in GF diet can modulate the insulin response. Diets based on different grains (CB) is rapidly absorbed into the intestine. Nevertheless, cereal-based diet is rich in dietary fibre positively affecting intestinal fermentation. This could have implications in populations of performance or working dogs as well as therapeutic impacts on the management of conditions such as diabetes mellitus.

## O301

### English and American Golden retrievers differentiation: from sperm morphometry to genomic data

Emanuele D'anza<sup>a</sup>, Arianna Bionda<sup>b</sup>, Luigi Liotta<sup>b</sup>, Mauro Ronchese<sup>b</sup>, Matteo Cortellari<sup>c</sup>, Sara Albarella<sup>a</sup>, Francesca Ciotola<sup>a</sup> and Paola Crepaldi<sup>c</sup>

<sup>a</sup>*Dipartimento di Medicina Veterinaria e Produzioni Animali, Università Federico II di Napoli, Napoli, Italy*

<sup>b</sup>*AMBULATORIO VETERINARIO REPROVETPOINT, Cordenons, Italy*

<sup>c</sup>*Dipartimento di Scienze Agrarie e Ambientali, Produzione, Territorio, Agroenergia (DiSAA), Università di Milano, Milano, Italy*

The identification of genomic and semen-related differences among dog breeds or varieties is pivotal for the improvement of the reproductive management of livestock species. Given their peculiar population structure, dogs represent an excellent animal model for this purpose. In particular, the Golden Retriever has to date only one British standard officially recognised by the FCI, but