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×), 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

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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

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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