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Genetics and Sustainability of Irish Wolfhound

Index

Supplementary documents accompanying the presentation by Prof. Maria Giuseppina Strillacci and Prof. Stefano Paolo Marelli at the FIWC 2026 Congress in Bologna, entitled "Genetic Characterization of Irish Wolfhound Dogs: A Worldwide Study of Genetic Variability and Inbreeding."

The original research papers based on this study are currently under review for publication in specialized scientific journals.

Introduction

Genetic characterization of Irish Wolfhound dogs: a worldwide study of genetic variability and inbreeding

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I believe it is quite evident that over the last few decades the public perception of the value of purebred dog breeding has suffered a certain decline. To a greater or lesser extent, depending on the canine culture of different countries, it has often proven difficult to make puppy buyers understand the importance of the pedigree as a guarantee of the dog's typicity — that is, the correspondence of its morphological and behavioural characteristics to the breed standard and, presumably, to the expectations of the owner who made their choice precisely with these characteristics in mind. In recent years, the debate surrounding animal welfare and canine genetic health has also brought increasing attention to the possible effects of selective breeding practices that are not adequately managed. In some cases, this has encouraged an oversimplified representation of the issue, whereby mixed-breed dogs are perceived as inherently healthier than purebred dogs. In reality, as also emphasized in recent scientific and institutional documents, a dog's health and welfare depend above all on the quality of breeding practices, the management of genetic variability, and responsible selection.

This scenario, combined with other factors — foremost among them changes in lifestyles — has led to the sometimes drastic reduction in the population size of many ancient and noble breeds, placing them at risk of extinction despite the constant dedication of many devoted breeders. In other breeds that have meanwhile become highly popular, one may instead observe selective drifts aimed at emphasizing characteristics particularly demanded by the market, sometimes at the expense of the dog's overall balance or consistency with the breed standard. It is not easy to counter broad cultural trends, but I believe that today it is necessary to promote an approach to breeding that is increasingly informed, transparent, and also grounded in the support of scientific research. Alongside the study and knowledge accumulated over the years and translated into good breeding practices, experience and intuition in selective choices, breeders today can also rely on advances in genomic research, guiding their decisions not only through phenotype-based evaluations, but also through genotype-based analysis.

Starting from these reflections, during the first months of 2024 I had the opportunity to discuss these issues with Professor Stefano Paolo Marelli, professor at the Faculty of Veterinary Medicine of the University of Milan and member of the FCI Scientific Commission, and together we launched an initial research project on the genome of the Irish Wolfhound, a breed that I bred for almost thirty years together with my wife Daniela. Professor Maria Giuseppina Strillacci, lecturer at the University of Milan in courses dedicated to the enhancement of animal breeds and to General Animal Husbandry and Genetic Improvement, promptly joined the working group. She conducted much of the analysis and drafted the scientific report, with the collaboration of Dr. Francesca Bernini and Dr. Carlotta Ferrari. In May 2024, the collection of saliva samples began from 96 Irish Wolfhounds bred in different geographical areas of the world, including Central Europe, Scandinavia, the British Isles, the United States, Canada, and Australia. I would like to thank, in addition to the researchers involved in the project, all the breed enthusiasts who collaborated in this important initial phase of sample collection. The dogs' DNA was extracted from the collected samples and subsequently sent to Scotland for genomic analysis; the resulting data were then processed at the University of Milan. For the outcomes of the research, the data from www.iwdb.org also proved extremely valuable, and the entire Irish Wolfhound community owes great gratitude to its founders and administrators for this resource.

This booklet aims to summarize this experience. It first contains the FCI's position on the subject, set out in two documents approved by its General Assembly in September 2024, the scientific report of the research, and several explanatory articles prepared by the researchers in order to make the findings more accessible to a non-specialist audience as well. I hope that our initiative may prove useful in achieving the objectives it set out to pursue and may represent a concrete contribution to the development of increasingly sustainable and informed breeding practices, encouraging further scientific research aimed at preserving this ancient and noble breed in its typicity, with the goal of improving its health, welfare, and longevity.

Use of genomic tools

Over the last 25 years, the field of genomic has revolutionised dog breeding, offering to dog owners, breeders and organisations a multiplicity of tools to breed and monitor their animals. This document presents the position of the FCI regarding the potential and limits of genomic tools for a sustainable management of dog breeds.

Genetic identification and parentage testing is one of the most widely used tool for dog breeding. Using international norms, it should be encouraged and generalised by breeding organisations and by the FCI. This would guarantee the reliability of pedigrees, which is crucial for the integrity of purebred dog breeding. Genetic identification and parentage testing can help to eliminate errors and fraud in pedigrees and provide a more accurate record of a dog's ancestry.

Genetic tests for inherited disorders or phenotypic traits can also be of wide interest for breeding. If well-used, those tests may help to monitor and select against health issues. They can be used to identify carriers of these genetic disorders, and to avoid breeding affected or at-risk dogs. This can help to reduce the incidence of these disorders in the breed, and to improve the health and welfare of the dogs. However, it is important to consider and prioritize tests that are reliable and relevant for a given breed in a given country, and to ensure that the tests used are reliable (Pegram et al. 2019). This means that the tests should be reviewed by experts and published in a scientific paper. Their applicability should be also validated for the population of interest. Indeed, a test relevant and reliable for a given dog population in a given country may be not necessarily relevant or reliable for the same breed in another country. The use of such tools should be integrated in breeding programmes considering the overall health, demographic, economic and governance challenge that the breed is confronted with.

Finally, genomics may support genetic monitoring of genetic diversity both at individual and breed level. Since medium and high-density marker sets have been made available, it is possible to assess genetic relationships and admixture among populations, while measuring genetic variability at individual and breed level, which may be useful to investigate the situation of a breed regarding genetic variability in relation to its health and its history (Donner et al. 2023) and need for potential actions to be taken. To conclude, the FCI wants to underline that if adequately used, the use of genomic tools in purebred dog breeding can have significant benefits for the health, welfare, and sustainability of breeding programs.

The FCI should encourage the use of genetic identification and parentage testing. With regard to genetic testing for hereditary disorders and phenotypic traits, as well as the monitoring of genetic variability, their use should only be encouraged after careful evaluation of the suitability of a given test for a targeted national breed population, taking into account its specific situation in terms of health and welfare, genetic variability and overall breed objectives.

By doing so, the FCI could help to improve the integrity of pedigrees, reduce the incidence of genetic disorders, and promote responsible and sustainable breeding programs.

Approved by the FCI General Committee in Amsterdam, September 2024, based on the recommendation of the FCI Scientific Commission.

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Breeding systems and dog health and welfare

This paper is dedicated to the memory of our colleague Ana Eugenia Vázquez Liévano, a great person, a friend whose invaluable contributions, vision, and dedication have been instrumental for the work of this commission.

This document follows a request from the FCI General Committee regarding the current state of knowledge on the impact of different breeding systems on the present and future health and welfare of puppies intended for future owners, with a specific focus on pedigree breeders. In other words, from a buyer's perspective, what are the potential benefits and issues associated with purchasing a pedigree dog compared to a puppy from other breeding systems? This brief paper first presents the main factors affecting health and welfare in dogs. It then examines the relationship between these factors and breeding systems in dogs. Finally, some proposals are discussed to improve the sustainability of pedigree breeding in terms of health and welfare.

FACTORS IMPACTING HEALTH AND WELFARE IN DOGS

Over the past few decades, animal health and welfare have become significant concerns, particularly for animals living in close proximity to humans, such as dogs.

The factors influencing the raising of these animals can be divided into two categories: those related to the environment in which they are raised, and those linked to their genetic makeup. Both of these factors are shaped by the decisions and practices of dog breeders.

FACTORS RELATED TO ENVIRONMENT

The environment in which a puppy is raised plays a crucial role in determining its future health and welfare. From the prenatal stage through to the critical socialization period, various environmental factors can profoundly influence the puppy's development (Dendoncker, 2019). During this time, the care and handling practices implemented by breeders are pivotal in shaping the puppy's physical, emotional, and behavioural well-being. For instance, the quality of prenatal care, including the mother's nutrition, stress levels, and overall health, can have lasting effects on the puppy's development.

Inadequate prenatal care may lead to issues such as low birth weight, developmental delays, and a predisposition to certain health conditions. Post-birth, the environment crafted by the breeder, including socialization practices and the timing of the homing period, continues to impact the puppy on multiple levels. Proper socialization during the early weeks of life is essential for fostering well-adjusted behaviour in adult dogs. Puppies exposed to a variety of stimuli, including different people, other animals, and various environments, are more likely to develop into confident and well-behaved adults. Conversely, insufficient socialization can result in undesirable behaviours like anxiety, fear, and aggression, which may negatively impact the dog's long-term well-being and its relationship with future owners. In some cases, this could even lead to the dog being given up (Kwan & Bain, 2013; Eagan et al., 2022).

Moreover, the physical environment where puppies are raised can introduce potential zoonotic risks, such as exposure to parasites, bacteria, and viruses that can adversely affect their health. Poor sanitation, overcrowding, and inadequate healthcare practices can exacerbate these risks, leading to long-term health issues that may impair the dog's future life. However, when breeders adhere to rigorous healthcare protocols, including timely vaccinations, deworming, and regular veterinary check-ups, these risks can be significantly mitigated. This proactive approach not only ensures the immediate well-being of the puppies but also sets the foundation for a healthier and more resilient adult dog.

GENETIC FACTORS

A dog's genetic background significantly influences not only its behaviour but also its health and overall welfare. Hundreds of diseases are either directly determined or influenced by genetic factors. Some inherited disorders are linked to specific phenotypic traits in dogs (Asher et al., 2009), while others are inherited independently of the carrier’s morphology (Summers et al., 2010). In dogs, breed differentiation plays a crucial role in shaping individual differences in morphology, behaviour, and health.

There are significant variations across breeds in terms of morbidity and the risk of developing certain disorders. The concept of a breed is complex, even in the dog world, where purebreeding—breeding within a closed population known as a breed—has been considered the standard for many decades (Leroy et al., 2023). According to the FCI, a dog is considered purebred when its pedigree includes a minimum of 3 complete generations registered in FCI recognized studbooks or appendices to the studbooks. However, this definition can be misleading in the context of this discussion, as two puppies from the same litter may share the same genetic background, yet one may not be considered purebred if it has not been registered. For simplicity, we will differentiate between pedigree dogs (i.e., purebred dogs as defined by the FCI), look-a-likes, and crossbreds. A look-a-like is defined here as a dog that matches a breed-specific morphology but does not have a pedigree (Van Zeeland & Beerda, 2015). This category includes actual purebred dogs without papers and crossbreds that resemble a specific breed. Crossbred dogs can also include designer dogs, which result from intentional mating between two different breeds, as well as undetermined crossbred individuals.

Since breeds are the result of multiple generations of selective breeding aimed at achieving specific goals (Pongrácz & Dobos, 2024), the behaviour of a pedigree dog is generally expected to be more predictable than that of a crossbred dog. In terms of health, comparative studies have shown that certain breeds are at a higher risk for specific disorders when compared to crossbred dogs (Bellumori et al., 2013; Donner et al., 2018; Forsyth et al., 2023).

This increased risk may be due to the breed's particular morphology or the random spread of a specific disorder within the breed. However, these studies suggest that being a purebred or pedigree dog is not necessarily associated with an overall higher prevalence of disorders.

When comparing pedigree dogs with look-alikes, Van Zeeland & Beerda (2015) did not find that look-a-likes were less affected by certain genetic disorders, such as hip dysplasia (HD) and elbow dysplasia (ED), than their pedigree counterparts.

This suggests that look-a-like dogs may share the same genetic issues as pedigree dogs. In addition to its role in the spread of inherited disorders, the impact of inbreeding on health and welfare can be assessed at multiple levels. Bannasch et al. (2021) demonstrated that breeds with higher levels of inbreeding exhibit greater morbidity compared to those with lower inbreeding levels.

On an individual level, research by Leroy et al. (2015) has shown that inbred dogs tend to have reduced longevity. This suggests that, from a buyer's perspective, puppies with lower levels of inbreeding should be preferred.

When considering either behaviour or health, there is generally some heterogeneity in trait expression within a given breed. This is an important consideration because, depending on the modes of inheritance and expression, as well as the tools available (such as behavioural assessments, health phenotypic or genetic tests), reputable breeders can work to reduce the risk of a puppy developing undesirable traits in the future.

BREEDING SYSTEMS AND THEIR RELATIONS WITH FACTORS AFFECTING HEALTH AND WELFARE

In differentiating breeding systems, the literature often contrasts small-scale producers (occasional or hobby breeders) with more intensive producers, such as professional or commercial breeders, whose kennels are often referred to as puppy farms or puppy mills (McMillan et al., 2011; Wauthier & Williams, 2018; Dendoncker, 2019). It is challenging to assess the relative importance of small-scale versus large-scale breeders, both in terms of the number of breeders and the number of puppies produced. Several studies suggest that while breeding is a hobby or sporadic activity for the majority of breeders (IBF et al., 2021; Santos et al., 2021), the significance of large-scale breeders in terms of the number of dogs produced tends to be underestimated, especially when accounting for unregistered or illegal breeders.

It is important to note that both small- and large-scale breeders encompass a wide range of production practices and profiles.

However, studies generally indicate that puppies raised in commercial establishments are more likely to suffer from illnesses and poor socialization (McMillan, 2017; Wauthier et al., 2018). Examining practices beyond the scale of production, Dendoncker (2019) found that while large-scale breeders typically provide a less enriched environment for puppies, they tend to be more rigorous in biosecurity measures, including vaccination, pest control, quarantine, and facility hygiene. This may eventually be linked to the fact that incidence and morbidity for parasitic and infectious diseases may increase with animal density (Grellet et al., 2014), thereby raising awareness among large-scale breeders about these issues.

Another way to classify dog breeders is by considering their breeding practices and the use of pedigree dogs. Blackman et al. (2020) proposed differentiating between commercial breeders, pedigree hobby dog breeders, and occasional breeders. Pedigree breeders are primarily defined by their production of pedigree dogs, meaning dogs registered under a recognized studbook. While the majority of pedigree breeders are non-commercial, this is not always the case (Leroy et al., 2007), and not all occasional or hobby breeders are necessarily pedigree breeders. Registration under a studbook facilitates the quantification of pedigree breeders. For instance, Wang et al. (2018) found that among a sample of 50 countries, pedigree breeders contribute between 0% and nearly 80% of the total dog population, depending on the country, with an average contribution of 20%. Aside from providing certification of breed origin, sourcing a puppy from a pedigree breeder does not, in theory, guarantee the health or behaviour of the dog.

However, several national canine organisations either record information on certain health conditions or behavioural tests in the pedigree or impose specific requirements for breeding, such as health screenings or inbreeding limits (Wang et al., 2018). In general, pedigree breeders are not required to apply specific practices for the environment where puppies are raised besides the ones imposed by national legislation. Outside of pedigree dogs, it is relatively easy for buyers to find a look-alike puppy that resembles a specific breed type (IBF et al., 2015). Therefore, sourcing a non-pedigree dog should not be expected to offer particular advantages in terms of health.

DISCUSSION

From a buyer's perspective, several factors must be considered to ensure that a puppy has the potential to exhibit optimal behaviour, health, and welfare. One of the most significant decisions is whether to choose a crossbred puppy or one that matches a specific breed phenotype (whether pedigree or look-alike). Selecting a breed-specific phenotype increases predictability regarding both adult morphology and behaviour. However, while current literature suggests that a purebred or pedigree dog is not inherently associated with health issues, many breeds are known to have higher prevalences of specific diseases.

Therefore, it is crucial for prospective owners to verify that the breeder has taken necessary precautions to minimize the risk of these diseases, such as requesting up-to-date health certificates when available. Choosing a crossbred dog can help reduce the risk of inbreeding depression, as crossbreeds generally have a more diverse genetic background. On the other hand, opting for a pedigree dog over a look-alike typically provides assurance regarding the genetic origins of the puppy and its predictability in terms of phenotype expression. While pedigree breeders are often not large-scale producers, registration with a recognized studbook does not generally guarantee specific health and welfare practices (IBF et al., 2015), unless the corresponding National Canine Organisation has implemented stringent rules and quality standards.

From the perspective of an FCI national canine organisation, if the goal is to demonstrate that pedigree puppies have a higher likelihood of better health in their future lives compared to non-pedigree dogs, then specific measures must be implemented to ensure this. Provision of information about the health and behaviour of the dog and its relatives, whether in the pedigree or online, can offer some degree of assurance. It is essential that this information, along with the associated rules and requirements, be presented to the public clearly and transparently to avoid any confusion. The National Canine Organisation can effectively provide training for pedigree breeders to ensure they have basic knowledge of breeding systems, as well as the necessary requirements for maintaining a healthy, socially appropriate, and well-managed breeding environment. Ultimately, ensuring robust quality standards and transparent communication, along with implementing effective breeding schemes aimed at improving health, will help build trust and enhance the well-being of pedigree dogs.

APPROVED BY THE FCI GENERAL COMMITTEE, AMSTERDAM, SEPTEMBER 2024

Breeding systems and dog health and welfare (Position of the FCI Scientific Commission)

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The Irish Wolfhound: what genetics tells us about the breed today

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A collaborative research project was carried out under the leadership of Prof. Maria G. Strillacci (Principal Investigator) together with Prof. Marelli and Dr Bernini at the Department of Veterinary Medicine and Animal Sciences (DIVAS) of the University of Milan, was carried out in partnership with the Sighthound Club of Italy and with the support of the Federation of Irish Wolfhound Clubs. By combining academic expertise and the active involvement of breed organizations, the study aimed to provide a deeper understanding of the genetic background of the Irish Wolfhound (IW) and to support more informed and sustainable breeding practices at an international level

The IW is a famous and ancient dog breed known for its unique combination of strength and gentle temperament, often described by breeders as "lambs at home, lions in the chase". Today, these dogs take part in sports like lure coursing and racing, which allow them to express their natural speed, agility, and endurance in a safe and controlled way. Originally bred by the ancient Irish Celts to hunt wolves and deer, Irish Wolfhounds have a long and prestigious history, with written records dating back to 391 A.D. Over the centuries, they were highly valued as hunting companions and even given as royal gifts. However, by the 19th century, the breed was close to extinction.

It was revived thanks to careful crossbreeding efforts led by Captain G.A. Graham[1], using related breeds such as the Scottish Deerhound, along with Mastiff, Borzoi and Great Danes. Since the late 1800s, when the breed standard was established, detailed pedigree

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[1] *Denise Flaim. Irish Wolfhound History: Behind the Ancient Breed of Ireland. https://www.akc.org/expert-advice/dog-breeds/irish-wolfhound-history-behind-the-breed/ (2023).*

records have been kept. While these records are useful for managing breeding and preserving the breed, they also reveal a downside: limited genetic diversity due to inbreeding and past population bottlenecks (i.e., periods in which the population size was drastically reduced, leading to a loss of genetic diversity). Today, modern genomic technologies are helping researchers go beyond pedigree data, offering more precise tools to understand genetic diversity and improve the health and sustainability of the breed.

WHY STUDY GENETICS IN IRISH WOLFHOUNDS?

Modern dog breeds, especially those with a small population size, often face a common challenge: reduced genetic diversity. This can increase the risk of inherited diseases and may affect overall health, fertility, and long-term sustainability of the breed.

Traditionally, breeders rely on pedigrees to manage inbreeding. However, pedigrees only show expected relationships. Today, genomic tools allow us to look directly at the DNA and understand what is really happening at the genetic level.

In this study, the DNA of 96 IWs from 23 countries using a high-density SNP chip (a tool that scans hundreds of thousands of genetic markers across the genome) was analysed. This allowed us to answer three main questions:

- How much genetic diversity is present in the breed?
- Are dogs closely related to each other?
- Are there specific regions of the genome that have been strongly selected?

A GENETICALLY UNIFORM BREED WORLDWIDE

One of the most interesting results of our study is that IWs from different parts of the world are genetically very similar to each other. When we compared dogs from multiple countries, they did not form separate national groups but instead clustered together (Figure 1A).

This reflects the long-standing international exchange of breeding animals and indicates that the breed functions as a single global population rather than as distinct regional subpopulations.

This pattern becomes even clearer when our data are compared with previously published datasets. In Figure 1B, the same 96 dogs analysed in this study are combined with 247 Irish Wolfhounds from Shannon al., (2015)[2]. In this combined analysis, our IWs fall within the same genetic space as the larger dataset, meaning they do not form a separate group but are part of the same overall population.

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[2] *Shannon, L. M. et al. Genetic structure in village dogs reveals a Central Asian domestication origin (2025). Proc. Natl. Acad. Sci. U. S. A. https://doi.org/10.1073/pnas.1516215112*

This further confirms that IWs worldwide are genetically very similar and share a common genetic background, regardless of their country of origin. Despite this global connectivity, the breed remains numerically small. Registration data show that in North America around 800–970 dogs are registered each year (data from IWCA), while in countries such as Italy the numbers are often below 50. This highlights that, although widely distributed, the IW is still a relatively rare and potentially vulnerable breed.

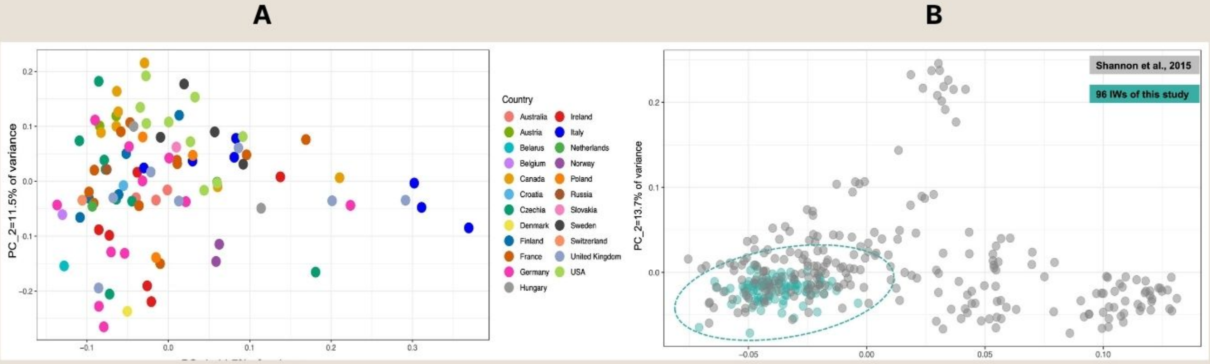

Figure 1. Principal component analysis (PCA) of IW samples (modified from Bernini et al., 2026[3]): (A) PCA showing the genetic distribution of the 96 individuals analysed in this study, coloured according to country of origin. (B) PCA including the same 96 dogs together with 247 Irish Wolfhounds from Shannon et al. (2015).

Consistent with its history, the breed shows relatively low genetic diversity and high levels of homozygosity[4] (average homozygosity and heterozygosity values are 0.85 and 0.15, respectively). In practical terms, this means that many regions of the genome are identical on both chromosomes within individuals and often shared across dogs, reflecting a limited gene pool. This reflects past bottlenecks and the limited number of founders used to rebuild the breed. However, an important and somewhat reassuring finding is that there is little evidence of recent inbreeding. Most of the 96 analysed dogs, are only distantly related to one another, and only a small number of pairs show close relationships (genomic kinship[5]), such as siblings or parent-offspring.

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[3] *The article has been submitted and is currently under peer review in the journal Scientific Reports.*

[4] ***Homozygosity** refers to the condition in which an individual carries two identical copies of a DNA variant (allele) at a given genetic locus, one inherited from each parent. In contrast, heterozygosity indicates the presence of two different alleles at the same locus. High levels of homozygosity are often associated with reduced genetic diversity and can result from inbreeding or population bottlenecks, whereas higher heterozygosity generally reflects greater genetic variability within a population.*

[5] ***Genomic relatedness** (or genomic kinship) refers to the degree of genetic similarity between individuals, estimated directly from DNA data rather than from pedigree records. It measures how much of the genome two individuals share due to common ancestry. Unlike pedigree-based relatedness, which relies on expected relationships, genomic relatedness captures the actual proportion of shared genetic material, providing a more precise assessment of how closely individuals are related.*

WHAT ARE ROHs, AND WHY DO THEY MATTER?

A key part of the study focused on something called Runs of Homozygosity (ROH). Runs of homozygosity (ROHs) are long stretches of DNA where both copies inherited from the parents are identical. These regions are particularly informative because their 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, whereas long ROHs are usually the result of more recent matings between closely related individuals. In the IW, our results show a clear pattern: there are many short ROHs, but very few long ones, and virtually no extremely long segments. This is an important finding, as it indicates that most of the inbreeding present in the breed is not recent, but rather dates back to the past. In other words, the genetic structure we observe today is largely shaped by historical events, such as population bottlenecks.

Another interesting aspect of the analysis concerns the presence of shared genomic regions, often referred to as "ROH islands," within the IW population. These are stretches of DNA that are found in a large proportion of individuals: in our study, some were present in at least 85% of the dogs, and a few in all of them (100%).

These shared segments likely reflect traits that were strongly selected during the breed's development or genomic regions inherited from the original founders. These are like "genetic signatures" of the breed, segments that have been passed down through generations and have become fixed over time.

Notably, some of these regions are also found in other hunting or working breeds, suggesting that they may be linked to functions or characteristics important for performance, morphology, or behaviour. From a health perspective, these regions are also of interest. Some of the genes located within them have been associated, in humans or in other dog studies, with conditions such as cancer, heart diseases, and neurological disorders. This does not mean that these genes necessarily cause disease in IWs, but it does highlight specific areas of the genome that may play an important role in health, longevity, and disease susceptibility. They provide a useful starting point for future research and may, in the long term, help support more informed and sustainable breeding decisions.

What do these results mean in practice for breeders of the IW?

Overall, the picture that emerges is both reassuring and informative. The breed is characterized by relatively low genetic diversity, largely as a consequence of historical bottlenecks and the limited number of founders used during its reconstruction. At the same time, there is no strong evidence of recent inbreeding, suggesting that current breeding practices are generally effective in avoiding close matings and in maintaining a certain level of genetic stability.

Despite this positive aspect, some critical points remain. The overall gene pool is still restricted, and the effective population size is relatively small. This means that, even in the absence of close inbreeding, genetic diversity can gradually decrease over time if not carefully managed. For this reason, breeding strategies should continue to focus on preserving as much genetic variation as possible. In practical terms, this includes limiting the overuse of popular sires, maintaining diversity among breeding lines, and promoting the exchange of animals across countries. In a globally interconnected breed such as the IW, international collaboration plays a key role in preserving genetic variability. The study also highlights the added value of genomic tools compared to pedigree-based approaches alone. Genomic data allow a more precise estimation of relatedness and inbreeding, capturing the actual genetic relationships among individuals rather than expected ones. Looking ahead, the integration of genomic information with pedigree records and health data will be essential to support more informed breeding decisions. Such an approach can contribute to reducing the risk of inherited diseases, preserving genetic diversity, and improving the overall health and longevity of the breed.

CONCLUSIONS

Although the IW remains genetically constrained due to its history, current breeding practices appear to be moving in a positive direction. The challenge for the future will be to consolidate these efforts by combining traditional breeding knowledge with modern genomic insights, ensuring the long-term sustainability and health of this historically important breed.

Pedigree Analysis of the Irish Wolfhound: Insights into Inbreeding and Population Structure

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Modern dog breeds are closed populations shaped by selective breeding. While this process has fixed desirable traits, it has also reduced genetic diversity and increased levels of relatedness within breeds. Managing this balance between selection and genetic variability is one of the key challenges in canine breeding today.

The modern Irish Wolfhound (IW) was reconstructed in the late 19th century from a limited number of founders, following the near disappearance of the original population of large hunting dogs historically used for wolves and other game. As a result, the breed does not represent a continuous lineage from these early dogs, but rather a reconstructed population derived from a small number of individuals and, in part, from crosses with other large breeds. This process generated a strong founder effect, meaning that the current population originates from a restricted genetic pool. The subsequent use of closed studbooks has further limited the introduction of new genetic material, reinforcing genetic isolation and increasing the degree of shared ancestry among individuals. Consequently, the breed is characterised by reduced genetic diversity and relatively high relatedness, factors that may influence health, fertility, and longevity. 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.

INBREEDING AND ITS IMPLICATIONS

Inbreeding is an inherent feature occuring when related individuals are mated, increasing the probability that offspring inherit identical copies of genes from both parents (Wright 1922[1], Falconer & Mackay, 1996[2]). 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 effects on traits such as fertility may appear limited, while other traits such as disease susceptibility and lifespan may be more strongly affected. For this reason, monitoring inbreeding remains a key component of responsible breeding strategies.

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 (Table 1). Pedigree analysis also helps detect population trends such as bottlenecks and the overuse of specific individuals. However, pedigree-based estimates have limitations. They depend on the completeness and accuracy of recorded ancestry and assume that founders are unrelated. As a result, they may underestimate true inbreeding.

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[1] *Wright, S. (1922). Coefficients of inbreeding and relationship. The American Naturalist, 56(645), 330-338.*

[2] *Falconer, D.S. and Mackay, T.F.C. (1996) Introduction to Quantitative Genetics. 4th Edition, Addison Wesley Longman, Harlow.*

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

Table 1. Inbreeding Levels Classification (Leroy et al., 2006)

MATERIALS AND METHODS

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

RESULTS

Out of the total population, 553 individuals (23.61%) were identified as inbred (Table 2).

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[3] *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.*

F	Inbred subjects (N)	Inbred/tot population (%)	Inbred/tot inbred population (%)
0.00 < F <= 0.05	386	1648	6980
0.05 < F <= 0.10	117	500	2116
0.10 < F <= 0.15	39	167	705
0.15 < F <= 0.20	7	30	127
0.20 < F <= 0.25	3	13	54
0.25 < F <= 0.30	0	0	0
0.30 < F <= 0.35	1	4	18
Total	553	2361	10000

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

The majority of inbred individuals (69.8%) showed low inbreeding levels (F ≤ 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.

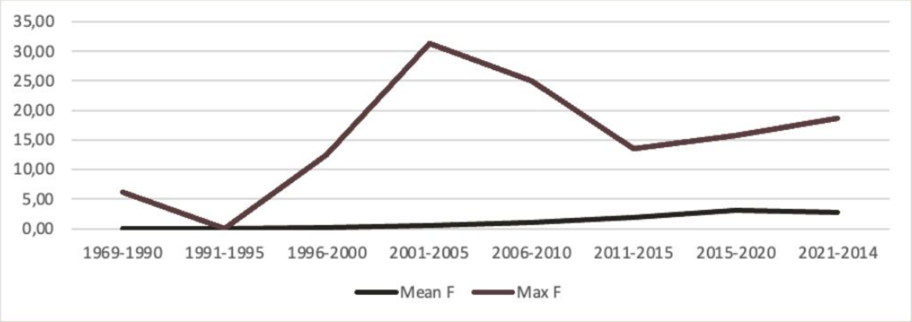

Figure 1. Mean and maximum inbreeding coefficient (F_{ped}) across birth-year clusters

DISCUSSION

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.

However, 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.

CONCLUSIONS

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.

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

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In the second part of the study, the genealogical structure, longevity, and main causes of death in Irish Wolfhounds were analyzed through an international pedigree reconstruction.
The pedigrees of 96 reference dogs previously studied at the genomic level were reconstructed, involving animals from 23 countries. For each dog, the following data were collected:

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

The main objective was to understand how pedigree structure, inbreeding, and the distribution of ancestors may influence health and survival within the breed.
In simple terms, the study 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?

Main Findings

A HIGHLY INTERCONNECTED POPULATION

By integrating the pedigrees of the initial 96 subjects, a highly interconnected population of 2,343 genealogically related dogs emerged. For some individuals, the pedigree reconstruction extended beyond 11 generations, reaching a maximum of 14 generations. This remarkable genealogical depth made it possible to evaluate not only direct family relationships, but also how certain ancestors have influenced the genetic structure of the modern population over time. The analysis showed that many Irish Wolfhounds repeatedly share the same ancestors and that, in several cases, the same dog appears multiple times within the same pedigree through different lineage branches. This phenomenon, known as pedigree collapse, is fairly common in dog breeds developed from a relatively limited number of breeding animals.

The study also demonstrated that some sires (and some dams) had a much greater influence than others, contributing significantly to the current genetic structure of the breed. This phenomenon is also typical of selected canine populations and is known as the popular sire effect. Both the breeding dogs with the highest direct number of offspring and those that left the greatest “genealogical impact” across subsequent generations were identified.

In an ideal theoretical situation, considering five completely independent generations, each dog should have 62 unique ancestors. In the sample of 96 Irish Wolfhounds analyzed, this would correspond to a theoretical total of 5,952 different ancestors. However, the genealogical analysis revealed a very different reality: the total number of unique ancestors observed was only 2,247, as shown in Figure 1. This finding highlights the frequent recurrence of the same bloodlines within the population and the resulting reduction in the breed’s genetic variability.

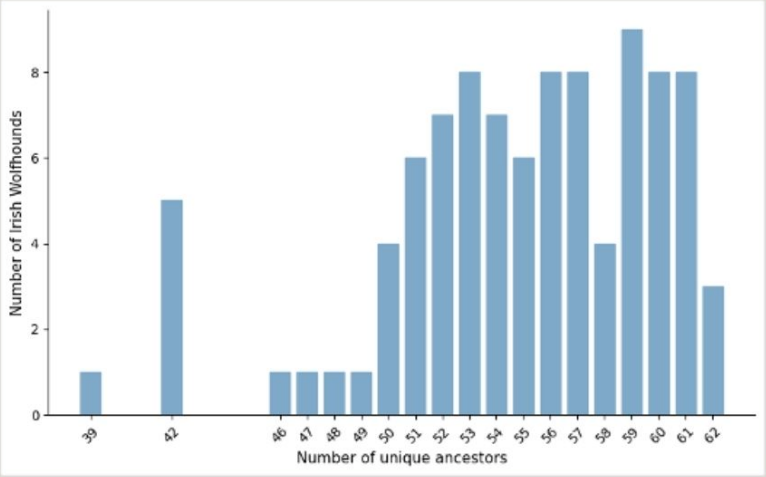

Figure 1. Number of ancestors per dog.

The study also showed that the effective population size (Ne) was low (Ne = 45), a value that is typical of breeds in which only a limited number of breeding animals are actually used. In simple terms, this means that, from a genetic perspective, the population behaves as if it were composed of approximately 45 individuals contributing genes to the following generations. A reduced effective population size may, over time, promote the loss of genetic variability and an increase in inbreeding.

HOW LONG DOES AN IRISH WOLFHOUND TYPICALLY LIVE?

The survival analysis section of the study examined a large number of individuals within the analyzed population. In particular, complete birth and death dates were available for 1,052 dogs, which were used to estimate the breed's longevity. The survival analyses, however, included a total of 1,267 Irish Wolfhounds, also taking into account dogs that were still alive at the time of the study or for which a date of death was not yet available. These individuals, referred to as "censored" in survival analysis, are included through a standard statistical procedure that allows researchers to use all available information without biasing the results. To evaluate changes in longevity over time, the dogs were divided into three generational groups: those born before 1990, between 1990 and 2005, and after 2005. The analysis was performed using Kaplan–Meier survival curves, statistical tools widely used in human medicine as well to compare survival probabilities between different groups over time.

The results showed that most of the Irish Wolfhounds included in the study died between 6 and 10 years of age. Females showed slightly better survival than males, with a higher proportion reaching ages beyond 9–10 years (Figure 2).

No significant differences were observed between the different generations considered. In other words, dogs born after 2005 do not appear to live, on average, longer than Irish Wolfhounds from earlier generations. This suggests that, despite changes over time in breed management and selection, average longevity has remained relatively stable.

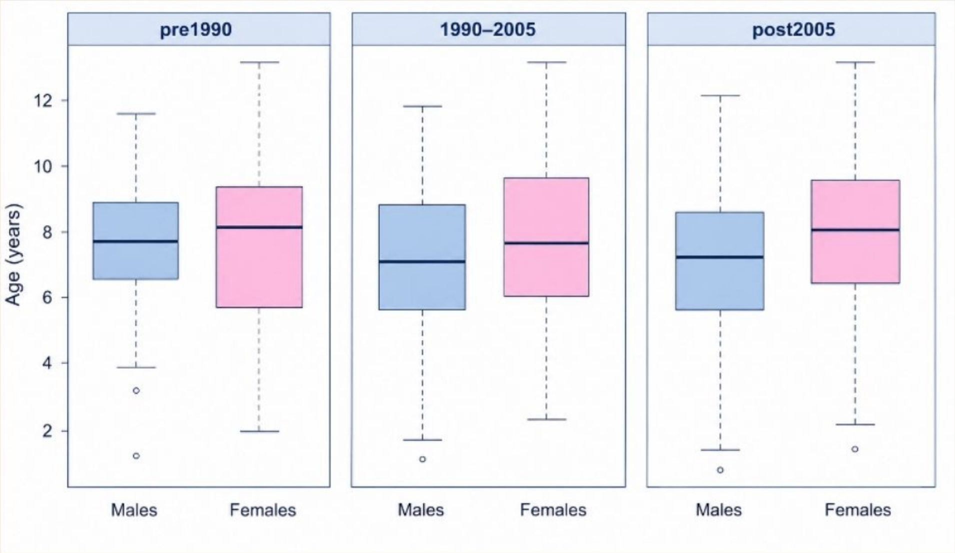

Figure 2. Distribution of Irish Wolfhound longevity by sex and birth period.

MAIN CAUSES OF DEATH

Information on cause of death was available for approximately 30% of the studied population. Although complete data were missing for many individuals, it was still possible to identify clear trends regarding the main health issues in the breed.

Among all recorded causes of death, neoplastic diseases were the most frequent. In particular, osteosarcoma accounted for about 17% of known deaths, while other types of cancer represented an additional 14%. Overall, nearly one third of documented deaths was linked to neoplastic conditions. Cardiac diseases (approximately 12%) and respiratory disorders (around 10%) were also significantly represented in the studied population. Gastrointestinal problems, typical of giant breeds, were also commonly observed. One of the most interesting findings is that some diseases appear to recur more frequently within specific genealogical lines. To explore this, the pedigrees of

two representative individuals were reconstructed in detail: an exceptionally long-lived Irish Wolfhound that lived almost 12 years, and a dog that died from osteosarcoma. In both cases, the respective pedigrees included ancestors—often repeatedly used as breeding animals—with the same cause of death, suggesting that health, longevity,
and susceptibility to certain diseases may also be influenced by the genealogical structure of the breed.

The study also highlighted an important point regarding inbreeding. Coefficients of inbreeding calculated using pedigree data alone were not directly associated with survival. However, it emerged that many pedigrees tended to underestimate the true level of genetic relatedness among individuals. In fact, about 76% of dogs showed an inbreeding coefficient of zero, yet many of these had shallow or incomplete genealogies.

Genomic analyses performed on the 96 reference dogs showed instead that several individuals who appeared “lowly inbred” from a pedigree perspective still exhibited high levels of genetic homogeneity. In practice, a dog may appear minimally related based on pedigree information alone, but still be genetically very similar to other members of the population when DNA is analyzed directly.

This finding highlights how important it is today to integrate pedigree data with genomics in studying health and managing breeding in Irish Wolfhounds. Pedigrees remain a fundamental tool, but on their own they may not fully capture the true level of genetic variability within the breed.

Conclusions

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WHY THIS RESEARCH IS IMPORTANT FOR THE FUTURE OF THE BREED

Taken together, the two studies provide a much more complete picture of the modern Irish Wolfhound population. On one hand, the genomic analysis made it possible to directly observe the dogs' DNA and assess the breed's actual level of genetic variability. On the other hand, the genealogical and demographic study showed how bloodlines have been structured over time and how certain ancestors have had a particularly strong influence on the current population.

One of the most interesting insights from this integrated approach concerns the relationship between pedigree data and genomics. Traditionally, breeders rely on pedigrees to assess relatedness and inbreeding, but these tools describe theoretical relationships and depend heavily on the completeness of available genealogical records. Genomic analyses, however, have shown that some individuals who appear to be only distantly related based on pedigree data still exhibit high levels of genetic homogeneity when their DNA is directly analyzed. In other words, pedigree and genomics should not be seen as alternative tools, but as complementary ones. Pedigrees help reconstruct the history of bloodlines and understand the population's genealogical structure, while genomics provides a more precise measure of the actual genetic variability within the breed.

The results confirm that the modern Irish Wolfhound is a highly interconnected genetic population at an international level. This is likely the result of the breed's history, past population bottlenecks, and the repeated use of a limited number of highly influential breeding lines. Nevertheless, the study did not reveal strong signals of recent inbreeding, suggesting that modern breeding practices are generally avoiding very close matings. However, preserving the remaining genetic diversity within the breed remains essential. In practical terms, this means continuing to limit the overuse of a small number of popular sires, encouraging international exchange between different bloodlines, and progressively integrating genomic tools into breeding strategies and reproductive management. These studies therefore represent not only an important scientific snapshot of the breed, but also a concrete foundation for developing more sustainable breeding programs focused on health, longevity, and the preservation of genetic diversity in the Irish Wolfhound.

POSSIBLE FUTURE DIRECTIONS OF THE RESEARCH

The results obtained open the door to several future developments. One of the main goals will be to further expand the number of studied subjects by integrating genealogical, genomic, and clinical data from an increasing number of breeders and countries.

In the future, it will be particularly interesting to investigate the relationship between specific genetic lines and breed-related diseases, such as osteosarcoma, cardiomyopathies, and certain immune or respiratory disorders. The integration of genomic data with health records could in fact help identify regions of DNA associated with increased disease susceptibility or, conversely, greater longevity.

Another possible direction involves the development of genomic tools that can be directly applied in breeding management, helping breeders select mating pairs not only based on pedigree information, but also on the actual genetic compatibility between individuals.

In the long term, collaboration between universities, breed clubs, and breeders will be essential to build increasingly comprehensive databases and to translate this scientific knowledge into practical tools for safeguarding health and ensuring the future sustainability of the Irish Wolfhound.

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