

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^a

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 glycemic and insulin response in healthy dogs. Fifteen adult neutered healthy dogs (mean age 5.00 ± 1.30 years; body weight 21.1 ± 5.36 kg; and BCS 4.20 ± 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 (~ 10 mL) at recruitment and at the end of each

nutritional phase. To measure dogs' post-prandial glycemic 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 glycemic 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^a, Arianna Bionda^b, Luigi Liotta^b, Mauro Ronchese^b, Matteo Cortellari^c, Sara Albarella^a, Francesca Ciotola^a and Paola Crepaldi^c

^a*Dipartimento di Medicina Veterinaria e Produzioni Animali, Università Federico II di Napoli, Napoli, Italy*

^b*AMBULATORIO VETERINARIO REPROVETPOINT, Cordenons, Italy*

^c*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

there is also another morphotype, commonly called 'American', which presents differences in coat colour and body size and structure. Recent evidence on differences in sperm quality parameters in relation to the colour variants of the Arctic fox prompted us to investigate the possible differences in terms of semen morphology and genomics in *Canis Familiaris*. 20 Golden Retrievers, 10 English aged 5.4 ± 3.5 and 10 American aged between 2.8 ± 2.2 were enrolled for this study. Semen was collected by manual stimulation after 3 days of abstinence, the second fraction of the ejaculate were used for quantitative and qualitative analysis. Sperm counts were performed with the Makler Counting Chamber. 100 spermatozoa, each ejaculate, were observed in bright field under a Nikon Eclipse 80i microscope (100 \times), captured with a digital camera (Nikon DS-Ri1) and analysed with the software SCA[®] CASA System and Nis Elements Imaging Software 4.00.02 (Nikon, Tokyo, Japan) for the measurement of head area, perimeter, max and minimum feret. After appropriate quality control, 230K SNPchip data were used to assess the genomic differences between American and English dogs through population structure and selection signature (FST, XP-EHH, and ROH) analyses. Fitting semen morphologic parameters with a mixed model, differences between the varieties were found for minimum feret, perimeter, and roughness, with higher values in English dogs. American and English Golden retrievers were well distinguishable also from a genomic perspective. Eleven genes were identified as the most differentiating both by FST and XP-EHH analyses. Moreover, the two groups presented very different homozygosity scores for 109 genes. Some of these genes play an important role in spermatocyte development and functionality, possibly accounting for the observed differences in sperm morphology. In addition, several of them have been previously related to dog behaviour, size, and coat colour.

O150

Resistance versus susceptibility to *Leishmania*: genetic differences in a population of English Setter dogs

Riccardo Moretti^a, Stefania Chessa^a, Margherita Profiti^a, Annamaria Uva^b, Alberto Tarducci^a, Andrea Zatelli^b and Paola Sacchi^a

^aDipartimento di Scienze Veterinarie, University of Turin, Turin, Italy

^bDipartimento di Medicina Veterinaria, University of Bari, Bari, Italy

Leishmaniosis is a parasitic disease caused by kinetoplastid protozoa belonging to the genus *Leishmania*, which is transmitted to vertebrates via infected female phlebotomine sand flies. The main causative agent of canine leishmaniasis in Europe is *L. infantum*, which is highly diffused in the Mediterranean area and causes a

spectrum of clinical signs that varies greatly from asymptomatic/mild to a very severe disease in dogs. The natural susceptibility or resistance to *Leishmania* infection is the result of complex interactions between the parasite and the host immune system. These interactions are due to the differences among individuals, and their genetic asset. Various genetic mutations in different breeds have been suggested as potential genetic markers to be used in the study of *L. infantum* infection resistance/susceptibility. Aim of this study was to evaluate the genotype of 4 SNPs (CBD1 gene), described as associated with resistance (rs852670798 and rs853079810) or susceptibility (rs850814192 and rs851268228) to *L. infantum* infection, in a cohort of 12 English Setter dogs, raised sharing the same habitat (private hunting dogs kept in outdoor kennel) and same repellent treatment for leishmaniasis vector (phlebotomine sand flies), but with different responses to this infection. The dogs in this study were 10 males and 2 females, age ranging between 1 to 13 years (mean age ~6 years). Four age classes (with three dog each) were defined and identified as I to IV: age ≤ 2 years old, 2 < age ≤ 4 years old, 4 < age < 8 years old, and age ≥ 8 years old. Of these dogs, sampled during spring 2021, 8 animals were positive to the ELISA test for *L. infantum* infection, while 4 animals were negative. A preliminary analysis of the obtained data showed no correlation between the different haplotypes found in the cohort and the ELISA test result (p -value = 0.49). Nevertheless, as suspected, a quadratic association between the age of the animal and the ELISA test result was found (R^2 of the model = 35.2%, p -value = 0.05). A follow-up on the cohort will be performed and the animals will be re-evaluated in the following infectious seasons to separate the effect of the age from the genetic one. Furthermore, the samples were genotyped using a high density SNP chip and we are testing different SNP-based approaches to investigate other possible genetic effects on resistance/susceptibility of *L. infantum* infection.

O245

Use of lactic acid bacteria in forage production of Alto Sannio area

Costantino Caturano, Patrizio Tremonte, Silvia Jane Lombardi, Antonella Fatica, Elena Sorrentino and Elisabetta Salimei

Di AAA, University of Molise, Campobasso, Italy

The aim of this study was to validate biotechnological innovations capable of enhancing the relationship between forages used in dairy cattle farming and sustainability and biodiversity of Alto Sannio Area (BN). For this purpose, a microbial culture appropriately isolated and selected from the natural bio-reserves Area was used in hay making. Honeybee foragers (*Apis mellifera ligustica* S.), as indices of environmental quality, were used for the isolation of lactic acid bacteria. The isolated strains were