

Book of Abstracts of the 1st EAAP Companion Animals Workshop



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Milan - Italy
14-16 May, 2025

Welcome to the 1st EAAP Companion Animals Workshop in Milan, 14 – 16 May 2025

On behalf of the Organizing Committee, it is our honor and pleasure to welcome you to the 1st EAAP Companion Animals Workshop, scheduled for May 14th to 16th, 2025, in the vibrant city of Milan, Italy. This event presents a unique opportunity to bring together scientists, researchers, and professionals from across Europe and beyond, focusing on the latest advancements and future directions in companion animal science.

The workshop will offer a comprehensive scientific program covering critical topics. Discussions will center on recent breakthroughs in pet genetics and breeding, particularly on how genomics can improve health, longevity, and welfare. The role of nutrition will also be explored, with insights into how dietary strategies and nutrigenomics can optimize pet health and performance. Additionally, the behavior and welfare of companion animals will be a major focus, addressing both scientific developments and ethical considerations.

The One Health approach will also be a key theme, emphasizing the interconnection between human, animal, and environmental health. Furthermore, the public's perception of companion animals and their evolving role in society will be critically examined, as these aspects are increasingly shaping policies, research, and market trends.

Milan, with its dynamic and international atmosphere, offers an inspiring venue for this meeting. Participants will not only engage in a stimulating scientific program but will also have the opportunity to explore the city's rich cultural heritage, world-class cuisine, and vibrant social scene.

We are confident that the 1st EAAP Companion Animals Workshop will be an exciting event, fostering collaboration, knowledge exchange, and innovation. We look forward to welcoming you to Milan for a productive and inspiring experience.

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The European Federation of Animal Science (EAAP)

The main aims of the EAAP are to promote, by means of active co-operation between its members and other relevant international and national organisations, the advancement of scientific research, sustainable development and production systems; experimentation, application and extension; to improve the technical and economic conditions of the livestock sector; to promote the welfare of farm animals and the conservation of the rural environment; to control and optimise the use of natural resources in general and animal genetic resources in particular; to encourage the involvement of young scientists and technicians. More information on the organisation and its activities can be found at www.eaap.org.

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The European Federation of Animal Science (EAAP) has close established links with its sister organizations of American Society of Animal Science (ASAS), American Dairy Science Association (ADSAS), Canadian Society of Animal Science (CSAS) and Asociación Latinoamericana de Producción Animal (ALPA) and is also member of the World Association for Animal Production (WAAP).



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Industry members

EAAP started in 2023 a new initiative to create closer connections between European livestock industries and the animal science network. Therefore, the “EAAP Industry Club” was shaped with the specific aim of bringing together the important industries of the livestock sector with our European Federation of Animal Sciences. All companies dealing with animal production (nutrition, genetic, applied technologies, etc.) are invited to join the “EAAP Industry Club” because industries will have opportunity to increase their visibility, to be actively involved in European animal science activities, and to receive news and services necessary to industries. In addition, through the Club, industries will enlarge their scientific network and will receive specific discounts on sponsoring activities

The industries that already joined the “EAAP Industry club are:



The Club gives:

Visibility • Company name and logo at EAAP website and all relevant documents • Slides with name and logo at Official Events • Priority links with EAAP Socials • Invite, through EAAP dissemination tools and socials, people to events organized by your company • Information disseminated through a brand new Industry Newsletter • Networking • Joining the Study Commissions and Working Groups • Suggest topics to be considered for Annual Meetings Scientific Sessions • Organize Professional Panel through the EAAP platforms • Economic Benefits • One free registration to each Annual Meeting and at every meeting organized by EAAP • Five individual memberships at no cost • Many possible discounts (-30%) to increase company visibility through: EAAP Newsletter, EAAP website, EAAP Annual Meetings and workshops • Support young scientist by sponsoring scholarships named by the company • Co-Organize and sponsor webinars.

Make yourself more visible within the livestock industry via the animal science network!

For more information, please contact eaap@eaap.org.

Scientific programme

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An Ancient DNA perspective on the origins and spread of domestic cats in EuropeC. Ottoni¹¹ *University of Rome Tor Vergata, Department of Biology, Via Cracovia 1, 00133 Rome, Italy*

From wild animals to pest controllers and finally to pets, the evolutionary success of domestic cats is indisputable. However, cats are understudied, especially if compared with other domesticates and their wild relatives. Zooarchaeological and genetic evidence demonstrated that domestic cats originated from the North African and Near Eastern wildcat, *Felis silvestris lybica*. The interaction between humans and cats most likely started 11 thousand years ago in the Neolithic Levant. More recently, ancient mitochondrial DNA evidence suggested that domestic cats spread to Southeast Europe as early as 4,400 BCE, however their dispersal to the rest of Europe is controversial due to the paucity of data. We will present the results of the genetic analyses conducted on 225 cat remains from archaeological sites in Europe and Anatolia, resulting in 70 low-coverage genomes spanning a period of more than ten millennia from the 9th millennium BCE to the 19th century CE. We also generated 17 low- to high-coverage (~0.7- to 18-fold) genomes of present-day and museum wildcats from Italy, Bulgaria and north Africa, regions previously unexplored in terms of wildcat genetic diversity at the genome level. This comprehensive genomic time transect enabled us to evaluate existing hypotheses about the origins and spread of cats in Europe and shed more light on the evolutionary history of wild and domestic cats and their complex interactions with humans across time.

Session 1

Theatre 2

Cats are not small dogs; dogs are not big cats!L. Lyons¹¹ *College of Veterinary Medicine, University of Missouri, Veterinary Medicine & Surgery, E109 Vet Med, 1520 Rollins Street, 65211 Columbia, United States*

Cats and dogs are distinct animals although both are beloved companions and family members. The ancient divergence between canid-like and felid-like carnivores occurred millions of years ago, leading to different physiologies and metabolisms. Cats are obligate carnivores whereas dogs are omnivorous. The domestication process has also been different. Dogs are perhaps the oldest domesticate, initiating when humans were still hunter-gatherers, 10's to 100's of thousands of years ago, while wildcats began the process of domestication only after humans became farmers, some 10,000 years ago. The wild progenitor of the dog is considered extinct, while several wildcat subspecies can still introgress their genetics into domestics, potentially adding new genetic diversity to random bred cat populations. While most breeds developed from region populations of random bred cats, most random bred dogs are a concoction of a variety of breeds. Breed development has also been different. Cats have had less selective pressures as their form and function was and still is as required for a vermin hunter, while dogs were pressured into becoming better hunters for different types of prey or to have different guarding and herding abilities. Cat breeds have developed only since the late 1800's, mainly for aesthetic Mendelian traits but dog breeds have developed over hundreds of years for mainly complex traits that affect behavior and performance. The stud books for cats are more open, thus, crossbreeding and the new founders is an ongoing, leading to more genetic diversity. Hence, less than 50 cat breeds are well defined as compared to hundreds of dog breeds. Cats and dogs also have some similar but also fairly different genetic maladies. Cats have a high degree of renal disease, while dogs are prone to cancer. With mandatory genetic testing, most cat genetic diseases could be eradicated, whereas many genetic maladies are more fixed in dog breeds and would require significant long-term management approaches. Although both cats and dogs have grave concerns for increased brachycephalic conditions, their associated syndromes are fairly different. Thus, breed and health management in cats and dogs need to consider different approaches, since cats are not small dogs.

Dog breed assignment using the ISAG panel of genetic markers and machine learning approachesM. Zorc¹, P. Dovc¹¹ University of Ljubljana, Biotechnical Faculty, Jamnikarjeva 101, 1000 Ljubljana, Slovenia

Dogs exhibit a wide range of genetic diversity, spanning from well-documented purebred populations to mixed-breed dogs with unknown or partially known ancestry. Understanding the genetic background of mixed-breed dogs is crucial for predicting traits related to appearance, behavior, and health. In this study, we explored the potential of machine learning to infer breed composition using a standardized panel of genetic markers. Publicly available genomic data from various dog breeds were analyzed, and classification models including logistic regression, support vector machines, k-nearest neighbors, and neural networks were applied to predict breed identity. Our findings highlight the effectiveness of computational approaches in identifying breed-specific genetic patterns and assigning ancestry with high confidence. This method provides valuable insights for owners of mixed-breed dogs seeking to understand their pets' genetic heritage. Additionally, it contributes to broader applications in veterinary care, breed conservation, and responsible pet ownership by improving breed identification accuracy. The integration of advanced computational tools with genetic data enhances our ability to decode canine ancestry and refine our understanding of breed-related traits.

From Tradition to Recognition: Characterizing the Maltese Hunting Dog (Kelb tal-Kaċċa ta' Malta) in Support of Its PreservationA. Bionda¹, V. Florida², S. Boccuni³, C. Shoemake³, P. Crepaldi¹, G. Attard³, L. Liotta²¹ Milan University, Department of Agricultural and Environmental Sciences, Via Celoria 2, 20133 Milan, Italy,² Messina University, Department of Veterinary Sciences, Viale Palatucci, 98168 Messina, Italy, ³ University of Malta, Department of Rural Sciences and Food Systems, -, 2080 Msida, Malta

The Maltese Hunting Dog (Kelb tal-Kaċċa ta' Malta, KTKM) is deeply rooted in Malta's hunting tradition, with historical records tracing its presence back to the 16th century. Despite the absence of official recognition, this breed has been preserved and selectively maintained over centuries, thanks to the dedication of breeders. This study aimed to characterize the phenotypic and genomic features of 24 KTKM individuals to support their official recognition and conservation. Morphological analyses defined the KTKM as a mesocephalic and mesomorphic breed, characterized by large pendulous ears, a "Braque"-type face, and a short coat with white-patched pheomelanin colouration. Genomic comparisons with 46 dog breeds consistently revealed the KTKM's unique genetic identity and high uniformity, placing it near pointing dogs while highlighting ancient connections with the Maltese Pharaoh Hound. Moreover, despite the small population size and geographic isolation, KTKM displayed relatively low levels of genomic inbreeding. Effective population size was 76, with a trend dropping 12 generations ago. To identify potential introgressed genomic regions, local ancestry inference was performed against nine historically, phenotypically, or genomically relevant breeds. Several emerged regions were associated with key morphological traits -e.g., coat color and length, ear shape, and size-, behaviour, and physical or cognitive abilities important for hunting tasks. In conclusion, the KTKM emerges as a genetically distinct and uniform population belonging to the pointing dog group. Its moderate inbreeding levels and unique genomic characteristics support the possibility of preserving the breed through dedicated conservation efforts. This study underscores the critical need to protect the KTKM's genetic diversity and cultural heritage, providing a foundation for its official recognition and long-term preservation.

Analysis of genomic diversity in the Slovak Cuvac dog

H. Vostra-Vydrova¹, B. Hofmanová¹, N. Moravcikova², R. Kasarda², L. Vostry¹

¹ Czech University of Life Sciences Prague, Kamýcka 129, 165 00 Prague, Czech Republic, ² Slovak University of Agriculture in Nitra, Tr. Andreja Hlinku 2, 949 76 Nitra, Slovakia

Loss of genetic diversity negatively affects most of the modern dog breeds. The genetic diversity of dog breeds is usually evaluated based on pedigree analysis. However, the study of the genetic diversity of dog breeds using genomic data has been analyzed so far. The Slovak Cuvac's breed characteristics conform to the type of mountain dog, with a firm constitution, impressive appearance, and thick white coat. The Slovak Cuvac was bred to guard property and herds of sheep. Because the population is closed, there is a concern about the loss of genetic variation. Pedigree records, collected since 1925, when the breed was founded, contain information on 17 thousand animals. Our main objective in this study was to analyze the genomic diversity (estimated by genomic inbreeding and current and historical effective population size) of the Slovak Cuvac population. The population's forty most important individuals, selected based on pedigree analysis, were analyzed based on high throughput SNP array genotypes. The hidden Markov model framework was used to estimate total genomic inbreeding (FRZ) array genotypes. The hidden Markov model framework was used to estimate total genomic inbreeding (FRZ). In addition, depending on the number of generations taken into account, inbreeding coefficients from 3rd to 24th generations were computed (from FRZ3 to FRZ24). The mean value of genome-based inbreeding coefficients FRZ was 0.21, with minimum and maximum values of 0.1521 and 0.3084. The significant mean value was also estimated for genomic inbreeding FRZ24 (0.17). The 24 generations taken into account with an expected generation interval of 5 years goes back to the time of the breed's foundation. Another significant mean value of inbreeding was estimated for FRZ3 (0.03), which represents current inbreeding. The estimated genomic effective population size (N_e) was relatively high (59). However, an examination of historical N_e indicated a decline between 17 and 8 generations, from 57 to 36 individuals. These results provide valuable insights for future breeding programs of the Slovak Cuvac dog breed genetic diversity management. This research was supported by the projects SV24-14-21360 and APVV-20-0161, APVV-17-0060.

Session 2

Theatre 1

Genomic technologies and their application to combat hereditary diseases in dogs

T. Leeb¹

¹ University of Bern, Institute of Genetics, Bremgartenstrasse 109a, 3001 Bern, Switzerland

Genomic technologies and their application in dogs have massively improved during the last 20 years. Today, we have high quality reference genome assemblies from several individual dogs together with comprehensive functional annotation. Massively parallel genotyping by either array- or sequence-based methodologies facilitate positional approaches to identify trait-controlling variants such as genome-wide association studies and linkage analyses. Re-sequencing individual dog genomes has become widely available at affordable prices and thousands of publicly available genomes help to distinguish common neutral variants from rare deleterious variants. The available genetic toolkit enables the fast identification of pathogenic variants that cause new hereditary diseases in dogs. In my presentation, I will review the current state of the art in canine medical genetics. This will include some representative examples on the discovery of disease-causing or disease-predisposing genetic variants complemented by an update on ongoing efforts to improve the quality and harmonize reporting in genetic research and diagnostics. I will then move on to present strategies how the available technologies can be applied in the daily breeding practice to promote the health and wellbeing of dogs.

Cell-based Tools for Advancing Canine Genetics Research

C. Abeykoon¹, M. Jackson¹, T. Watson¹, S. Meek¹, L. Adamson¹, S. Boyle², G. T. Bergkvist¹, T. Burdon¹, J. J. Schoenebeck¹
¹ University of Edinburgh, The Roslin Institute and Royal (Dick) School of Medicine, Easter Bush Research Campus, EH25 9RG Midlothian, United Kingdom, ² University of Edinburgh, MRC Human Genetics Unit, Institute of Genetics and Cancer, Western General Hospital, EH4 2XU Edinburgh, United Kingdom

Dog population genetics studies have revealed a myriad of genetic variants that are associated with disease and traits. However, assigning causality to alleles of interest is extremely challenging in non-laboratory animal species like dogs, especially when cases are rare and access to biological material for characterisation is limited. Induced pluripotent stem cells (iPSCs) are an essential and inexhaustible biological resource for circumventing these limitations. As a self-renewing population of cells amenable to genetic manipulation and lineage differentiation, iPSCs are an ideal tool to explore the effects of genetic variation conspecifically. Currently, the production of canine iPSCs from adult cells is inefficient and reproducibility is poor. Here we describe our progress to overcome these limitations. Using transposon-based, doxycycline regulatable reprogramming factors, we attempted to reprogramme skin fibroblasts derived from a Labrador retriever, the same dog sequenced to produce the ROS_Cfam_1.0 genome assembly. Theorising that a major limitation to reprogramming success was the proliferative capacity of starting adult cells, we overexpressed SV40 large T antigen to create the cell line LAB1-Tag. Critically, this cell line is immortalised in a doxycycline-dependent manner and sequence-based inference of karyotypes indicates LAB1-Tag is normal. Unlike their primary parental cells, LAB1-Tag cells were competent to produce putative iPSC colonies following transfection with a cocktail of reprogramming factors. We will provide updates on our ongoing iPSC characterisation that describe our iPSCs' pluripotency and competence to differentiate.

Diagnosis of canine myxomatous mitral valve disease: Development of a novel microRNA based platform

J. May¹, E. Hanks¹, R. Coultous¹, P. Capewell², J. Palarea-Albaladejo³, J. Duker-Mcewan⁴

¹ MI-RNA, Animal Health, Scotland's Rural College, EH9 3JG Edinburgh, United Kingdom, ² University of Glasgow, School of Molecular Biosciences, College of Medical, Veterinary and Life Sciences, College of Medical, Veterinary & Life Sciences Wolfson Medical School Building, G12 8QQ Glasgow, United Kingdom, ³ University of Girona, Department of Computer Science, Applied Mathematics and Statistics, C/ de la Universitat de Girona, 6 Campus Montilivi, 17003 Girona, Spain, ⁴ University of Liverpool, Small Animal Clinical Science, Chester High Road Neston, CH64 7TE Liverpool, United Kingdom

Background: Myxomatous mitral valve disease (MMVD) is a common and progressive canine heart disease. The presence of heart murmur and current cardiac biomarkers are useful in MMVD cases but are not sufficiently discriminatory for staging an individual patient. Objectives: In dogs, to answer the question: can analysis of a blood sample by a novel microRNA based platform, when compared to the current gold standard of echocardiography, effectively distinguish between dogs with MMVD and healthy controls? Methods: A prospective case-control study was performed to obtain blood samples from dogs diagnosed with MMVD and healthy controls. The diagnosis of MMVD was made by a cardiology specialist after a cardiac evaluation including echocardiography. Blood samples were analysed for the expression profile of 15 microRNA markers. Machine learning algorithms were trained aiming to discriminate between these two groups and their predictive performance was objectively assessed by repeated cross validation. Model classification accuracy was assessed using ROC AUC (receiver operator characteristic area under the curve), accuracy, sensitivity and specificity. Results: Seventy-seven client owned dogs were recruited (36 myxomatous mitral valve disease; 41 controls). For diagnosis of MMVD compared to controls a sensitivity of 0.83 [95% CI 0.69-0.91], specificity of 0.92 [0.78-0.97], AUC-ROC of 0.94 [0.89-0.99] and accuracy of 0.87 were achieved using the k-nearest neighbours (KNN) algorithm. Conclusions and clinical importance: This proof of concept study has demonstrated the use of microRNA expression profiles combined with probabilistic predictive modelling to discern canine MMVD cases from healthy controls.

Perspectives on polyunsaturated fatty acid supplementation for improved immunity in healthy, chronically ill and aging dogs

C. Barroso¹, A. Cabrita¹, A. Fonseca¹

¹ REQUIMTE, LAQV, ICBAS, School of Medicine and Biomedical Sciences, University of Porto, Rua de Jorge Viterbo Ferreira, 228, 4050-313 Porto, Portugal

Dogs are currently considered family members, and their owners are increasingly demanding food with high nutritional and functional values that benefit pets' health. Polyunsaturated fatty acids (PUFA) are nutrients considered to improve immune responses and mitigate inflammation associated with various diseases across different age groups. To assess the scientific evidence supporting these claims, a literature review was conducted using peer-reviewed articles sourced from PubMed and Web of Science databases. The analysis included *in vivo* studies (n = 25) examining the impact of PUFA supplementation on immunity and inflammation in healthy, chronically ill and aging dogs. The dietary supplementation with fish oil, particularly rich in long chain omega-3 PUFA [eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA)] in healthy young and elderly dogs have been shown to modulate the inflammatory response. The use of hemp oil, rich in linoleic and alpha-linolenic acids, demonstrated immunomodulatory effects by increasing serum interferon (IFN)-gamma and immunoglobulin M. In dogs with cancer, cardiovascular and dermatological diseases, supplementation with fish oil or EPA and DHA reduced the production of prostaglandin E2 (PGE2) and pro-inflammatory cytokines, including interleukin-6 and tumor necrosis factor (TNF)-alpha. Despite the promising results, variations in PUFA inclusion levels, duration of supplementation and outcome measures, highlight the need for further research, namely focused on novel sustainable PUFA sources, determining the optimal balance between n-3 and n-6 PUFA, evaluating the long-term effects and elucidating the molecular mechanisms underlying the potential benefits of the various PUFA. Such insights will be critical for the development of therapeutic diets aimed at promoting anti-inflammatory effects and enhancing immunity in both health and disease. This work received financial support from the PT national funds (FCT/MECI) through the project UID/50006 – Laboratório Associado para a Química Verde – Tecnologia e Processos Limpos.

Session 2

Theatre 5

Milk is good for all ages: development of antioxidant DHA-loaded milk fat-derived nanocarriers

J. Albuquerque¹, A. Cabrita², F. Soares¹, A. Granja¹, C. Nunes¹, A. Fonseca², S. Reis¹

¹ LAQV, REQUIMTE, Faculty of Pharmacy, University of Porto, Rua Jorge Viterbo Ferreira 228, 4050-313 Porto, Portugal, ² LAQV, REQUIMTE, School of Medicine and Biomedical Sciences, University of Porto, Rua Jorge Viterbo Ferreira 228, 4050-313 Porto, Portugal

As our pets' lifespan increases it becomes even more important to promote their health and quality of life in older ages. Docosahexaenoic acid (DHA) is a long-chain omega-3 polyunsaturated fatty acid (PUFA) considered fundamental in the development and performance of the nervous system. Studies have shown that dietary fortification with DHA can improve cognitive, memory, psychomotor and retinal functions in growing animals. Furthermore, DHA can attenuate negative effects of brain ageing and dementia, possesses anti-inflammatory and immunomodulatory properties, and has been found to be effective in the management of osteoarthritis, cancer, kidney and cardiovascular diseases. Typically, fish oil is included in pet food as a source of omega-3 PUFA, but due to their instability and high propensity to oxidize and degrade over time, antioxidants are commonly added. The development of nanocarriers (NC) using components collected from milk with inherent antioxidant activity comprise a novel strategy to encapsulate DHA, thus improving its stability and bioavailability. The milk fat-derived NC were produced using organic solvent-free methods used in food technology and loaded with DHA. The NC presented two populations, with diameters around 200 and 600 nm, which are optimal dimensions for oral administration and intestinal absorption of lipid-based particles. The NC possessed a zeta potential value of -20 mV, translating a good colloidal stability, and maintained their properties for at least 10 months of storage at room temperature. Developed NCs are resistant to gastrointestinal conditions, with concentrations up to 2.5 mg/mL of NC being non-cytotoxic and non-hemolytic. DHA-load NCs exhibit considerable antioxidant activity. The antioxidant activity of the NC themselves, suggest their potential to be used as antioxidants and enabling the development of feed additives with multiple functional properties. Funding: This work received financial support from national funds (FCT/MCTES) through the project PTDC/BAA-AGR/4923/2021.

Organic selenium yeast reduces TK6 cell mutation frequency: implications for companion animal health

K. Horgan¹, J. Keenan², R. Murphy¹

¹ Alltech, Research, Summerhill Rd, A86X006 Dunbooyne, Ireland, ² Dublin City University, School of Biotechnology, Glasnevin, D09 V209 Dublin, Ireland

The aging process is highly responsive to diverse environmental influences, such as chronic inflammation, infectious diseases, and nutrition. Environmental hazards can result in spontaneous tumour development in dogs. Whilst dogs naturally develop the same cancers as humans, they do so much more quickly. Numerous studies have shown people on low selenium diets have a higher incidence of many cancers than those on higher selenium diets. Mutagenesis is a crucial step in the carcinogenesis process. To date, studies investigating mammalian systems have focused on DNA damage endpoints, demonstrating selenium's ability to alter the expression of genes involved in genotoxicity protection which result in reduced DNA damage. Such studies demonstrate, selenium's capability to reduce the negative impacts of reactive oxygen species (ROS). However, to date no in vitro functional mutation-based assays assessing selenium's capabilities in reducing mutational frequencies have been conducted. The TK6 gene mutation assay was used as a functional endpoint to compare mutation frequency (MF) after -treatment of lymphoblastoid cells with inorganic sodium selenite (SS) or organic forms of selenium including selenized yeast (SeY), selenomethionine (SM) and methylselenocysteine (MSC). Both the form and concentration of selenium affected MF. At low concentrations (0.5 and 2.5 mM), no form of selenium alone had an influence on mutation rate. With cisplatin as the mutagen, at 2.5 mM but not at 0.5 mM, only SeY significantly reduced MF by 29%. Selenoprotein expression, antioxidant activity and p53 expression are implicated in selenium antimutagenic activity. While GPX1 and GPX4 were similarly elevated after selenium treatment, SeY increased redox potential (elevated GSH, reduced ROS) while selenite increased oxidative stress (increased ROS, lower GSH). These results complement previous genotoxic studies demonstrating SeY as a safer supplement than inorganic selenite and implicate GSH as another factor involved in the antimutagenic activity of SeY and warrants further investigation.

Session 3

Poster 1

Leveraging genomics for modern dog breeding and conservation: the Sicilian Mastiff case study

K. Seghrouchni^{1,2}, M. Barbato¹, A. Bionda³, S. Frattini², L. Liotta¹

¹ Università degli Studi di Messina, Dipart. di Scienze Veterinarie, Polo Universitario dell'Annunziata, 98168 Messina, Italy, ² Vetogene ENCI-servizi, Viale Ortles 22/4, 20139 Milano, Italy, ³ Università degli Studi di Milano, Dipart. di Scienze Agrarie e Ambientali - Produzione, Territorio, Agroenergia, Via G. Celoria 2, 20133 Milano, Italy

The Sicilian Mastiff (Mannara dog) is an ancient breed that has been an integral part of Sicilian pastoral life as a livestock guardian. However, unregulated crossbreeding has threatened its genetic integrity. About 100 new individuals are registered in the herdbook annually, bringing the breed head count to around 700. To mitigate extinction risks, conservation efforts resulted in the breed recognition as a native Italian breed by the Italian Kennel Club in March 2023, marking a crucial step towards achieving international recognition. This shift affirms the breed's distinct lineage and enables structured breeding programs, genetic health screenings, and phenotypic evaluations to preserve its integrity. Here we employ genomic tools, specifically SNPchip-based analyses through MyDogDNA®, to assess the genetic diversity, wellness, and health of the breed by investigating inbreeding levels, hereditary diseases, and breed distinctiveness. As a first survey, we genotyped 22 dogs. The breed's heterozygosity levels range from 0.24 to 0.42, with the tested group averaging 0.41, indicating moderate genetic variability. Over 250 genetic conditions were screened, identifying three carriers of progressive retinal atrophy (PRCD) and one carrier of adult-onset deafness (intergenic). Further, associations with key phenotypic traits such as coat color, presence of hind dewclaws and ear shape, were also found. Our results offer a preliminary genetic characterization of the breed, contributing to conservation efforts, and will be instrumental toward the Sicilian Mastiff's official recognition as a historically significant Italian breed.

Architecture of Ancestral Genomic Components in the Sicilian Mastiff

P. Crepaldi¹, A. Bionda¹, V. Floridia², M. Barbato², L. Liotta²

¹ Milan University, Agricultural and Environmental Sciences, Via Celoria 2, 20133 Milano, Italy, ² Messina University, Veterinary Sciences, Viale Palatucci, 98168 Messina, Italy

The Sicilian Mastiff (or Mannara dog), is an indigenous Sicilian livestock guardian dog (LGD) breed with approximately 700 registered individuals. Formal recognition as a distinct breed was conferred by the Italian Kennel Club in 2023 and efforts to attain international recognition are ongoing. Previous studies have identified the Maremma and the Abruzzes sheepdog as the closest relative of the Sicilian Mastiff, highlighting a shared history and overlapping functional characteristics typical of LGDs. Thus, investigating the genetic makeup of the Sicilian Mastiff becomes essential to safeguarding and enhancing its cultural heritage and role in Sicilian pastoralism. In this study, the genetic investigation of 12 Sicilian Mastiffs revealed significant divergence from other breeds, while also confirming a close genetic relationship with the Maremma sheepdog. Therefore, local ancestry inference analyses were performed to identify genomic regions potentially influenced by the Maremma sheepdog, in comparison with other European and Mediterranean LGD breeds. Several genomic regions exhibited strong introgression with the Maremma sheepdog. Among the genes within highly introgressed (99th percentile) regions identified in at least three of these comparisons, several were associated with traits characteristic of LGD. These traits included behavioral attributes such as aggression towards strangers, morphological features such as drop ears, and physical attributes enhancing their guarding abilities. These findings support the hypothesis that centuries of selective pressures shaped the Sicilian Mastiff, highlighting its genetic and cultural value for pastoral communities. To explore the Sicilian Mastiff's genetic evolution and adaptability, extensive sampling is being conducted to assess changes in its genetic variability and structure over the past decade. During this period, breeders have been encouraged to adopt more stringent and informed selection practices. This longitudinal approach aims to provide valuable insights into the impact of modern management practices on the genetic profile of the breed.

Genetic Characterization of Irish Wolfhound Dogs: A Worldwide Study of Genetic Variability and Inbreeding

M. G. Strillacci¹, M. Poli², S. P. Marelli¹

¹ Università degli Studi di Milano, Veterinary Medicine and Animal Science, Via Dell'Università, 6, 26900 Lodi, Italy, ² Sighthound Club of Italy, Via per Tavernaro, 3, 38121 Trento, Italy

The Irish Wolfhound (IW) is a canine breed characterized by phenotypical traits far from the *Canis lupus familiaris* species' normotype. Notably, its giant size is among the breed's most recognizable features and, as reported in the scientific literature, is associated with a reduced lifespan. In addition, well-documented genetic bottlenecks in the breed's history have significantly shaped its genomic landscape, contributing to its limited genetic variability and health challenges. This study aimed to investigate the genetic diversity and inbreeding levels in this breed. A total of 96 IW dogs collected from 23 countries worldwide were genotyped using the Illumina CanineHD Bead-Chip, annotated according to the CanFam3.0 genome assembly. Genetic variability was assessed through metrics such as observed and expected heterozygosity (He and Ho), allelic richness, and effective population size (Ne). The genetic relationships among the sampled dogs were analyzed using principal component analysis (PCA). In addition, Runs of Homozygosity (ROHs) were detected, and the level of inbreeding was evaluated by estimating FROH coefficients using a dedicated tool. Our findings revealed similar Ho and He values (average values: 0.3 and 0.32) and a high proportion of ROHs across the genome (mean number of ROHs: 300). No ROHs in the longest class (>16 Mbp) were identified. The average FROH was 0.28 with minimum and maximum values of 0.11 and 0.41. PCA revealed no genetic sub-structuring among the sampled dogs, indicating a largely homogeneous global population. This study underscores the need for breeding strategies that prioritize the maintenance of genetic diversity to mitigate the negative effects of inbreeding on health and lifespan. Incorporating genomic information into breeding programs can help reduce inbreeding rates and promote the long-term sustainability of the Irish Wolfhound breed. Acknowledgments The authors gratefully acknowledged the breeders and the Federation of Irish Wolfhound Clubs (FIWC) for supporting this study.

Genetic variability of Croatian Shepherd Dog estimated with a pedigree data – a preliminary studyI. Djurkin Kušec¹, K. Gvozdanović¹, I. Bošković¹, B. Petric², Ž. Radišić¹¹ Faculty of Agrobiotechnical Sciences Osijek, Vladimira Preloga 1, 31000 Osijek, Croatia, ² “Croatian Shepherd Dog” kennel klub Đakovo, Zvečaj II, 31400 Đakovo, Croatia

The Croatian Shepherd Dog is an autochthonous Croatian breed whose historical references date back to 1374, when its appearance was first described. Its phenotype has remained unchanged to this day. Despite the lack of systematic cynological management, the breed has been preserved, albeit with a very small population size, which led to it being classified as an endangered population by the FAO (DAD-IS) in 2019. The breed is known for its exceptional herding instincts and is also used in rescue operations and various dog sports, including agility competitions. Although the Croatian Shepherd Dog has an ancient ancestry, there is currently no comprehensive data on its genetic diversity, population structure or level of inbreeding. To fill this knowledge gap, we conducted a high-resolution genomic study to assess population structure and compare genomic data with genealogical records from pedigrees. The results presented here are based on genealogical data spanning six generations from 40 individuals genotyped with HD SNP microarrays. Each dog's data set included its identification number, sex, date of birth and the identification data of its parents, grandparents, and great-grandparents. The pedigree structure analysis was carried out using the CFC software. A total of 362 dogs were analysed with 201 (55.5%) being inbred. The inbreeding coefficient ranged from 0.05% to 28.07%, with an average inbreeding coefficient of 5.5% among the inbred individuals. The average relatedness was 7.42%, indicating moderate genetic similarity within the population. In order to preserve genetic diversity and mitigate potential inbreeding-related risks, a responsible breeding programme and continuous genetic monitoring needs to be implemented.

Guess the Wild: Habitat Prediction Model for Wildcat in ItalyS. Comazzi¹, C. Polce², M. Longeri¹, M. Maini³, R. Milanese¹, F. Mattucci⁴, E. Velli⁴, R. Caniglia³, R. Cazzolla Gatti³¹ University of Milan, Veterinary Medicine and Animal Science, via dell'Università 6, 26900 Lodi, Italy, ² Independent consultant, Varese, 21100 VA, Italy, ³ Alma Mater Studiorum University of Bologna, Biological, Geological and Environmental Sciences, Piazza di Porta San Donato 1, 40126 Bologna, Italy, ⁴ Italian Institute for Environmental Protection and Research (ISPRA), Unit for Conservation Genetics (BIO-CGE), Via Cà Fornacetta 9, 40064 Ozzano dell'Emilia, Italy

The European wildcat (*Felis silvestris silvestris*) is under significant threat from habitat fragmentation, environmental changes, and interaction with domestic cats (*Felis silvestris catus*). The two subspecies can interact with the effect of genetic introgression and disease transmission. Little is known about wildcats' overall demographic and conservation status in Italy especially due to their elusive behavior and insufficient monitoring projects. Camera trap images and biological samples were collected from an Italian Northeastern region (Friuli) where the presence of the wildcat has long been reported. A predictive habitat distribution model has been developed to help with ongoing trap installation/sample collection and assess the potential presence of human (and thus domestic cats) settlements in potential wild areas. The model used two types of environmental predictors: land use/land cover and topography and was designed to include all currently available wildtype phenotypic occurrences from peninsular Italy (n.69). The model included a sample of 50 phenotypically wildcat occurrences collected in Friuli from camera traps or carcasses in 2024. The model's prediction ability compared to the sample data will drive the next sample collection campaign for both wild and domestic cats and integrate the future genomic analysis on samples of both species.

SLC35D1 frameshift variant in Weimaraner and Wirehaired Slovakian Pointer: A genetic risk factor for a form of steroid-responsive meningitis-arteritis (SRMA) and hyperostosis?

A. Letko¹, K. Matiasek², D. Schweizer¹, C. Drögemüller¹

¹ University of Bern, Bremgartenstr. 109A, 3012 Bern, Switzerland, ² Ludwig-Maximilians-Universität, Veterinärstr. 13, 80539 Munich, Germany

SRMA is an immune-mediated, non-infectious inflammatory condition of young-adult dogs commonly observed in breeds like Weimaraners (WEM) and German Wirehaired Pointers (GWP). The acute form typically presents with fever and neck pain. While genetic predisposition is suspected, specific risk factors remain unclear. Hyperostosis encompasses several self-limited disorders causing inflammation of soft tissues leading to fever, lameness, and consequent discomfort signs during bone proliferation. GWP are prone to craniomandibular osteopathy, while WEM often develop hypertrophic osteodystrophy. Various inheritance modes were postulated, suggesting heterogeneity across breeds. In a previous study of a WEM with hyperostosis, a rare heterozygous variant in the SLC35D1 gene, encoding a nucleotide-sugar transporter involved in chondroitin sulfate biosynthesis, was reported as likely pathogenic. To further investigate, we evaluated the variant allele frequency in a larger cohort of WEM and Wirehaired Slovakian Pointers (WSP), a breed that arose from crossing WEM, GWP, and Bohemian Wirehaired Pointer. The newly reported young-adult WSP cases showed recurrent unexplained fever episodes, hindlimb lameness and SRMA. We genotyped 135 WEM, 51 GWP and 29 WSP. The variant allele was absent in the GWP cohort but found at a relatively high frequency of 0.2 in WEM without detailed medical records. All 6 SRMA-affected WSP were heterozygous for the variant and extended pedigree analysis revealed they belonged to one pedigree with multiple WEM sires. The variant was detected in only 8 WEM in a recent study that screened over 200,000 purebred dogs of various breeds. Our findings suggest that the SLC35D1 variant may be a genetic risk factor for SRMA and hyperostosis in these breeds. Further studies are needed to explore the dominant allele's role and assess potential underdiagnosis due to the condition's self-limiting nature. Understanding breed genetic predispositions may reduce the incidence of the disorder and improve the quality of life for affected dogs and their owners.

Session 3

Poster 7

Differential expression of microRNAs in descended and undescended canine testicles

J. Nowacka-Woszek¹, A. Kajdasz^{1,2}, I. Szczeral¹, M. Stachowiak¹, M. Switonki¹

¹ Poznan University of Life Sciences, Wolynska 33, 60-637 Poznan, Poland, ² Institute of Bioorganic Chemistry of the Polish Academy of Sciences, Noskowskiego 12/14, 61-704 Poznan, Poland

Cryptorchidism is a major disorder of sex development in dogs. Recent studies have shown that the expression of protein-coding genes is significantly altered in undescended testes (Stachowiak et al., PNAS, 2024). In this study we aimed to compare global microRNA expression in the testicles of unilateral cryptorchid and control dogs. Global ncRNA levels was analyzed by RNA sequencing (RNA-seq) in undescended (UD) and descended (D) testicles of cryptorchid dogs (n = 9) and scrotal testicles (C) of control dogs (n = 8). Validation of selected miRNAs was conducted in a larger cohort (26 UD, 26 D, 25 C) using ddPCR. Comparison of UD and D testes revealed 224 differentially expressed miRNA genes (DEGs), with 118 meeting the criteria of $FDR < 0.05$ and $-1.5 < \log_{2}FC > 1.5$ (8 up- and 110 downregulated). Similarly, comparison of UD and C testes identified 200 DEGs, with 102 meeting the same criteria (9 up- and 93 downregulated). Using the TargetScan database, we identified potential target sequences for these miRNAs in the 3'UTRs of mRNA DEGs. Target sequences were found in numerous protein-coding genes, including those implicated in testicular cancer, e.g. upregulated TP53 in UD testicles has a target site for the downregulated cfa-miR-122, while the downregulated KLF4 contains multiple target sites for upregulated miRNAs (e.g. cfa-miR-25, cfa-miR-26, cfa-miR-34 etc). We further selected the top ten up- and top ten downregulated miRNAs and compared their expression with the top ten up- and top ten downregulated mRNAs reported in earlier studies (Stachowiak et al., 2024). The UD vs. D comparison revealed four downregulated miRNAs (cfa-miR-8831, cfa-miR-449a, cfa-miR-34b, and cfa-miR-449b) with the targets in the 3'UTR of the upregulated PDGFRA, and downregulated cfa-miR-15b, which targets the upregulated GOS2. Such relationships were not observed in the UD vs. C comparison. In conclusion, the altered expression of miRNAs contributes to the dysregulated expression of protein-coding genes in undescended testes. [Financed by the National Science Centre, Poland, grants 2018/29/B/NZ9/01065, 2023/51/B/NZ9/01165]

Exploring gonadal dysgenesis in dogs with disorders of sex development using spatial transcriptomics

J. Nowacka-Woszuk¹, S. Hryhorowicz², J. Suszynska-Zajczyk^{1,2}, M. Knaur², A. Lukomska¹, N. Sowinska¹, I. Szczerebal¹, M. Switonski¹

¹ Poznan University of Life Sciences, Wojska Polskiego 28, 60-637 Poznan, Poland, ² Institute of Human Genetics, Strzeszynska 32, 60-479 Poznan, Poland

Disorders of sex development (DSD) are a heterogeneous group of congenital malformations characterized by dysgenetic gonads, which may have an increased risk of cancer development (e.g. undescended testes). In this study we applied spatial transcriptomics approach to analyze descended and undescended testes from two DSD dogs—one with isolated unilateral cryptorchidism and another with complex DSD, including cryptorchidism—and a control male dog. The Visium Spatial Gene Expression protocol (10x Genomics) was applied to study tissue sections placed on the slides, fixed, stained with hematoxylin and eosin, and permeabilized for different lengths of time. After selection of the optimal permeabilization time mRNA was released, barcoded, and converted into cDNA for library preparation. Sequencing was performed using the Illumina NextSeq 2000 platform, and data processing and visualization were conducted with SpaceRanger and Loupe Browser software. Our analysis identified altered mRNA expression in specific testicular cell types in undescended testes, including early spermatids, spermatocytes, spermatogonial stem cells, late spermatids, as well as Leydig and Sertoli cells. Among candidate genes associated with cryptorchidism (INSL3, CYP17A1, WT1, and AMH), elevated mRNA levels were observed in undescended testes. For genes linked to testicular cancer (KIT, KLF4, DMRT1, SALL4, GATA4, INHA, and CLPTM1L), expression levels varied significantly between descended and undescended testes, with changes dependent on gene function. Additionally, genes belonging to heat shock protein families (e.g., HSPA8, HSPB1, HSPD1, and HSPA5) were upregulated in undescended testes, likely due to elevated temperature in these gonads. This study highlights the potential of spatial transcriptomics to uncover transcriptomic profiles at cells resolution in a spatial context, significantly advancing our understanding of the molecular basis of cryptorchidism in dogs. [Financed by the National Science Centre, Poland, grant no. 2023/51/B/NZ9/01165]

Session 3

Poster 9

A rare SNP in the 3'UTR of the AMH gene in a tortoiseshell Maine Coon tomcat with disorder of sex development (38,XX; SRY-negative)

J. Nowacka-Woszuk¹, I. Szczerebal¹, A. Szabelska-Beresevicz¹, J. Zyprych-Walczak¹, P. Parma², K. Ropka-Molik³, M. Jankowska³, T. Nowak¹, M. Stachowiak¹, N. Rogalska-Niznik¹, M. Switonski¹

¹ Poznan University of Life Sciences, Wojska Polskiego 28, 60-637 Poznan, Poland, ² University of Milan, Via Celoria 2, 20133 Milan, Italy, ³ National Research Institute of Animal Production, Krakowska 1, 32-083 Balice, Poland

The occurrence of disorders of sex development (DSD) represents a significant health issue in cats. Testicular XX (SRY-negative) DSD is a very rare condition in this species. In this study, a tortoiseshell Maine Coon tomcat with male external genitalia, scrotally located gonads, low serum testosterone and elevated anti-Müllerian hormone (AMH) levels underwent genetic analysis. Initial tests revealed the presence of XX sex chromosomes and the absence of the SRY gene. The DSD tomcat and its parents were analyzed using whole-genome sequencing. It was hypothesized that the disorder could be caused by a recessive pathogenic variant, manifesting phenotypically only in female cats. Thus, the study focused on identifying homozygous SNP genotypes in the affected cat that were heterozygous in its parents. Seven candidate variants were identified, including two SNPs in the 5'- and 3'-UTR of AMH and five missense SNPs in ORC1, DOCK8 (two SNPs), PRKAR1A, and TMEM186. Variants in five genes—except for AMH—were excluded, as similar genotypes were also detected in control cats. Further analysis, prompted by the elevated serum concentration of AMH, focused on SNPs in the 5'-UTR (A>G) and the 3'-UTR (G>A) of AMH. The 5'-UTR SNP showed no significant impact on secondary structure or functional motifs. PCR-based analysis of AMH transcripts confirmed that only a short transcript (ENSFCAT00000036376.3) is present in feline testicles, localizing the G>A substitution to the 3'-UTR. In silico analysis revealed that this SNP alters the target sequence for miR-5571 expressed in mammalian testicles, potentially affecting AMH expression. We conclude that the homozygous AA genotype in the 3'-UTR of AMH is associated with elevated serum levels of the encoded hormone in the studied XX DSD tomcat. [Financed by statutory funding 506.534.05.00 from the Faculty of Veterinary Medicine and Animal Science, Poznan University of Life Sciences, Poland]

Sequence analysis of SOX9 gene in a cohort of French bulldogs with disorder of sex development (XX DSD, SRY-negative)

J. Nowacka-Woszuk¹, S. Albarella², B. Slaska³, W. Nizanski⁴, S. Dzimira⁴, N. Sowinska¹, M. Mikolajczak⁵, M. Sobczak¹, Z. Sawicz¹, I. Szczerbal¹, M. Switonski¹

¹ Poznan University of Life Sciences, Wojska Polskiego 28, 60-637 Poznan, Poland, ² University of Naples Federico II, Via Delpino 1, 80127 Naples, Italy, ³ University of Life Sciences in Lublin, Akademicka 13, 20-400 Lublin, Poland, ⁴ Wroclaw University of Environmental and Life Sciences, Norwida 25, 50-375 Wroclaw, Poland, ⁵ Vet-Med Clinic, Plac Sokola 7, 62-002 Suchy Las, Poland

The SOX9 gene, which acts downstream of the Y-linked SRY gene, is a key transcription factor involved in sex development and it plays a pivotal role in the formation of fetal testicles. There are numerous reports on disorders of sex development (DSD), characterized by virilization (e.g. enlarged clitoris) and the presence of testes or ovotestes, in dogs with XX karyotype and the absence of the SRY gene. This study aimed to analyze the copy number of the SOX9, as well as its coding and 5'UTR sequences. A total of 26 XX (SRY-negative) DSD French Bulldogs were included. Gene copy number was determined using digital droplet PCR (ddPCR), and sequence analysis was performed using the Sanger method. In a single XX DSD case three copies of the SOX9 gene were detected. Notably, this dog also exhibited skeletal defects and is the first reported case of an XX DSD dog with skeletal anomalies. This finding aligns with the known role of SOX9 in chondrogenesis. The 90% of the coding sequence revealed no variants, while the 5'UTR showed two known variants: a 3 bp insertion/deletion (CCT/-, rs852828782) and a T>C SNP (rs22704771). At the indel site (c.-226-224del), two DSD dogs had a heterozygous genotype, while the remaining cases were homozygous for the insertion (ins/ins). For the SNP (c.-36T>C), the genotype distribution was CC = 15, CT = 8, and TT = 3. Interestingly, the dog with three copies of SOX9 was heterozygous at both polymorphic sites. In conclusion, an elevated number of SOX9 copies appears to be a rare cause of XX DSD in French Bulldogs. The observed 5'UTR variants are unlikely to have a pathogenic role in the development of DSD. [Financed by statutory funding 506.534.05.00 from the Faculty of Veterinary Medicine and Animal Science, Poznan University of Life Sciences, Poland]

Variation of faecal microbiota in dogs during ageing

B. Stefanon¹, F. Baloue¹, P. Mongillo², N. McCarthy³, A. Paradis³, C. De Rivera³

¹ University of Udine, Agrofood, Environmental and Animal Science, via delle Scienze, 33100 Udine, Italy, ² University of Padova, Comparative Biomedicine and Food Science 16, 35020, Viale dell'Università, 35020 Legnaro, Italy, ³ Transpharmation, Canada Ltd, P.O. Box 248, N1M 2W8 Fergus ON, Canada

The composition of the gut microbial population fluctuates during life and changes are expected with ageing. However, several confounding factors have to be considered, since breed, diet, onset of degenerative disease and environmental situations can affect the gut microbiota and are not easy to control on longitudinal study. In this research, fecal samples from 150 Beagle dogs housed in the same kennel and fed the same diet were collected in a 30 days span time and analysed for microbiota composition. Dogs were grouped as young (30 dogs, from 20 to 46 months), adult (44 dogs, from 47 to 92 months) and old (76 dogs, 93 to 168 months). After DNA extraction, the V3-V4 hypervariable regions of the 16S rRNA gene were sequenced in a 250 PE mode with Illumina Novaseq platform. FASTQ files were uploaded in QIIME2 for taxonomic annotations, based on the greengene classifier, trained on the amplified regions. The alpha and beta diversities did not vary between young, adult and old groups of dogs. The analysis of LDA Effect Size (LEfSe) on the relative abundances of taxa showed significant differences for the Burkholderiales, Erysipelotrichaceae, and Clostridiales in young dogs. The taxa of S24_7, Peptococcus, Ruminococcaceae, Bacteroidales, Peptostreptococcus, Eubacterium and Lachnospira significantly differ in adult dogs, whilst Sutterella and Clostridium prevailed in old dogs. The observed shifts of the relative abundance of these taxa with ageing suggest that the gut microbiota can be regulated by ageing, although the meaning of these changes deserves further investigation.

The role of the National Rescue Dog Unit in search and rescue operations in Slovenia

P. Dovc¹, M. Velikonja², K. Skulj², M. Zorc¹

¹ University of Ljubljana, Biotechnical Faculty, Jamnikarjeva 101, 1000 Ljubljana, Slovenia, ² Cynological association of Slovenia, Commission for rescue dogs, Zapoge 3D, 1217 Vodice, Slovenia

Search and rescue (SAR) dogs are indispensable in locating missing persons across diverse environments. In Slovenia, the National Rescue Dog Unit (NRDU) operates under the Cynological Association of Slovenia, which is a member of the Fédération Cynologique Internationale (FCI), and is a member of the International Search and Rescue Dog Organisation. The NRDU has developed the national education and training program for search and rescue teams which contains nine theoretical exams for handlers and, according to FCI rules, 15 practical exams for SAR teams. As an integral part of the national civil protection system, the NRDU participates in search and rescue missions. All work is conducted on a voluntary basis, with handlers dedicating significant amount of time to training and emergency response. Since its establishment in 1957, the members of the NRDU have participated in 957 SAR missions, with a notable increase in recent years. In 2024, the unit has responded to 59 missions, underscoring its growing importance and capability in addressing emergencies. During the history of the NRDU, the breed composition changed significantly. In summary, 48 distinct breeds were represented, but also a significant number of mixed-breed dogs. The most common breeds include Labrador Retrievers (106), Mix-breed dogs (87), Golden Retrievers (42), Border Collies (40), German Shepherds (35), Australian Shepherds (31) and Flat Coated Retrievers (28). Although the Labrador Retrievers were very frequently used for a long period, at present there is no strong breed preference and the present population of dogs in NRDU shows a wide variety of middle-size dog breeds. In total, female dogs (56%) slightly outnumber males (44%), however, in some breeds, the dominance of females is present (Flat Coated Retriever, Labrador Retriever, and Malinois). The dogs reach the readiness and stability to participate in SAR actions on average soon after three years of age and stay working in the unit until the age of eight years. However, if dogs are in good condition and do not have health issues, they can continue to work in the unit even longer.

Session 3

Poster 13

Therapy dogs: bringing smiles and comfort to people in need

M. Zorc², U. Ivanovič¹

¹ The Slovenian Association for Therapy using Animal Assistance, Ambassadors of Smiles, Knobleharjeva ulica 21, 1000 Ljubljana, Slovenia, ² University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Jamnikarjeva 101, 1000 Ljubljana, Slovenia

Therapy dogs play an essential role in improving the quality of life for individuals of all ages by providing companionship, emotional support, and facilitating rehabilitation. The Slovenian Association for Therapy using Animal Assistance, Ambassadors of Smiles, has dedicated its mission to enhancing the everyday lives of elderly individuals, the lonely, the sick, and people with special needs. Operating in various institutions and through individual home visits, the association aims to bring moments of joy and relief to those facing pain, sadness, or isolation. The association is a non-profit organization that emphasizes professional education and research in animal-assisted therapy. Therapy dog-handler pairs undergo specialized training, rigorous testing, and annual veterinary checks to ensure the highest standards of safety and quality. These certified pairs conduct therapy sessions in kindergartens, schools, eldercare homes, and rehabilitation centers. Activities range from interactive therapy sessions to tailored programs aimed at reducing anxiety, improving communication, and fostering motor skills. Since its foundation in 2005, the society has expanded its scope to include a variety of therapy programs such as reading with dogs, relieving fears of animals, and supporting individual rehabilitation plans. The association's work has been recognized as being in the public interest and as a humanitarian initiative, making it a vital part of Slovenia's healthcare and educational systems. With an ever-growing team of dedicated volunteers and therapy pairs, the association continues to bring smiles to thousands, highlighting the transformative power of animal-assisted therapy.

Anthropomorphism in the relationship between dog and humanE. Jastrzębska¹, A. Pawłowska¹, P. Kur¹¹ University of Warmia and Mazury in Olsztyn, Department of Horse Breeding and Riding, Oczapowskiego 2, 10-719 Olsztyn, Poland

Anthropomorphization is giving animals characteristics, thoughts, emotions and beliefs typical of humans. Such behavior affects the relationships between people and animals, but also the well-being of animals. The aim of the study was to analyze the impact of anthropomorphization on the relationships between dogs and humans. For this purpose, a study was conducted in the form of an online survey, to which 340 people responded. The results of the own research indicate that respondents are characterized by anthropomorphic behavior towards their own animals, which may affect the level of well-being of dogs. Despite the fact that some features of animals may resemble a child's appearance, caregivers should be aware that their animals are not small children. Putting on clothes, difficulty in refusing additional food, carrying in a bag are factors that reduce the level of well-being. On the other hand, anthropomorphic thinking results in greater empathy towards animals. It can therefore influence caregivers in such a way that they will provide their animals with better care. Scientific evidence should be reflected in decision-making and the way animals are treated. Animals have different needs and show emotions differently, which is why people should be aware of this in order to treat them appropriately and fulfill their behavioral needs.

The effect of inbreeding on litter size in the Czech Spotted DogB. Hofmanova¹, M. Chladkova¹, H. Vostra Vydrova¹, L. Vostry²¹ Czech University of Life Sciences Prague, Department of Ethology and Companion Animal Science, Kamycka 129, 165 00 Prague 6, Czech Republic, ² Czech University of Life Sciences Prague, Department of Genetics and Breeding, Kamycka 129, 165 00 Prague 6, Czech Republic

The Czech Spotted Dog is an autochthonous breed not yet recognized by the FCI (Federation Cynologique Internationale). The breed was created in the mid-20th century for laboratory purposes and is currently used mainly as a companion animal. It is a medium-sized, undemanding breed with a calm temperament and typical spotted patterns. Given that it is a small, closed population, inbreeding is used to a certain extent, which can sometimes lead to inbreeding depression. Significant negative consequences of inbreeding include decreased reproductive performance. Therefore, the study aimed to analyze the reproduction results and assess the influence of inbreeding on the litter size in this breed. Information on a total of 313 litters registered in the years 2009 – 2021 was included in the analysis. The average litter size was six puppies (minimum 1, maximum 13). Wright's coefficient of inbreeding, calculated from 4 generations of ancestors, was used as a criterion for the intensity of inbreeding. The values of the inbreeding coefficient ranged from 0 to 18.75%. The influence of maternal and litter inbreeding was evaluated using a general linear model, including other factors (age of a dam/parity, age of a sire, and season of birth of the litter). The results show that maternal inbreeding negatively affects litter size more significantly than direct inbreeding of the litter. In dams with an inbreeding coefficient higher than 6.25%, a statistically significant decrease in litter size was observed, and the negative effect of inbreeding was confirmed even when inbreeding was included in the model as a continuous variable. Another statistically significant factor influencing litter size was the parity when the second and third litters were the most numerous. The influence of the sire's age and season was not confirmed. Given that the ability of dogs to reproduce and raise numerous and healthy litters is an important prerequisite for successful breeding, it is necessary to follow measures to minimize inbreeding and thus maintain a healthy and sustainable population.

Why do we want a Maltipoo? Exploring the ownership of this popular designer breed

S. Boero¹, S. Cannas¹, C. Palestrini¹, A. Garegnani¹, G. V. Berteselli¹

¹ University of Milan, Department of Veterinary Medicine and Animal Science, Via dell'Università 6, 26900 Lodi, Italy

“Designer breed” refers to a deliberate cross between two purebred dogs, aimed at merging desirable traits from both parent breeds. Designer breeds are gaining popularity in Italy. This study aimed to explore various aspects of owning a designer dog. A descriptive analysis was carried out using an online questionnaire. Seventy-eight Maltipoo (Maltese x Poodle) owners (MPOs) took part in the survey. 93.6% were women, 38.5% were aged 45–54. 61.5% reported living in urban areas. Most MPOs (57.7%) lived in apartments without gardens; 55.1% of households were composed of 2–3 people. Most MPOs reported no minor children in their household (55.1%). 61.5% of MPOs acquired their dog from a breeder. Notably, 65.4% of owners did not research information about the breed before acquisition; for the rest (34.6%), the primary source of information was the breeder (44.4%). Gastrointestinal issues were reported in 27% of dogs, and overall health of dogs was rated as excellent by 67.9% of MPOs. About expectations versus reality, 74.4% of MPOs found veterinary costs aligned with expectations, while 20.5% found them higher than anticipated. Exercise required by the dog was as expected for 82.1% of MPO, although 12.8% found it higher. Behavioural expectations were met for 65.4%. Additionally, 78.2% of MPOs were satisfied with their decision to purchase a Maltipoo. Dog appearance was a main motivation for 64.1% of MPOs. Maltipoo’s goodness for children and suitability as a companion pet were the most influencing factors (51.3% and 78.2% respectively). Breed popularity was influential for 15.4%. Despite the high cost of a Maltipoo, this factor was non-influential for 43.6%. The crossbreeds’ reputation for good health was important for 34.6% of owners, as well as long lifespan (38.5%). The results suggest that most MPOs were satisfied with their choice. Dog’s appearance, suitability for living with children and as companion dog emerged as influencing factors in owners’ decision, as well as beliefs on longevity, and better health of designer breeds. This study is a foundation for future research on designer breeds phenomenon in Italy.

Session 3

Poster 17

Understanding Grief Experiences of Pet Loss Among African Americans

M. Whitney¹

¹ Walden University, PhD Candidate, Human Services, Washington Ave S, 55401 Minneapolis, United States

Disenfranchised grief responses and associated stigma from pet loss have been documented among researchers; however, the unique lived experiences of African American adults facing pet bereavement have been underrepresented in research. This qualitative phenomenological study aimed to deepen the understanding of grief responses after pet loss, specifically focusing on African Americans’ experiences of human–pet bereavement. Grounded in the dual process model of coping with bereavement, which emphasizes the oscillation between loss- and restoration-oriented coping strategies, this study explored how African American pet owners experience and make meaning of grief following pet loss. A phenomenological design was employed with a purposeful sample of 23 African American adults in the Midwest United States who had lost a pet during adulthood. Data were collected through semistructured interviews and analyzed using thematic analysis, which reflected the lived experiences of participants through eight primary themes: (a) familial bonds and pet relationships, (b) anticipatory grief, (c) disenfranchised grief, (d) grief confrontation, (e) grief avoidance, (f) post-loss social support, (g) grief inequities, and (h) spiritual and emotional growth. Findings from this study can inform human services researchers and professionals in developing culturally relevant public health policies, programs, and practices. Such contributions not only enhance support systems within diverse cultural contexts but also have significant implications for positive social change by addressing inequities in bereavement care and fostering inclusive approaches to grief support.

Pets in Switzerland – Overview and trends derived from national registry recordings

U. Heikkilä¹, K. Ueda¹, J. L. Morchetti¹, C. Beglinger¹, S. Rieder¹

¹ Identitas AG, R&D, Stauffacherstrasse 130A, 3014 Bern, Switzerland

Companion animals occupy an ever-increasing place in many societies and countries around the world. With over 550'000 dogs, nearly 800'000 registered cats and about 110'000 equids, Switzerland holds a wide diversity of pet animal species within its borders. However, very little official data is available for all other companion animals so far. The majority of pet owners and keepers are female: 65% in the case of dogs, about 70% in cats and equids. Approximately 86% of dog owners keep one dog, whereas this value amounts to 61% in cats and 54% in equids, respectively. Switzerland counts about 6 dogs per 100 permanent residents, 18 cats and one equid. Given these numbers Switzerland belongs to the rear end of European countries regarding dogs per inhabitant but is among the leaders in the case of cats, and average in the case of equids. Unsurprisingly, the highest density of dogs and cats are found in urban areas such as Geneva or Basel, whereas equids are usually kept in a more rural setting. Nearly 40'000 dogs have been imported in 2021, during the pandemic, meanwhile this number decreased to only about 24'000 last year. Imports of cats are at a much lower level of about 9'000 slightly increasing over recent years. In equids imports decreased from approximately 3'800 before the pandemic to roughly 3'000 in 2024. Up to nearly 6'000 dogs and 1'400 equids got exported in the mentioned time period. The leading import and export countries for all three species into and from Switzerland are Germany and France. No export data is available for cats so far, as identification, registration and notification are not mandatory in the latter species. We see a distinct increase of smaller dog breeds over time. Organized breeding is less popular in cats than in the other two animal species. However, some breeds such as Main Coon, British Shorthair and Bengal gain in popularity. About 2'000 dogs are trained as professional guardian dogs for the police, army etc., and about 500 as livestock protection dogs. The gross product of the companion animal sector in Switzerland is an estimated 9 billion Swiss francs, with important shares coming from feed and holding costs. More information can be found on our open data platform "Animal Statistics".

Session 3

Poster 19

Sustainability challenges in the Italian pet sector

P. Crepaldi¹, A. Bionda¹, L. Liotta²

¹ Milan University, Agricultural and Environmental Sciences, Via Celoria 2, 20133 Milano, Italy, ² Messina University, veterinary Sciences, Viale Palatucci, 98168 Messina, Italy

Italy is home to 8.8 million dogs and 10 million cats, with an additional 1-2 million stray dogs and 2.5 million stray cats. Despite only 15% of dogs and < 1% of cats have a registered pedigree, the purebred animal market valued at €165-350 million per year. The Italian pet food industry generates €3 billion annually, selling 673,000 tons of pet food. Beyond food, Italians spend €100 million/year on cat litter and €85 million on accessories. A rough estimate for the impact of pet food sector alone is 1.4-3.8 Mt CO₂e, accounting for 5-12% of agricultural emissions. It consumes 0.13-0.28 km³ of freshwater, equal to 0.8-1.7% of agricultural water use, while occupying 6-9% (1-1.5MHa) of Italy's total agricultural area. Our pilot survey describes 60 Italian dogs and 56 Italian cats. Among dogs, 45% were purebred, including 15% with unregistered pedigrees, while 86% of cats were mixed-breed. Regarding diet, 73% of cat owners provided both dry and wet food, primarily poultry and fish-based, while 65% of dog owners fed only dry food, with ruminant proteins (beef, lamb) as the most common, followed by poultry and fish. Monthly food expenses ranged from €13-58 per cat and €35-60 per dog. Litter usage for cats varied between 4-10 kg per month, costing €5-19, but only 23% of owners purchasing litter chose biodegradable materials. Annual veterinary and medication costs ranged from €64-170 for cats and €160-400 for dogs. Additional costs included pet sitters, boarding, accessories, grooming, training, and insurance. These findings highlight economic and environmental challenges in pet ownership. Sustainable pet care requires multidisciplinary expertise, genetic management, and alternative proteins to reduce the pet food carbon footprint. Life Cycle Assessment should be applied across the supply chain, with environmental certification on packaging to promote sustainable choices. Italy should foster scientific innovation while ensuring environmental responsibility and ethical animal care. The future challenge is sustainable breeding and management of pets, safeguarding biodiversity and animal welfare within a One Health approach.

Supplemental effect of probiotic on growth performance, nutrient digestibility, and blood profile in beaglesS. Cho^{1,2}, Y. Cho³, J. W. Jang^{1,2}, I. H. Kim^{1,2}¹ Dankook University, Animal Biotechnology, 119, Dandae-ro., 31116 Cheonan, South Korea, ² Smart Animal Bio Institute, 119, Dandae-ro., 31116 Cheonan, South Korea, ³ Proxenrem, C&V Research Center, Osongjeup, 28160 Cheongju, South Korea

Dogs have been cohabiting with us for thousands of years. They are the major human companions. The health and well-being of companion animals, just as their owners, depend on the gut microbes. Providing proper care and a nutritionally balanced diet to companion animals is recognized as a part of our responsibility to maintain the health and well-being of pets. Herein, we conduct research to evaluate the effect of dietary *Bacillus subtilis* probiotics (strain pb2441) on beagle's overall health. A total of 8 dogs with an initial body weight (BW) of 5.44 ± 0.28 kg were assigned to one of three dietary treatments in a 3×3 replicated Latin square design for 4 weeks. The experimental diets were as follows: 1) a normal commercial diet (CON); 2) a high-calorie diet (TRT1); and 3) a high-calorie diet supplemented with PB2441 (4×10^7 cfu/ml/day per kg of the BW) probiotic (TRT2). Growth performance indicators such as BW, average daily gain (ADG), and body condition score (BCS) were measured at the initial and the end of weeks 2 and 4. Serum parameters, including glucose, triglyceride, total cholesterol, low-density lipoprotein, high-density lipoprotein, alanine aminotransferase, aspartate aminotransferase, and cortisol levels were measured at the initial and the end of week 4. Additionally, the nutrient digestibility of dry matter, nitrogen, and energy was measured at the end of week 4. Data were analyzed using the GLM procedure of SAS and Duncan's multiple range test was performed to determine the significance between means. The inclusion of probiotic supplementation to a high-calorie diet significantly increased ($P < 0.05$) the BW of the beagle at week 4. Also, trend to improve ($P < 0.1$) ADG during weeks 2-4. Notably, dogs receiving a probiotic diet exhibited significantly lower ($P < 0.05$) BCS and total cholesterol levels compared to the control group. Based on these findings, we suggest that adding probiotics (4×10^7 cfu/ml/day per kg of the BW) to high-calorie diet would be beneficial to enhance the growth performance and to reduce the body condition score in beagles.

Session 3

Poster 21

A Preliminary investigation on the effect of dietary glucan from *Aureobasidium pullulans* in Beagle healthS. Cho^{1,2}, J. W. Jang^{1,2}, D. Min³, I. H. Kim^{1,2}¹ Dankook University, Animal biotechnology, 119, Dandae-ro, 31116 Cheonan, South Korea, ² Smart Animal-Bio Institute, 119, Dandae-ro, 31116 Cheonan, South Korea, ³ Cosmax Pet Co. Ltd., 106, Goryeomsandan-ro., 17794 Pyeongtaek, South Korea

β -Glucans affect the immune system and have antitumor activity; therefore, they are being investigated as immunomodulator adjuvants. Herein, we aimed to investigate preliminary research on the effect of a specific β -glucan (Exopolysaccharide), derived from *Aureobasidium pullulans* SM-2001 on growth performance, nutrient digestibility, fecal microbial, and blood profile in beagle dogs. A total of eight beagles with an initial body weight of 10.70 ± 1.79 kg were assigned to one of two dietary treatments: 1) CON, Basal diet; 2) TRT, CON + β -glucan (180 mg/day) for ten weeks. Each treatment has 4 replications, with 1 animal per replication. Growth performance (average daily feed intake, daily gain, and body condition score) was measured at initial and at the end of the trail. Additionally, nutrient digestibility (dry matter, nitrogen, and energy), fecal microbiota (*Lactobacillus* and *E. coli*), and blood profile (calcium, phosphorous, vitamin D, parathyroid hormone, alkaline phosphatase, osteocalcin, C-reactive protein, insulin-like growth factor-1 (IGF-1), growth hormone, lactate, creatinine, insulin, total protein, albumin, ferritin, lactate dehydrogenase (LDH), and immunoglobulin (IgG) levels) were measured at the end of the trail. All data were analyzed using the GLM procedure of SAS. A T-test was performed to know the statistical difference between the treatments. Beagles fed a diet supplemented with 180 mg/day glucan had significantly increased calcium, IGF-1, growth hormone, IgG, and WBC levels in serum than the CON control group ($P < 0.05$), suggesting that glucan supplementation has a positive impact on immune function and bone health in beagles. Furthermore, no adverse effects were observed on growth performance, nutrient digestibility, or fecal microbiota, indicating that the glucan supplement is safe and well-tolerated. Based on these findings, we suggest that adding 180 mg/day glucan would be beneficial for enhancing the immune response and promoting overall health in beagles

Therapeutic Effects of Hovenia Dulcis Thunb Extract on beagles' liver healthJ. W. Jang^{1,2}, S. Cho^{1,2}, D. Min³, I. H. Kim^{1,2}¹ Dankook University, Department of Animal Biotechnology, 119, Dandae-ro, 31116 Cheonan, South Korea,² Smart Animal Bio Institute, 119, Dandae-ro, 31116 Cheonan, South Korea, ³ Cosmax Pet Co. Ltd., 106, Goryeomsandan-ro., 17794 Pyeongtaek, South Korea

Hovenia dulcis Thunb. (Rhamnaceae), also known as oriental raisin tree, is used in traditional herbal medicine. Its extracts have been reported to show various pharmacological effects such as hepatoprotection, antitumor, anti-atopic dermatitis, anti-lipid peroxidation, anti-steatotic, anti-inflammatory, and antiallergic activities. To date, no reports have existed on the therapeutic effects of *hovenia dulcis* thunb (HDT) extract on beagles. Thus, this study investigated the beneficial effects of HDT on liver health in beagle dogs. A total of 8 beagles with an initial body weight of 9.21 ± 0.76 kg were assigned to one of two dietary treatments in a 2×2 Latin square for 10 weeks. The test treatments were as follows: CON, basal diet; TRT, CON + 90 mg/day HDT extract. The growth performance (average daily feed intake, daily gain, and body condition score) was measured at initial, week 4, 6, and 10. The fecal and serum samples were collected in weeks 4 and 10 for metabolomic and 16S rDNA analysis, respectively. All data were analyzed using the GLM procedure of SAS. There were no changes in the growth performance, while metabolic pathway analysis using the KEGG database revealed significant alterations in Pyrimidine, Histidine, beta-Alanine, pantothenate and CoA biosynthesis, sulfur, primary bile acid biosynthesis, Taurine and hypotaurine levels. The extract from the HDT resulted in beneficial changes in the abundance of core microbial communities, particularly in the abundance of bacteria such as *Collinsella intestinalis* and *Allobaculum stercoricanis*, and in the production of SCFAs such as butyrate. These changes likely contributed to a more balanced gut-liver axis, thereby improving liver function through better bile acid metabolism, reduced inflammation, and improved lipid metabolism. From this, we suggest that adding 90 mg/day HDT extract to beagles' diet would be beneficial to enhance gut and liver health without disrupting the overall microbial community.

Session 3

Poster 23

Dietary inclusion of hydrolyzed feather meal on nutrient digestibility and fecal quality in adult dogsR. Armone¹, F. Balouei², A. Randazzo¹, V. Nava³, A. F. M. Alizzi¹, M. Barbato¹, B. Stefanon², B. Chiofalo¹¹ University of Messina, Veterinary Sciences, Via Palatucci, 98168 Messina, Italy, ² University of Udine, Agri-food, Environmental and Animal Science, Via delle Scienze, 206, 33100 Udine, Italy, ³ University of Messina,

Biomedical, Dental and Morphological and Functional Imaging Sciences, Via Consolare Valeria, 1, 98125

Messina, Italy

There is increasing interest in alternative protein sources to enhance the sustainability of agri-food systems. This study assessed the response of healthy dogs to a diet including 7% hydrolyzed feather meal, by evaluating nutrient digestibility and fecal quality. Eight dogs (four adult female and four adult male English Setters) were fed two extruded isoenergetic, isonitrogenous, and isolipidic commercial kibble diets over 45 days. The PM diet contained poultry meal as source of proteins of animal origin (160 g/kg of feed), whereas the HFM diet included 90 g/kg of poultry meal and 70 g/kg of hydrolyzed feather meal. Fecal consistency scores (FCS) were assessed, and fecal samples were collected and analyzed for chemical composition, organic acids and biogenic amines at days 0, 3, 7, 15, and 45. Nutrient digestibility was also calculated. A generalized linear mixed model was used to analyze significant differences between groups, where each focal analytical parameter served as response variable, Diet (PM or HFM), Time and their interaction (DxT) as fixed effects, and the experimental phase as random variable. Statistical significance was assumed at $\alpha = 0.05$. Throughout the study, FCS remained optimal, ranging from 2.2 to 2.5 for both diets. The Diet had a significant effect on the digestibility of dry matter, starch, and organic matter ($P < 0.01$), whereas the DxT interaction had no significant effect on nutrient digestibility ($P > 0.05$). The concentration of all organic acids in feces were significantly affected by the Diet ($P < 0.001$). The DxT interaction significantly influenced organic acids ($P < 0.001$) except for acetate ($P > 0.05$). Both the Diet and the DxT interaction had significant effect on all biogenic amines ($P < 0.01$). This preliminary study suggests that dogs can adapt to moderate concentrations of hydrolyzed feather meal while maintaining nutrient digestibility.

Application of the E-tongue for evaluating fecal biogenic amines in dogs fed hydrolyzed feather mealF. Accetta¹, R. Arnone¹, A. R. Di Rosa¹, B. Chiofalo¹¹ University of Messina, Veterinary Sciences, Via Palatucci, 98168 Messina, Italy

Previous studies have shown that electronic sensory technologies (E-eye, E-tongue, E-nose) can serve as effective and rapid alternatives to official analytical methods for evaluating petfood digestibility. In this study the impact of substituting 7% of poultry meal with hydrolyzed feather meal on digestive processes was investigated using the E-tongue to detect fecal biogenic amines in adult dogs. Six adult female English Setter dogs were divided into two groups and fed two different commercial kibble diets over a 45-day period. The control group (CTR) received a diet based on poultry meal as the protein source, while the treated group (TRT) was fed a diet consisting of a mix of poultry meal and hydrolyzed feather meal. A crossover experimental design was applied. Fecal samples were collected on Day 0 and after 3, 7, 15 and 45 days, and analyzed using a potentiometric E-Tongue (α Astree, Alpha MOS, Toulouse, France) equipped with seven chemical sensors. Biogenic amines were also quantified by high-performance liquid chromatography with fluorescence detection. The dataset was subjected to statistical analysis using Discriminant Function Analysis (DFA) to assess the effect of time (Days 0, 3, 7, 15, 45) for each diet, and the effect of diet (TRT vs. CTR) independently of time. Additionally, a data fusion approach was applied to validate the instrumental sensory results through quantitative identification of catabolites, using traditional chromatographic analyses. The DFA plot generated from the E-tongue sensor signals revealed a clear separation between the CTR and TRT groups, with the maximum Discrimination Index (DI = 100) on Days 0, 3, and 15, and a DI of 95 on Days 7 and 45. The TRT group exhibited the highest levels of putrescine and cadaverine at all time points, while the CTR group showed the highest levels of spermine on Days 0, 3, and 45. These findings were consistent with the results obtained from chromatographic analysis. Data confirm that the E-tongue technology is a reliable and rapid alternative to traditional methods. Its application is particularly valuable for assessing the impact of dietary strategies on gastrointestinal health.

Optimizing Canine Nutrition: Evaluating Legumes, Wheat, and Quinoa as Dietary ComponentsJ. Litzenger¹, N. Paßlack², E. M. Saliu¹, J. Schulze Holthausen¹, J. Zentek¹¹ Institute of Animal Nutrition, Veterinary Medicine, Königin-Luise-Str. 49, 14195 Berlin, Germany, ² Chair of Animal Nutrition and Dietetics, Veterinary Medicine, Schönleutnerstraße 8, 85764 Munich/Oberschleißheim, Germany

The inclusion of plant-based feed and cereals in canine diets and suitability of cereals is questioned, with growing demand for so-called "pseudo-cereals". This feeding study evaluated diets containing either poultry protein or a combination of pea and bean protein concentrate, with or without the addition of a conventional cereal (processed wheat flakes) or a pseudo-cereal (quinoa). The study followed a three-factorial design, with carbohydrate source (wheat or quinoa), protein source (animal or plant-based) and dietary protein concentration (meeting or exceeding essential amino acid requirements by 1.5 times) included. After a three-week adaptation period, feces, urine, and blood samples were collected in the fourth week. Statistical analysis included three-factorial ANOVA and Tukey's test ($p < 0.05$). The dietary protein source significantly influenced ($p < 0.001$) the microbial diversity in feces, with animal protein diets yielding the highest microbial richness. Animal protein diets increased the fecal presence of Fusobacteria ($p < 0.001$), while plant protein diets promoted Actinobacteria ($p = 0.040$). Urinary pH varied based on diet composition. Dogs fed wheat and poultry protein had lower urinary pH values (5.73–6.30) compared to those fed quinoa (7.20–7.47). An exception was observed when wheat was combined with plant protein at a higher protein dosage, leading to a pH of 7.42. As expected, urinary nitrogen concentrations increased with higher protein intake. Protein source had minor effects on hematological parameters, but serum urea and albumin concentrations were significantly influenced by dietary protein content ($p < 0.001$; $p = 0.004$). Notably, alanine aminotransferase (ALT) activity increased with quinoa-containing diets compared to wheat-based diets ($p = 0.017$), and higher bilirubin levels were observed ($p = 0.031$). Alkaline phosphatase (ALP) activity was elevated with quinoa consumption ($p = 0.030$) but decreased with higher protein intake compared to an adequate protein supply ($p < 0.001$). Conclusion: The choice of protein source, dietary protein concentration, and carbohydrate type influences key physiological parameters, including hematological markers, urinary pH, and fecal microbiota composition in dogs.

Effect of a diet with reduced levels of phenylalanine and tyrosine on coat pigmentation in adult white-coated dogs

A. Ruggiero¹, M. Fantinati², C. Caterino¹, B. Piccirillo¹, A. Vastolo¹, M. I. Cutrignelli¹

¹ Università degli studi di Napoli, Department of Veterinary Medicine and Animal Production, Via F. Delpino, 1, 80137 Naples, Italy, ² Farmina Pet Food, R&D, Via Nazionale delle Puglie, 41, 80035 Nola, Italy

The coat pigmentation is determined by the relative concentration of two pigments: eumelanin and pheomelanin, both synthesized from the amino acid tyrosine (Tyr). The latter can be metabolized directly from the diet or synthesized by hydroxylation of the essential amino acid phenylalanine (Phe). Although the synthesis of pigments is genetically determined, the concentration of the aforementioned nutrients may influence melanogenesis. The present double-blind study was conducted on a group of 12 healthy Maltese dogs, 8 males and 4 females (age 5.6±2.3 years; body weight 2.78±0.37 kg; BCS 3.9±0.4 on a 9-point scale). The subjects were randomized in 2 groups homogeneous for gender, BCS, body weight, and age. For the purpose of the study, two isocaloric, iso-protein diets, identical in composition, were formulated with different levels of Phe and Tyr: a high-amino acid control diet (Phe 4.63 g/Mcal + Tyr 3.66 g/Mcal) and a low-amino acid test diet (Phe 2.21 g/Mcal + Tyr 1.52 g/Mcal). The trial lasted 25 weeks (3 of washout and 22 of dietary trial). Spectrophotometric (Spectro-guide® 45/0 gloss, BYK Gardner) evaluation of coat colour in 4 distinct areas of the body (left shoulder, right shoulder, withers and rump) was performed on a monthly basis. According to the international standard for colourimetry (CIE Lab), a uniform colour is characterised by a brightness axis L*; a red-green colour axis a*; and a yellow-blue colour axis b*. A significant reduction ($p < 0.01$) of the wither's parameter a* was observed from week 15 onwards in the test group, suggesting decreased synthesis and deposition of pheomelanin in the hair shaft. This was also reflected in a macroscopically visible improvement. This finding suggests that reducing the dietary levels of the amino acids (Phe and Tyr) involved in melanogenesis can reduce the presence of off-white discoloration areas, with decreased degree of reddening, on the coat of adult white-coated dogs.

Session 3

Poster 27

Towards a scientific standard of dentition

A. Bionda¹, L. Liotta², P. Crepaldi¹

¹ Milan University, Department of Agricultural and Environmental Sciences, Via Celoria 2, 20133 Milan,

Italy, ² Messina University, Department of Veterinary Sciences, Messina University, Viale Palatucci 13, 98168 Messina, Italy

Dog breed standards provide a description of the facial region, with details on muzzle and teeth. However, there is significant variability in details provided, e.g. according to the breed's country of origin, and in the tolerance to deviations from a complete dentition. In light of this, we evaluated 341 dog breed standards approved by the Fédération Cynologique Internationale (FCI). The cranio-facial ratio was absent in 31% of the standards, including many brachycephalic breeds. By contrast, almost all breeds in Group 1 (Sheepdogs and Cattle Dogs) included this information. Groups 2 (Molosses, Pinscher, and Schnauzer) and 9 (Companion and Toy Dogs) displayed the greatest variability and the lowest average ratios, whereas Group 6 (Scent Hounds) and 10 (Sighthounds) were more homogeneous, with predominantly meso-dolichocephalic breeds. Scissor bite was accepted in 93% of the breeds and considered a disqualifying fault in only 6%. However, 13% of Group 2 and 38% of Group 9 preferred an undershot bite. PM1 and M3 were the most tolerated missing teeth, being allowed in 18% and 13% of the standards, respectively. Groups 1, 7 (Pointing dogs), and 4 (Dachshunds) were the most permissive regarding dental agenesis. Conversely, no breeds in Group 8 (Retrievers, Flushing, and Water Dogs) allowed missing teeth. The lack of scientific data on dental agenesis in dogs limits the ability to define breed standards objectively. Studies comparing the prevalence of missing teeth across breeds and mixed-breed dogs are necessary to determine whether this trait represents a genetic defect or an evolutionary adaptation to domestication and dietary changes. Such studies could also justify different levels of tolerance across breeds or groups. In conclusion, significant variability exists among dog breed standards in describing dentition and muzzle conformation and, in the context of conformation dog shows, judges often interpret these traits inconsistently across breeds and countries. A harmonized collection of data and evaluations and a more uniform and scientific approach to defining breed standards are essential for ensuring a fair and welfare-oriented canine evaluation.

On the necessity and impossibility of breeding working dogsP. Arvelius¹¹ Private, Edavägen 31, 74193 Knivsta, Sweden

Dogs have proven to be enormously useful for military and police work. However, animals well suited for these tasks have since long been in short supply worldwide. To function well in service, dogs are required to be both healthy and mentally strong. The latter typically requires high levels of confidence (nerve stability, hardness, courage) and engagement (competitiveness, hunting drive, prey drive, liveliness). These traits often make the dogs demanding to handle, and less suited outside a professional working environment. Naturally, hobby breeders usually have other breeding goals than what is optimal for service. Furthermore, setting up and running a breeding program takes a long time and requires substantial investments, and the market is unstable. The consequence is that few, if any, large commercial breeding programs exist. Only occasionally, governmentally financed organisations set up breeding programs large enough to allow for systematic selection of new breeding animals among the dogs produced, thereby making possible a genetic progress without unreasonable inbreeding-related risks. The few programs that have existed were typically shut down within one or few decades, also when they were successful. The reason was usually decision makers lacking knowledge and engagement, or not having enough sense of long-term responsibility versus short-term savings. The fact that the very same mistake of cancelling well-run breeding programs happens over and over again, resulting in a decreased capacity for military and police organisations, calls for actions to prevent it from continuing to happen. An organisation such as EAAP can play a role in such actions by, for example, providing best practice and scientifically based information directed at decision makers; facilitating collaborations between breeding programs; arranging platforms for education, discussion and exchange of experience among breeding managers; advocating the essential importance of involving animal breeding expertise.

No evidence of increased stress levels of service dogs, signal dogs and therapy dogs in comparison to family dogs without special tasksL. Huber¹, S. Mliner¹, S. Bruckner¹, K. Weissenbacher¹¹ Messerli Research Institute, University of Veterinary Medicine Vienna, Veterinaerplatz 1, 1210 Vienna, Austria

Service dogs support people with motor disabilities, work together with their owners on a daily basis and are confronted with sometimes challenging tasks. The task of signal dogs for diabetic people is to perceive and signal changes of the human metabolism such as hyper- and hypoglycemia. Because they are on constant alert they can do this even before humans perceive any symptoms. Therapy dogs get deployed specifically to get in contact with different types of people and provide help with their presence one or two times a week. Although an increasing number of research projects about both the methods and the benefits of various kinds of assistance dogs for humans have been conducted, we still suffer from a lack of knowledge about the well-being and challenges for the dogs themselves. This is important because stress may eventually lead to chronic diseases in these dogs. In two studies, the cortisol levels in the saliva of service, signal and therapy dogs have been compared with family dogs with no special tasks to find out whether their stress level is elevated. As cortisol levels can vary greatly over the course of a day, the samples were taken three times a day for seven consecutive days. Because travelling to the lab may be itself stressful, the measurements were taken by the human partners or caregivers in their homes. Results show that there is no significant difference between saliva cortisol levels of signal, therapy and family dogs, with working stress values being similar to those of normal stress. This suggests that signal dogs for diabetic people do not suffer from a higher cortisol level than therapy dogs and normal family dogs. Surprisingly, we found that service dogs for people with motor disabilities had even lower cortisol levels than family dogs. Possible reasons could be the regulated daily routine of service dogs and a strong trust between humans and dogs, which may result in lower stress levels.

The effects of PTSD-assistance dogs' work on their salivary cortisol levels and their handlers' Quality of life

K. Gerwisch¹, K. Weissenbacher¹, M. Proyer³, R. Palme², L. Huber¹

¹ Messerli Research Institute, University of Veterinary Medicine, Vienna, Comparative Cognition, Veterinärplatz 1, 1210 Vienna, Austria, ² University of Veterinary Medicine, Vienna, Department of Biological Sciences and Pathobiology, Veterinärplatz 1, 1210 Vienna, Austria, ³ University of Vienna, Department of Education, Porzellangasse 4, 1090 Vienna, Austria

Assistance dogs for people with Posttraumatic Stress Disorder (PTSD) support their handlers by performing tasks that help mitigate symptoms such as intrusive thoughts, emotional numbing, dissociation, flashbacks, and hyperarousal. While limited research exists on the impact of PTSD-assistance dogs on their caregivers' quality of life (QoL), most studies focus on American war veterans, with few addressing the welfare of the dogs themselves. In our study, we examined the QoL of PTSD-assistance dogs' handlers (N=24) in Austria and Germany through a qualitative online questionnaire based on the Capabilities Approach. We also explored whether PTSD-assistance dogs (N=9) experience distress by measuring their salivary cortisol levels. Samples were collected by the handlers three times a day on seven consecutive days. We then compared the cortisol levels to those of companion dogs (N=8) and diabetic-signal dogs (N=9), whose workload is similar to that of PTSD-assistance dogs (values measured in a prior study by Simone Bruckner, 2019). Our hypotheses were: PTSD-assistance dogs positively impact their handlers' condition. PTSD-assistance dogs' cortisol levels are higher than those of companion dogs but similar to those of diabetic-signal dogs. Results showed that PTSD sufferers' QoL can be improved by having an assistance dog, e.g. by enhancing social interactions. However, new social barriers, such as access issues, might emerge. Surprisingly, PTSD-assistance dogs exhibited significantly lower salivary cortisol levels than the control groups. We concluded that a positive relationship between PTSD-assistance dogs and handlers can reduce stress on both sides, and well-tuned training can prevent stress in the dogs' daily lives.

Session 4

Theatre 4

Genetic parameters of personality traits in dogs based on behavioral assessment and questionnaire information

E. Strandberg¹, K. Nilsson¹, K. Svartberg¹

¹ Swedish University of Agricultural Sciences, Department of Animal Biosciences, P O Box 7023, 75007 Uppsala, Sweden

A new behavior and personality assessment in dogs (BPH) was created in Sweden in 2012. Since the start of BPH, questionnaire data based on an extended version of C-BARQ have been collected to describe the everyday behavior of dogs. Our aim was to estimate heritability and genetic correlation for personality traits based on BPH or questionnaire data for eight breeds: American Staffordshire Terrier, Golden Retriever, Labrador Retriever, Lagotto Romagnolo, Nova Scotia Duck Tolling Retriever, Perro de Agua Español, Rhodesian Ridgeback, and Staffordshire Bullterrier. The number of BPH records ranged from 862 for Lagotto Romagnolo to 2462 for Labrador Retriever. Average heritability across all breeds was 0.21 for Sociability, 0.22 for Playfulness, 0.16 for Non-social fearfulness, 0.26 for Aggressiveness, and 0.22 for Boldness; all traits defined based on BPH. The genetic variation between breeds was larger than the genetic variation within breeds for Sociability, Playfulness, and Boldness. Estimates of heritability for questionnaire traits were more variable, owing to fewer observations, and averages ranged from 0.06 to 0.28. The genetic correlation between BPH traits, on the one hand, and corresponding questionnaire traits, on the other hand, was consistently high: between Sociability and Stranger-directed interest (average 0.93) and Stranger-directed fear (-0.89); between Playfulness and Human-directed play interest (0.77); between Non-social fearfulness and Non-social fear (0.77); between Aggressiveness and Stranger-directed aggression (0.57); and between Boldness and Stranger-directed interest (0.78) and Stranger-directed fear (-0.80). Often, we could also see that a measure at BPH involving human interactions also extended to measure reactions to interactions with other dogs, e.g., a strong genetic correlation between Sociability and Dog-directed interest (0.58). In summary, selecting dogs based on traits defined at BPH is expected to result in behavioral changes not only when measured at BPH but also changes in everyday behavior in an expected way.

Not just for fun - Cognitive tests can predict dog's everyday behaviorK. Tiira^{1,3}, S. Junntila¹, A. Valros¹, K. Mäki²¹ University of Helsinki, Department of Production Animal Medicine, P.O. Box 66, 00014 Helsinki, Finland,² International Partnership for Dogs, <https://dogwellnet.com/>, - -, Finland, ³ smartDOG Ltd, Pietilänkatu 5, 11130 Riihimäki, Finland

A huge amount of cognitive research has been done on dogs, but does the research only tell us about the dog's behaviour in the test room, or does it reflect the dog's behaviour in everyday life? Dog cognition research has been characterised by very small sample sizes, studies have rarely considered the genetic background of the subjects, and all breeds have been combined, assuming that there are no differences between breeds. We used the results of the commercial smartDOG test battery to investigate whether adult and puppy cognitive test scores are associated with dog behaviour in everyday life (C-BARQ, DIAS). We were also interested in the possible predictability of puppy tests (administered at 4-7 months of age) on adult behaviour. Many cognitive traits appear to be relatively stable from 5 months of age or show some improvement with age. In adult dogs (N=987), several cognitive tests were associated with everyday trainability, impulsivity, learning speed and problem behaviour. In addition, certain cognitive tests in puppies (N=227) were able to predict adult characteristics such as trainability, impulsivity, energy level and fearfulness. Breeds differed in many cognitive test sections and, most importantly, on cognitive traits that influence trainability, impulsivity and problem behaviour. Females show better inhibitory control and more human-oriented behaviour than males – also traits strongly associated with trainability. Preliminary results from heritability analyses of several cognitive traits (based on actual smartDOG test data) will be presented at the meeting.

How do Danish dog owners use cages for their dogs?H. Proschowsky¹, I. Czycoll¹, L. M. Jønsson¹, D. J. Laurents¹, P. Sandøe^{1,2}¹ University of Copenhagen, Dep. of Veterinary and Animal Sciences, Groennegaardsvej 8, 1870 Frederiksberg, Denmark, ² University of Copenhagen, Dep. of Food and Resource Economics, Rolighedsvvej 23, 1958 Frederiksberg, Denmark

The use of cages for managing companion dogs seems to be on the rise and gives rise to controversies. However, numbers on how many dog owners use cages, to which extent and for what purposes they use them are lacking. To get an overview of the current situation, a questionnaire was created and distributed via social media to Danish dog owners. A cage was defined as a small, demarcated area for indoor use, where the dog has limited freedom of movement (e.g. transport cages, playpens, or built-in furniture cages). The questionnaire consisted of 18 questions covering information about the dog, the cages and their use. The respondents were also asked about their views on different use of cages and about actions undertaken to accustom their dog to the cage. A total of 3201 owners responded and nearly half of them (47%) used the cage daily. Family dogs, sports dogs and show dogs were most prevalent and 57% of the dogs were between one and five years old. A total of 73.5% used a cage for transportation "often" or "very often" while cages were used in relation to dog shows by 38% and for training activities by 36% of the owners. 26% of the owners put their dog in a cage for the night or during home alone time. The weighted average for use of cages was 23.2 times per month and 4.3 hours per day. When asked what the cage could provide, 79% of the owners agreed with the statement "the cage is a safe and familiar place for my dog". 29% of the dog owners had not trained their dogs to the cage. The data from the present study will be subject to further statistical analysis to identify relevant linkages. There are currently very few data-based studies in the field, but a recent French/Israeli study reported a quarter of the dog owners using cages. The higher number in the present Danish study may be due to the fact that the study was based on convenience sample and the responding dog owners may have been more interested in the use of cages than the average. This study adds to literature to form a baseline for further trials including observational studies to provide guidelines for the use of cages for dogs.

Brachycephalic phenomenon. The dark fascination of flat faced dogsS. Boero¹, S. Cannas¹, C. Palestirini¹, A. Garegnani¹, G. V. Berteselli¹¹ University of Milan, Department of Veterinary Medicine and Animal Science, Via dell'Università 6, 26900 Lodi, Italy

This study aimed to investigate dog-human relationship, behavioural features, health status perception, motivations and satisfaction of owning brachycephalic dog. The study reports a large-scale online survey with valid responses from 320 Brachycephalic dogs' owners (BDOs) (French and English bulldog, Pug), and 408 Non-brachycephalic dogs' owners (NBDOs). To explore relationship quality and behavioural traits "Dog-Owner Relationship Scale" (DORS) and "Canine Behavioral Assessment and Research Questionnaire" (CBARQ) were used. Specific questions on owner's motivations, perception, and satisfaction were also included. Dog-Owner interaction (DOI) and Perceived Emotional Closeness (PEC) scores were significantly higher in BDOs (DOI: 4.31+/-0.4; PEC: 4.55+/-0.44) ($p \leq 0.05$). The Perceived Cost (PC) score was higher in NBDOs (3.84+/-0.44) ($p \leq 0.05$). Considering only the BDOs, the PEC score was higher in owners who chose these breeds for their character ($p \leq 0.05$); the PC and DOI score were related to health check status ($p \leq 0.05$). The mean scores of Trainability ($p < 0.001$), Excitability ($p = 0.003$) and Separation-related behaviours ($p = 0.024$) were significantly higher for BDOs. Comparing the brachycephalic breeds, Pug obtained the higher score for Excitability ($p = 0.007$), Separation-related behaviours ($p = 0.005$), and Attachment/attention seeking ($p = 0.011$). Character was the main motivation for acquiring these breeds (94.1%). 81% of BCOs assessed the dog's health status from good to excellent, despite breed-related disorders' occurrence (respiratory and gastroenteric diseases). Additionally, the satisfaction of BDOs with specific aspects (veterinary costs, physical activity level, interaction, and dog behaviour) met the expectations. The neotenic appearance of a dog can impact the perception of its behaviour and relationship quality. The cuteness effect elicits increased attention and a willingness to care for these individuals. Psychological mechanisms play a significant role in under-recognizing poor welfare and normalizing breed-related problems. By grasping the complexity of the brachycephalic phenomenon, successful implementation of strategies to address welfare issues can be achieved.

Session 5

Theatre 1

EU Commission proposal on the welfare of dogs and cats and their traceabilityP. Gomez Garcia¹, A. Gavinelli¹, M. Raebisch¹¹ EU Commission, DG SANTE, Rue Froissart, 1030 Bruxelles, Belgium

EU Commission proposal on the welfare of dogs and cats and their traceability. The European Commission adopted in 2023 the first ever proposal for a Regulation on the welfare of dogs and cats and their traceability[1]. The data supporting this legislative proposal is summarized in a Staff Working Document[2] (SWD), based on the input from initiatives under the EU Platform on Animal Welfare[3], an EFSA report [4], the EU Enforcement Action on illegal trade of cats and dogs[5], stakeholder consultations and a 2023 Eurobarometer were 74% of EU citizens consider that companion animals should be better protected.[6] Three key issues were identified. First, the un-harmonized single market, due to the lack of EU rules creates an uneven playing field for operators. Secondly, the suboptimal level of welfare of dogs and cats. Thirdly, the limits of the existing traceability system for dogs and cats. The proposal is structured around several pillars. Chapter II lays down obligations for operators of establishments breeding, keeping and placing dogs and cats on the Union market, including pet shops and shelters. General welfare requirements tailored to each type of establishment, and specific requirements apply. Chapter III covers the traceability of dogs and cats placed on the Union market or supplied in the Union. All dogs and cats, including those imported from third countries, must be identified by microchips and registered in interoperable national databases. Chapter V requires third countries importing dogs and cats into the Union to comply with EU requirements or equivalent. The Council agreed on a negotiating mandate on the proposal in June 2024. [8] Negotiations with the European Parliament are ongoing. [1] EUR-Lex – 52023PC0769 – EN – EUR-Lex[2] SWD(2024) 88 final[3] Platform conclusions[4] Scientific and technical assistance on welfare aspects related to housing and health of cats and dogs in commercial breeding establishments – 2023 – EFSA Journal – Wiley Online Library[5] EU Enforcement Action on illegal trade[6] Attitudes of Europeans towards animal welfare[7] EUR-Lex – 02017R0625-20220128 – EN – EUR-Lex[8] 2023/0447(COD)

Breeding Healthy Pets: supporting sustainable dog and cat breeding in Flanders

E. Beckers¹, B. J. G. Broeckx², S. Janssens¹, N. Buys¹

¹ Center for Animal Breeding and Genetics, KU Leuven, Department of Biosystems, Kasteelpark Arenberg 30, 3001 Leuven, Belgium, ² Laboratory of Animal Genetics, UGent, Department of Veterinary and Biosciences, Heidestraat 19, 9820 Merelbeke, Belgium

Cats and dogs suffer from numerous genetic diseases, sometimes linked to breed standards, and many breeds have low genetic diversity. Flanders (Belgium) aims to establish a sustainable breeding policy for dogs and cats, by focusing on two main objectives: 1) reducing the frequency of disease-causing variants and the prevalence of genetic diseases without known causal variants and 2) maintaining or potentially increasing the genetic diversity of breeds. To achieve these goals, the Animal Welfare Department of the Flemish Government introduced a breeding decree, defining conditions for issuing pedigrees. The scientific project “Breeding Healthy Pets”, funded by the Flemish Government, was launched to support the decree through research. Amongst others, the project recommends mandatory screening tests for each breed and offers breeding advice for genetic diseases. Starting January 1st, 2025, dogs and cats born in Flanders can only receive a pedigree from a recognized (Flemish) pedigree organization if the parentage is confirmed through DNA testing and the animal is bred according to the approved breeding program. The latter includes mandatory tests, accompanying breeding advice, and measures supporting genetic diversity. Currently, five pedigree organizations (two for dogs and three for cats) are recognized by the Flemish government, with 2 more applications pending. Fifty-five breeding programs have been approved for 74 breeds and breed varieties. In the coming months and years, Breeding Healthy Pets and the Flemish Government will develop a central database to store animal information (date of birth, sex, breed, etc.), pedigree information, and screening results. In the long term, we aim to include SNP information in this database and integrate a selection tool. This tool will enable breeders to assess the genetic suitability of parent combinations based on relatedness, test results, and compliance with the approved breeding program.

Session 5

Theatre 3

Monitoring legal skull criteria for brachycephalic dogs in the PetScan diagnosis registration system

H. Fieten¹, E. De Boer¹, L. Vree¹, M. A. Van Hagen¹

¹ Fac. of Vet. Med., Utrecht University, Clinical Sciences, Yalelaan 108, 3584 CM Utrecht, Netherlands

In the Netherlands, breeding dogs with a high risk of health or welfare issues related to extreme conformational traits is prohibited. To endorse breeding of healthy dogs, six criteria related to skull conformation were legally implemented in 2019 to provide clear guidelines to dog breeders on the prevention of health and welfare issues. These criteria include: no abnormal breathing sounds in rest, open nostrils, cranio-facial ratio (CFR) > 0.3, absence of a nasal fold irritating the eyes, limited visibility of the white of the eye and the possibility to close the eyes completely. An interactive scoring form for these six criteria was included in the diagnosis registration system PetScan. PetScan is implemented in practice management systems of veterinary clinics and is used to record patient diagnoses and the six skull criteria. General patient information including age, sex, breed, origin of the dog and whether the dog was bred with a FCI pedigree is also recorded. The data collected through PetScan facilitates monitoring of the effect of legal implementation of the criteria in the Dutch population of brachycephalic dogs. Currently, these skull criteria were recorded for 832 dogs. The top 3 most common breeds recorded were the French bulldog (n=192), cross-breed (n=108) and Chihuahua (n=63). The majority of dogs (64.5%) were bred in the Netherlands. The percentage of dogs that violated the criteria varied from 0% in Rottweilers to 100% in pugs and English bulldogs. For Shih-Tzu's and Chihuahua's the CFR of dogs bred with an FCI pedigree was significantly lower than dogs that were bred without pedigree. In the Shih-Tzu's that were born in the Netherlands, there was a significant increase in median CFR from 0.24 to 0.31 in dogs that were born before implementation of the criteria (n=32) and dogs born thereafter (n=7). In French bulldogs, there was no significant difference. Registration of skull criteria by veterinarians via the PetScan system provides breeders, veterinarians and policy-makers, with a powerful monitoring tool for effect of implementation of breeding criteria. Population effects in improvement of skull conformation upon implementation of guidelines differs between breeder communities.

The Kennel Club's Efforts in Managing Pedigree Dog Breeds: Strategies for Long-Term SustainabilityJ. Ilska¹¹ *The Kennel Club, Health, 10 Clarges Street, W1J 8AB London, United Kingdom*

The world of pedigree dog breeding has undergone significant changes over the past few decades. The selection goals in this field have evolved from primarily functional traits such as herding or hunting, to those that focus on appearance, temperament and health. While the selection for appearance and temperament is largely subjective, with a lack of phenotypic datasets, selection for health benefits has grown rapidly, allowing for enhanced volumes of health test results. The structure of the industry has also transformed, from a few large kennels that produced the majority of a breed's population, to a large number of small-scale breeders, each with only a few breeding animals and often breeding just once. This makes management strategies developed and tested in livestock, such as optimum contribution methods, difficult or even impossible to implement in pedigree dog breeding. In the absence of a single decision-maker for each breed, the responsibility for managing breed populations is often placed on kennel clubs, which serve as registration bodies for pedigree dogs. The Kennel Club in the United Kingdom (KC) is the oldest such organisation, founded in 1873. Currently, the KC recognises 224 breeds, with the electronic database containing records for nearly 12 million dogs. In this talk, we will explore the data collected by the KC, and its application in the context of pedigree dog population management. We will discuss the available health testing tools and the progress achieved through them to date, as well as introduce the first standardised approach to health test prioritisation, referred to as the Health Standard. Further, we will examine the structure of the pedigree dog population and the changes it has undergone over the last three decades, based on meta-analyses of within-breed estimates for a range of demographic parameters, including trends in population size, the percentage of dogs used in breeding, the use of purpose-bred and imported dogs in breeding, as well as statistics related to litter sizes. We will conclude by outlining our approach to the management of genetic diversity and the challenges it presents, given the nature of pedigree dog data.

Session 6

Theatre 2

Managing genetic variation in dog breeds – from a practical and organisational point of viewS. Malm Persson¹, H. Skarp¹¹ *Swedish Kennel Club, Dept. for Breeding and Health, Box 771, 191 27 Sollentuna, Sweden*

Dog breeding is generally conducted in closed populations, which over time inevitably leads to increased inbreeding and reduced genetic variation. There are several ways in which Kennel Clubs and breeders can help preserve genetic diversity, e.g., by avoiding popular sire effects and close inbreeding, as well as unnecessary breeding restrictions and too strict thresholds for breeding animals. In many breeds, there are opportunities for a more efficient use of genetic variation within the population. In Sweden, each breed should have a Breed-Specific Breeding Strategy, considering all aspects in the breeding goal, with health being the top priority. In addition, kinship indices are applied as a breeding tool in several breeds. However, in some breeds, efforts to preserve genetic variation within the breed have proven insufficient. Lack of genetic variation and/or widespread health problems can make it difficult or impossible to achieve the breeding goals. In these breeds, adding genetic variation may be required for long-term sustainable breeding. There are different approaches to increasing genetic variation in a breed. What approach is best suited may vary depending on the situation and conditions in the breed concerned. In some cases, some unregistered individuals that can contribute with valuable genetic variation may be added to the breed register through exemption registration. Another option for broadening the gene pool may be to allow mating between closely related breeds, by redefining the breeds as varieties of the same breed instead of separate breeds. Moreover, outcrossing or an open breed registry may be applied to add genetic variation to the population. The Swedish Kennel Club recently developed guidelines to support the increasing number of Breed Clubs that wish to implement projects to increase genetic variation. Efforts to increase genetic variation are long-term commitments that require planning, collaboration, and committed breeders. Currently, the Cavalier King Charles Spaniel Club in Sweden is conducting an outcrossing project, and several of the Swedish Scent Hound breeds have opened their breed registries towards other Scent Hound breeds.

Fit2Breed: a new platform to support sustainable breeding of dogs

H. Fieten¹, C. Limpens¹, L. Vree¹, L. Karssen²

¹ Faculty of Veterinary Medicine, Clinical Sciences, Yalelaan 108, 3584 CM Utrecht, Netherlands, ² PolyKnomics BV, Het Vlaggeschip 61, 5237 PA 's Hertogenbosch, Netherlands

Purebred dog populations face considerable problems regarding inbreeding and a high incidence of hereditary diseases. However, the increasing availability of data from screening programs, DNA tests and SNPs, and pedigree data allow for the creation of powerful tools to improve health in companion animal populations. Nevertheless, properly integrating and making good use of these data has proven to be challenging for breeders. We have developed Fit2Breed, a web-based platform for population analysis, management and breeding advice. Its purpose is to help breeders pick the best match for their bitch based on genetic, pedigree and disease data, while at the same time offering guidance and education, for example, by offering an interactive visualisation of the animal's pedigree. Fit2Breed compiles all available genetic and disease information on the dogs to predict disease risk for future pups. It also considers population data to minimize the spread of the disease genes in future generations. Fit2Breed currently has two modules: one for Genotype matchmaking and one for Pedigree matchmaking. The Genotype matchmaking module calculates genetic kinship. In Pedigree matchmaking, kinship is based on the available pedigree information. After filtering based on the clinical and DNA test results, the presented stud dogs are ranked based on kinship with the bitch. The platform is now available for its first breed, the Nederlandse Kooikerhondje, with currently 35,000 dogs and 500 active users. For this breed, Fit2Breed analyzes clinical data on patellar luxation and hereditary eye disease (ECVO screening) and DNA test results on Hereditary Necrotizing Myelopathy, Polymyositis and von Willebrand Disease. For the Kooikerhondje breed, we assessed the breed's coefficient of inbreeding, disease allelic frequencies and incidences of diseases prevalent in the breed. The breed has an average coefficient of inbreeding of 33%, higher than what is reported for other breeds, which has stabilized since the year 2000. Allelic frequencies for hereditary necrotizing myelopathy and von Willebrand disease have been reduced since screening started, making them no longer a problem in the breed.

Session 6

Theatre 4

The ambiguous role of DNA-testing in dog breeding

H. Proschowsky¹, C. Bruun¹, P. Sandøe^{1,2}, M. Fredholm¹

¹ University of Copenhagen, Dep. of Veterinary and Animal Sciences, Groennegaardsvej 8, 1870 Frederiksberg, Denmark, ² University of Copenhagen, Dep. of Food and Resource Economics, Rolighedsvej 23, 1958 Frederiksberg, Denmark

DNA testing in dog breeding has significantly enhanced the health status of many breeds suffering from Mendelian inherited diseases. Notably, it has helped address the challenge of late clinical onset and enabled the identification of carriers. However, many dog breeders tend to see the use of DNA tests as a magic bullet to deal with all heritable diseases at the cost of other, more traditional breeding tools, which often are needed to solve the problems. Here, we use Intervertebral Disc Disease (IVDD) as an example to discuss this challenge. IVDD is a painful and potentially fatal condition, which currently affects 1 out of 5 Dachshunds. The risk is correlated with the number of calcified intervertebral discs, which is highly heritable. In Denmark, a breeding program based on a radiographic evaluation of the number of calcified discs supplemented with Estimated Breeding Values (EBVs) has been running for around 20 years with good results, especially in wire-haired Dachshunds. In 2017, an insertion of an FGF4 retrogene on CFA12 was identified as responsible for the chondrodystrophic phenotype and associated with the risk of developing disc herniation in chondrodystrophic breeds, and a commercially available DNA test was developed. Many breeders are in favor of using this DNA test instead of the more laborious alternative, but this could potentially have deleterious effects on the breed. The frequency of the FGF4 risk allele is extremely high in the Danish long- and smooth-haired populations, and a significant association between the FGF4 retrogene insertion and the disc calcification status has only been demonstrated in the wire-haired population. Considering this, it can be argued that, at least in Denmark, the FGF4 retrogene insertion on CFA12 cannot stand alone as a risk indicator. Relying on the DNA test will have an irreversible effect on the Dachshund breed, excluding far too many healthy dogs from breeding. Thus, using a combination of calcification status and Estimated Breeding Values remains the most reliable breeding scheme for disc herniation in Dachshunds, despite many breeders wanting to use DNA tests as a quick fix.

Scientific data on cat management by the members of the Italian National Feline Association: preliminary data

B. Paddalino^{1,2}, C. Manetti³, F. Serena⁴, G. Ballotta³, M. Cunto³, D. Zambelli³

¹ Southern Cross University, Faculty of Science and Engineering, Military Road, 2480 Lismore, Australia, ²

University of Bologna, Department of Agricultural and Food Sciences, viale Fanin 46, 40127 Bologna, Italy,

³ University of Bologna, Department of Veterinary Medical Sciences, Via Tolara di Sopra 50, 40064 Ozzano

(Bo), Italy, ⁴ ASL Toscana Centro, Via dei Cappuccini 79, 50053 Empoli, Italy

The European Commission requested a report from the European Food Safety Authority to summarize the scientific evidence on the management and welfare of cats and dogs. While data from Northern European breeder associations were available, no data were found for Italy. Thus, this study aimed to collect data on the management, reproduction, and welfare of cats kept by members of the Italian Feline Breeder Association (ANFI). The authors developed an ad hoc questionnaire and distributed it via email to ANFI members (n = 2500). Currently, 239 responses, accounting for 1505 cats, have been analyzed. Most of the breeding centres were located in Northern Italy (63%), and 72% of breeders kept their cats only indoors. Fortunately, 85% of the cats had access to natural light, and those kept under artificial lighting were exposed to more than 8 hours of light daily (72%). Cats were mostly kept freely (96%), with no breeders using multi-tier cages. The majority of breeders were highly experienced (10+ years), with only 7% breeding more than one breed and just 7% breeding for profit. The median size of breeding centres was small (median = 6 cats, min = 1, max = 36). Almost half of the cats were fed only commercial food, one-third had supplemental home food, and only 5% were fed BARF or alternative diets. Vaccinations and genetic screenings were regularly conducted (94% and 89%, respectively), while deworming occurred less frequently (78%), and semen checks and artificial insemination were even rarer (17% and 4%, respectively). Drugs to control pregnancy were used by 41% of breeders. The response and completion rates currently stand at 10% and 76%, respectively, but data collection is still ongoing, and further analysis will be performed. Two reminders will be sent out to emphasize the importance of collecting data to identify welfare concerns and suggest better policies for cats kept in Europe.

Session 6

Theatre 6

Transition to SNP Genotyping for Parentage Verification: Practical Challenges

L. Van De Goor¹

¹ VHLGenetics, Agro Business Park 100, 6708 PW Wageningen, Netherlands

Parentage verification in dogs has been a standard practice for over a decade. In 2006, the International Society for Animal Genetics (ISAG) introduced a recommended STR marker panel for this purpose, commonly referred to as the ISAG2006 panel. This panel, consisting of 22 markers, was widely adopted by genotyping laboratories worldwide. As cross-border breeding increased, the exchange of ISAG2006 DNA profiles between laboratories became routine. These profiles are typically shared as PDF files, with receiving laboratories manually entering the genotypes into their database. While this process is labor-intensive, it is manageable given the limited number of markers involved. In 2020, ISAG recommended a new SNP marker panel for parentage verification, known as the ISAG2020 panel. This ISAG2020 panel, comprising over 200 SNP markers, enables laboratories to include, in one test, SNP markers that provide insight into genetic diversity, characteristics and diseases. Consequently, several kennel clubs and their partner laboratories have transitioned from ISAG2006 to ISAG2020 in recent years. However, this transition has introduced significant logistical challenges. The large number of SNP markers makes manual data entry from PDF files impractical, time-consuming and prone to errors. Despite the clear advantages of the ISAG2020 panel, no international electronic system has been developed to exchange these DNA profiles. As a result, many dogs are genotyped by multiple laboratories, leading to confusion among breeders and increased costs—issues that have generated dissatisfaction within the breeding community. To address these issues, an ideal solution would involve the development of an international platform where laboratories and kennel clubs can securely upload and download ISAG2020 DNA profiles, with appropriate access authorizations. Alternatively, a more immediately feasible approach could be for genotyping laboratories to agree on a standardized file format for exchanging ISAG2020 DNA profiles. This 1st EAAP Companion Animals Workshop provides an excellent opportunity to initiate discussions on establishing an international electronic exchange system for ISAG2020 DNA profiles, ultimately benefiting breeders, kennel clubs, laboratories, and the wider canine genetics community.

Brachycephalic heritage breeds in Italy: analysis of studbook entry dataS. P. Marelli¹, M. G. Strillacchi¹, G. Berteselli¹, M. Polli¹, S. Cannas¹¹ University of Milan, Department of Veterinary Medicine and Animal Science, via dell'università 6, 26900 Lodi, Italy

The aim of the present research is to analyse entry data from the only official Italian Studbook, maintained by the Ente Nazionale della Cinofilia Italiana (ENCI) on behalf of the Italian Ministry of Agriculture, for three extreme brachycephalic breeds: English Bulldog (EB), French Bulldog (FB), and Pug (PG). These ancient and well-known breeds are popular worldwide due to their phenotypical traits; however, their characteristic head morphology raises significant welfare concerns, particularly regarding respiratory issues. This study analysed ENCI breed entry data (N) from 2014 to 2023. An aggregated dataset for the three breeds combined (EB+FB+PG = Three Breeds, TB) was calculated, along with the total number of entries for all registered breeds (All Breeds, AB). Data were processed using Microsoft® Excel® and SAS® software. Statistical analysis included the calculation of means, standard deviations, linear trend lines with slope coefficients (SC), and the coefficient of determination (R²), as well as annual average percentage variation (AAPV) and the 5-year and 10-year mean AAPV (M5AAPV and M10AAPV). The TB population represents 3.9% (N=55276) of the total AB entries. Within the TB population, the distribution was as follows: EB 33.37%, FB 53.91%, and PG 12.73%. EB showed the strongest constant population decline, with a slope coefficient of -123.08 and R² = 0.86 (10 yrs). The M5AAPV revealed negative growth for EB, PG, TB, and AB, while FB showed a positive variation of 2.26%. Our findings highlight a general decline in TB puppy registrations in Italy, alongside distinct breed-specific trends. Population studies based on entry data provide valuable information for developing protection strategies for heritage breeds. Health, welfare, and biodiversity conservation should be the primary goals in breeding heritage canine breeds. Given that pedigree dogs account for a maximum of 18.42% of the total Italian canine population, health and breeding strategies should also be extended to non-pedigree dogs.

Session 7

Theatre 1

Why do people keep dogs, cats and other companion animals?P. Sandøe^{1,2}, T. Bøker Lund¹, S. Springer³¹ University of Copenhagen, Department of Food and Resource Economics, Rolighedsvej 23, 1958 Frederiksberg C, Denmark, ² University of Copenhagen, Department of Veterinary and Animal Sciences, Grønnegårdsvej 8, 1870 Frederiksberg C, Denmark, ³ University of Veterinary Medicine, Messerli Research Institute, Veterinärplatz 1, 1210 Vienna, Austria

Most animals kept by humans are production animals, typically kept by a small minority in large numbers per unit. Companion animals, in contrast, are typically kept in small numbers per household by a large proportion of the population. While these animals mostly do not provide material goods, they may offer valuable services such as hunting or guarding, in the case of dogs, and pest control, in the case of cats. Still, most companion animals primarily have the purpose of giving their owner company, support, and something to care about. However, there are major differences between cultures, between different parts of the human population, and between species when it comes to the purpose of keeping companion animals and the relation between the owners and their animals. We will address these variations based on two different representative surveys: Of companion animal ownership conducted in Denmark in 2021, and of dog and cat ownership conducted in Austria, Denmark and the United Kingdom in 2022. The first serves to compare differences in the reasons why Danish families choose to have dogs, cats and rabbits, and the other looks at differences relating to nationality of owners and species (cats or dogs) when it comes to various indicators of how much people care about their animals. The main findings are: First, in Denmark dogs and cats are primarily acquired for adult owners, while rabbits are mostly acquired for children. Secondly, for all three species, for a minority of owners essential social support (“The animal helps me through hard times” / “I would be lonely without it”) is the prime reason for keeping the animal. However, more than one out of five dog owners keep their companions primarily for pursuing joint activities. When it comes to indicators of attachment, earlier studies have found that people were much more attached to dogs than to cats, but our study finds that while this is still the case in Denmark, in the UK the level of attachment to the two species is very close.

Pet Caregiver Burden: The Role of Attachment, Pet Health, and Care Support

S. Joo¹, M. S. Chun¹

¹ *Seoul National University, College of Veterinary Medicine, Veterinary Humanities and Social Science, Gwanakro 1, 08826 Seoul, South Korea*

Pets contribute significantly to their owners' emotional well-being and companionship; however, caregiving responsibilities can also impose substantial burdens. This phenomenon, often referred to as "caregiver burden," encompasses a range of physical, emotional, and temporal strains (Zarit, 1980; Kogan et al., 2022). This study investigates pet caregiver burden in South Korea, focusing on the interplay of caregiver characteristics, pet health, the human-animal bond, care support, and veterinary services. An online survey of 766 primary pet caregivers revealed that 47.8% were male and 52.2% female, predominantly over the age of 50, with 80% owning dogs. In terms of pet health, 70% were healthy, while 16.8% had acute or curable illnesses, and 11.2% were chronically or terminally ill. The study assessed attachment levels to pets using the Lexington Attachment to Pets Scale, which yielded an average score of 50.91 (SD=9.28). Higher levels of attachment were observed among female caregivers, younger individuals, those caring for multiple pets, and caregivers of pets experiencing health challenges ($p < 0.05$). Caregiver burden assessed using the 7-item Burden Interview (Spitznagel et al., 2019), showed a significant correlation with pet health status. Caregivers of pets with acute or curable illnesses reported the highest levels of burden, indicative of the stress imposed by unpredictable care demands, such as administering medications and managing urgent veterinary visits (Spitznagel et al., 2017). These short-term, intensive caregiving obligations can disrupt daily routines and augment stress levels. Regression analysis identified significant predictors of caregiver burden, including pet health, caregiver gender (male), and the relative youth of caregivers and pets. Frequent veterinary consultations were associated with increased burden, possibly reflecting the heightened stress of managing pet health care concerns. Additionally, lower emotional support significantly amplified caregiver burdens. Attachment levels mitigated perceived burdens, indicating a protective effect of the human-animal bond (Indirect effect: -0.015, BootLLCI: -0.033, BootULCI: -0.001). This study underscores the dual nature of pet caregiving—both rewarding and burdensome. It highlights the need for targeted interventions to support caregivers, emphasizing the interplay of emotional, social, and health-related factors in shaping their experiences.

Session 7

Theatre 3

The role of monocular cues in dogs perception of three-dimensionality

A. Broseghini¹, V. Bevilacqua¹, C. Guérineau¹, L. Marinelli¹, P. Mongillo¹

¹ *University of Padua, Department of Comparative Biomedicine and Food Science, Viale dell'Università 16, 35020 Legnaro, Italy*

Understanding depth perception in dogs is crucial for interpreting their behavior, optimizing their environments, and advancing comparative visual cognition. A previous study by our group showed that dogs can use a combination of linear perspective and shading to infer tridimensionality from pictorial cues in two-dimensional images. Here we examined the individual contribution of the same two monocular, pictorial cues, in three experiments, involving a total of 84 dogs (46 females, 38 males; mean age \pm SD = 4.2 \pm 2.1 years). Using a violation of expectation paradigm, we measured dogs looking time – as a proxy for surprise – after observing a ball rolling onto an apparatus and then disappearing into a real hole or rolling over a fake hole, where either perspective lines or shading mimicked those of the real hole. Linear perspective alone did not elicit surprise, suggesting it is insufficient to elicit depth perception (Wald Chi-square = 2.012, $p = 0.152$), nor did low contrast shading (Wald Chi-square = 0.977, $p = 0.442$). However, high contrast shading successfully induced depth perception (Wald Chi-square = 7.405, $p = 0.006$), with longer looking times in the illusory condition (estimated mean \pm std. error: 8.12 \pm 1.22 s) compared to the real condition (6.11 \pm 0.97 s). Results suggest that dogs can perceive depth from 2D images, but the effectiveness depends on the specific pictorial cues used. Shading appears to be a more salient depth cue for dogs compared to linear perspective when presented individually. These findings have implications for understanding visual processing in dogs and optimizing visual stimulus presentation in canine cognitive tests. Further research is needed to elucidate the mechanisms and ecological relevance of different pictorial depth cues in canine vision, as well as to explore the integration of multiple cues in depth perception.

“You own a rabbit, you buy a hutch”: Understanding public perception of companion rabbit ownership and accommodation requirements

N. Powdrill-Wells¹, F. Cooke¹, S. Ryan¹, J. Thornett¹, K. Stoneman¹

¹ Woodgreen Pets Charity, Pet Services, Kings Bush Farm, London Road, Godmanchester, PE29 2NH Cambridgeshire, United Kingdom

Despite companion rabbits in the United Kingdom being protected by the Animal Welfare Act 2006, rabbit owners often fail to provide for the basic needs of their rabbits. Many rabbits spend their lives in inappropriate accommodation. Rescue centres are also inundated with requests to admit relinquished rabbits, but often struggle to find new homes for them. In this study, we interviewed forty-nine people attending community events about their views of rabbit ownership, and their awareness of suitable rabbit accommodation. Interview data were analysed through reflexive thematic analysis. Participants held differing views surrounding keeping rabbits as companion animals, and perceptions of rabbits as a species varied significantly. Whilst 63% of participants had owned rabbits previously, 71% of those were unlikely to consider rabbit ownership in future, mainly due to the realities of rabbit care. Tradition and the influence of social norms were cited as key influences on perceptions of appropriate rabbit care. Participants reflected on their awareness of good practice rabbit accommodation and expressed surprise at the space recommended. Many participants would seek advice about appropriate accommodation provision from their pet acquisition source. Challenges regarding provision for the environmental needs of rabbits were highlighted, particularly relating to competing human lifestyle factors like space constraints in human homes. Our research findings identify the complexities of rabbit ownership and potential conflicts with owner lifestyles. Traditional perspectives surrounding rabbit suitability as children’s pets remain and may detrimentally affect how the species is viewed. The visibility of good practice rabbit housing is important in changing existing views of suitable rabbit care and acquisition sources can play a key role in promoting good practice. This presents a challenge for animal welfare organisations, as promoting positive rabbit welfare is likely to lead to fewer homes for rabbits. With a mismatch between rabbit needs and what society can provide, the future of companion rabbits in the United Kingdom is uncertain.

Session 8

Theatre 1

Alternative proteins in canine nutrition

J. Zentek¹

¹ Institute of Animal Nutrition, Veterinary Medicine, Königin-Luise-Str. 49, 14195 Berlin, Germany

The feeding of dogs and cats is undergoing significant transformation due to various influences, including ethical concerns, environmental considerations, and scientific advancements. Alternative protein sources are increasingly used for pet nutrition, it is necessary to evaluate their nutritional adequacy, digestibility, and potential benefits or drawbacks. The domestication process has led to adaptations in both dogs, influencing their digestive systems and requirements. While dogs have developed a greater ability to digest plant-based components, cats remain obligate carnivores. The presentation reviews conventional animal-based protein sources, such as meat, offal, dairy products, and eggs, as well as novel protein alternatives, including insect proteins, plant-based proteins, and hydrolyzed protein sources. Insect proteins, particularly from black soldier flies and mealworms, offer a high-quality and sustainable alternative with favorable amino acid profiles. Plant-based proteins, such as soy, lupins, and peas, require careful processing to reduce anti-nutritional factors and improve digestibility. The potential of hydrolyzed proteins is also discussed in the context of reducing allergenicity and improving bioavailability. Additionally, vegetarian and vegan diets for dogs and cats are discussed, highlighting key studies on their impact on animal health, nutritional sufficiency, and associated risks. While some vegetarian diets may meet the requirements with proper formulation, vegan diets for cats pose significant nutritional risk due to essential nutrient deficiencies. The presentation concludes that while alternative protein sources can be viable under specific conditions, careful formulation and scientific validation are necessary to ensure they meet the nutritional needs and well-being of companion animals.

Evaluation of *Hermetia illucens* larvae meal as the main protein source in a digestibility trial for cats

G. Bussone¹, L. Penazzi¹, A. Schiavone¹, U. Ala¹, L. Prola¹

¹ University of Turin, Veterinary Medicine, Largo Paolo Braccini 2, 10095 Grugliasco, Italy

Insect meal is an innovative and sustainable protein source for both human and animal consumption. Despite challenges in consumer acceptance, research highlights its potential in animal diets. With growing human and pet populations, the demand for protein sources continues to rise, making alternative ingredients essential¹. Insects offer a highly digestible protein source with a balanced amino acid and lipid profile, as demonstrated in previous studies^{1,2}. An additional benefit of novel protein sources is their potential use in hypoallergenic diets³, particularly for animals requiring elimination trials due to gastrointestinal conditions. This study aimed to evaluate the nutritional composition and digestibility of a commercial insect-based dry food for adult cats. Eight healthy adult cats participated in a digestibility trial, divided into two groups receiving either an insect-based or lamb-based control diet. Both diets were formulated to be isoenergetic and isonitrogenous. The study followed a crossover design: four cats started on the control diet, and four on the insect diet, switching after a 30-day washout period on a standard maintenance diet. After a 10-day adaptation phase, total fecal collection over seven days allowed for in vivo digestibility assessment. Results showed significantly higher digestibility ($p < 0.05$) of dry matter (DM) and organic matter (OM) in the insect-based diet ($79.84\% \pm 2.5$ and $83.42\% \pm 2.0$, respectively) compared to the control diet ($76.13\% \pm 3.0$ and $79.54\% \pm 2.7$, respectively). Crude protein (CP) digestibility was also significantly higher ($p = 0.001$) in the insect diet ($79.12\% \pm 2.6$) versus the lamb diet ($71.28\% \pm 4.1$). However, DM digestibility values were lower than expected, likely due to high hair content in feces, which previous studies suggest⁴ can underestimate DM digestibility by about 6%. This study confirms that insect protein is a highly digestible and sustainable alternative, showing promising results compared to traditional hypoallergenic meat-based diets for cats. References Bosch G et al., J Nutr Sci. 2014; 2.Reilly LM et al., J Anim Sci. 2022 3.Keřińska-Pacelik J & Biel W., Animals. 2022 Seong H., Thesis, 2017

The Role of Nutritional Management in Enhancing Welfare of kennel dogs. An Evidence based approach towards education and communication

M. G. Cappai¹, G. Coppa²

¹ Università degli Studi di Sassari, Medicina Veterinaria, via Vienna 1, 07100 Sassari, Italy, ² Comune di Cagliari, Canile Comunale, via Po 57, 09121 Cagliari, Italy

Proper feeding management is integral to enhancing the welfare of kennelled dogs, addressing both their physical health and psychological needs. Therefore, individual nutritional assessment shows up to be a starting point to evaluate health and welfare of hosted dogs. However, very few is reported as to the nutritional needs and management of kenneled dog, where clinical, hygienic and behavioural aspects are involved in the daily practice. In the year 2022, a cooperation between the municipal kennel of the city of Cagliari and the Nutrition Desk of the Veterinary Teaching Hospital of the University of Sassari (Sardinia, Italy) was started. Gaps about the knowledge of the nutritional state of dogs and feeding management were aimed to be cleared, along with the need to increase the public awareness and the education of future veterinary surgeons on the topic. The nutritional screening of dogs and the feeding practices adopted in the kennel pointed out a series of management aspects, worth of being considered in the complexity of kennel running. A considerable proportion of dogs potentially adoptable turned out to be overweight (73.3% with a Body Condition Score, BCS > 3.5), of which 23.5% were diagnosed as obese (BCS > 4.5). The rest of dogs were considered in adequate body condition according to age, gender and size. The nutritional assessment was noted on purposely created reports, associated with the ID records of the kennel. Marked importance was attributed to the fecal quality, both as an animal based measure and indicative of hygiene, requiring personnel commitment in case of disorders of digestive function (wrong provision? stress?). A series of aspects were accounted for the evaluation of the most appropriate feeding management: a) heterogenous composition of the box as to mass and size; b) dominance and risk of undernourishment of other dogs; c) neutering and spaying are default conditions and often correlate with body weight increase. Adoptable dogs could be accompanied with a personalized nutritional sheet and a booklet developed for the appropriate feeding management at home and for the conduct in urban environment.

Evaluation of *Tenebrio molitor* Meal as a Sustainable Protein Source for Pet Food: In Vitro Digestibility and Antioxidant Capacity

M. R. Dametti¹, S. Frazzini¹, I. Ferri¹, M. Dell'Anno¹, B. Canala¹, E. Fusi¹, L. Rossi¹

¹ University of Milan, Department of Veterinary and Animal Sciences, Via dell'Università, 6, 26900 Lodi, Italy

The pet food industry has witnessed remarkable growth, driven by a rising pet population and an urgent need to identify sustainable protein sources to replace conventional ingredients with high environmental costs. Insects, particularly *Tenebrio molitor* (TM), represent a promising alternative due to their low resource requirements, reduced greenhouse gas emissions, and favorable feed conversion ratios. Additionally, TM is rich in proteins and essential amino acids, lipids, and bioactive compounds with potential nutritional and functional benefits. This study investigates the in vitro digestibility and antioxidant activity of TM larvae meal in comparison with fishmeal, aiming to explore its suitability as a sustainable pet food ingredient. To evaluate its nutritional potential, TM larvae and fish meals were analyzed for dry matter, crude protein (CP), lipid content, and ash using standard AOAC methods. In vitro digestibility was assessed through a two-step gastric and intestinal simulation process. Total protein and lipid digestibility was expressed as the percentage of residual material post-digestion. Antioxidant capacity was evaluated via the ABTS assay, using water extracts and expressed in μM Trolox equivalents. Statistical analyses were performed using non-parametric tests, and significance was set at $p < 0.05$. TM meal exhibited a total digestibility of $52.56 \pm 6.62\%$, compared to $75.32 \pm 2.90\%$ for fish meal. No significant difference was found between insect and fish meal digestibility (Tukey's test). Crude protein content was $43.02 \pm 1.39\%$ for TM meal and $71.60 \pm 5.47\%$ for fish meal, with post-digestion values of $86.60 \pm 1.33\%$ and $89.76 \pm 3.74\%$, respectively. Lipid digestibility was $82.94 \pm 5.89\%$ for TM meal and $94.73 \pm 2.65\%$ for fish meal, with no significant difference (Dunn's test). Antioxidant activity was significantly higher in TM meal ($2143 \pm 142.1 \mu\text{M}$ Trolox eq) compared to fish meal ($1092 \pm 134.3 \mu\text{M}$ Trolox eq) ($p = 0.0397$, Dunn's test). These findings highlight TM larvae meal's potential as a sustainable, nutritionally adequate protein source and as a functional ingredient for pet food.

Session 8

Theatre 5

Characterization of the gut mycobiome of companion animals

E. Scarsella¹, G. Jospin¹, D. Reyes¹, H. H. Ganz¹

¹ AnimalBiome, 2945 Webster St Fl 2, 94609 Oakland, United States

The gut microbiome plays a vital role in maintaining the health of cats and dogs. However, little is known about the composition and diversity of fungi in the gastrointestinal tracts of domestic cats and dogs. This study characterized the gut mycobiome of cats and dogs using full-length ITS sequencing of fecal samples. A total of 670 canine fecal samples were sequenced, including 643 from customer submissions with owner reported health metadata and 27 from verified healthy dogs. Additionally, 139 feline fecal samples were sequenced, comprising 122 from customer submissions and 17 from verified healthy cats. The most abundant fungal taxa identified in dogs included *Cladosporium herbarum*, *Cyphellophora reptans*, *Cynicomyces guttulatus*, *Issatchenkia orientalis*, *Saccharomyces cerevisiae*, *Candida albicans*, *Malassezia pachydermatis*, and *Trichosporon asahii*. The main taxa found in cats were *Cynicomyces guttulatus*, *Saccharomyces cerevisiae*, *Cyphellophora reptans*, *Cryptococcus neoformans*, *Clitopilus baronii*, and *Sarocladium dejongiae*. We calculated the alpha diversity index for both cats and dogs. A Kruskal-Wallis test was subsequently employed to compare alpha diversity between the verified healthy subjects and a cohort of customer-derived samples with a range of health conditions reported but not verified. For both feline and canine cohorts, no statistically significant difference in alpha diversity was observed between the verified healthy population and the general populations. This result, however, was anticipated, owing to the limited sample size of healthy subjects within each cohort. Furthermore, a comparative analysis was performed on a subset of samples subjected to both 16S and ITS sequencing. Despite the study's limitations, including a small sample size of healthy animals and numerous samples from a general population of animals, these findings offer new insights into the composition and diversity of feline and canine gut mycobiomes. Further studies are necessary to provide a more comprehensive understanding of companion animal mycobiomes.

Nutritional knowledge and evolving human-animal relationships: growth trends in the pet food market over the last years

M. I. Cutrignelli¹

¹ Department of Veterinary Medicine and Animal Production, University of Naples Federico II, Via Federico Delpino 1, 80137 Naples, Italy

In Europe, approximately 50% of households own at least one pet, with dogs, cats, birds and unconventional mammals being the most common. These data reflect as pets are considered as members of the family unit, and the interest of owners in the health and welfare of their animals has steadily increased in recent decades. Concurrently, there is a growing interest in the diet/health relationship. The pet-food industry is distinguished from other segments of feed industry by its resilience in the face of various challenges, including rising raw material and energy costs, and the global COVID-19 pandemic. Over the past 30 years, pet-food sector has demonstrated a consistent upward trend in production, in terms of the quantity manufactured annually and the total revenue generated. The industry has witnessed the introduction of specific diets designed to meet the unique nutritional needs of specific life stages or breed, and formulated with novel ingredients, predominantly protein or starch sources. Furthermore, pet-food is now readily available through a diverse range of sales channels, including specialist retailers, large-scale distribution networks, and online marketplaces. This expansion has resulted in a complex and often perplexing landscape for consumers. Meanwhile, there has been an increase in the production of snacks or supplements dedicated to pet gratification or for dental health or to increase palatability. However, if these products are not considered part of the daily ration, they could be misused, increasing the risk of obesity and diabetes. Consequently, a growing number of pet owners who adhere to specific nutritional trends or philosophies are opting for more natural or holistic diets, leading to an increased presence of novel diets characterised by the presence or absence of nutrients or ingredients (e.g. grain-free, gluten-free, single-protein, vegetarian or raw diets). The development of diets based on scientific knowledge has contributed to enhancing the wellbeing and health of pets, thereby increasing their lifespan. However, it is imperative to emphasise the importance of consulting a nutritionist to ascertain the most suitable diet and ration for each animal.

Session 8

Theatre 7

Functional ingredients in dogs nutrition

A. Ruggiero¹, A. Vastolo¹, M. Ferrara¹, T. Montefusco¹, M. I. Cutrignelli¹, D. Bergero²

¹ Università degli studi di Napoli, Department of Veterinary Medicine and Animal Production, Via F. Delpino, 1, 80137 Naples, Italy, ² Università degli studi di Torino, Department of Veterinary Science, Largo P. Braccini, 2, 10095 Grugliasco, Italy

Probiotics, are becoming increasingly important in global companion animal breeding. Probiotics are defined as “live microorganisms, which when administered in adequate amounts confer a health benefit on the host” in terms of improvement of fecal consistency, gut health and modulating the immune system. This double-blinded study was designed to evaluate the effects of *Bacillus coagulans* on gut health in adult dogs. Specifically, 14 neutered healthy dogs, 5 females and 9 males (age 6±3 years, BW 30.70±6.93 kg, BCS 5.94±1.9 on a 9-point scale) were recruited and divided into two homogenous groups. All dogs were fed the same commercial diet. The trial lasted 42 days (7 of adaptation and 35 of supplementation). Both groups daily received a supplement (10 g/animal) of maltodextrin (CTR) or *B. coagulans* 1×10⁹ CFU/animal (TRT). Feed intake was daily registered, while BW and BCS were evaluated at the beginning and at the end of the trial. Fecal quality was assessed using a 7 points scale fecal score_FS. Fecal samples were collected weekly to evaluate pH, DM, and fecal metabolites such as: short chain fatty acids_SCFA, NH₃ and lactic acid. In addition, *B. coagulans* colonies were identified using MALDI-TOF mass spectrometer (MALDI Biotyper® Sirius), according to the manufacturer’s instructions (Bruker Daltonics), on supplements and groups fecal pool at the beginning and at the end of the trial. No significant differences were observed along the trial or between the groups for BW, BCS and feed intake. Along the trial a progressive improvement of fecal quality was observed in TRT group (FS from 2.4 to 2.1/7 and DM from 31.9 to 28.9%; SCFA from 186 to 197 mmol/l) compared to CTR (FS from 3.0 to 2.5/7 and DM from 29.3 to 29.6%; SCFA from 196 to 182 mmol/l). The presence of *B. coagulans* was confirmed only in TRT group fecal samples. These preliminary results suggest a beneficial effect of *B. coagulans* on the gut health of dogs potentially lead to improved health and well-being, probably due to an increase in the beneficial microbial population.

Chemical Composition and Oxidative Stability of Dog Food: Insights into Nutritional Quality

T. Pirman¹, J. Salobir¹, A. Levart¹

¹ University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Jamnikarjeva 101, 1000 Ljubljana, Slovenia

Oxidative stability of dog food is crucial for maintaining, especially the quality of fats and oils. It prevents harmful oxidative processes that could lead to the formation of free radicals and toxic compounds while preserving the freshness, aroma, and palatability of the food. Adding natural or synthetic antioxidants such as vitamins E and C, BHT/BHA, as well as natural extracts, helps protect nutrients, particularly sensitive unsaturated fatty acids, extends shelf life, and positively impacts dogs' health. We analysed several dry foods for adult medium-sized dogs. The dog foods were selected according to price range and had the legally required information on the declaration. All foods were purchased and analysed in independent triplicates. The composition of the selected foods was analysed based on the proximate analysis, additionally mineral content, fatty acids (FA) composition and vitamin E were determined. The degree of fat oxidation was monitored at different time intervals by measuring the primary (lipid peroxides) and the secondary oxidation product (malondialdehyde.) The obtained results were compared with the declared values. The analysis revealed that most dog foods complied with NRC, AAFCO, and FEDIAF recommendations for key nutrients, except for K in two mixtures and EPA+DHA in three mixtures. Regarding minerals, excess Zn levels were detected in several mixtures, while regulatory limits for Fe, Mn, and Cu were not exceeded, and n-3 PUFA content was higher in more expensive mixtures. None of the foods showed signs of oxidation after opening and during the measurement period (27 weeks). The findings highlight that while most dog foods meet regulatory standards for essential nutrients, variations in mineral and fatty acid content underscore the need for careful selection to ensure optimal nutritional quality. The oxidation assessment showed that oxidative stability is effectively maintained across different price ranges.

Session 9

Theatre 1

Diseased by design or fit to function? Using scientifically informed selection to breed the companion dogs of the future

R. Packer¹

¹ Royal Veterinary College, Hatfield, AL97TA Herts, United Kingdom

Over the past century, artificial selection has moulded the domestic dog into an extraordinary array of body shapes. This variation has been driven by anthropocentric desires, creating breeds to fulfil diverse human lifestyle niches. While some conformations were originally selected to enhance specific physical functions (e.g., hunting, guarding), data suggest that today's canine conformations predominantly persist to satisfy human aesthetic preferences within companion roles. This shift has led to an uncoupling of form and function, resulting in increasing selection for exaggerated conformations. The past two decades of scientific discovery in canine health and welfare has revealed the severe disease burden associated with selecting for phenotypes outside of the biological limits of the domestic dog. These "extreme conformations" occur where appearance diverges so significantly from the ancestral form that resultant dogs commonly suffer from poor health and welfare. Scientific evidence now shows that > 60 canine disorders directly result from extreme conformations, with data generated to identify physical characteristics to avoid, and establish safe conformational ranges for breeders to aim towards to protect canine welfare. New data suggest that outcrossing breeds with extreme phenotypes (e.g., extreme brachycephaly) results in rapid, marked health and welfare gains. However, progress towards achieving 'innately healthy' body shapes is hindered by the modern pedigree dog breeding paradigm. Qualitative data suggest that continued focus on breed purity inhibits judicious outcrossing to replenish phenotypic/genetic diversity, along with breed standards and show-ring decisions that promote extreme conformations as desirable, impeding improvements. Paradigm-shifts are urgently required by international stakeholders to align breeding decisions with modern science and reverse the anthropogenic harms of aesthetic selection and its negative effects on canine welfare, even if this is at the expense of appearance. Shifting societal norms regarding ethically acceptable body shape for dogs is crucial to ensure that today's companion dogs can enjoy the long and healthy lives they deserve in this modern function.

General pedigree tracking of recessive disease-causing alleles in dogs

R. Craddock¹, M. Janes¹, A. Martin¹, C. Mellersh², J. Iliska³, P. Wiener¹, S. Smith⁴, G. Gorjanc¹

¹ University of Edinburgh, Roslin Institute, Easter Bush Campus, EH25 9RG Midlothian, United Kingdom, ² University of Cambridge, Canine Genetics Centre, Department of Veterinary Medicine, CB3 0ES Cambridge, United Kingdom, ³ The Kennel Club, Clarges Street, W1J 8AB London, United Kingdom, ⁴ University of Edinburgh, Global Academy of Agriculture & Food Systems, Easter Bush Campus, EH25 9RG Midlothian, United Kingdom

Genetic testing identifies asymptomatic carriers (dogs carrying one copy of a recessive disease-causing allele) and late-onset diseases for specific hereditary conditions. The Kennel Club, UK (KC) records the genetic test results for individual dogs with pedigree information to monitor disease-causing alleles. However, genetic testing is not widely adopted by dog owners. The KC addresses this by assigning hereditary status to progeny with parents known to be clear (no copies of the disease-causing allele) or affected (two copies of the disease-causing allele). Still, a high proportion of registered pedigrees lack tracking of disease-causing alleles. This study evaluates the use of probabilistic pedigree-based inference for tracking disease-causing alleles. Two recessive monogenic eye conditions within five KC-registered breeds were analysed, aiming to (1) use state-of-the-art methods to propagate available genetic test results to all recorded dogs in the pedigree, (2) estimate genotype and allele frequencies over time, and (3) provide insights into the consequences of breeding decisions on gene flow. Results suggest that current methods underestimate the disease-causing allele trajectories for dogs born after genetic test introduction. For instance, dogs born in 2021 across the five breeds report up to 0.091 higher disease-causing allele frequencies with inferred genotype probabilities than with only genetic tests and hereditary status. This reflects probabilistic inference's ability to consider the entire pedigree, diluting the reporting preference for clear dogs. Additionally, we identified an instance of the popular sire effect and inbreeding increasing the dissemination of a disease-causing allele through partitioning the inferred genetic trends by sires. Overall, this study will better inform breeding decisions for reducing monogenic recessive diseases in KC-registered dogs.

Session 9

Theatre 3

Extreme breed standards and inbreeding situation as a reason for the critical health situation in many dog breeds.

O. Vangen¹

¹ Norwegian University of Life Sciences, Department of Animal and Aquacultural Sciences, PO Box 5003, N-1432 Aas, Norway

Over the last 10 years, many scientific reports have documented the alarming health situation for many dog breeds. Two main problems with the pure breeding of the many dog breeds are breed standards, breeding show dogs in extreme directions and the high level of inbreeding in many breeds. There seems to be different paths to follow in order to improve this situation; Use of laws and regulations to improve the in order to control dog breeding. Examples of such are The European Parliament and Council on recommendations for ethical dog breeding 2020 (mass data and breeding values for health and functionality, large scale databases, more use of mental tests and more focus on inbreeding increase). Another even stronger regulation is the Norwegian example: The Norwegian high court banned in 2023 breeding of King Charles Cavalier Spaniel in Norway due to the breed's critical health situation. For another breed, the High Court have decided that for English bulldog, only dogs with lowest grade of BOAS are allowed for breeding. The court decided the breeding practice to be a violation of the Animal Welfare Act. It is alarming that dog breeding issues had to be taken to court in order to change direction of the breeding practice. It is regarded as not only a failure to the kennel club breeding system but also a failure to implement animal breeding and genetics theory into the "dog breeding world". Increasing the knowledge and scientific inputs into the "dog breeding world". In July 2023, 71 Norwegian scientist and persons linked to science signed a summons published in a national newspaper, to raise awareness on the unhealthy situation in dog breeding. Scientists in breeding and genetics can contribute by publishing and presenting data, statistics and new knowledge on health issues correlated to extreme conformation and/or inbreeding levels practices. The presentation will deal with the latest scientific reports on inbreeding developments in dog breeds, as well at reports on health problems related to unbalanced breed standard selection decisions.

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