Programme & Abstracts

12th International Conference on

Canine and Feline Genetics and Genomies



ICCFGG2024 Helsinki — Finland

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Welcome to the 12th International Conference on Canine and Feline Genetics and Genomics

Helsinki is the capital and most populous city in Pinland. It is located on the shore of the Gulf of Pinland and serves as the seat of the Uusimaa region in southern Pinland. More than 675,000 people live in the municipality, and 1.6 million in the metropolitan area. Helsinki is a vibrant city and the country's most significant center for politics, education, finance, culture, and research.

This International Conference has a tradition of alternating between Europe and the United States, and the Helsinki conference follows the successful meeting in Huntsville, Alabama, US, in 2022. The conference has evidenced many breakthroughs and milestones in the fields of canine and feline genetics, including the development of outstanding resources for genetic, genomic, and functional genomics research coupled with exciting studies in inherited diseases, cancer, behavior al and morphological traits, evolutionary biology, genome architecture and related areas in dogs and cats.

This time in Helsinki, we have planned a full plate of fascinating presentations based on 115 submitted abstracts. We will skip the workshop day — preceding the official conference - to avoid overlapping presentations and have spread the official program over the 3,5 days. The Scientific Organizing Committee has selected 40 for oral presentations, with all other abstracts being presented at one of the three poster sessions. Additionally, fifteen posters from mostly young scientists will be highlighted in poster flash talks.

We also have two inspiring keynote speakers: Aarne Palotie, MD, PhD, is the research director of the Human Genomics program at the Institute for Molecular Medicine Finland (FIMM) at the University of Helsinki. His research utilizes the unique Finnish population and health care to improve our understanding of the genetic component underlying common diseases. Guillaume Bourque is a Professor in the Department of Human Genetics at McGill University, and his research interests are in comparative and functional genomics with a particular emphasis on applications of next-generation sequencing technologies and transposable elements.

The social program includes a Sunday night reception at the Little Pinland and, on Tuesday, June 11, a gala dinner at the Restaurant Saaristo, located on the Klippan island in front of South Harbour. Saaristo is one of Helsinki's most imposing and traditional restaurants, and it includes a short boat trip to get there.

Again, we are very grateful to our main sponsor, Nestle Purina, who has supported and made this event possible for the last 20 years. My team and I look forward to welcoming you to Helsinki and enjoying an exciting and collaborative scientific conference.

Enjoy the conference, and welcome to Helsinki!

Best wishes,

Hannes Lohi





On behalf of Nestlé Purina PetCare Company, we are pleased to welcome you to Helsinki, Pinland for the 12th International Conference on Canine and Feline Genetics and Genomics. Nestlé Purina PetCare Company is honored to sponsor this prestigious scientific gathering, continuing our tradition of supporting advancements in pet health since the conference's inception. We trust that this event will continue its tradition of excellence in sharing and promoting scientific advancements that help dogs and cats live longer and healthier lives.

We extend our gratitude to the scientific committee for their dedication to maintaining the conference's high standards. Special thanks go to the local organizing committee for their tireless efforts in ensuring a smooth event. Our appreciation extends to all supporters and contributors who have made this conference possible. We are especially thankful to the researchers and presenters for their invaluable contributions to enhancing the lives of pets.

With over a century of experience in animal nutrition research, Purina is committed to pioneering petcare innovations. Our global team of over 400 scientists and experts, along with our eight dedicated research and development centers and facilities, continues to lead way in advancing pet nutrition.

Through collaborations with researchers worldwide and innovative partnership in academia and industry, we strive to drive breakthroughs in petcare. We look forward to the opportunities for knowledge exchange and future collaboration at this conference.

Thank you for joining us in Helsinki. Your participation is crucial to driving scientific progress in the field of pet genetics and genomics. Together, we can anticipate exciting breakthroughs that will positively impact the lives of pets worldwide.

Sincerely,

Johnny Li, Ph.D. Senior Principal Scientist Nestlé Purina Research Ebenezer Satyaraj, Ph.D. Director of Molecular Nutrition Nestlé Purina Research

Conference Ethics

The International Canine and Feline Genetics and Genomics Conference encourages scientists to present and discuss preliminary data prior to scientific publication. Presentation of research findings is a major factor for the success of the conference. In order to maintain conference integrity and participation, we stress that information presented here should be treated as preliminary work and out of respect for the authors, should only be used with the authors' permission.

In order to maintain the high quality of the conference we would like to inform all attendees of the following policies:

- We ask that new information obtained at this conference will not be used, for either research or commercial purposes, without permission from the authors.
- The abstracts in the conference program booklet cannot be cited.
- Publication of studies presented here in peer-reviewed journals is of course highly encouraged.

Breaches of confidentiality and common sense ethics will ultimately interfere with the pre-publication free flow of information and discussion expected of our conference and endangers the spirit of the conference.

We all thank you for your understanding and attention to this matter.



Conference committees

Scientific organizing committee

Hannes Lohi, University of Helsinki, Finland Jennifer Meadows, University of Uppsala, Sweden Jeffrey Schoenebeck, Roslin Insitute, Scotland, UK Christophe Hitte, University of Rennes, France Greg Barsh, Hudson Alpha, US Adam Boyko, Cornell University, US Eva Furrow, University of Minnesota, US Leigh Anne Clark, University of Georgia, US Claire Wade, University of Sydney, Australia Qinghong (Johnny) Li, Nestle Purina Research, US

Local organizing committee

Hannes Lohi, University of Helsinki and Folkhälsan Research Center Marjo Hytönen, Folkhälsan Research Center and University of Helsinki Mikko Peltonen, Faculty of Veterinary Medicine Nanna Mourujarvi-Rosenlöf, University of Helsinki Confedent International

Presentation awards

The scientific organizing committee will select six graduate or postdoctoral student talks and posters (3+3) for best presentation awards (250€ each) in the conference.

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Mt-ND5 DNA variability in wildcats living in Central Italy Protected Areas

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¹University of Bologna, Dept. BiGeA, ²Ecology Consultant, Varese, ³University of

Milan, Dept. Veterinary Medicine & Animal Science

Poster session 1

The European wildcat (Felis silvestris silvestris, Schreber 1777) is a medium-sized felid distributed heterogeneously throughout Europe: from the Iberian Peninsula to the Caucasus and up in north in Scotland. Despite the generally stable trend of the population, it is included in the "strictly protected" species in Europe. In Italy, the reserved behavior of this felid together with its small distribution, particularly in the central regions of the peninsula, has prevented the collecting of data, hence little is known about its demographic situation and genetic status. This study provides a preliminary view of the genetic variability of the European wild cat, based on 21 tissue samples of dead subjects neighboring or inside Central Italy Protected Areas. These individuals were phenotypically classified as wildcats by experts (park guards and/or veterinarians) and the DNA of their samples was extracted. Preliminary analyses on mitochondrial NADH subunit 5 (MT-ND5) by sanger sequencing have been conducted. A total of four haplotypes have been identified having: 71% a DW1 (Domestic Wildcat hybrid) haplotype, 14% a DW4 haplotype, 10% a W (Wildcat) haplotype and 5% (one individual) a D3 (Domestic) haplotype. Overall, the Haplotype diversity (HD) was 0.48095 with a Nucleotide diversity (π) = 0.00318 (computed using DNASP version 6.12.03). Furthermore, a meta-analysis has been conducted by comparing these results with those reported by other authors in these Italian regions. The results align, to some extent, with the reported introgression of domestic cat genes into European wildcat populations, which is occurring along with habitat loss and fragmentation.