

Book of Abstracts of the Ist EAAP Companion Animals Workshop



Book of Abstracts No. 37 (2025)
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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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The Croatian Shepherd Dog is an autochthonous Croatian breed whose historical references date back to 1374, when its appearance was first described.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, ²Independent 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

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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.