

The Irish Wolfhound

What genetics tells us about the breed today

*A collaborative genomic study for a
healthier and sustainable future of the breed*



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CONGRESSO - FIWC 2026

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PROJECT OVERVIEW

Phase 1 – Genetic characterization

- Breeders (23 countries)
- Sighthound Club of Italy
- Federation of Irish Wolfhound Clubs (FIWC)
- UNIMI- DIVAS



divas
DIPARTIMENTO DI MEDICINA
VETERINARIA E SCIENZE ANIMALI

Phase 2 – Pedigree, inbreeding, and longevity analysis

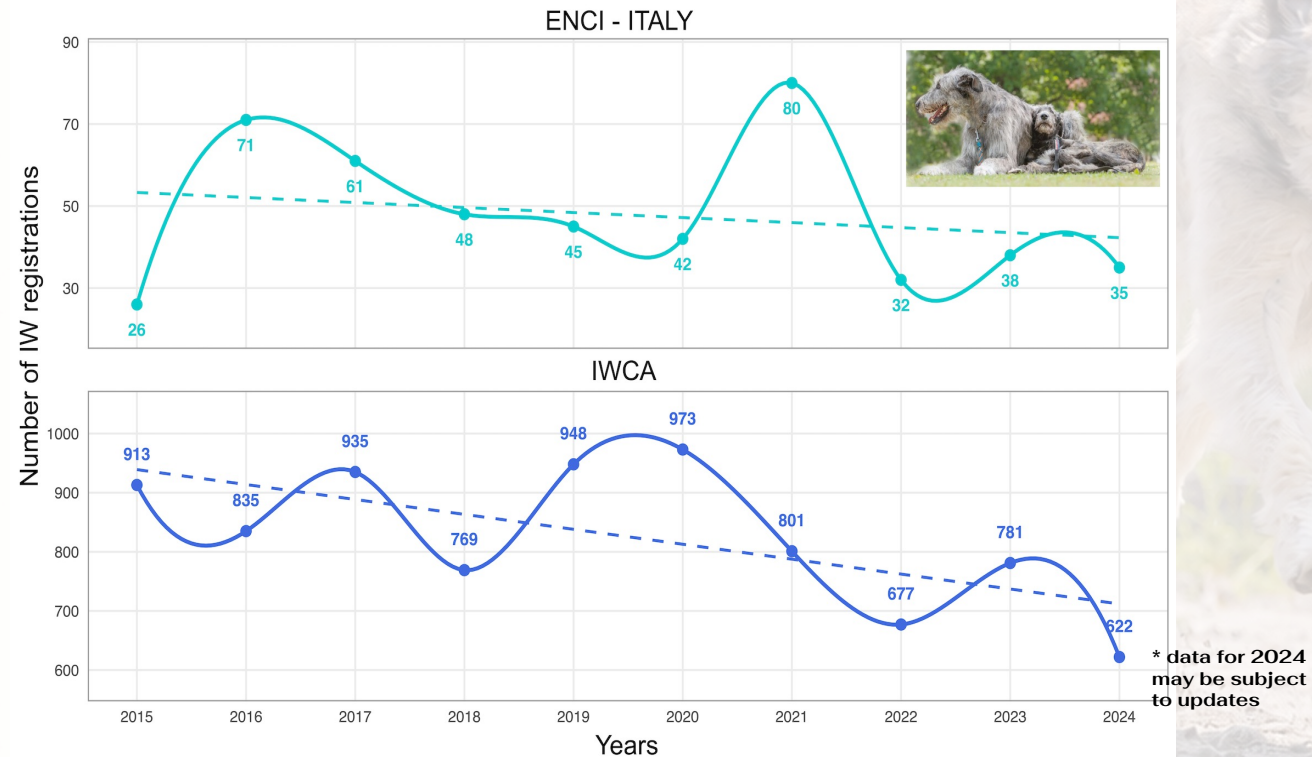
- Irish Wolfhound Database
- Irish Wolfhound Club of America



IRISH WOLFHOUND
CLUB OF AMERICA

WHY STUDY IRISH WOLFHOUND GENETICS?

- The breed has a long history, but its numbers dropped dramatically during the two World Wars → Today's population remains relatively small.



* data for 2024
may be subject
to updates

What is DNA?

DNA (Deoxyribonucleic Acid) is the genetic material of every living organism

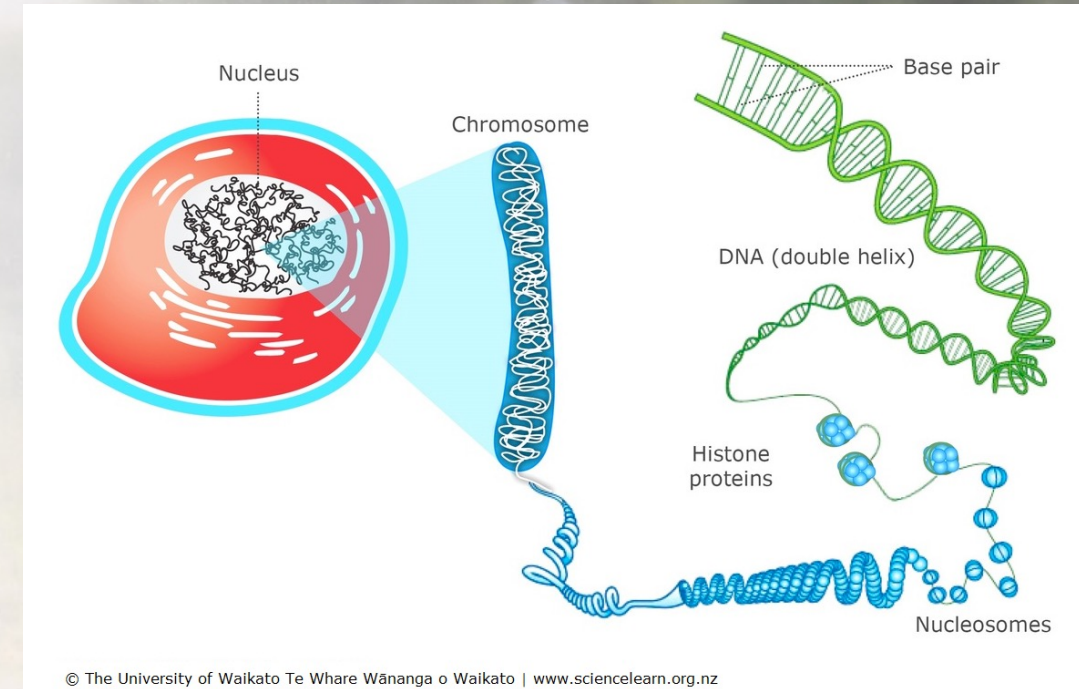
- It contains the biological instructions needed for growth, development, and reproduction
- DNA is a double helix organized into genes and chromosomes

DNA is composed of **millions of bases** = “4 letters” → **A, T, C, G**

A **SNP** (Single Nucleotide Polymorphism) is a **variation in one single DNA base**

- One letter changes = one SNP

About 20 million SNPs differ among individuals



SNPs: small genetic differences with big importance

LOCUS: SPECIFIC POSITION OF VARIATION

From mother → AAGCAT
From father → AAGCGT

Heterozygous → Different versions inherited from each parent

From mother → AAGCAT
From father → AAGCAT



From mother → AAGCGT
From father → AAGCGT



Exonic SNPs → may affect phenotype
Intronic/intergenic SNPs → markers of genetic variability

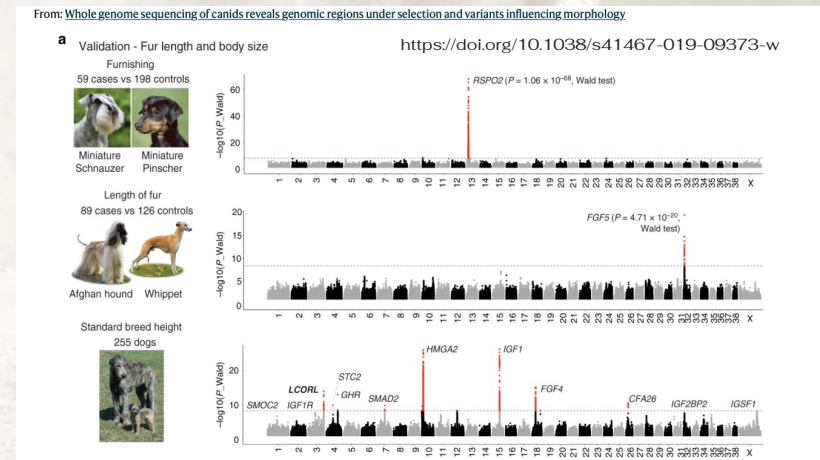
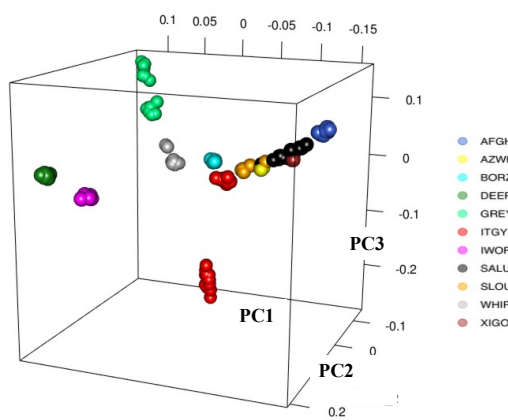
Homozygous: → Same version inherited from both parents

- More heterozygosity = more genetic variability
- More homozygosity = less variability and potentially more inbreeding

How do we analyze genetics diversity?



A SNP chip is a tool that reads hundreds of thousands of SNPs at the same time



- scans the genome and identifies homozygous and heterozygous regions
- captures genetic variability and diversity both within and among breeds

Into the IW genomic part of the project

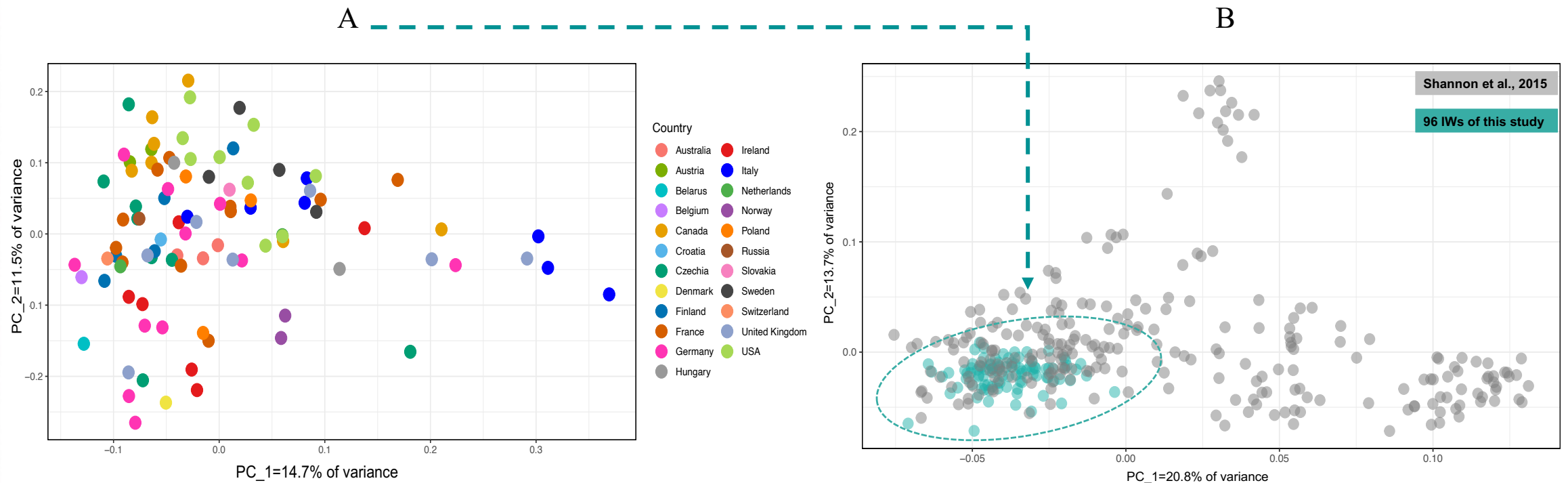
96 IWs from 23 different countries (buccal swaps collection)

SNP chip: Illumina CanineHD BeadChip (230K SNPs) - ROS_Cfam_1.0 reference genome

PCA - plots of diversity

Unique cluster → indicating a single global breeding population.

Homozogosity vs heterozygosity
0.85 vs 0.15



Runs of Homozygosity (ROH)

Long stretches of DNA where both copies inherited from the parents are identical (No heterozygous SNPs are present).

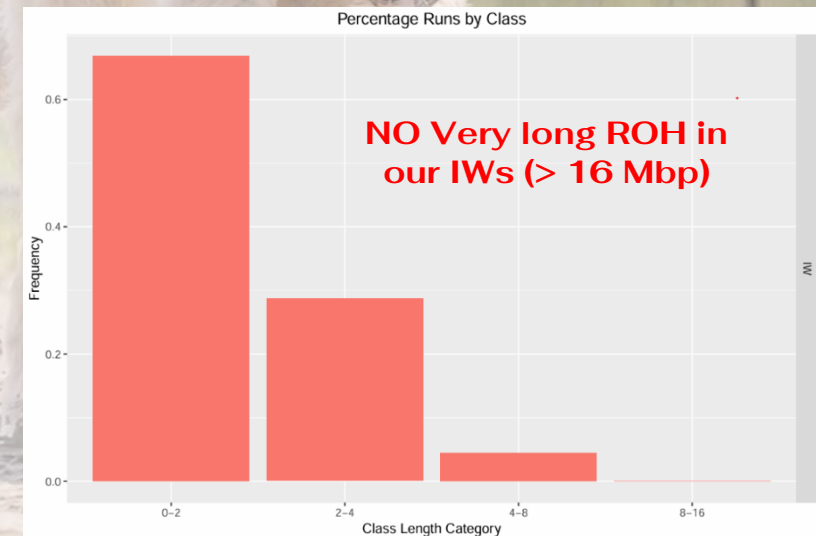
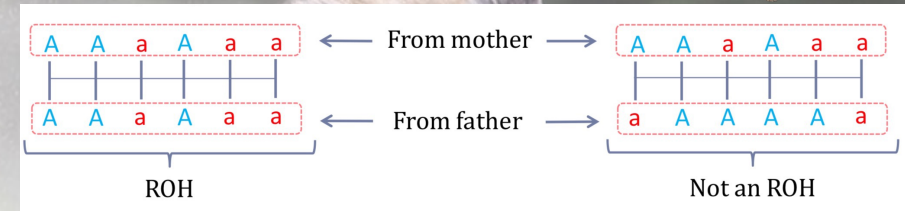
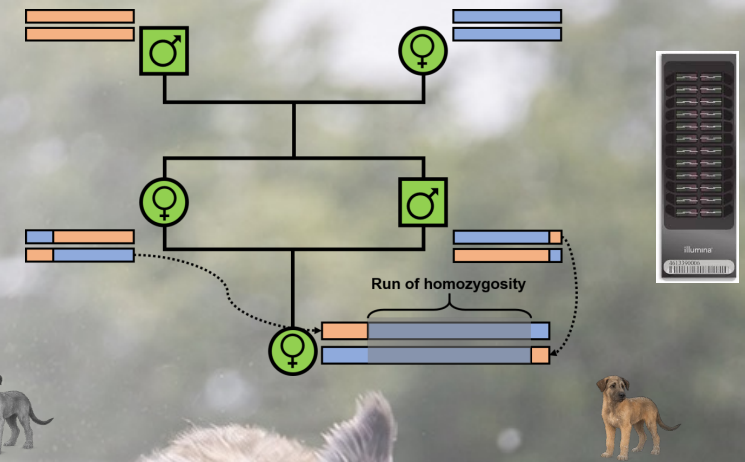
ROH length tell us about when inbreeding occurred in the history of a population.



Short ROHs typically reflect more ancient inbreeding events, dating back many generations.

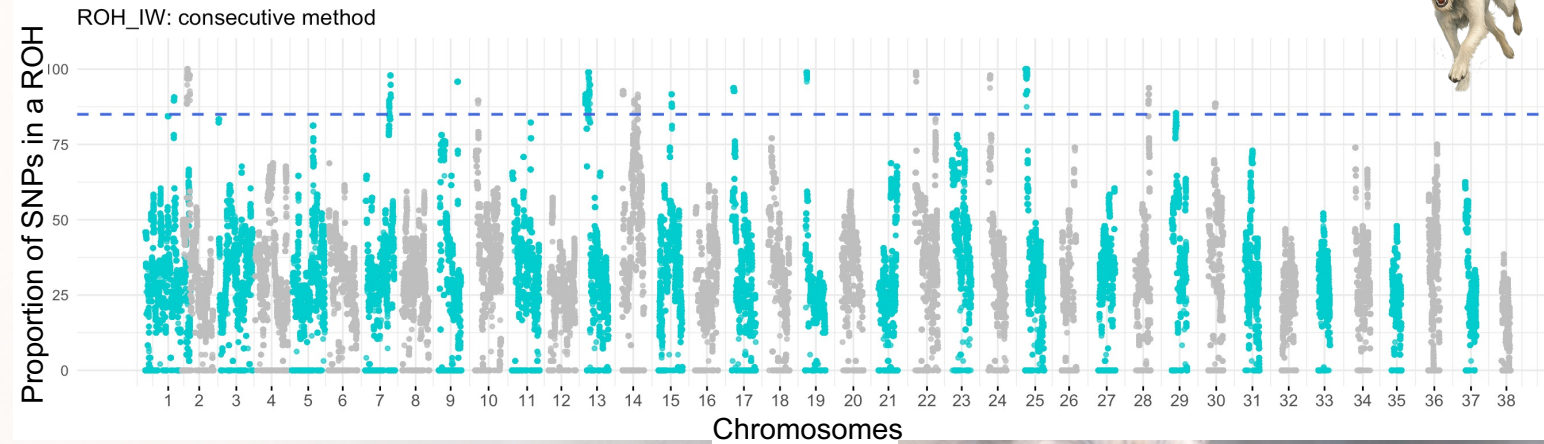
Long ROHs are usually the result of more recent matings between closely related individuals.

Our results indicate that **most of the inbreeding present in the breed is not recent, but rather dates back to the past**



Runs of Homozygosity (ROH)

ROH islands → shared genomic regions within the IW population



In our study, some were present in at least 85% of the dogs, and a 3 in all of them (100%).



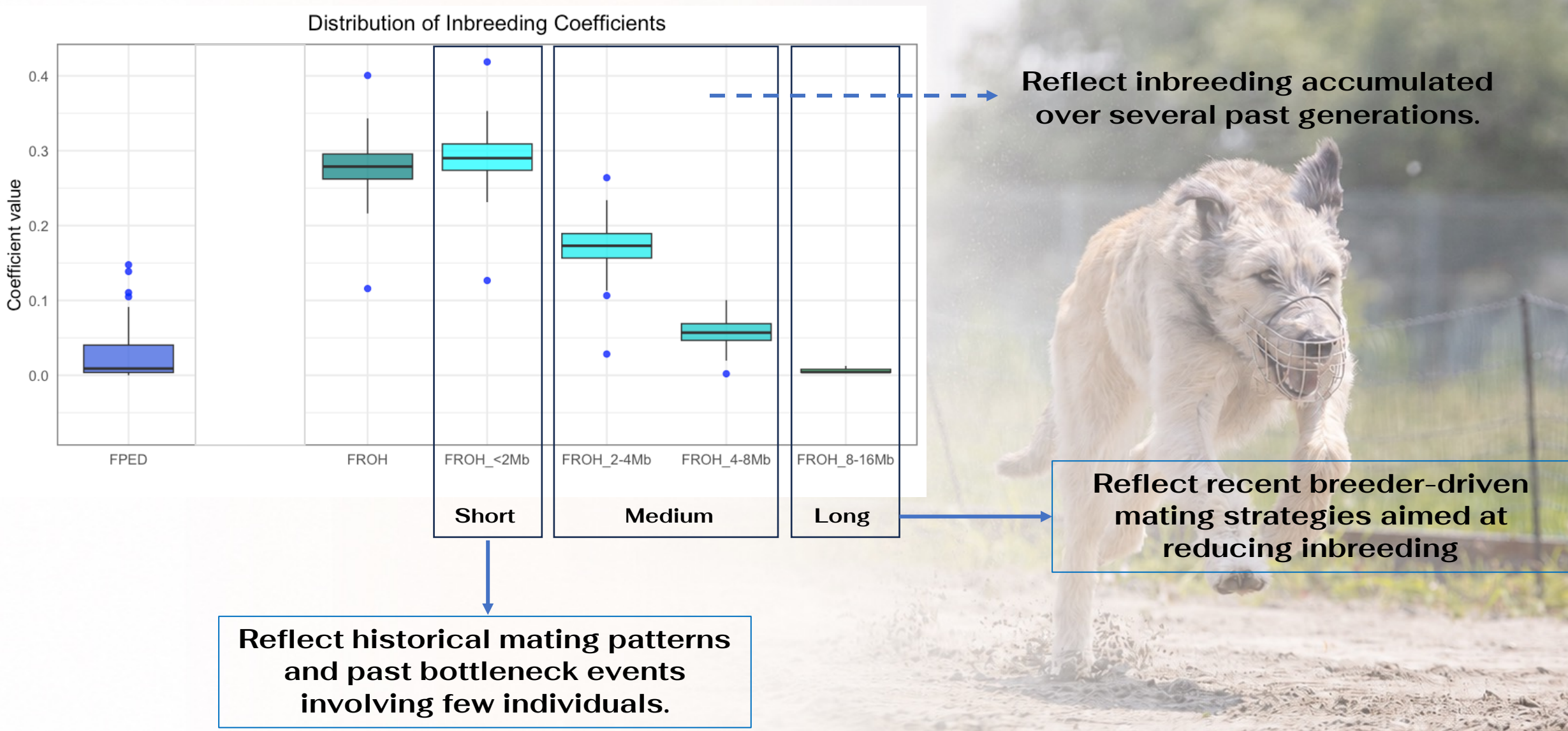
“Genetic signatures” of the breed, segments that have been passed down through generations and have become fixed over time.



Found in other hunting or working breeds, suggesting that they may be linked to functions or characteristics for performance, morphology, or behaviour

Some of the genes located within them have been associated with conditions such as cancer, heart diseases, and neurological disorders.

Genomic inbreeding coefficients (ROH)

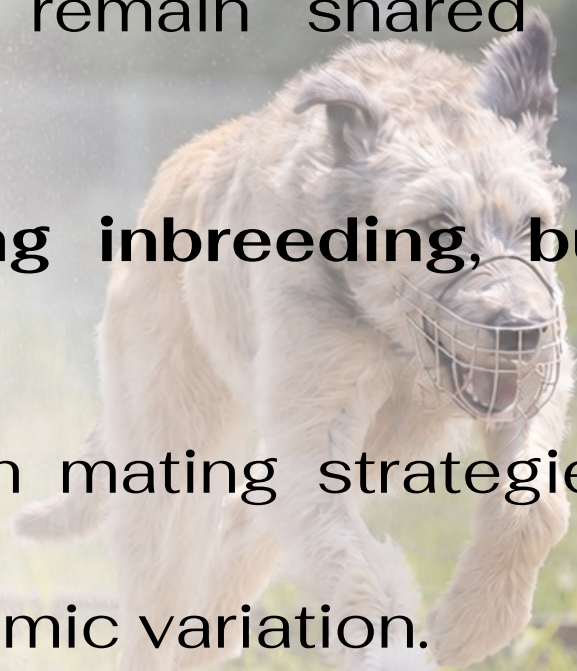


CONCLUSIONS

1. Recent breeding strategies appear effective in limiting recent inbreeding.
2. However, large portions of the genome remain shared in homozygosity across the breed.

The main challenge is no longer reducing inbreeding, but preserving the remaining genetic diversity.

1. Lost diversity cannot be recovered through mating strategies alone.
2. Future efforts → maximizing the existing genomic variation.
3. Further studies could investigate whether genes located within highly shared ROH regions contribute to the major causes of morbidity and mortality (including longevity) observed in the breed.



Second part of the project

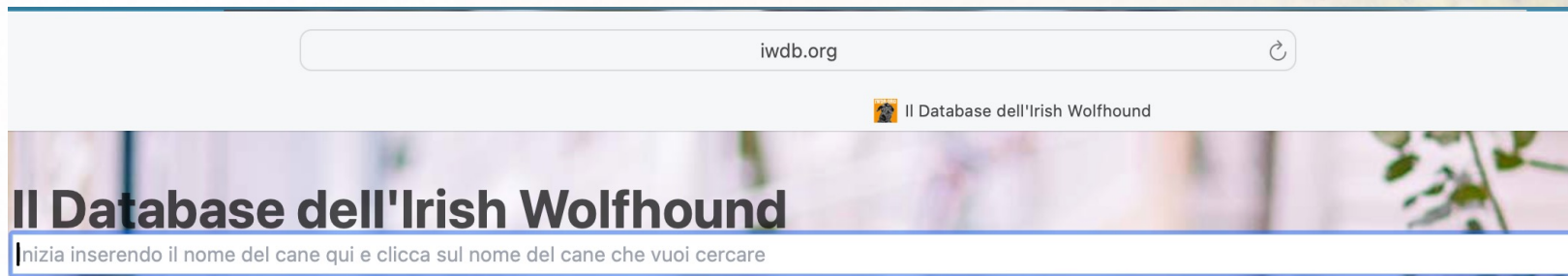
Irish Wolfhound: Genealogy, Longevity and Health of a Unique Breed

We aimed to answer three major questions:

- How closely related are the “bloodlines” of these 96 dogs in reality?
- Does inbreeding affect longevity?
- Do certain diseases appear to recur more frequently in specific family lines?

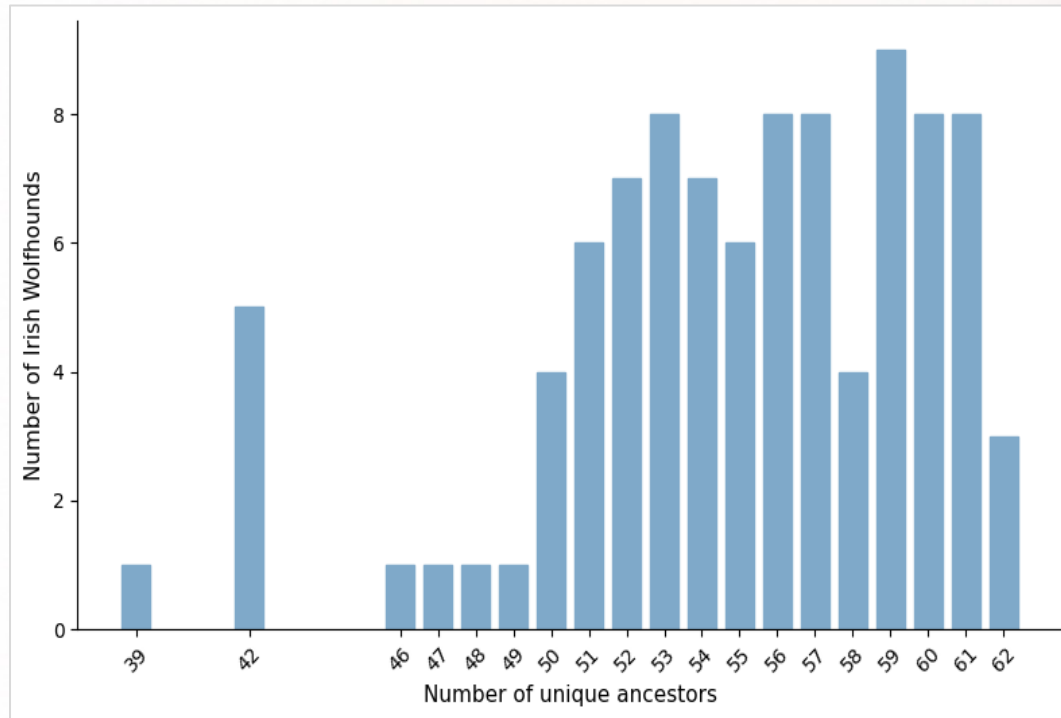
For the 96 dogs:

- genealogical data (five complete generations);
- dates of birth and death;
- information on the cause of death.

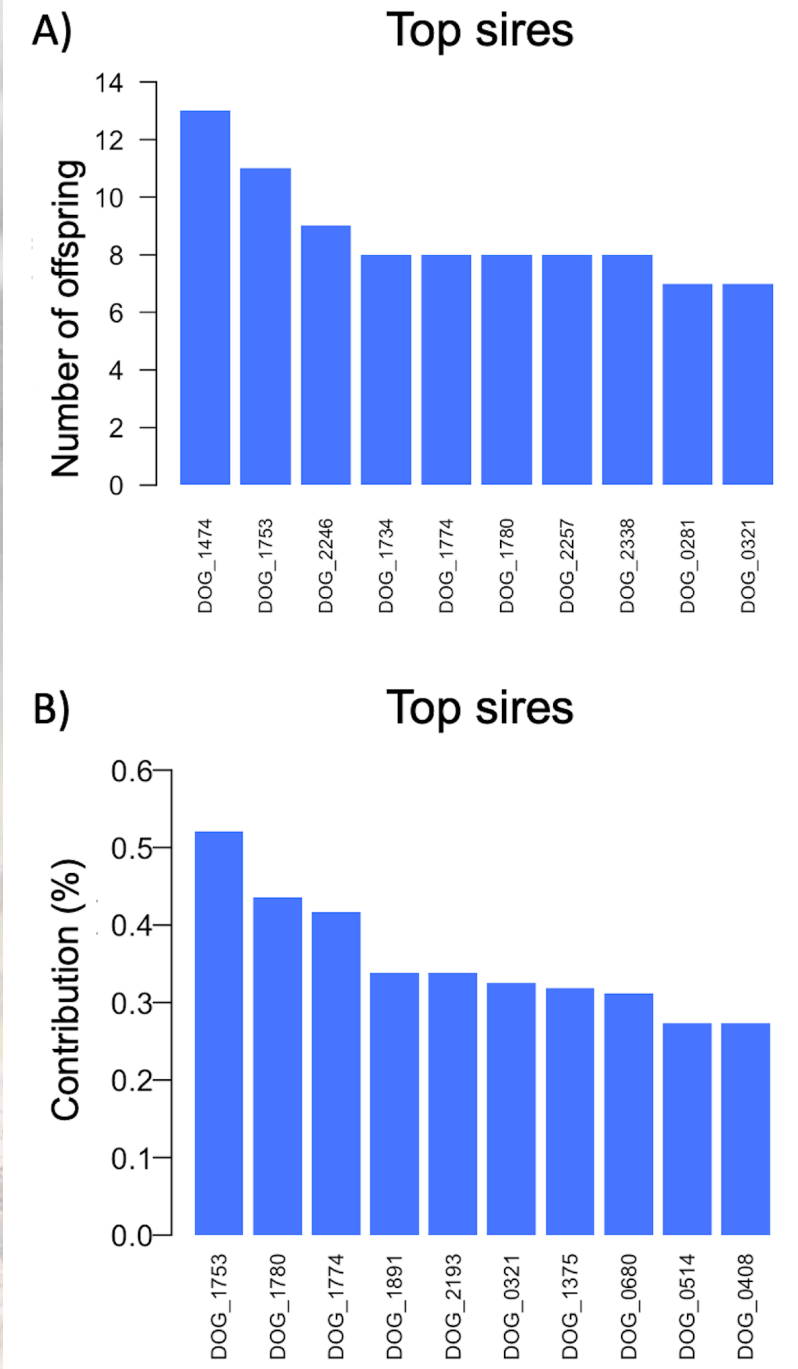


96 dogs → Theoretical n. of different ancestors: 5,952
Our dataset → 2,247

Genealogical redundancy → recurrences of some sires.

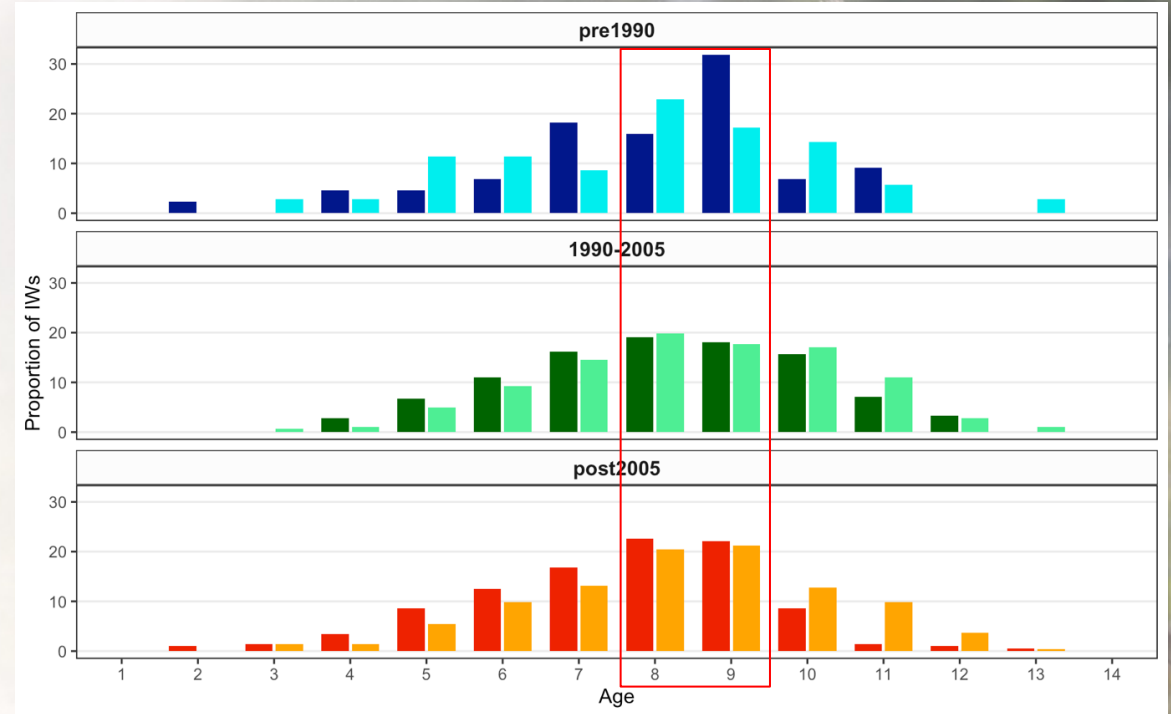
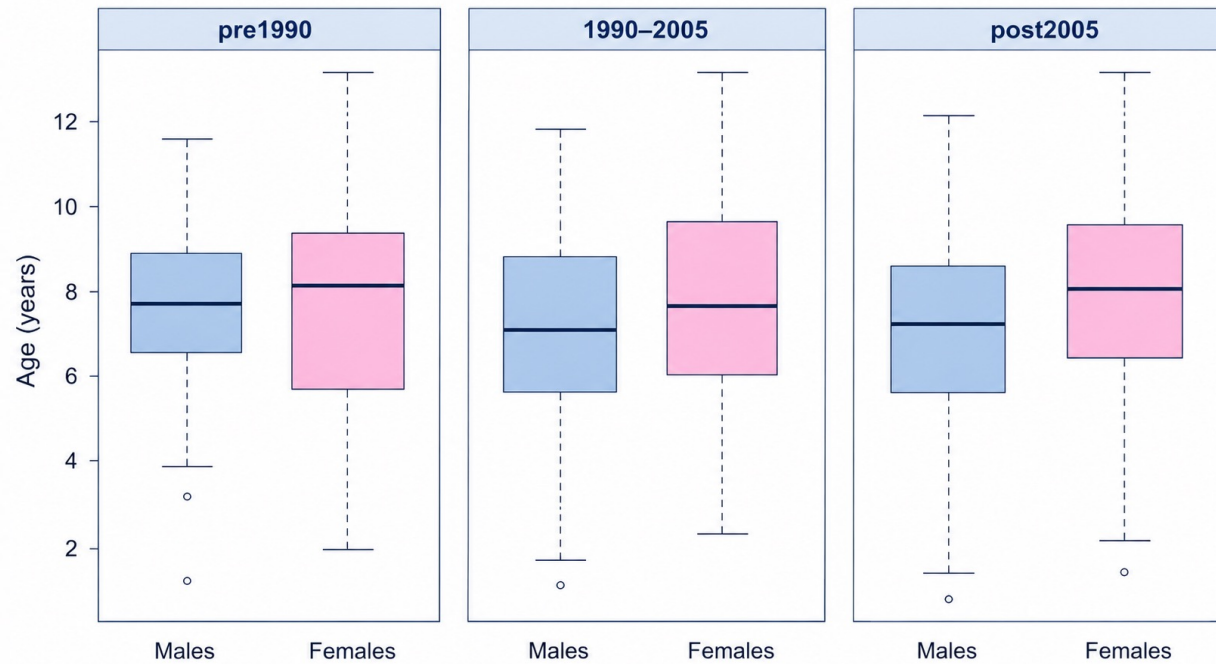


Popular sire effect: some sires had a much greater influence than others, contributing significantly to the current genetic structure of the breed.



Longevity (life-span)

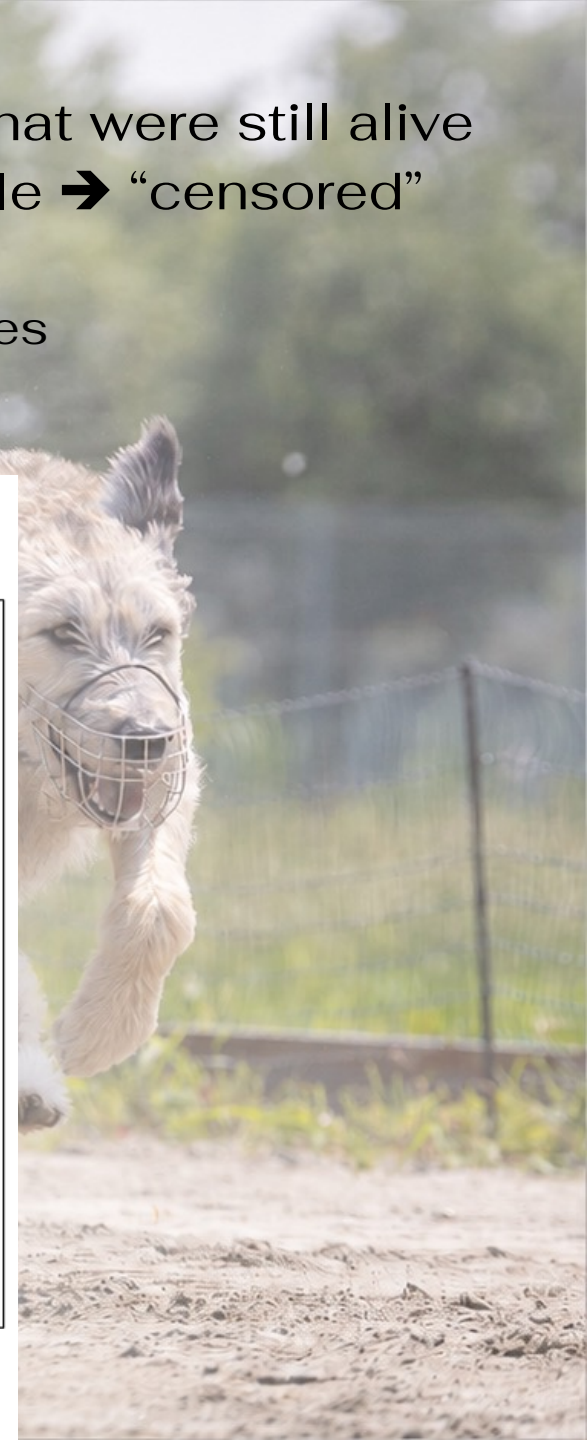
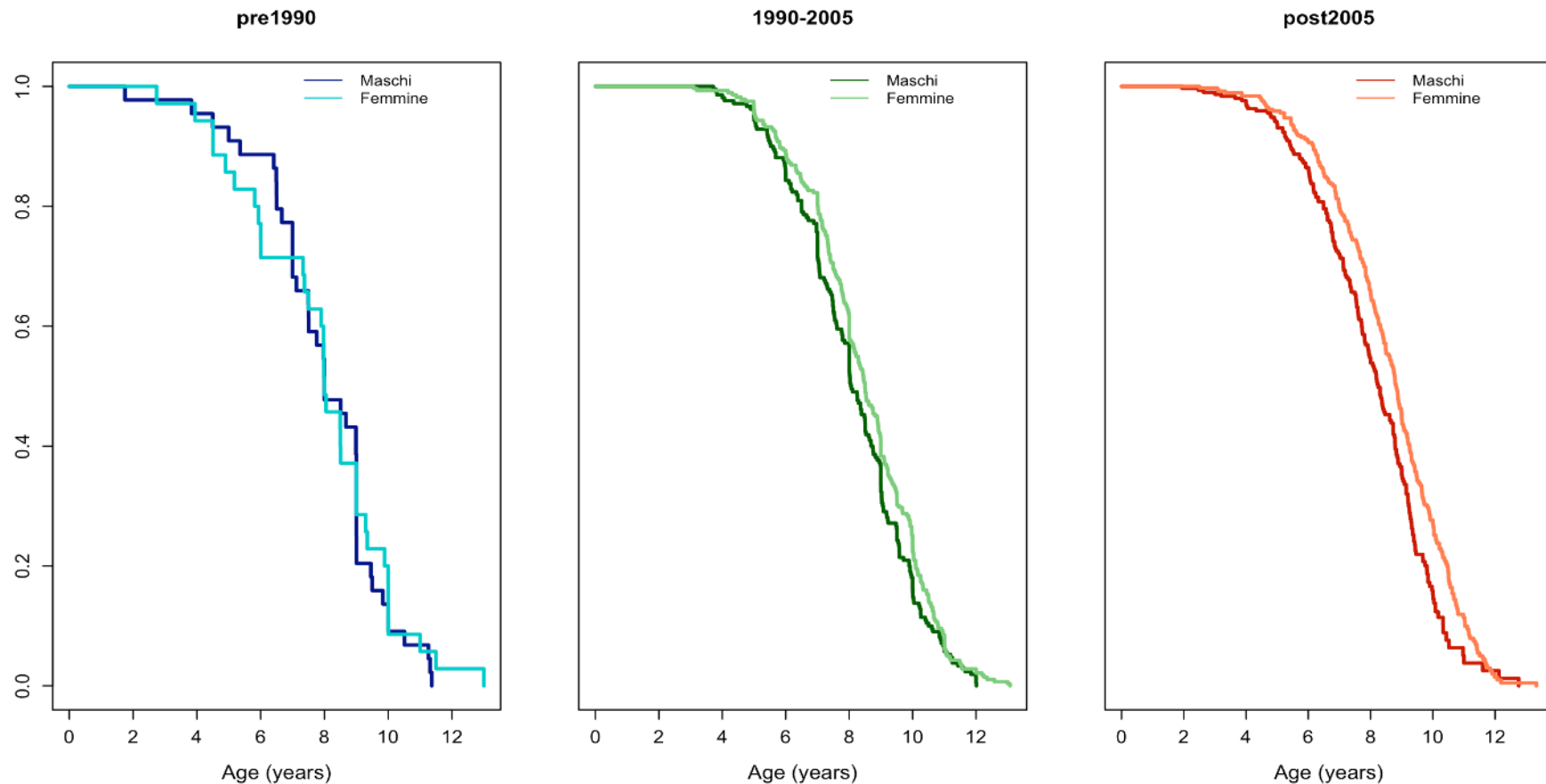
Complete birth and death dates were available for **only 1,052 dogs** (dataset 2247 + 96 → 2343).



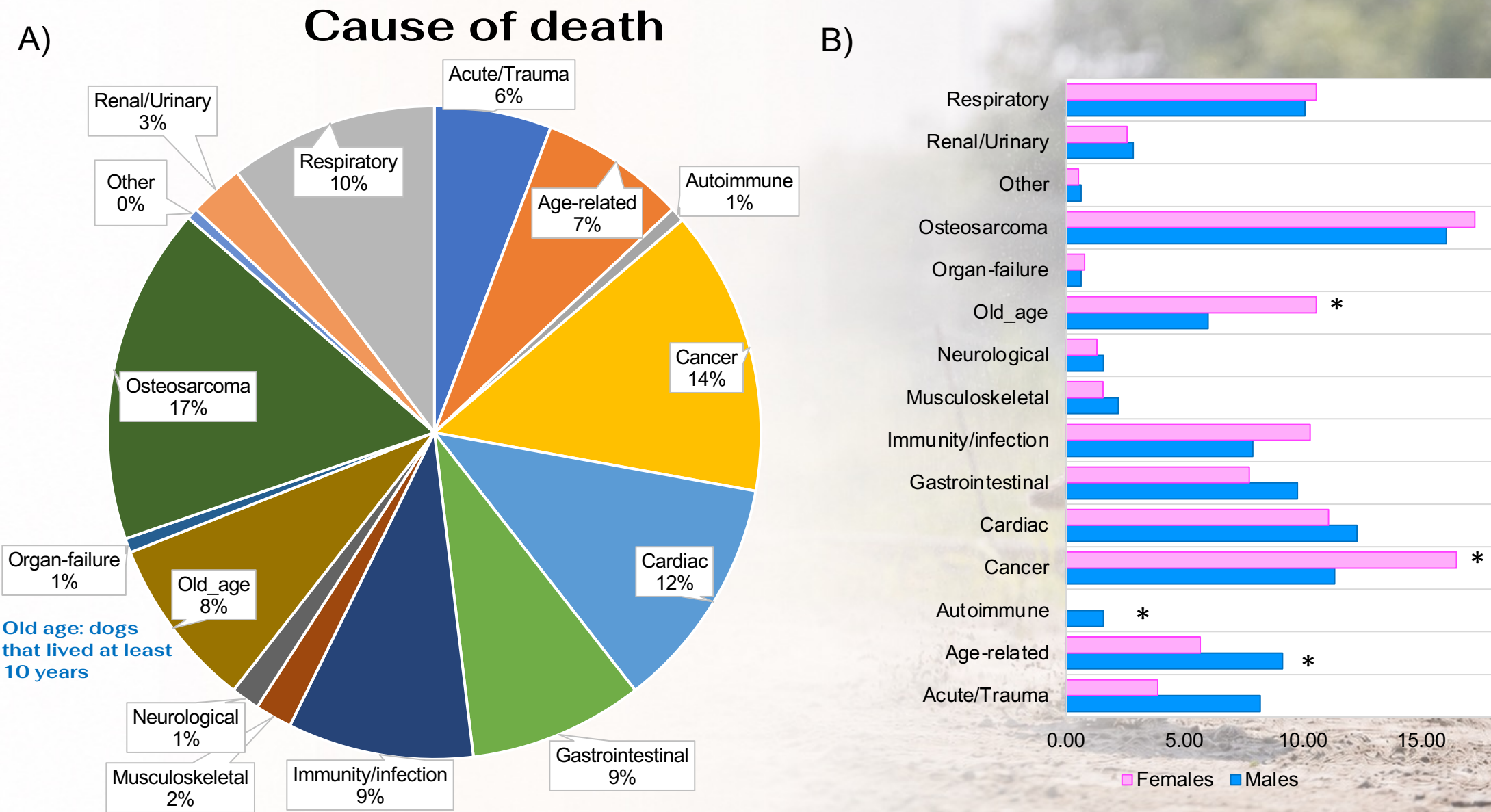
No significant differences were observed between the different generations considered.

Survival analyses → a total of 1,267 IWs: we also considered dogs that were still alive at the time of the study or for which a date of death was not yet available → “censored”

Females showed slightly better survival than males



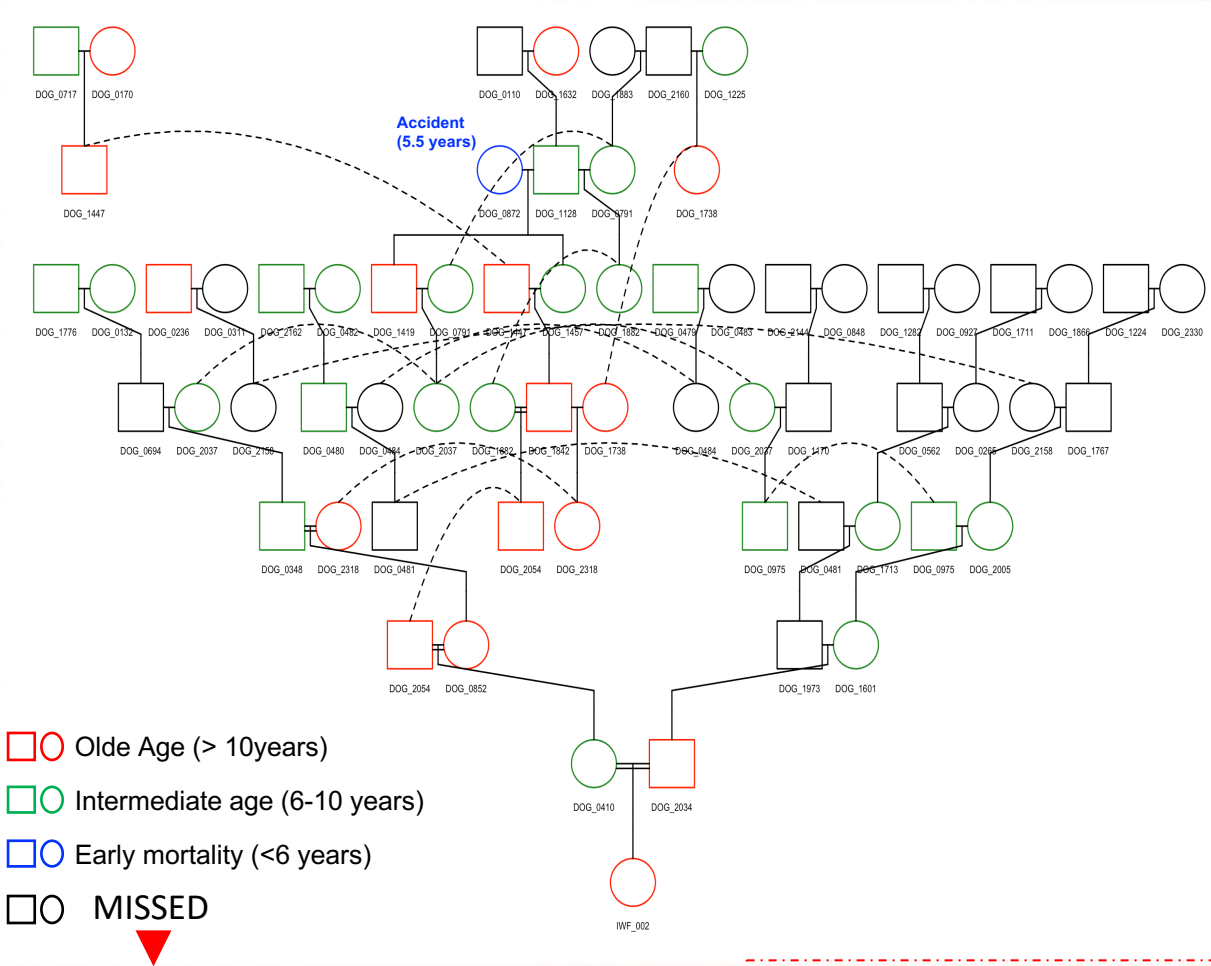
Dataset → n = 2,343 → Missing category (n = 1,291 without cause of death)
(low proportion are still alive)



Phenotype Tracking Through Familial Cause-of-Death (COD) Records

Longevity (life-span)

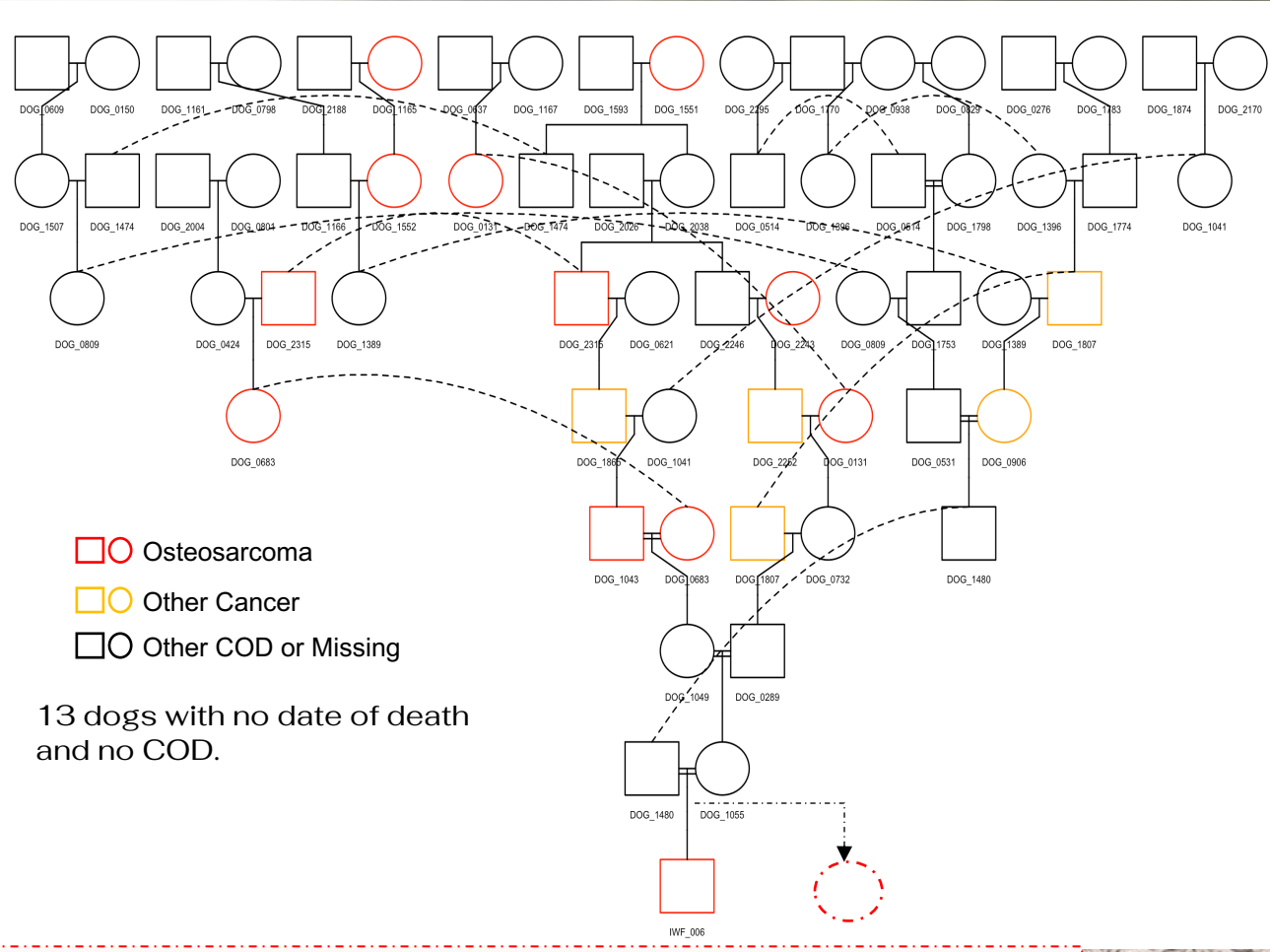
53 ancestors (62)



22 with no date of death and no cause of death.

Osteosarcoma

52 ancestors (62)



13 dogs with no date of death and no COD.

Could we one day predict at least part of a dog's expected lifespan based on information from its ancestors?

TAKE-HOME MESSAGE & FUTURE PERSPECTIVES



DATA TODAY, HEALTHY TOMORROW

Building a sustainable future for the Irish Wolfhound



*Preserve the breed.
Improve health.
Extend life.*

1. DATA IS THE FOUNDATION

Breeders play a key role by recording and sharing information about their dogs.



Pedigree information
ancestry, relatives



Health data
diseases, longevity, treatments



Genomic data
genotyping, genetic diversity



All data stored in breed databases
accurate • secure • shared

2. FROM DATA TO TOOLS

High-quality data enable research to develop tools that support breeders.



Inbreeding estimation
pedigree & genomic



Detection of hidden relatedness
more accurate risk assessment



Mating recommendation tools



Selection for health, longevity and diversity

3. BETTER BREEDING DECISIONS

Using the right tools helps breeders to:



Manage inbreeding and preserve genetic diversity



Reduce risk of inherited diseases



Improve puppy health and longevity



Safeguard the future of the Irish Wolfhound



4. TOGETHER FOR THE FUTURE

A collaborative approach is essential to conserve the breed and make it healthier and longer-lived.



BREEDERS

Provide accurate data, use tools responsibly, and share for the good of the breed.



VETERINARIANS

Support health monitoring, diagnosis, and data collection.



RESEARCHERS

Transform data into knowledge and develop practical tools for breeders.



CLUBS & KENNEL CLUBS

Promote collaboration, responsible breeding and data sharing initiatives.



The Irish Wolfhound carries the genetic signature of its historical bottlenecks, but modern breeders are successfully limiting recent inbreeding. The next challenge is preserving the remaining genetic diversity while continuing to improve health and longevity through international collaboration and data sharing.



Many thanks to all who made this project possible



PROJECT LEADERSHIP, COORDINATION & DATA ANALYSIS



M.G. STRILLACCI



S.P. MARELLI



M. POLI

DATA ANALYSIS SUPPORT



C. FERRARI



F. BERNINI

♡ *A special thanks to* ♡

**THE BREEDERS WHO CONTRIBUTED SAMPLES AND INFORMATION
FOR THE 96 IRISH WOLFHOunds INCLUDED IN THE STUDY.**

Your collaboration, trust, and passion for the breed
are at the heart of this work.



**THANK YOU TO THE IRISH WOLFHOund BREED CLUBS
AND ORGANIZATIONS FOR THEIR SUPPORT AND FOR PROMOTING
COLLABORATION AMONG BREEDERS AND RESEARCHERS.**

