



UNIVERSITÀ DEGLI STUDI DI MILANO
DIPARTIMENTO DI MEDICINA VETERINARIA
E SCIENZE ANIMALI

Pedigree Analysis of the Irish Wolfhound:

Insights into Inbreeding and Population Structure

Stefano Paolo Marelli, Marcello Poli

Prof. Dr S.P. Marelli, MSc, PhD: stefano.marelli@unimi.it



Domestication: FEAR & AGGRESSIVENESS

Human societies – specific functions – **Functional landraces**

Phenotypic clustering:

dogs that looked and behaved similarly were preferentially bred together, gradually increasing within-group genetic similarity.

Over time, **geographic isolation** and **human preference for specific traits** reduced gene flow between dog groups, causing the first measurable increases in population structure and inbreeding levels.

Introduction



IRISH WOLFHOUND

- FCI BREED STANDARD NO. 160





GENERAL APPEARANCE:
Of great size and commanding appearance, commanding, strong but with exuberant and where most capricious appearance, the breed height the Wolfhound is commanding, strong but gracefully built.

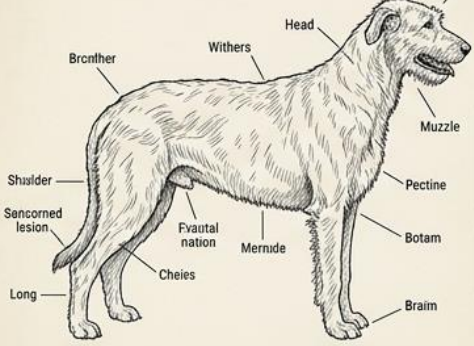
HEAD:
Long and flat.
Muzzle moderately.
Muzzle moderately long.

HEAD:
Long and flat.
Muzzle moderately.
Muzzle moderately long.

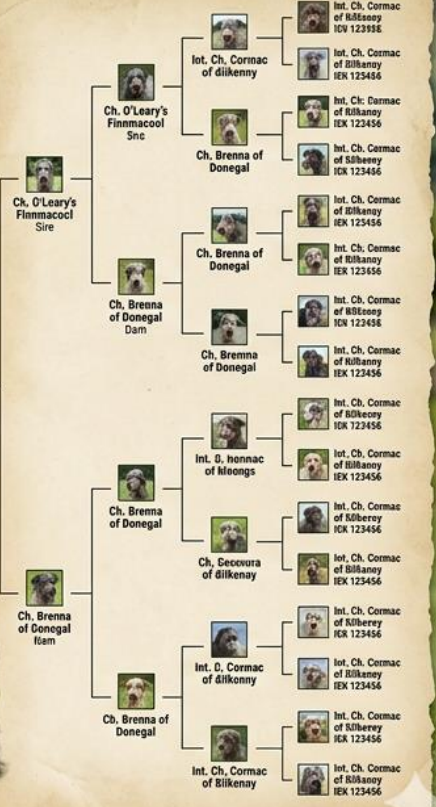
HEIGHT AT WITHERS:
Minimum for Dogs: 79 cm;
for Bitches: 71 cm.

WEIGHT:
... not less than 54.5 kg for dogs.

COAT:
Rough, hard, and wire-haired. The ane coat is renewable in a haired suvumard arent the coat tonitadie vvxs coat ins close moon created.



PEDIGREE



The modern concept of the dog breed emerged in the 19th century with the establishment of kennel clubs and closed studbooks, which formalized breed definitions based on **conformation standards** and restricted breeding to registered individuals.

Pedigree

The transition to **closed breeding** systems caused a dramatic **increase in inbreeding** because gene flow from outside populations was effectively stopped, and all individuals within a breed began to share a finite set of founders.

Many modern breeds exhibit **high levels of relatedness** even among apparently unrelated individuals, due to repeated use of popular sires and genetic bottlenecks during breed formation

The Irish Wolfhound has a complex origin that combines:

- ❖ ancient canine lineages
- ❖ cultural reconstruction
- ❖ severe modern genetic bottlenecks

One of the most genetically distinctive giant dog breeds



Historical records suggest that large “**wolf-hunting dogs**” existed in Ireland as early as antiquity and the early medieval period, where they were used for hunting wolves, elk, and large game, and were highly valued as status animals.

These early Irish Wolfhounds were not a single standardized breed in the modern sense but rather a functional population of large hunting dogs with **shared morphology and working behaviour**, maintained through selective breeding within **regional landraces** .

With the extinction of wolves in Ireland and social changes in the 18th–19th centuries, the original functional population declined sharply, leading to a near **disappearance** of the historical Irish wolfhound type.

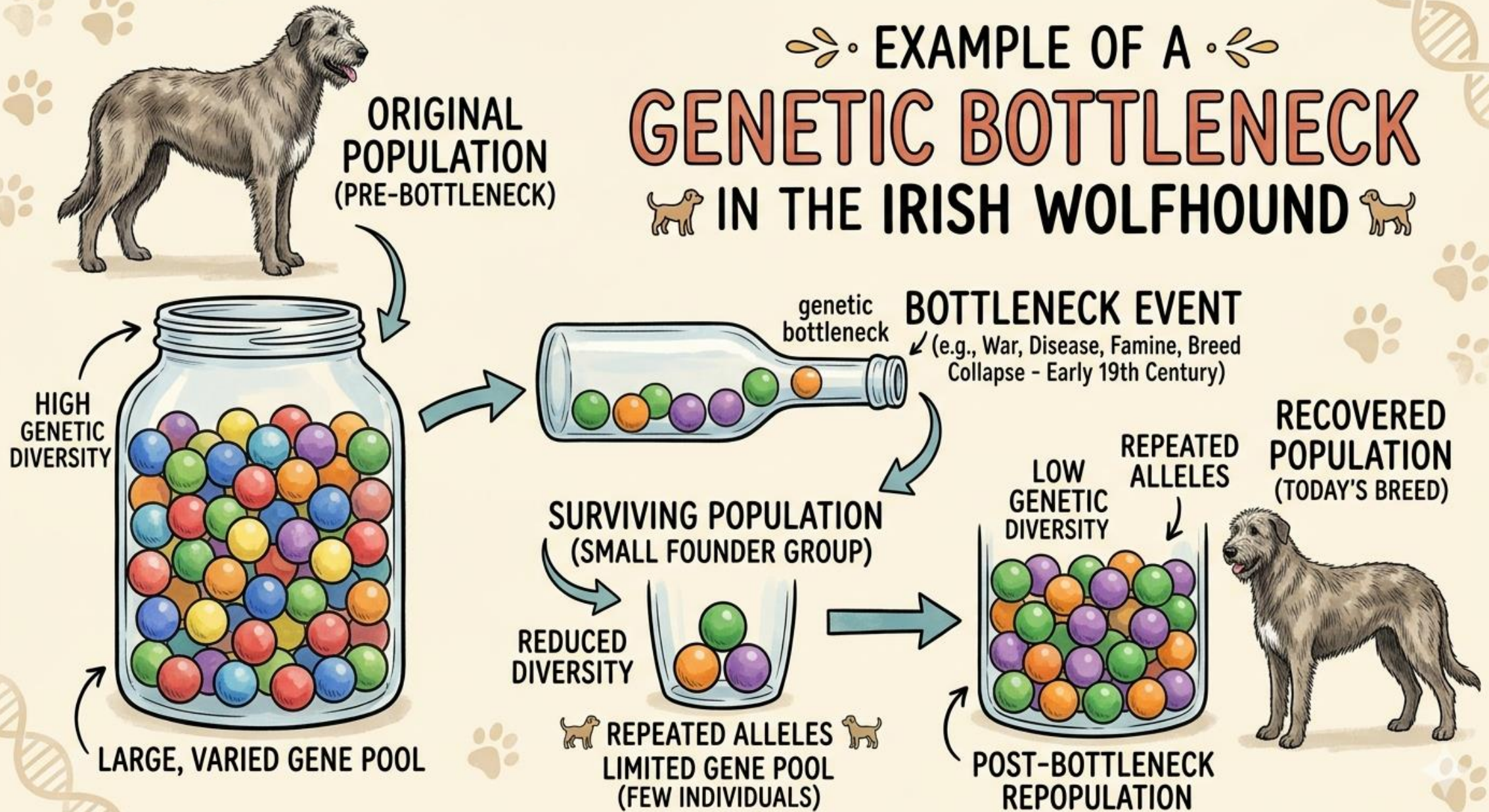
The modern Irish Wolfhound breed was reconstructed in the late 19th century primarily through the efforts of breeders such as Captain George Augustus Graham, who aimed to “**restore**” the ancient wolfhound type using surviving large dogs and **crossbreeding** with breeds such as the Great Dane and Scottish Deerhound.

This **reconstruction** means that the modern breed is not a direct continuous genetic lineage from ancient Irish wolfhounds but rather a reconstructed composite breed derived from **multiple source populations**.

The use of a **limited number of founding individuals** during this reconstruction created a strong founder effect, where the entire modern population descends from a small genetic base

A **genetic bottleneck** occurs when a population undergoes a severe reduction in effective size, leading to loss of genetic variation and increased genetic drift.

EXAMPLE OF A GENETIC BOTTLENECK IN THE IRISH WOLFHOUND



The Irish Wolfhound experienced at least **two major bottlenecks**: the historical near-extinction of the original functional population and the 19th-century breed reconstruction using few selected founders.

These bottlenecks drastically reduced **effective population size (N_e)**, increasing relatedness among individuals and accelerating the accumulation of inbreeding across generations.



IRISH WOLFHOUND: Effective Population Size (N_e), Increase of Inbreeding and Conservation Limits

FAO DAD-IS guidance for the management of animal genetic resources

INBREEDING INCREASE PER GENERATION

FAO Formula:

$$\Delta F = \frac{1}{2N_e}$$

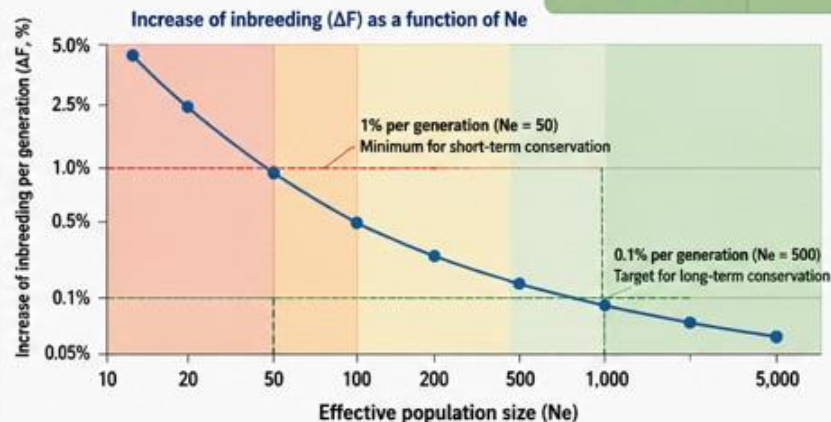
where:

ΔF = increase in inbreeding coefficient per generation

N_e = effective population size

Why N_e is important for the Irish Wolfhound?

- N_e reflects the number of animals effectively contributing genes to the next generation.
- Small N_e leads to faster increase in inbreeding (F) and loss of genetic diversity.
- Maintaining an adequate N_e is essential to preserve health, fertility and long-term viability of the breed.



RELATIONSHIP BETWEEN N_e AND INBREEDING INCREASE

Effective population size (N_e)	Increase of inbreeding per generation ($\Delta F = 1/2N_e$)	Interpretation (FAO DAD-IS)
$N_e < 50$	$> 1.0\%$	Very high risk Not acceptable for conservation (inbreeding increases too fast)
$N_e = 50$	1.0%	Minimum acceptable level for short-term conservation
$N_e = 50 - 100$	$0.5\% - 1.0\%$	Risk zone – loss of genetic diversity accelerates
$N_e \geq 100$	$\leq 0.5\%$	Better – reduction in rate of diversity loss
$N_e \geq 500$	$\leq 0.1\%$	Recommended target for long-term conservation

CONSERVATION LIMITS (FAO DAD-IS)



$N_e < 50$

Inbreeding increases $>1\%$ per generation. High risk of inbreeding depression, loss of fertility, and accumulation of deleterious alleles.



$N_e 50 - 100$

Loss of genetic diversity is rapid. Active management required.



$N_e \geq 100$

Maintains diversity better, but still monitor inbreeding.



$N_e \geq 500$

Recommended goal for long-term conservation of the breed.

RECOMMENDATIONS FOR THE IRISH WOLFHOUND



Monitor pedigrees and control inbreeding (COI).



Use genomic tools (SNP chips, ROH) to estimate realized inbreeding.



Balance contributions of sires and lines (avoid popular sire effect).



Integrate health screening and longevity data in breeding decisions.



Aim to maintain or increase N_e toward ≥ 100 , and ideally ≥ 500 for long-term sustainability.

SOURCE

FAO. *In situ* Conservation of Livestock and Poultry. Guidelines for the Management of Animal Genetic Resources. DAD-IS (Domestic Animal Diversity Information System). FAO, Rome.

Relevant sections:

- FAO, 1992. Breeding strategies for *in situ* conservation.
- FAO, 2000. DAD-IS Guidelines.



Maintaining an adequate effective population size ($N_e \geq 100$, and ideally ≥ 500) is the most effective way to limit inbreeding, preserve genetic diversity and ensure the long-term health and viability of the Irish Wolfhound.



UNIVERSITÀ
DEGLI STUDI
DI MILANO

Pedigree data are central to inbreeding estimation and, more broadly, to genetic management in purebred dog populations

Dog breeds operate within **closed studbooks**, meaning all individuals descend from a **finite set of founders**

Pedigree records especially valuable for understanding genetic structure and managing diversity

The **depth and completeness of pedigree** records directly influence the accuracy of inbreeding estimates, as shallow pedigrees tend to underestimate true inbreeding.

Inbreeding is an inherent feature occurring when related individuals are mated, increasing the probability that offspring inherit identical copies of genes from both parents

From a genetic perspective, this leads to **increased homozygosity**. While this can help stabilise desired traits, it also increases the risk of expressing deleterious recessive alleles and can contribute to inherited disorders.

The impact of inbreeding is not always uniform. In some cases, its **negative** effects on traits such as **fertility** may appear limited, while other traits such as **disease susceptibility** and **lifespan** may be more strongly affected.

Monitoring inbreeding remains a key component of responsible **breeding strategies**.

Inbreeding is an inherent feature of modern purebred dog breeding, arising from the intentional mating of **related individuals** to **stabilize desirable phenotypes**.

While this practice has enabled the fixation of breed-specific traits, it has also **reduced genetic diversity** and increased the expression of **deleterious recessive alleles**.

From a population genetics perspective, inbreeding **increases homozygosity** and **reduces allelic variation**, thereby elevating the risk of inbreeding depression, a phenomenon associated with reduced fitness, fertility, and health.

In this context, monitoring inbreeding and preserving genetic variability are essential for ensuring the **long-term sustainability** of the breed.

This can be effectively supported by **integrating** traditional pedigree analysis with modern genomic tools.

The most widely used measure of inbreeding is the **Coefficient of Inbreeding (COI)**, which estimates the probability that two alleles at a given locus are identical by descent.

Traditionally, COI is calculated using pedigree data (F_{ped}).

This approach is valuable because it allows breeders to track ancestry, identify common ancestors, and estimate expected inbreeding levels before mating

F Range (%)	Description
0–5%	Low inbreeding, typically corresponding to matings between unrelated or very distantly related individuals
5–10%	Moderate inbreeding, often reflecting distant linebreeding within a closed population
10–20%	High inbreeding, associated with repeated use of related individuals or closer common ancestry
20–25%	Very high inbreeding, representing close consanguineous matings with a high probability of homozygosity

Pedigree data were analysed to evaluate the genetic structure of the Irish Wolfhound population.

The complete five-generation pedigrees of **96 Irish Wolfhounds** were analysed.

When combined into a single pedigree dataset, this resulted in a total of **2,343 individuals**, including all known ancestors.

Pedigree completeness was assessed using the number of **equivalent complete generations (ECG)**, with a mean value of 6.39, indicating a good depth of genealogical information.

F_{ped} were calculated using the CFC population genetics tool (Sargolzaei, 2005).

These coefficients represent the probability that two alleles in an individual are **identical by descent** based on pedigree records.

Sargolzaei et al., (2005). A new indirect method for computing inbreeding coefficients in large populations. Journal of Animal Breeding and Genetics, 122(5), 325-331.

Table 2. Inbreeding coefficient (F_{ped}) distribution (N; %)

F	Inbred subjects (N)	Inbred/tot population (%)	Inbred/tot inbred population (%)
$0.00 < F \leq 0.05$	386	16.48	69.80
$0.05 < F \leq 0.10$	117	5.00	21.16
$0.10 < F \leq 0.15$	39	1.67	7.05
$0.15 < F \leq 0.20$	7	0.30	1.27
$0.20 < F \leq 0.25$	3	0.13	0.54
$0.25 < F \leq 0.30$	0	0.00	0.00
$0.30 < F \leq 0.35$	1	0.04	0.18
Total	553	23.61	100.00

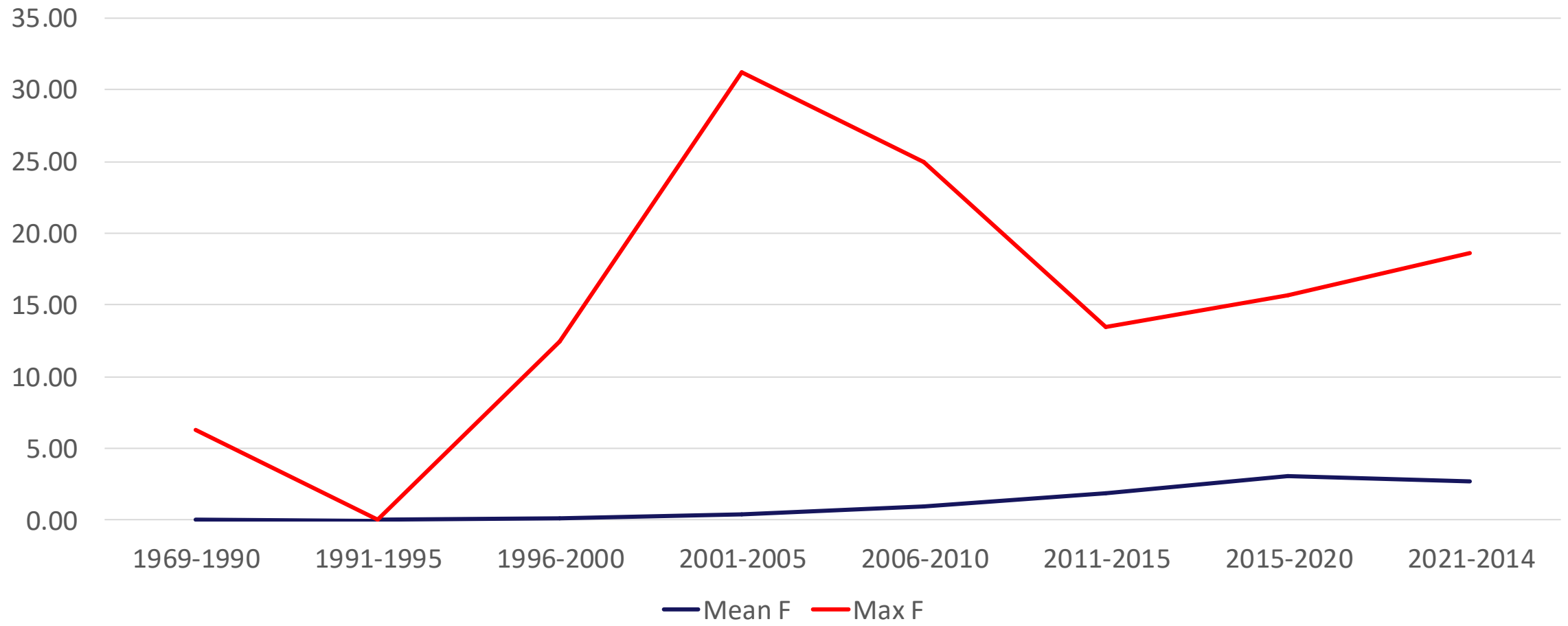
The majority of inbred individuals (**69.8%**) showed low inbreeding levels (**$F \leq 5\%$**). Only one individual presented a very high inbreeding coefficient (**above 30%**).

The **overall average inbreeding coefficient** of the population was **0.92%**, while the average among inbred individuals was 3.92%.

The population included **716 founders** and **1,627** individuals with **both parents known**.

Analysis over time showed generally **low average inbreeding levels**, with occasional **peaks** in specific periods.

Figure 1. Mean and maximum inbreeding coefficient (F_{ped}) across birth-year clusters



The analysed population shows relatively low average inbreeding levels, with most individuals falling below commonly used warning thresholds (**mean value < 5%**).

This suggests that, overall, breeding practices have avoided excessive consanguinity.

The presence of inbreeding peaks and the limited genetic base of the breed highlight the importance of **continued monitoring**.

Even moderate levels of inbreeding can accumulate over generations, particularly in closed populations.

The Irish Wolfhound remains **genetically constrained** due to its historical bottlenecks and founder structure. For this reason, maintaining genetic diversity should remain a priority.

The Irish Wolfhound represents a valuable case study in the management of genetically constrained dog populations.

Although current inbreeding levels appear generally low, **the breed's narrow genetic base and historical bottlenecks require ongoing attention.**

Pedigree analysis remains a fundamental tool for monitoring population structure and guiding breeding decisions.

However, genomic approaches, such as the estimation of inbreeding through runs of homozygosity (ROH), may provide a more accurate measure of realised genetic variation.

The integration of pedigree and genomic data therefore represents a promising direction for improving the management of genetic diversity

Sustainable breeding strategies will depend on:

continuous monitoring,

informed decision-making, and

collaboration within the breeding community

to preserve both the health and the identity of this iconic breed.

THE IRISH WOLFHOUND

HERITAGE, SCIENCE AND RESPONSIBLE STEWARDSHIP



A VALUABLE CASE STUDY

The Irish Wolfhound represents a valuable case study in the management of genetically constrained dog populations. Although current inbreeding levels appear generally low, the breed's narrow genetic base and historical bottlenecks require ongoing attention.



PEDIGREE ANALYSIS: A FUNDAMENTAL TOOL

Pedigree analysis remains a fundamental tool for monitoring population structure and guiding breeding decisions.



GENOMIC INSIGHTS: A MORE ACCURATE PICTURE

Genomic approaches, such as the estimation of inbreeding through runs of homozygosity (ROH), may provide a more accurate measure of realised genetic variation.



INTEGRATION OF PEDIGREE AND GENOMIC DATA

The integration of pedigree and genomic data therefore represents a promising direction for improving the management of genetic diversity.



CONTINUOUS
MONITORING



INFORMED
DECISION-MAKING

SUSTAINABLE BREEDING FOR THE FUTURE

Sustainable breeding strategies will depend on continuous monitoring, informed decision-making, and collaboration within the breeding community to preserve both the health and the identity of this iconic breed.



COLLABORATION
WITHIN THE COMMUNITY



PRESERVING HEALTH
AND IDENTITY

HONORING THE PAST, GUIDING THE FUTURE



UNIVERSITÀ
DEGLI STUDI
DI MILANO

☘GO RAIBH MAITH AGAT☘

