DAY PROGRAM

THURSDAY, JUNE 4th, 2026

THE CONGRESS
SPEAKERS & TOPICS

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Maria Giuseppina Strillacci & Prof. Stefano Paolo Marelli

DAY PROGRAM

BIO:

Maria Giuseppina Strillacci is an Associate Professor at the Department of Veterinary Medicine and Animal Science (DIVAS) of the University of Milan. With a PhD in Animal Production and degrees in Animal Science and Veterinary Medicine, her expertise focuses on animal genetics applied to livestock improvement, with a particular emphasis on cattle, poultry, and companion animals. She is responsible for the molecular genetics lab and leads the bioinformatic analysis of her research group. Her current research focuses on the analysis of structural variants to identify genomic variation among breeds and their adaptation to changing environments. She has gained solid academic and research experience, including a period as Honorary Associate/Fellow at the University of Wisconsin-Madison. She has participated in numerous international and national research projects, collaborating with institutions in Mexico, Canada, Iran, and Israel. Her research interests include the evolution and biodiversity of animal breeds, gene expression analysis, the identification of candidate genes for hereditary diseases, and genomic structural variation. She is the author of over 69 publications in peer-review journals. She coordinates and participates in funded research projects, demonstrating leadership and skills in managing work groups. She possesses technical skills in both the laboratory (nucleic acid isolation, PCR, sequencing) and bioinformatic analysis (population genetics, sequence analysis, association analysis).

GENETIC CHARACTERIZATION OF IRISH WOLFHOUND DOGS: A WORLDWIDE STUDY OF GENETIC VARIABILITY AND INBREEDING

Abstract: Unraveling the Genetics of the Irish Wolfhound

The Irish Wolfhound (IW) is a canine breed characterized by phenotypic traits that differ significantly from the normotype of Canis lupus familiaris. Its giant size is one of its most distinctive features and, as noted in scientific literature, is associated with a shorter lifespan. This unique breed also carries a history of genetic bottlenecks, which have impacted its health and reduced its genetic diversity.

In our study, we analized 96 Irish Wolfhounds from 23 countries using high-density genomic tools to investigate their genetic variability and levels of inbreeding. We examined how similar or different these dogs are at the DNA level, focusing on genomic regions that are identical due to shared ancestry—known as “runs of homozygosity” (ROHs).

Here’s what we found so far/first results?

Genetic diversity is relatively low, with average heterozygosity around 0.3;

there is no clear genetic sub-structuring within the population;

some genomic regions were shared by 100% of the dogs, likely as a result of selection and mating practices over time;

no ROHs longer than 16 Mbp were detected, which may reflect historical, rather than recent, inbreeding;

genomic inbreeding levels (FROH) ranged from 11% to 41%, indicating moderate to high inbreeding. We are now investigating potential links between causes of death and pedigree/genomic data. By connecting genetic insights with health outcomes, we aim to support better breeding strategies that prioritize genetic diversity and long-term health for this breed.