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Improving animal welfare in Italian Holstein and Jersey cattle through selection for longevity

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Abstract

The concept of longevity in the domain of animal science constitutes a complex trait that can be approached from diverse perspectives. The debate surrounding the optimal duration for a cow to stay in a herd remains under discussion, given that the typical lifespan of a cow in a herd is between two and a half to four years, which is significantly shorter than its natural maximum lifespan. Consequently, the primary objective for dairy farmers is to determine the optimal herd life, balancing the need to maximise the farm revenue and the genetic progress, while sustaining animal welfare. The present thesis investigated these aspects within the framework of the National Breeders Association of Italian Holstein, Brown and Jersey dairy cattle (ANAFIBJ). The ultimate objective of this project was to develop two new models for the routine genetic evaluation of longevity in Italian Holsteins and Jerseys. The following sections offer a concise summary of these findings.

Chapter 1 provides a comprehensive overview of the various approaches to measuring longevity across Interbull countries, with a particular focus on the Italian Jersey and Holstein breeds. Additionally, a brief description is provided of the existing routine genetic evaluations of longevity in Italian Holsteins.

The second chapter details the research undertaken for the Italian Jersey breed, which involved the establishment of a novel genetic evaluation. Prior to 2023, the Italian Jersey population was not subject to the implementation of an official selection index. The concept of longevity was analysed as stayability, defined as the ability of cows to survive to a specific calving event. Furthermore, genetic and phenotypic correlations between stayability and other important traits under selection were estimated.

In Chapter 3, an analysis to compare various longevity approaches in Holstein cows was conducted, with the objective of identifying the most effective strategy for extending their lifespan. This study constituted a preliminary investigation in which a selection of models and approaches were tested to identify the most suitable for this large population. The analysis encompassed

functional longevity and true longevity. The findings indicated that functional longevity should be prioritised.

Chapter 4 provides a comprehensive analysis and development of a new genetic index for the Holstein breed. The index utilised a 9-trait stayability approach with the objective of achieving survival at third lactation. Furthermore, different phenotypic indicators were developed to predict stayability starting from the first lactation, from somatic cell count and from morphology traits.

Chapter 5 provides the general conclusions of the work. This thesis demonstrates that longevity selection should be approached with caution to ensure understanding and effective exploitation of the genetic potential in modern dairy cattle farms. Animal survival is dependent on their well-being; indeed, the primary factors contributing to voluntary culling are diseases and health concerns. Consequently, by breeding animals that have a longer life, we also select for health and well-being.

Riassunto

Il concetto di longevità nel campo della zootecnia costituisce un carattere complesso che può essere affrontato con diverse prospettive. Il dibattito sulla durata ideale della permanenza di una vacca nella mandria è ancora oggetto di discussione, poiché la permanenza tipica di una vacca in una mandria è compresa tra due anni e mezzo e quattro, significativamente inferiore alla sua naturale massima espressione. Di conseguenza, l'obiettivo primario degli allevatori di bovini da latte è quello di determinare la durata ottimale della vita della mandria, bilanciando la necessità di massimizzare il reddito dell'azienda agricola e il progresso genetico, pur mantenendo il benessere degli animali. La presente tesi ha studiato questi aspetti nell'ambito delle razze iscritte all'Associazione Nazionale Allevatori di Bovini da Latte Holstein, Bruna e Jersey Italiani (ANAFIBJ). L'obiettivo finale di questo progetto era quello di sviluppare due nuovi modelli per la valutazione genetica di routine della longevità delle razze Holstein e Jersey italiane. Le seguenti sezioni offrono una sintesi concisa di questi risultati.

Il capitolo 1 fornisce una panoramica completa dei vari approcci alla misurazione della longevità nei paesi Interbull, con particolare attenzione alle razze Jersey e Holstein italiane. Inoltre, viene fornita una breve descrizione delle attuali valutazioni genetiche di routine della longevità nella Holstein italiana.

Il secondo capitolo descrive in dettaglio la ricerca intrapresa per la razza Jersey italiana, che ha comportato la creazione di una nuova valutazione genetica. Prima del 2023, la popolazione Jersey italiana non era infatti sottoposta a una selezione ufficiale per questo carattere. Il concetto di longevità è stato analizzato come capacità di sopravvivenza, definita come la capacità delle vacche di sopravvivere fino a uno specifico evento di parto. Inoltre, sono state stimate le correlazioni genetiche e fenotipiche tra la capacità di sopravvivenza e altri importanti caratteri oggetto di selezione.

Nel capitolo 3 è stata condotta un'analisi per confrontare vari approcci alla longevità nelle vacche Holstein, con l'obiettivo di identificare la strategia più efficace per prolungarne la durata della vita.

Questo studio è servito come indagine preliminare per identificare il modello che più si adatta alle peculiarità della popolazione, e l'analisi ha incluso un confronto tra la longevità funzionale e la longevità reale. I risultati hanno indicato che la longevità funzionale dovrebbe essere considerata prioritaria.

Il capitolo 4 fornisce un'analisi completa e lo sviluppo di un nuovo indice genetico per la razza Holstein. Questo indice, con un approccio di sopravvivenza basato su 9 periodi singoli, mirava alla sopravvivenza alla terza lattazione. Inoltre, sono stati sviluppati diversi indicatori fenotipici per prevedere la permanenza a partire dalla prima lattazione, dal conteggio delle cellule somatiche e dalle caratteristiche morfologiche.

Il capitolo 5 fornisce le conclusioni generali del lavoro. Questa tesi dimostra che la selezione della longevità dovrebbe essere affrontata con cautela per garantire la comprensione e lo sfruttamento efficace del potenziale genetico nelle moderne aziende da latte. La sopravvivenza degli animali dipende dal loro benessere; infatti, i fattori primari che contribuiscono all'abbattimento volontario sono le malattie e i problemi di salute. Di conseguenza, allevando animali che hanno una vita più lunga, selezioniamo anche la salute e il benessere.

Chapter 1:
General introduction

The objective of this thesis was to develop or update the routine genetic evaluation of longevity in Italian Jersey and Holstein dairy cows. The present chapter is dedicated to the introduction of fundamental definitions and the international and national context. Furthermore, it provides a comprehensive overview of the current Italian Holstein and Jersey populations. The final section delineates the issues inherent in the prevailing genetic routine evaluation of longevity in Italian Holsteins, and provides a motivation for the development of a novel model.

The definition of longevity

Dairy cattle longevity is a highly valued trait that has been extensively studied over the last decade (Heise et al., 2016; De Vries, 2017, 2020; Dallago et al., 2021), given its crucial impact on both animal welfare and farm profitability. The optimal duration of a cow's productive life remains a subject of ongoing debate. Currently, the typical herd life of a commercial dairy cow ranges between 2.5 and 4 years (De Vries, 2020; Schuster et al., 2020), which contrasts sharply with the species' natural life expectancy of 20 years or more. The concept of the profitability of older cows was described as early as 1959 by Snook, who highlighted that retaining mature animals significantly increases milking herd revenues due to their higher production capacity. Indeed, defining the optimal time a cow should be kept in the herd is frequently complex and contingent upon multiple interacting variables. As outlined by Schuster et al. (2020), these variables can be categorised into intrinsic factors - such as milk yield, health status, and reproductive performance - and extrinsic factors, including milk prices, rearing costs, and the availability of replacement heifers.

In the scientific literature, the concept of longevity is multidimensional and has been defined in several ways to reflect these culling dynamics. A widely accepted metric is 'productive life', typically defined as the number of days from first calving until culling (Caraviello et al., 2004; Raguz et al.,

2011). Another common approach used in genetic evaluations is 'stayability' (STAY), defined as a binary trait indicating the success or failure of an animal to remain in the herd until a specific time point, such as a subsequent lactation (Hudson and Van Vleck, 1981; Hardie et al., 2021).

The length of time a cow remains in the herd is ultimately dictated by voluntary and involuntary culling decisions. Accurate evaluation of longevity is often hindered by erroneous or imprecise recording of culling reasons. When analysing specific populations, such as the Jersey breed, Norman et al. (2022) reported that culling (excluding sales for dairy purposes) accounted for 30.1% of all herd exits in 2021. The primary reasons for these removals were low milk production, reproductive failure, locomotion issues, udder problems, and mastitis. Importantly, these culling patterns shift dynamically according to parity order. For instance, Khansefid et al. (2021) demonstrated that voluntary culling for low milk production is highly prevalent during the first lactation, whereas involuntary culling due to reproductive failure and health issues gradually increases in subsequent parities. This dynamic suggests that survival should be evaluated as distinct, genetically correlated traits depending on the parity order (Holtsmark et al., 2009; Heise et al., 2016; Pritchard et al., 2013; Khansefid et al., 2023).

To accurately define these dynamics in genetic evaluations, longevity is typically partitioned into 'true' and 'functional' traits. In this context, 'true stayability' considers the raw ability of a cow to delay any culling, reflecting the farmer's overall perception of the cow's value regardless of the removal reason. Conversely, 'functional stayability' - originally described by Ducrocq (1987) - specifically targets the animal’s ability to delay involuntary disposal. Because culling reasons are often poorly recorded on farms, functional longevity is conventionally estimated by adjusting the analysis for the cow's milk yield relative to her herd mates, thereby isolating her intrinsic fitness from the farmer's economic decision to cull based on milk volume (Heise et al., 2016).

Economic aspects of longevity and genetic trade-offs

The importance of longevity in dairy cattle is fundamentally tied to the economic success of the farming operation. The primary objective for a dairy farmer is to ensure that a cow remains in the

milking herd long enough to generate sufficient profit to recover her rearing costs. Raising replacement heifers imposes a significant financial burden, representing one of the highest variable expenses on a dairy farm. Numerous studies indicate that rearing a heifer cost approximately €2.50 per day, a figure highly susceptible to the volatility of feed prices (Akins and Hagedorn, 2016; Hutchison et al., 2017). In Italy, for instance, simulations demonstrate that average feed costs alone increased from €22.9/ton in 2015 to €32.8/ton in 2023 (CLAL, 2024). Consequently, total rearing costs have drastically surged. For Holstein cattle, the total expense of raising a heifer from birth to 24 months - considered the ideal age for first calving - is currently estimated at approximately $2,650 (Lactanet, 2019). This financial risk is further exacerbated by early attrition; between 8% and 19% of cows die or are culled before completing their first lactation, representing a profound and unresolved economic loss (Bach, 2011; Brickell et al., 2011).

Because of these high initial investments, a dairy cow typically reaches her economic break-even point only between her second and third lactation (Lactanet, 2019; Gambonini et al., 2022). From the third lactation onwards, the revenue generated from milk sales minus the daily maintenance costs translates into true profit, as the initial rearing debt has been fully amortized. Therefore, maintaining a good proportion of older, mature cows is highly advantageous for farmers. Mature animals not only increase the milking herd's overall profitability due to their higher physiological production capacity, but they also reduce the annual replacement costs. Recent bio-economic modelling by De Vries (2020) suggests that the ideal average number of lactations in a herd to maximize profitability is five, ranging from four to six depending on specific herd inputs and replacement costs.

To mitigate rearing expenses and maximize the profitable period of a cow's life, farmers frequently adopt strategies aimed at reducing the age at first calving (AFC), thereby minimizing the unproductive rearing phase. Extensive research highlights a strong phenotypic and genetic relationship between AFC and subsequent longevity. For instance, a higher age at first calving has been shown to negatively affect stayability across parities, increasing the risk of early culling due to calving

difficulties or metabolic issues associated with over-conditioned older heifers (Rogers et al., 1991; Sherwin et al., 2016). Thus, an optimized AFC is a crucial precursor to a long and profitable productive life.

However, the pursuit of extended average herd life must be carefully weighed against the herd's genetic progress. Maximizing longevity inherently leads to an increase in generational intervals, which can slow down the integration of superior genetics into the milking herd. Due to the rapid adoption of genomic selection over the last decade, the rate of genetic gain for economically important traits has drastically accelerated. This acceleration widens the "genetic lag" between older, mature cows and incoming replacement heifers. Consequently, the average economically optimal productive lifespan is estimated to be slightly shorter today than in previous decades, as the opportunity cost of delaying the introduction of genetically superior heifers has increased (De Vries and Marcondes, 2020). Therefore, modern dairy operations face a complex dilemma: creating sustainable strategies and mating plans requires a delicate balance between extending longevity to amortize rearing costs and maintaining an optimal replacement rate to capture accelerated genetic progress.

Animal welfare, health, and environmental sustainability

Furthermore, dairy cow longevity is intrinsically linked to animal welfare and societal acceptance. The length of a cow's life is not merely an economic parameter; it serves as a global indicator of the herd's welfare status (Dallago et al., 2021). High rates of involuntary culling, particularly early in a cow's productive life, often reflect a high incidence of painful or debilitating conditions prior to removal (Rushen and de Passillé, 2013). Consequently, a short productive lifespan is frequently perceived by consumers as a symptom of intensive farming stress and poor animal welfare (De Vries, 2020). Thus, improving the ability of dairy farmers to keep animals healthy and comfortable for longer is increasingly demanded to maintain the social license of dairy production (von Keyserlingk et al., 2009).

A clear link between animal health and their length of life has been widely demonstrated (Pinedo et

al., 2014). Specific health traits, such as clinical mastitis, profoundly influence the productive life of dairy cattle and represent one of the primary reasons for premature culling (Neerhof et al., 2000). Because subclinical mastitis negatively affects both milk yield and milk quality, cows with repeatedly high somatic cell counts (SCC) face a significantly increased risk of being culled to avoid milk payment penalties (Samoré et al., 2003; Sewalem et al., 2006). Similarly, metabolic disorders represent major survival bottlenecks, particularly during the transition period and early lactation (Probo et al., 2018). Conditions such as clinical and subclinical ketosis - frequently monitored through milk beta-hydroxybutyrate (BHB) concentrations - and displaced abomasum drastically reduce survival probabilities by impairing the cow's early-lactation energy balance (Rostellato et al., 2021).

Because a cow's true longevity is only known at the end of her life, there is a strong need for early predictors of survival. In this context, morphological linear type traits evaluated during the first lactation are extensively used as early indicators of welfare, robustness, and longevity (Kern et al., 2015; Williams et al., 2022). Measures of physical conformation are phenotypically and genetically correlated with various health disorders (Pryce et al., 2000). Udder traits, specifically udder depth, fore udder attachment, and teat placement, have been identified as significant indicators of longevity due to their direct relationship with udder health (Nascimento et al., 2023). For instance, deeper udders and longer teats are closer to the ground, which increases the tendency for the udder to become contaminated with mastitis, inducing environmental pathogens or to suffer from mechanical injuries (Zavadilová et al., 2011). Additionally, feet and leg conformation traits (such as foot angle and locomotion scores) directly affect the animal's capacity to deambulate (Perez-Cabal et al., 2006). Poor locomotion and lameness constitute severe welfare issues that compromise feeding behaviour, milk production, and reproductive success, making them major drivers of forced culling (Khansefid et al., 2021).

Alongside health and conformation, reproductive performance is a critical determinant of cow longevity (Hardie et al., 2021). Failure to conceive, prolonged calving intervals, and an increased

number of unsuccessful inseminations are leading causes of involuntary culling worldwide, particularly in the later stages of lactation when milk yield naturally declines (Sewalem et al., 2008; Pinedo et al., 2010). Since reproductive failure is often a secondary consequence of underlying health issues, such as uterine diseases, lameness, or severe energy deficits, maintaining high fertility is synonymous with maintaining a healthy, resilient cow (De Vries et al., 2010).

Finally, extending the productive lifespan by improving health and welfare actively contributes to the environmental sustainability of the dairy sector. Rearing replacement heifers requires substantial resources, land, and feed, and accounts for up to 26% of the total enteric methane emissions of a dairy herd (Knapp et al., 2014). By extending the length of productive life, farmers can significantly reduce the annual replacement rate (De Vries, 2020). This decrease in the proportion of non-producing heifers drastically lowers the herd greenhouse gas emissions per kilogram of milk produced, demonstrating that optimising longevity is a highly effective strategy to promote a more sustainable and ethical global dairy industry (Grandl et al., 2019).

The genetic architecture of longevity and genetic progress

While management and environmental factors heavily dictate a cow's herd life, longevity is fundamentally a heritable trait. Historically, direct selection for longevity has been challenging due to its low heritability, which generally ranges between 0.01 and 0.10 depending on the specific trait definition and the statistical model used (Boettcher et al., 1999; Schuster et al., 2020; Hu et al., 2021). Despite this slow rate of genetic gain, cumulative improvements in longevity are permanent and highly valuable for the dairy industry.

Importantly, recent research has demonstrated that the genetic factors influencing survival are not static throughout a cow's life. Several studies have proven that survival in distinct parities can be considered as genetically different traits (Holtsmark et al., 2009; Pritchard et al., 2013; Heise et al., 2016; Khansefid et al., 2023). This dynamic genetic background is consistent with the shifting culling patterns observed across a cow's lifespan: voluntary culling for low production dominates the first

lactation, whereas involuntary culling due to fertility or health issues becomes the primary risk factor in later lactations (Heise et al., 2016; Khansefid et al., 2023). Therefore, evaluating survival at different stages of life as distinct but correlated traits is crucial for an accurate genetic evaluation.

However, the pursuit of an extended average herd life must be carefully weighed against the herd's overall genetic progress. Maximising longevity inherently leads to an increase in generational intervals, which can theoretically slow down the integration of superior genetics into the milking herd. Due to the rapid adoption of genomic selection over the last decade, the rate of genetic gain for economically important traits has drastically accelerated. This acceleration widens the "genetic lag" between older, mature cows and incoming replacement heifers. Consequently, the average economically optimal productive lifespan is estimated to be slightly shorter today than in previous decades, as the opportunity cost of delaying the introduction of genetically superior heifers has increased (De Vries and Marcondes, 2020).

Therefore, modern dairy operations face a complex dilemma: creating sustainable selection strategies and mating plans requires a delicate balance between extending longevity to amortise rearing costs and maintaining an optimal replacement rate to capture the accelerated genetic progress. To achieve this balance, breeding programmes require highly accurate genetic evaluations. However, properly modelling the genetic merit of survival over time and accounting for censored records - data from animals still alive at the time of evaluation - presents significant statistical and computational challenges, leading various countries to adopt different analytical approaches.

International Genetic Evaluations: the role of Interbull

Interbull: Organization, Mission, and Strategic Advantages

In order to bridge the gap between these diverse national methodologies, international frameworks have become essential for modern dairy cattle breeding. Indeed, the increasing globalization of the industry, driven by the extensive international trade of animals, semen, and embryos, now demands

a reliable way to compare the genetic merit of bulls evaluated in different countries. To address this challenge, Interbull was established as a permanent sub-committee of the International Committee for Animal Recording (ICAR), with the support of the European Association for Animal Production (EAAP) and the International Dairy Federation (IDF). Since 1996, the Interbull Centre, located in Uppsala (Sweden), has also been officially designated as the European Union Reference Centre (EURC) for Zootechnics (Interbull, 2026).

The core mission of Interbull is to promote the harmonization and enhancement of performance testing and genetic evaluation methods worldwide. Participating in the Interbull network offers overwhelming advantages for national breeding programs:

- objective global benchmarking: it allows dairy farmers and AI (Artificial Insemination) companies to select the most suitable bulls from a global population, evaluating their expected profitability within their specific national environment;
- standardization and quality control: to participate, countries must observe a strict Code of Practice and pass rigorous validation tests (e.g., genetic trend validation methods), which continuously forces national evaluation centres to upgrade and refine their statistical models;
- increased reliability: by sharing data internationally, the reliability of estimated breeding values (EBVs) for young or newly imported sires increases significantly, reducing the risk of bias associated with the empirical conversion formulas used in the past.

The international evaluations: MACE and GMACE

The fundamental statistical challenge in international evaluations is the presence of Genotype by Environment (GxE) interactions. Indeed, a bull whose daughters perform exceptionally well in a specific climate or management system might not rank equally well in another. Furthermore, different countries use different statistical models (e.g., survival analysis vs. linear models) and definitions for longevity. These two situations, often result in genetic correlations between countries to be lower

than 1 (Goddard et al., 2005). To solve this, Interbull abandoned simple conversion equations and implemented the MACE (Multiple-trait Across Country Evaluation) methodology. The statistical elegance of MACE lies in treating the same biological trait (e.g., longevity) measured in different countries as different, but genetically correlated, traits.

The most rigorous method of evaluating bulls for Interbull would be to process raw daughter phenotypes; however, this would be computationally unfeasible since it would require Interbull to model the heterogeneous fixed effects (herd-year-seasons) of every single country. Therefore, the MACE methodology uses the deregressed proofs (DRP) submitted by national evaluation centres as the dependent variable. The linear model is applied jointly across countries and incorporates three main components: the fixed effects of the evaluation country (to align differing national genetic bases), the genetic group of the bull (to account for selection among unknown parents), and the random sire effect. Crucially, the DRPs submitted by various nations are not equally reliable, thus they are weighted using the Effective Daughter Contribution (EDC). EDC adjusts for contemporary group structure, records per daughter, and the reliability of the daughters' dams (Mrode, 2014).

With the advent of the genomic era, Interbull expanded this framework to GMACE (Genomic MACE), providing international genomic evaluations for young bulls. GMACE integrates genomic information, allowing countries to share and compare the genomic breeding values of young, unproven sires on various national scales, fundamentally accelerating global genetic progress while accounting for international genetic correlations (Intebull Centre, 2026).

Global overview: member countries and national longevity models

Currently, 22 populations submit data to Interbull for the routine international evaluation of direct longevity, covering major dairy breeds including Holstein, Jersey, Brown Swiss, Guernsey, Red Dairy Cattle, and Simmental (Interbull Centre, December 2025 report https://interbull.org/ib/service_archives). However, to understand the methodological heterogeneity underlying these evaluations, the most comprehensive report is provided by the European Union

Reference Centre (EURC) for Zootechnics, which recently systematically analysed the genetic evaluation systems of 17 European member and associated countries (Nazari-Ghadikolaei et al., 2025). As MACE can process different national methodologies, the fundamental definition of longevity itself varies significantly across these 17 European nations; the longevity trait definitions mostly relies on the breeding goals and schemes Nations use in their national breeding objectives. According to the EURC, trait definitions can be rigorously categorized into four main classes:

1. *Length of productive life (LPL)*, applied by France, Switzerland, Poland, Slovenia, and the Germany-Austria joint evaluation (DEA). It's generally defined as the actual duration during which a cow remains in the lactating herd, ignoring the growth period. It is measured quantitatively, usually as the number of days (or months) from the date of first calving to the date of culling, death or censoring (Ducrocq et al., 1988);

2. *Survival across lactations or years*, applied by Belgium, Germany (DEU), the Nordic countries (DFS), Ireland, the Netherlands, the UK, and Norway. Here survival is analysed as a series of distinct traits that can be successive lactations (e.g. the ability to survive until the second, third or fourth lactation), or specific time segments (e.g. survival from the first to the second year, or up to the fifth year);

3. *Functional herd life*, utilized by the Czech Republic. It's defined as a cow's intrinsic ability to avoid involuntary culling due to health problems, infertility or diseases; this trait is obtained statistically by adjusting total longevity (true longevity) for the cow's production level compared to her contemporary group (Ducrocq et al., 1988);

4. *Risk of involuntary culling during a cow's lifetime*, explicitly adopted by Italy and Hungary. Longevity evaluations are based on proportional risk models, such as Weibull survival analysis, and they use a hazard function; indeed, they measure the instantaneous probability that a cow will suffer an elimination event unrelated to milk production at any point in her productive life.

Based on the EURC analysis, the precise statistical architectures of these national approaches for direct longevity are divided as follows:

- Countries employing survival analysis (proportional hazards models): they are the majority, 10 out of 17. Specifically:
    - France and Switzerland: both employ a single-trait sire-maternal grandsire survival analysis (ST S-MGS SA) model, applying a proportional hazards model with a piecewise Weibull baseline hazard distribution; this baseline is stratified according to the lactation stage within the lactation number (up to the sixth calving), minimizing the bias when compared with a single baseline.
    - Italy and Spain: both employ a ST S-MGS SA model for the Holstein breed, applying a standard proportional hazard function following a Weibull distribution; the difference is that Italy's approach encompasses the entire life cycle of an animal, whereas Spain's focuses exclusively to the third lactation.
    - Other SA adopters**:** The Czech Republic, Hungary, Poland, Slovenia, and the DEA consortium all employ variations of the Weibull proportional hazards model (either Sire or S-MGS models).
- Countries employing multiple-trait (MT) linear or stayability models:
    - Germany: employs a linear multiple-trait animal model (LM-MT-AM-BLUP) defining functional survival across nine consecutive periods strictly between the 1st and 4th calving.
    - Nordic Countries (DFS - Denmark, Finland, Sweden): they evaluate longevity using a multi-trait animal model (AM-MT), defining survival as five distinct traits representing longevity from year 1 to year 5.

    - Ireland and United Kingdom: Ireland employs a MT-AM BLUP focusing on survival to the next lactation up to the 6th parity, while the UK employs a bivariate AM scoring the number of lactations completed up to the 5th lactation.

- Countries employing random regression models:
    - The Netherlands: utilises a highly advanced single-trait random regression BLUP animal model (ST-RR-BLUP-AM) to calculate survival per month up to 72 months after first calving.
    - Belgium: evaluates survival over successive lactations using a random regression lactation survival animal model for all parities.
- Other non-European Interbull members: Canada employs the multiple-trait stayability approach (MT-AM BLUP across five biological periods), and Australia has recently updated its system to a multi-trait animal model defining survival across lactations based on discrete calving events. Conversely, the United States employs a single-trait BLUP animal model evaluating total months in the milking herd.

Italian Jersey and Holstein

The breeds

The management of herd books and genetic evaluations for the most widespread dairy breeds in Italy is officially conducted by ANAFIBJ (National Association of Holstein, Brown Swiss, and Jersey Breeders).

ANAFIBJ is, by its constitution, a non-profit Association. The core activities of the organisation are twofold: firstly, the selective breeding of the breeds, and secondly, the promotion, enhancement and dissemination of the Italian Holstein, Jersey and Brown breeds. The first attempt of recording data

started in 1922, but was only in the 1945 that the Association was established with the nomenclature 'Association of Italian Black-and-White Cattle Breeders'. The fundamental objective of the Association, as delineated in its founding documents, was to undertake functional checks and to maintain the National Herd Book. The establishment of the National Herd Book of the Italian Friesian occurred in 1956. The responsibility for the management of the breed's "Herd Book" was assigned to the then Ministry of Agriculture and Forestry, and the promotion of the selection of the breed itself was entrusted to the Central Technical Commission of the Herd Book, through the deliberative processes of that body. After some years, precisely in 1999, the organisation assumed responsibility for the Herd Book also for the Jersey breed. It's only in 2024 that ANAFIBJ was charged of managing Brow Swiss Herd Book as well.

Italian Holstein

The Holstein breed originated in the Friesland region, located between the Netherlands and Germany, an area with a mild climate that historically favoured pasture-based systems and forage production. Dutch settlers first introduced the breed to North America in 1621, but this initial population was entirely wiped out by a pleuropneumonia epidemic. Imports resumed in the late 1800s, forming a foundational base of about 8,000 animals from which the modern "Holstein Friesian" strain was heavily selected for high milk yields. In Italy, the modern population stems largely from the 1929 importation of the American sire *Carnation Producer* by the Torre in Pietra farm (Rome), now considered a key founding sire of the national population (Fusco, 1990).

The Holstein is a dolichomorphic animal, with a pronounced dairy aptitude, characterised by a lively temperament. The coat is typically black and white, although red and white is also recognised as a recessive trait. These are large-framed animals: adult females measure between 130 and 150 cm at the withers and weigh between 650 and 750 kg, while mature bulls can reach 1,200 to 1,300 kg. The average gestation length is 287 days, resulting in calves weighing between 40 and 50 kg or more. The skeletal framework requires a strong dorsal line and a properly sloped rump to facilitate calving and

provide adequate support for the mammary system, which must be firmly attached with a strong median suspensory ligament.

Figure 1 - SABBIONA TIKY, Champion of adult cows, National competition 2025; source ANAFIBJ

The Italian Holstein is the predominant and most widespread dairy breed in the country, with more than 1,150,000 cows breed in 8,500 herds, with an average of 131 cows/herd (ANAFIBJ, 2026). This accounts for 81% of Italian dairy cattle under test under test day control and 62% of the total Italian dairy herds (AIA, 2026). Because a significant proportion of the milk produced in Italy, approximately 49%, is destined for the production of Protected Designation of Origin (PDO) cheeses (ISMEA, 2025), historical breeding objectives for the Holstein breed heavily emphasised production traits, particularly milk yield, protein content, and fat content (Rostellato et al., 2022). However, selection criteria have progressively shifted. This is in line with global trends in the dairy industry,

where the aim is to achieve a more balanced breeding goal. ANAFIBJ has implemented composite national selection indices (such as PFT, IES, and ICS-PR; Figure 2) that increasingly incorporate

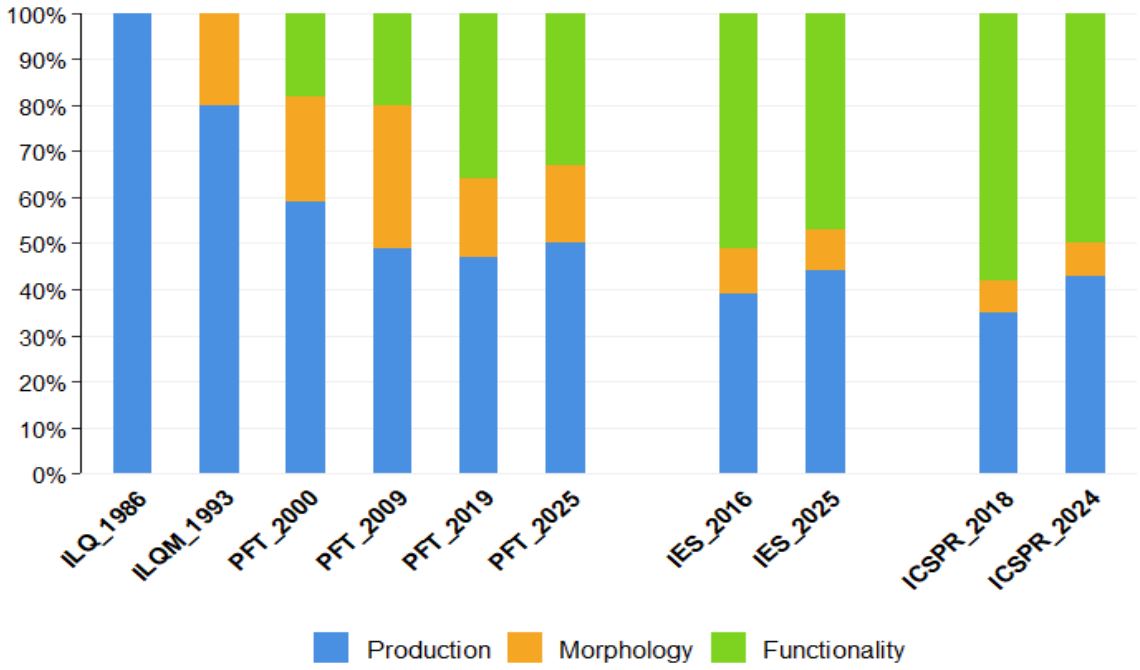

Figure 2 - Evolution of the breeding objectives for Italian Holstein

functional traits, health, and animal welfare, while maintaining focus on production (ANAFIBJ, 2026).

The Holstein breed has been selected for its ability to produce high volumes of milk, and it is now widely regarded as a leading milk producer; additionally, the Holstein has considerably incremented fat and protein content in its milk. The official average national milk production in 2024 was 10,977 kg, with 3.93% of fat and 3.42% of protein (ANAFIBJ, 2026). The annual increase in the milk yield

has been consistent, resulting in a mean of 30,535 kg for the year 2025. This remarkable production is complemented by an average herd life of 2.85 lactations (see Figure 3).

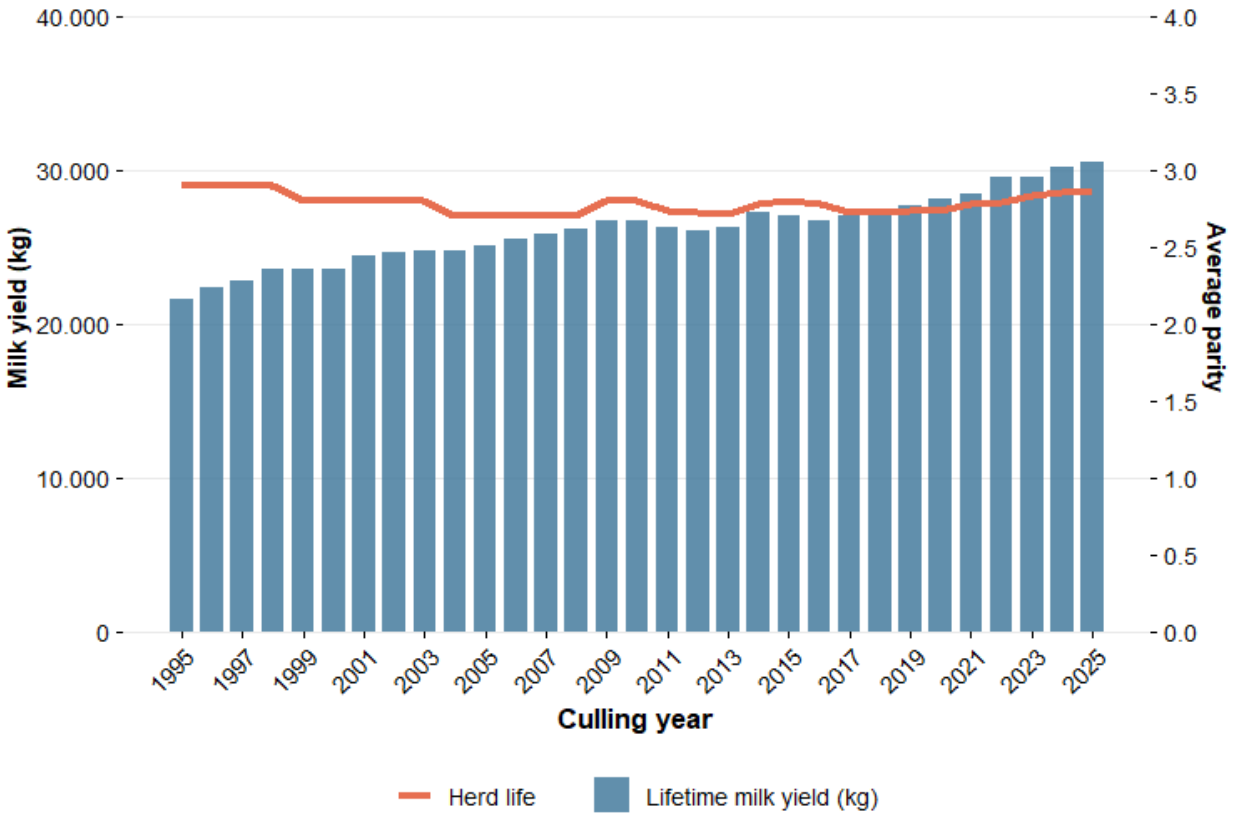

Figure 3 - Lifetime milk production and average herd life of Italian Holstein.

With regard to the culling of animals, AIA (Italian Associations of Breeders; AIA, 2026) also collects the events associated with animals during the routine test days, including culling. In the majority of cases, when a cow exits the herd, this movement is associated with a disposal code. In the estimation of the various stayability traits examined in this study, an investigation on registered culling causes was conducted. Consequently, the information regarding disposal reasons and the disposal date were retained when available. The disposal reasons presented in ANAFIBJ archives were the following: abortion (A), brucellosis (B), parasitosis (C), respiratory system (D), general disposed code (E), foot-and-mouth disease (F), digestive system (G), postpartum diseases (H), placental retention (I), vaccine (J), mastitis (K), reproductive system (L), natural calving (N), dystocia (P), sold for dairy purposes

(Q), dead in the farm (R), circulatory system (T), arthritis (U), age (V), fertility (W), production (X), foreign object (Y), lameness (Z).

Accounting for the disposal reasons, the 66.31% of the available disposal codes were different from E and R (5,170,559 animals). In view of the fact that not all disposal dates were associated with a disposal reason, this information was not utilised in the official evaluation to be presented in the following chapters. Nevertheless, these codes enabled a more comprehensive understanding of the disposal patterns within and between lactations. Over the years, the four most frequent disposal reasons were "sold for dairy purposes", "production", "fertility" and "mastitis", as it is shown in Figure 4. On the total of culled animals analysed, they accounted for the 35.6%, 26.3%, 11.8% and 5.45%, respectively. Consequently, looking at the culling causes, excluding the selling of alive animals, the main reasons to cull a cow have been imputed to production or health issues, regardless the parity order.

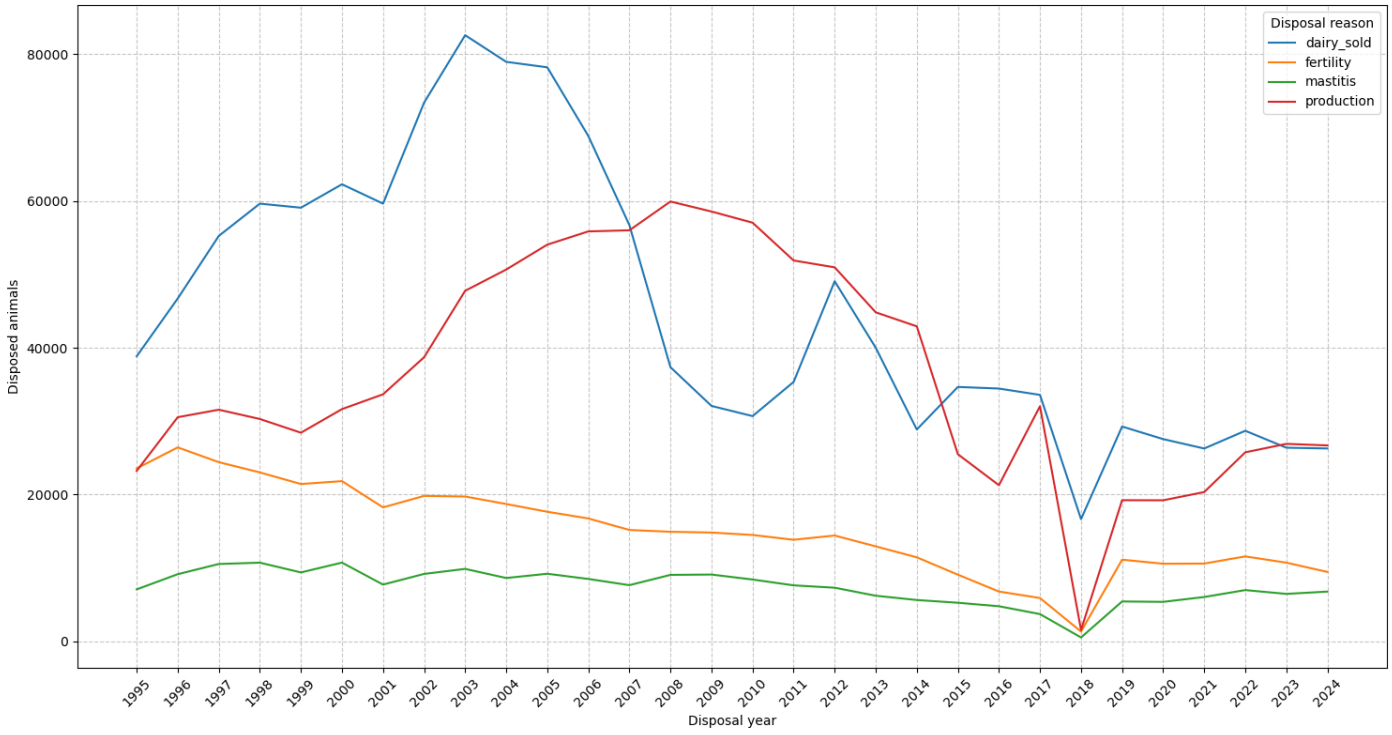

Figure 4 - Most frequent disposal reasons in Italian Holstein.

Looking in particular at each culling code, and within lactation, the trends in reference to days in milk (DIM) are diverse and are shown in Figures 5a-g. Regarding the cows sold for dairy purpose (Figure 5a), there are no substantial disparities in trends except for primiparous cows, which exhibit a considerable number of animals sold within 100 DIM. Thereafter, there is a realignment with other parity orders; in fact, there are slightly fewer bovines sold during the remainder of the lactation. Then, for the causes "digestive system" (Figure 5b) and "postpartum diseases" (figure not shown), the trend is similar: the greatest number of culled animals are within the first 50 days of lactation, a decreasing curve with a small pick again at the end of the lactation; small differences were found within parity orders, with the third lactation having the highest percentage of culled cows. A completely different pattern is shown for fertility (Figure 5c): the percentage of deceived cows sharply increased during the lactation and reached the maximum at approximately 350 DIM for all the parity orders; a second pick is shown also at the beginning of the lactation for the oldest cows. Accounting for production (Figure 5d), the majority of cows that are culled for low production could be found at the beginning of the lactation, before 60 DIM, and around 350 DIM, with a decrease amount in the extended lactations. Furthermore, it is noteworthy that primiparous cows are the most affected category for this cause. Similarly, the disposed animals because of ingestion of foreign objects had two picks before 50 DIM and around 350 DIM, but with higher variability (figure not shown). Lameness (Figure 5e) affected the first 75 DIM for each lactation, with a higher incidence for primiparous cows. Mastitis (Figure 5f) shows a different pattern: for primiparous cows, it revealed a pick before 50 days of lactation, and then a realignment with the other parity orders; multiparous cows conversely shoed the highest number of culled animals between 100 and 200 DIM. Last disposal cause investigated was those concerning the reproductive system (Figure 5g): a huge pick was found immediately after the calving, and a smaller one around 350 DIM. In summary, the timing and causes of culling vary significantly depending on the parity order of the cows. Primiparous cows have been observed to exhibit elevated levels of lameness and mastitis during the early stages of lactation. Furthermore, this category has been identified as the most susceptible to culling due to low production levels, exhibiting

distinct peaks at the commencement and conclusion of lactation. As bovines mature, there is a shift in the culling patterns exhibited, particularly with regard to udder health and reproductive performance. In contrast to primiparous cows, multiparous cows are predominantly culled due to mastitis during mid-lactation, and a peak in fertility is observed at the very beginning of the lactation.

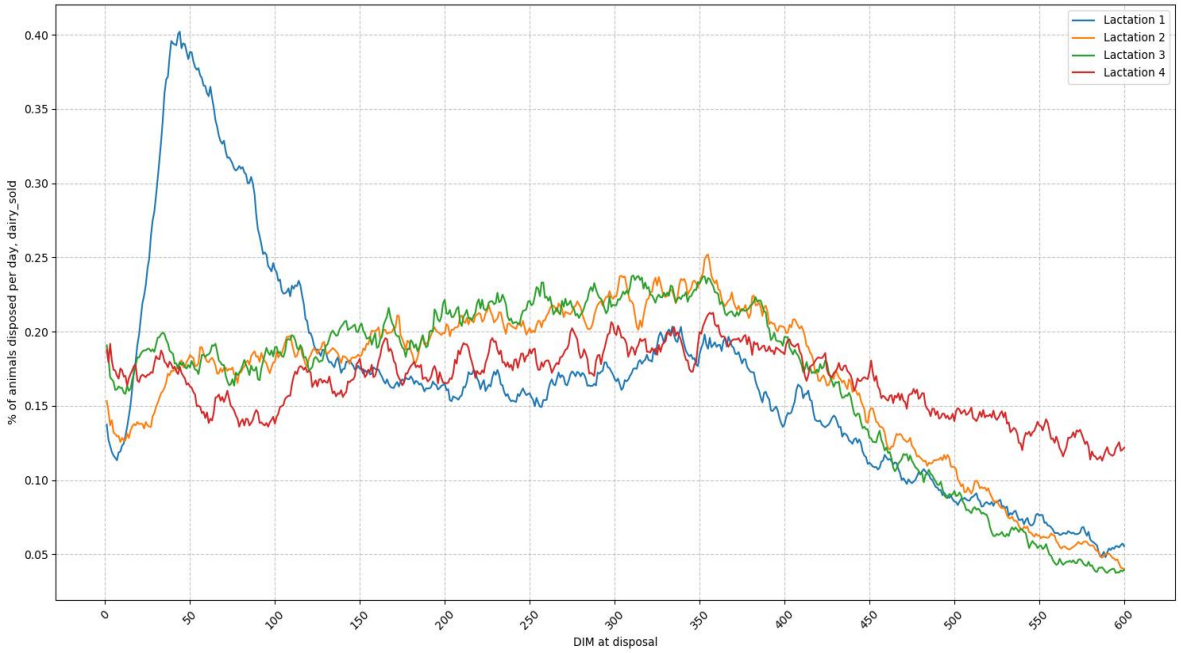

Figure 5a - Distribution of dairy cattle sold, by parity order.

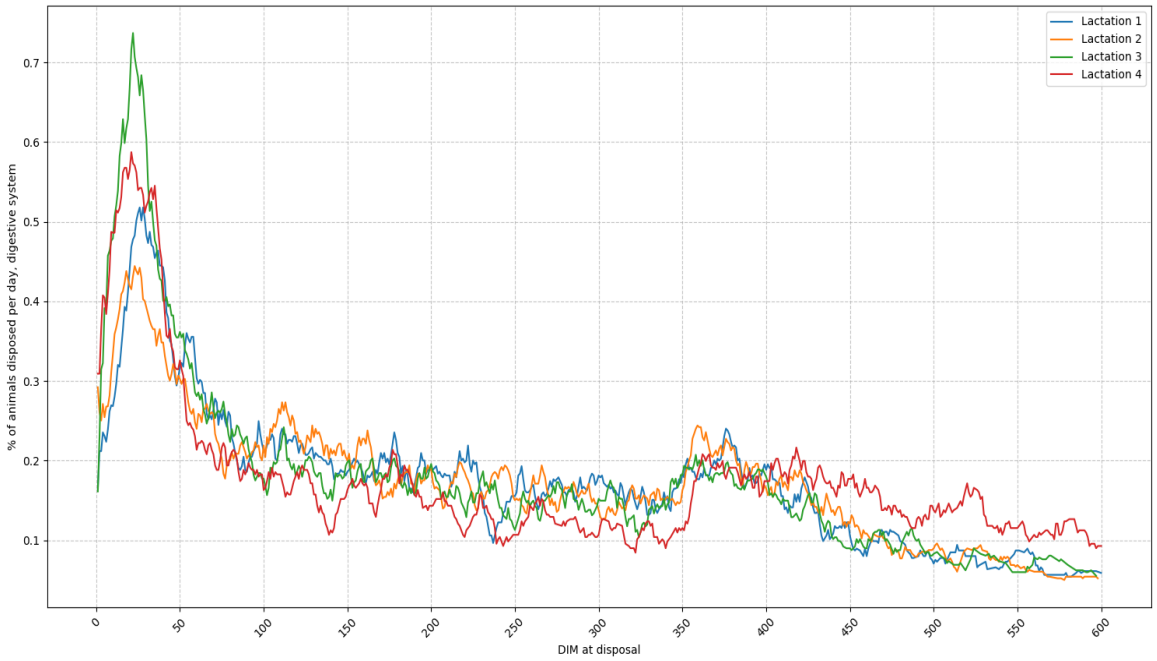

Figure 5b - Distribution of dairy cattle culled for digestive problems, by parity order.

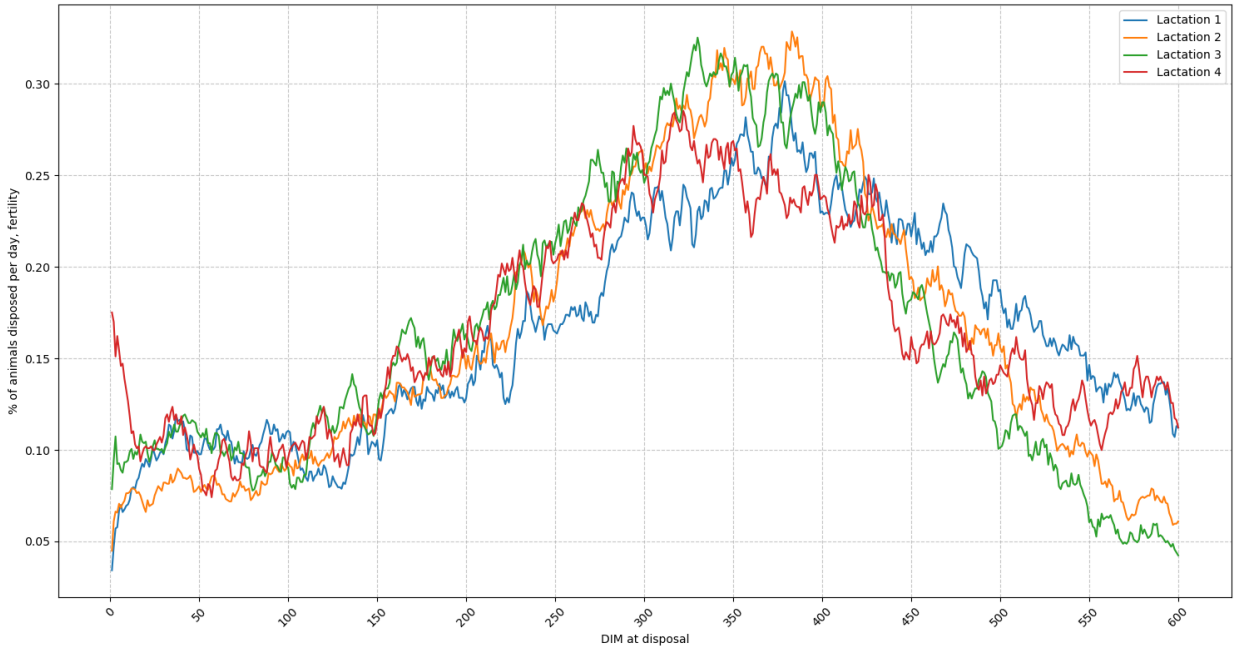

Figure 5c - Distribution of dairy cattle culled for fertility, by parity order.

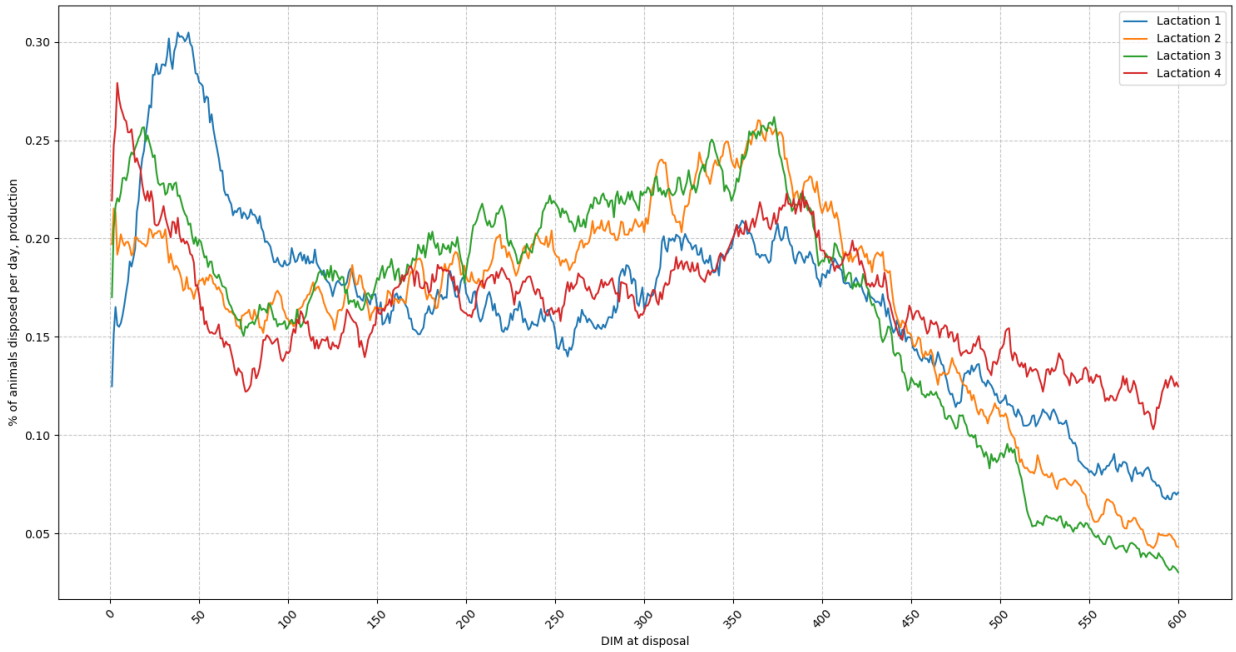

Figure 5d - Distribution of dairy cattle culled for low production, by parity order.

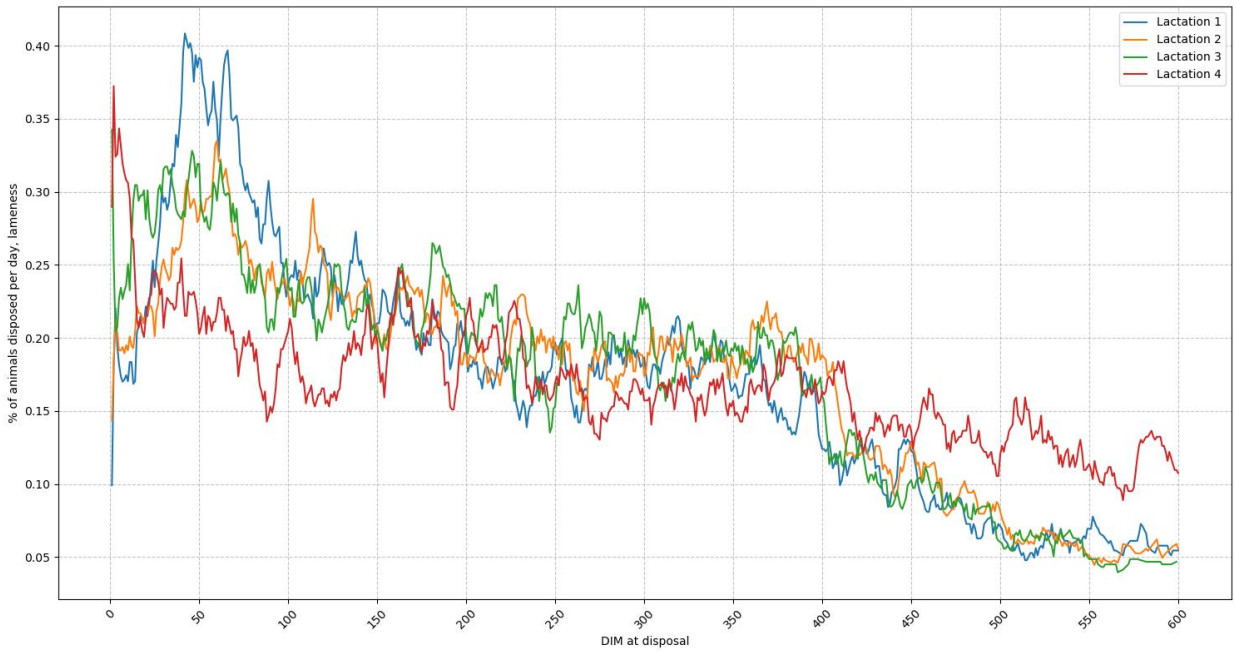

Figure 5e - Distribution of dairy cattle culled for lameness, by parity order.

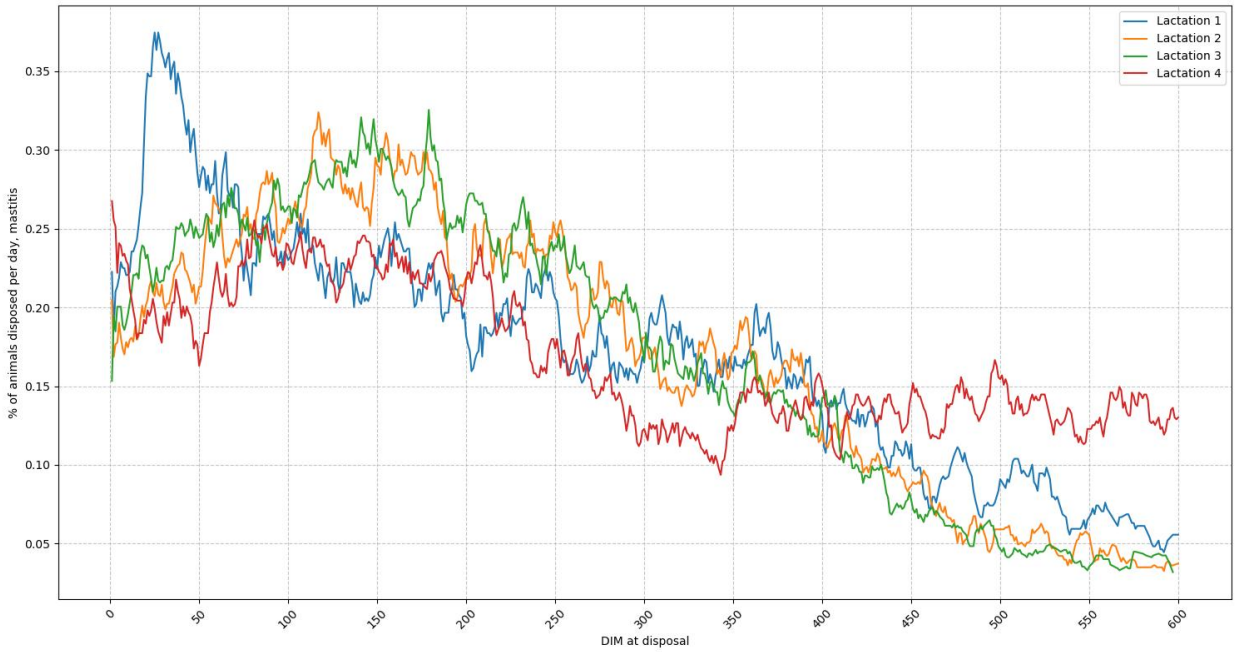

Figure 5f - Distribution of dairy cattle culled for mastitis, by parity order.

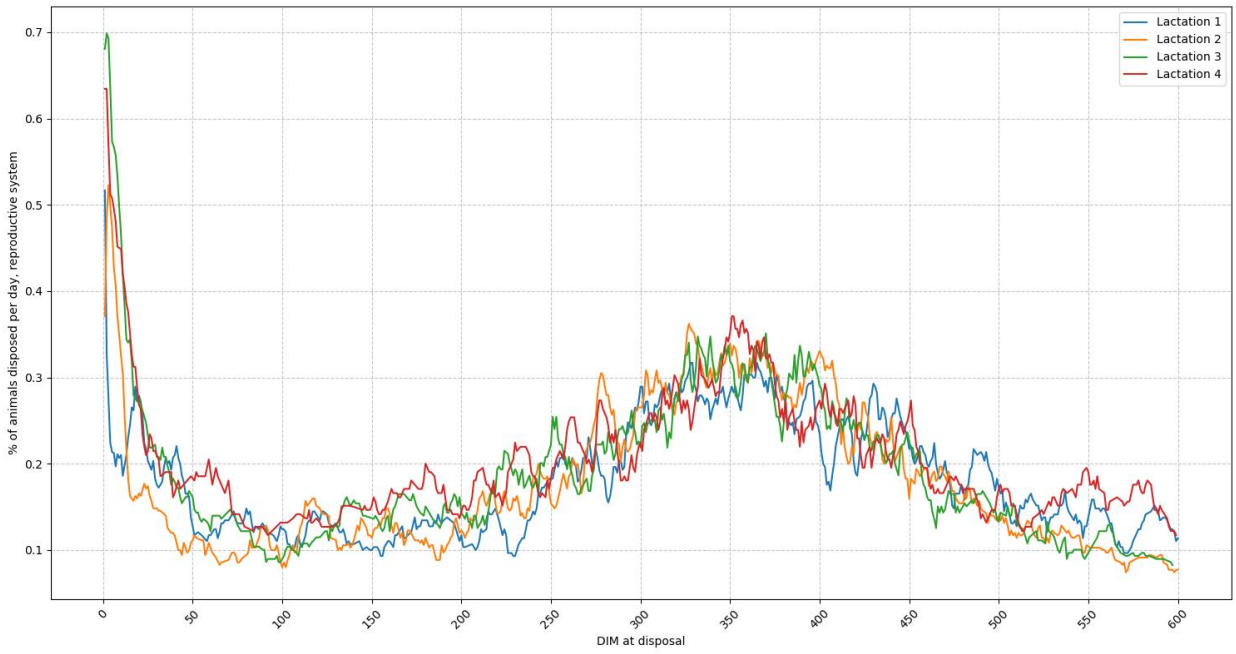

Figure 5g - Distribution of dairy cattle culled for reproductive problems, by parity order.

Italian Jersey

The Jersey breed is believed to have originated on the homologous island in the English Channel, located off the coast of France. It is hypothesised that these cattle are descended from domesticated Asian populations (Bos brachyceros) that migrated to Europe and subsequently interbred with native cattle from the French provinces of Brittany and Normandy (Huson et al., 2020). From the 1860s onwards, the breed experienced a period of significant export growth, driven by high international demand for its rich milk. This demand persisted until the onset of World War I, after which the distribution of the breed expanded to North America, Australasia, and Africa. In the contemporary era, the Jersey has become the second most prevalent dairy breed on a global scale, distinguished by its remarkable adaptability to varied climates and a range of production systems, including intensive and pasture-based methods (Huson, 2020).

In sharp contrast to the Holstein, the Jersey is an animal of remarkably small stature. Adult females reach 115-120 cm in height and a mature weight of approximately 400-450 kg. The coat ranges from

light brown and fawn to almost grey or dull black (mulberry), typically featuring a distinctive black nose bordered by a white muzzle (The cattle site, 2026).

Figure 6 - DOTTI VICTORIOUS SHARON ET, Champion of Dairy Show 2025; source ANAFIBJ

The Italian Jersey breed is a comparatively minor component of the national dairy sector, with a population of 7,000 cows in 840 herds, averaging 8.2 cows per herd (ANAFIBJ, 2026). This accounts for 0,45% of Italian dairy cattle under test under test day control and 6% of the total Italian dairy herds. The production is, in comparison to the Holstein production, less striking in terms of its quantity, yet it is of a higher qualitative nature. Figure 7 illustrates the trend over the past decade in milk yield, fat percentage and protein percentage of Italian Jersey cows. Due to the limited number of animals, a conventional genetic evaluation is currently performed for the Jersey. The extensive application of genomic data for routine selection indices remains to be achieved (ANAFIBJ, 2026).

Historically, no official selection index for complex functional traits like longevity has ever been applied to the Italian Jersey population. Nevertheless, breeding programmes for this breed are continuously evolving. There is a strong, ongoing effort to implement an increasing number of novel traits into the traditional valuation to specifically improve the functionality, robustness, and welfare

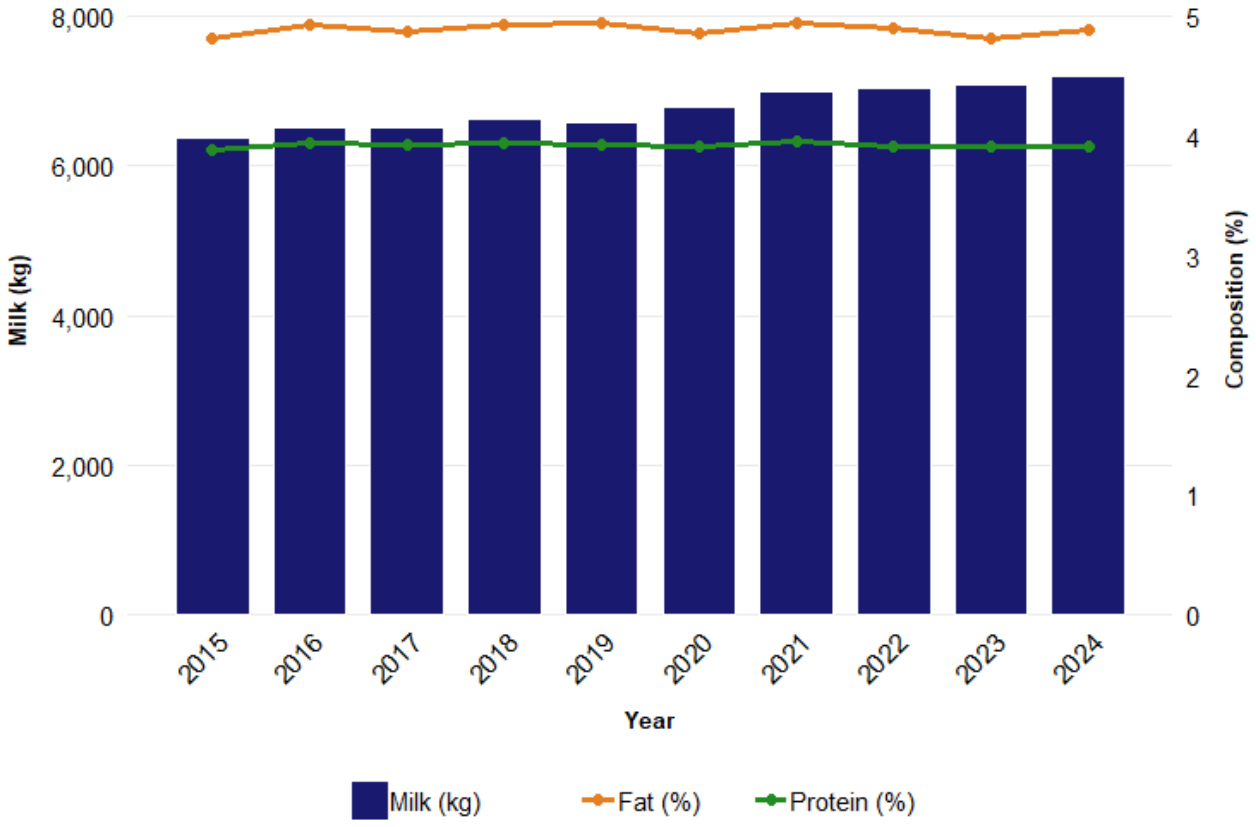

Figure 7 - Trends of milk kg, fat% and protein% in Italian Jersey.

of the Jersey cows, starting with routine longevity evaluations in this thesis.

Statistical model

For the Italian Holstein population, the focus on longevity is more established. An official routine genetic evaluation for functional longevity was implemented by ANAFIBJ in August 2001 (Canavesi et al., 2003). From a statistical perspective, the genetic evaluation of longevity poses challenges that traditional linear mixed models are unable to directly address. The primary obstacle is the presence of "censored" records; at the time of any genetic evaluation, a significant proportion of cows are still

alive and producing milk. For these animals, the true length of productive life is unknown, and their records only provide a lower bound of their eventual survival time (Ducrocq et al., 1988; Brotherstone et al., 1997). Treating censored records as completed, or projecting them based on simple linear regressions, leads to severe biases. Furthermore, survival data exhibit a highly skewed, non-normal distribution, and the environmental or physiological risk factors affecting a cow (e.g., herd size, stage of lactation, milk yield) change dynamically over her lifetime (Caraviello et al., 2004).

To overcome these limitations, the official Italian Holstein evaluation implemented by ANAFIBJ relies on Survival Analysis, specifically employing a Weibull proportional hazards model. The foundation of this methodology is the hazard function $\lambda(t)$, which represents the instantaneous probability (or risk) of a cow being culled at time t, given that she has survived up to that exact moment (Ducrocq et al., 1988). In the proportional hazards framework, the hazard of an individual cow is modelled as the product of two distinct components:

$$\lambda(t) = \lambda_{0,s}(t) exp\{\boldsymbol{x'}_m(t)\beta + \boldsymbol{z'}_m\boldsymbol{u}\}$$

The first component, $\lambda_{0,s}(t)$, is the baseline hazard function, which describes the underlying aging process and the general culling rate of the population over time. Adding the subscript s indicates that this baseline is stratified; instead of assuming a single underlying aging process for the entire population, specific baseline curves are defined for different strata (such as lactation number), allowing the Weibull shape and scale parameters to vary across a cow's productive life (Sewalem et al., 2004). The Weibull distribution is highly flexible and can model a hazard rate that remains constant, decreases, or increases as the animal ages (Ducrocq et al., 1988). The second component of the equation is a stress-dependent exponential function; the inclusion of (t) in the incidence vector indicates the use of time-dependent covariates $\boldsymbol{x'}_m$ (Sewalem et al., 2004). This allows the vector of fixed effects β to dynamically change over time, accommodating environmental or physiological risk factors - such as herd size or milk yield - that fluctuate throughout a cow's lifespan (Sewalem et al., 2004). The vector u represents the random variables, with $\boldsymbol{z'}_m$ as their associated incidence vector

(Sewalem et al., 2004). To process this highly complex mathematical framework, ANAFIBJ utilizes the 'Survival Kit', a specialized software originally developed by Ducrocq and Sölkner (1994), which allows the inclusion of a genetic covariance structure among individuals based on the additive relationship matrix (Canavesi et al., 2004).

In the specific operational model utilized by ANAFIBJ for the Italian Holstein breed, initially implemented in 2001 and substantially improved in 2004, the generic proportional hazards framework is adapted to capture national culling dynamics. Here, the baseline is assumed to follow a standard Weibull distribution, characterized by a scale parameter $\lambda_0(t)$ and a shape parameter $\rho = 2$. Instead of stratifying the baseline, the physiological stress of ageing and lactation is modelled within the exponential function as a piecewise constant time-dependent fixed effect, specifically defining the stage of lactation nested within the lactation number. Additional time-dependent fixed effects include the year-season of calving and the annual change in herd size, while the age at first calving is fitted as a time-independent fixed covariate (Canavesi et al., 2004). Regarding the random components $\boldsymbol{z}'_m$, the model accounts for a time-dependent herd-year-season effect (Canavesi et al., 2004). One critical implementation on the genetic evaluation was the upgrade from a simple sire model to a Sire-Maternal Grand-Sire (Sire-MGS) model; this structural improvement increased the estimated sire variance and the system's overall accuracy, leading to an estimated heritability of 0.097 on the normal scale (Canavesi et al., 2004)

To mathematically disentangle functional longevity from true longevity, the model corrects for the farmer's voluntary culling decisions. In the updated model, all lactation records - including short lactations in progress (< 30 days in milk) and closed short lactations - are projected to 305-day mature equivalents (Canavesi et al., 2004). Voluntary culling for production is then accounted for by incorporating within-herd-year deviations for milk yield, fat percentage, and protein percentage as piecewise constant time-dependent covariates (Canavesi et al., 2004). Lastly, the direct longevity estimated transmitting abilities obtained from this model are not published independently; rather, they

are combined with udder traits and feet and legs functionality to formulate the final official functional combined longevity index (Canavesi et al., 2004).

Transitioning to a new framework: limits of Survival Analysis and the Stayability approach

Computational and methodological limitations of Survival Analysis

Despite the Weibull proportional hazards model's historical efficacy in managing right-censored data and time-dependent covariates, its practical implementation in contemporary dairy breeding programmes has highlighted significant computational and biological limitations (Heise, 2017).

The primary challenge is the computational burden that occurs when moving from a sire model to a full animal model. In survival analysis, the genetic effect is modelled as a "frailty" term - a factor that multiplies the baseline culling risk, making it extremely complex to solve for millions of individual cows (Mészáros et al., 2013). Solving a non-linear proportional hazards model for millions of individual records requires highly complex numerical integration techniques (Ducrocq et al., 2001). While specialized software like the Survival Kit can efficiently resolve these equations for simple sire models, computing a full animal model, which requires incorporating the dense inverse of the additive genetic relationship matrix for all females, is computationally prohibitive under the timeframes required for routine national evaluations (Heise, 2017). This constitutes a critical methodological failure in the modern era, as the transition to an animal model is an absolute necessity to obtain estimated breeding values (EBVs) for cows, which form the foundation for genomic predictions using female reference populations.

Furthermore, as explicitly pointed out by both van Pelt et al. (2015) and Heise (2017), standard survival analysis relies on a major limiting assumption: it treats longevity as genetically the exact same trait throughout the entire productive lifespan of a cow. However, this has been shown to be untrue. Indeed, different studies show that the genetic correlation between survival in the first lactation and in the following differs from unity, with estimates ranging widely from 0.33 to 0.96

depending on the specific biological interval (Boettcher et al., 1999; Sewalem et al., 2007; Holtsmark et al., 2009; Heise et al., 2016; Pritchard et al., 2013; Khansefid et al., 2023). Consequently, since traditional survival models struggle to include genetic factors that change as a cow ages, they fail to accurately represent the true biology of longevity.

The global dairy breeding industry has undergone a significant change from the non-linear survival analysis towards multiple-trait linear models or random regression models, driven by the limitations imposed by computational capabilities. Germany, for instance, entirely dismantled its routine Weibull model in favour of a linear multiple-trait system specifically designed to natively accommodate the distinct genetic background of different survival periods and to enable the animal model. Similarly, the Netherlands adopted random regression models to dynamically capture the changing genetic variance over the lactation trajectory (van Pelt et al., 2015). Canada transitioned from a three-trait to a five-trait linear animal model to separately evaluate survival across discrete lactations (Sewalem et al., 2007), and New Zealand fundamentally utilizes a multiple-trait animal model for its longevity evaluations (van der Linde and de Jong, 2003).

The concept of Stayability

To address the statistical and computational limitations of modelling longevity as a single variable, the concept of "stayability" has been widely adopted in modern genetic evaluations. Stayability is strictly defined as a binary trait (coded as 1 for success, 0 for failure), reflecting an animal's ability to remain in the herd and survive until a predefined time point, such as a consecutive calving event (Hudson and Van Vleck, 1981; Hardie et al., 2021). Historically, earlier implementations defined stayability based on fixed chronological age milestones, such as survival to 36, 48, 60, or 72 months of age (Caraviello et al., 2004). A similar chronological approach is still widely used in beef cattle breeding, where stayability is both evaluated in months of age or complete calvings (Brigham et al., 2007; Brzáková et al., 2019; Callegaro et al., 2024). However, in contemporary dairy cattle evaluations, the chronological definition has evolved into a physiological one: productive life is now

methodically partitioned into discrete biological intervals, specifically evaluating the conditional survival from one parity to the next (Sewalem et al., 2007; Jamrozik et al., 2013).

From a quantitative genetics' perspective, the formulation of stayability is grounded in the threshold model theory (Dempster and Lerner, 1950; Gianola, 1982). This theory postulates that the observable binary phenotype (survival vs. culling) is the discrete expression of an underlying, unobservable, continuous variable termed "liability", which encompasses the cumulative sum of all genetic and environmental stresses acting on the cow (Heise, 2017). When this liability exceeds a certain biological or economic threshold, the failure (culling) occurs. While non-linear threshold models perfectly describe this binary nature, they are computationally intensive. Thus, multiple-trait linear models treating sequential stayabilities as genetically correlated traits have been proven as a highly effective and computationally superior approximation (Boettcher et al., 1999).

A major methodological challenge in longevity evaluations is the proper handling of "censored" records, i.e. data from cows that are still alive at the time of data extraction. In traditional single-trait linear models, the exclusion of these records or their projection can result in severe estimation bias. Within the framework of stayability, when combined with a multiple-trait parameterization, censoring can be managed. The lifespan of a cow is divided into a series of binary traits (e.g., survival from first to second lactation, second to third, etc.). Information derived from young, currently living animals is utilised to calculate the discrete intervals over which survival has been successfully achieved (coded as 1) (van Pelt et al., 2015). A focal point is that the stayability traits for subsequent, temporally distinct intervals are not treated as completed failures, but are rigorously set to "missing" within the incidence matrix (Sewalem et al., 2007; van Pelt et al., 2015). This mechanism relies on the genetic covariance structure established by older cows with complete records: the model uses these covariances to infer the genetic merit of the missing intervals for the younger cows. Statistically, this sequential binary approach acts like a discrete-time survival analysis. It takes full advantage of early-life data, making stayability an exceptionally robust setup for today's genetic evaluations.

Additionally, Sewalem et al. (2005) reported that genetic trends from a Weibull survival model seemed to be overestimated for young sires with a high amount of censored daughter information. Consequently, the multiple-trait linear framework helps circumvent the overestimation issues of non-linear survival models while simultaneously mitigating the truncation biases typical of older, single-trait linear approximations.

Advantages of linear trait models

Although the underlying biological nature of stayability is binary and conceptually grounded in threshold-liability theory, its multi-trait operational structure allows for a highly effective linear analysis. Evaluating sequential binary stayabilities via a linear model serves as a linear probability approximation. Avoiding extreme frequencies, this linear approach offers vast practical and computational advantages over traditional survival analysis frameworks.

First, linear models require a fraction of the computational time and resources. The extreme efficiency of linear models easily allows for the implementation of full animal models and the integration of genomic relationship matrices (Heise, 2017).

Second, linear models inherently support multiple-trait parameterization. By treating stayability at the 1st, 2nd, and 3rd lactation as separate but genetically correlated traits, the model perfectly captures the varying genetic determinism of survival as the cow ages (van Pelt, 2015).

Finally, despite the theoretical assertion that linear models are suboptimal for binary data due to the assumption of normally distributed residuals, extensive empirical research has demonstrated their practical robustness. Simulation studies have shown that the correlations between true and estimated breeding values derived from linear models are almost identical to those obtained from complex non-linear proportional hazards models (Holtsmark et al., 2009; Meuwissen et al., 2002). In practical routine evaluations, linear multiple-trait models have even been found to perform well in predicting the survival of daughters, largely due to their superior ability to accommodate multiple genetic

effects. Consequently, linear models applied to stayability traits are now considered a highly accurate, computationally superior, and genomically adaptable alternative to survival analysis.

Aims of this thesis

As previously stated, the traditional survival analysis models that were once utilised with great efficacy are now facing significant computational limitations and biological inconsistencies in the current genomic era. Contemporary linear models have proven to be a highly efficient, robust, and adaptable alternative. The present study was driven by a necessary shift in methodology, with the core objective being the development and implementation of a new linear-based genetic evaluation for longevity in the main Italian dairy breeds.

In order to achieve this aim, the research is divided into two principal practical parts, which are designed around the specific requirements of the national dairy sector. On one side, my focus was on the Italian Jersey breed. As no official selection index for longevity for this breed existed prior to the commencement of this project, the objective of this study was to construct a novel genetic evaluation, employing a multiple-trait stayability approach. On the other side, the work was focused on the significantly larger Italian Holstein population. The objective there was to revise and upgrade the existing Weibull proportional hazards system, which has been in utilisation since 2001, by replacing it with a faster and more straightforward linear framework.

The present thesis proposes a reinterpretation of the concept of longevity, emphasizing the notion of distinct stayability milestones rather than perceiving it as a singular lifelong trait. This approach aims to facilitate breeders with contemporary tools to reduce involuntary culling. This transition will ultimately assist farmers in enhancing the health, functionality and overall welfare of their dairy herds.

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Chapter 2:
Genetic evaluation of longevity in Italian Jersey

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Introduction

The aim of the present study was to develop a new routine evaluation for longevity in Italian Jersey. As stated in the general introduction, in the last decade, longevity has been widely studied, and it is still under investigation due to its importance for the dairy sector. In this study, we used the definition of 'stayability' (**STAY**), which is a binary trait for success or failure to remain in the herd until a given time point (Hudson and Van Vleck 1981; Hardie, Heins, and Dechow 2021). Since for Jersey cattle, there are fewer studies compared to other cosmopolitan dairy breeds, the aims of this study were multiple. First, to evaluate the Italian Jersey breed for longevity traits through a stayability approach. Second, to estimate correlations with other phenotypes in Italian background to allow further future investigation on the Jersey selection scheme.

Abstract

Longevity in animal science is a complex trait that can be approached in different ways. So far, for the Italian Jersey population, no official selection index is being applied. Thus, the present study aims to investigate the feasibility of an official routine genetic evaluation for longevity in this population. Longevity was analysed as stayability, meant as the ability of cows to survive to a specific calving event. Calving records for 20,724 cows were analysed. Phenotypically, longevity showed an average of 2.65 ± 1.62 lactations. Heritability was estimated with an animal model, which included the random effect of the contemporary group and the random animal additive genetic effect, fitted using a pedigree-based relationship matrix. Heritability estimates ranged from 0.050 ± 0.012 to 0.208 ± 0.022 for stayability traits, depending on the model. Stayability at the 4th lactation has been chosen to be the breeding objective, i.e. the minimum number of lactations a cow should show to have a successful productive life. Furthermore, genetic and phenotypic correlations between stayability and other traits undergoing selection such as milk, fat and protein yield, fat and protein percentage, type traits (e.g. foot angle, fore udder attachment, rear udder height, udder support, udder depth) and age at first calving (AFC) were estimated for cows' population. Generally, stayability showed a high genetic

correlation with production traits, fore udder, rear udder height, udder support and foot angle, while it was negligible with AFC. Longevity, as stayability, could be considered for routine genetic evaluations for the Italian Jersey population.

HIGHLIGHTS

- Longevity in dairy cows is important economically, socially and from an animal welfare standpoint
- Extending cattle longevity could enhance farmers' profit, and improve the social acceptability
- This study shows that selecting for stayability in Italian Jersey is feasible and that this trait

KEYWORDS
Genetic selection; stayability; longevity; dairy cattle

Material and methods

Data and edits

For this study, records on the Italian Jersey population were provided by the Italian Holstein, Brown Swiss, and Jersey Association (ANAFIBJ, Cremona, Italy). We considered only Jerseys born in Italy, showing a first calving event recorded later than the year 1997. Cows that changed their herd during their career or that had calving intervals shorter than 240 days were excluded. Furthermore, sires showing less than three daughters, herds with less than three cows, or fewer than two sires were discarded. We also determined as censored all cow records with a last calving event that happened less than 700 days before data extraction.

Stayability is a binary trait for success or failure to remain in the herd until a given time point (Hudson and Van Vleck 1981; Hardie et al., 2021). In this study, each calving was used to determine different periods. In particular, stayability from birth to second lactation, from birth to third lactation, from birth to fourth lactation, etc; stayability periods were labelled, respectively, as STAY2, STAY3, STAY4, STAY-n. Considering that stayability is a binary trait, it was coded as '1' to indicate animals that survived the period, and '0' otherwise.

After the first editing, 20,724 cows from 1,135 herds and offspring of 544 sires were present in the dataset, which will later be named **D-a**.

For Variance Components Estimation (**VCE**), stricter editing in addition to the aforementioned one was applied to avoid extreme or uncommon values and to ensure a more stable evaluation. Only cows born before 2018 were considered; moreover, animals with calving intervals longer than 700 days were excluded. Lastly, cows with intervals between the last calving event and any other registered event longer than 700 days were discarded. These specific edits were necessary to eliminate censored records and extreme outliers from the VCE population, as their inclusion would introduce substantial bias into the estimation of genetic parameters. As a result, we retrieved 15,569 cows, 457 sires, and 973 herds for the VCE step; this dataset will be labelled as **D-vce**.

Using the dataset D-vce, the assessment of the phenotypic stayability curve was carried out. We calculated culled animals across parity, stayability rate for each lactation as the average percentage of survived cows, average herdlife (the average numbers of lactations from first calving to culling), and replacement rate (annual percentage of herd replaced, assuming a calving interval of 365 days). Age at first calving (AFC) and productive traits (such as milk yield, fat kg and percentage, protein kg and percentage) were added to D-vce dataset. AFC was calculated as the difference in days between the day of first calving and the birthdate of the cows. It ranged between 517 days and 1113 days, that is between 17 and 36 months. All animals with AFC higher than 36 months were discarded, as a possible registration error, resulting in 15,550 animals; this dataset will be named as **D-afc**. Productive traits were collected during national routinely test days. Only records from the first lactation were considered to evaluate production as an early predictor of longevity and to ensure a standardized comparison across all contemporary groups. Furthermore, records with an effective DIM (days in milk) lower than 300 days were discarded to guarantee the accuracy of the conventional 305-d production projections. All the animals with no production at all, or at least one missing value, were discarded, resulting in 14,534 cows (data set **D-p**). One additional dataset was created merging

records for morphological traits (**D-m**); type traits evaluations were available only for primiparous cows, and cows were evaluated during national routinely test days. They were recorded as a linear score, ranging from 0 to 50, with an optimal value of 25 for almost all traits. All cows with missing data were discarded, resulting in 9,706 individuals for this last set.

Statistical analysis

To properly handle the variation of the trait, four models were compared. They will be labelled as **M1g** (M1, Gaussian), **M1t** (M1, threshold-liability), **M2g** (M2, Gaussian), **M2t** (M2, threshold-liability). The difference between M1 and M2 referred to the variable of the contemporary group (CG), while the difference within M1 and M2 referred to the statistical analysis applied.

Generally, the model equation used for all the analysis were defined as:

$$y_{ij} = \mu + CG_i + animal_j + e_{ij}$$

where: y_{ij} was the phenotype investigated (linearly for the Gaussian models or in terms of liability, for the threshold models), that were stayability to 2nd, 3rd and 4th calving, productive traits, AFC or morphological traits; μ was the intercept; CG_i was the random effect of ith contemporary group, and it was considered either as the herd of first calving (1009 classes, for models M1) or as the combination of herd and year of first calving (3929 classes, for models M2); $animal_j$ was the jth animal additive genetic effect with a pedigree of 27,687 animals, and e_{ij} was the random error. The effect of CG_i was fitted as random due to the data structure of the population, i.e. an uneven class frequency. Even though in this analysis an editing on representativeness of herds and sires has been applied, the risks of having an unbalanced representation of families within a herd was still present. Indeed, animals and herd estimates were not orthogonal, which lead us to fit effect as random.

The comparisons made had two aims: first, to test the different definitions of CG between M1 and M2; second, to compare the performances of the Gaussian (M1g or M2g) versus threshold-liability model (M1t or M2t), for both definitions of CG.

Variance components estimation

The pedigree of cows in the dataset D-vce was traced back to at least 4 generations. Unknown parents were assigned to phantom parent groups based on animal origin and year of birth (39 genetic groups), as described by Famula, Pollak, and Van Vleck (1983). Variance components were estimated with the Gibbs sampler THRGIBBS1F90 (Misztal et al. 2022) with 300,000 iterations, a burn-in of 100,000, and a thinning interval of 10. The same software was utilized for both the linear (Gaussian) and the threshold-liability model analyses. Specifically, the linear analysis was implemented using 'OPTION cat 0', which allows the program to perform linear analyses with the same computational efficiency as dedicated linear software. Convergence was assessed by visual inspection of the trace plots. The software uses flat priors for the variance components, by default. For the runs of analysis that showed poor convergence, a second run was carried out, using the same number of iterations while providing a stronger prior for the variance components. Here, the prior was stronger for the components that showed good convergence, poor for the others. This allowed better convergence of the Gibbs chains. The post-Gibbs analysis was performed with the software POSTGIBBSF90 (Misztal et al. 2022). An animal model was used; the additive genetic effect of the animal was fitted to the pedigree-based relationship matrix (A), and it was included as a random effect. An additional estimation, setting the 'option prior' to THRGIBBS1F90, was done to obtain better convergence for the M2g model. The formula was applied to values obtained from each iteration of the Gibbs sampler, the posterior mean was used as an estimate while the posterior standard deviation was used as an error.

Heritability (h2) was calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{cg}^2 + \sigma_e^2}$$

where σ_a^2 is the additive genetic variance, σ_{cg}^2 is the herd*year effect variance and σ_e^2 is the residual variance.

For h2 estimated with the threshold models, a transformation from the underlying to the observed scale was made, to make the results comparable. The formula used is the one of Dempster and Lerner (1950):

$$h^2_{obs} = \frac{h^2_{und} \; x \; Z^2_{ord}}{p \; x \; (1 - p \;)}$$

where h^2_{obs} is the heritability after the transformation on the observed scale, h^2_{und} is the heritability on the underlying scale, Z^2_{ord} is the ordinate height of the normal distribution at the threshold point corresponding to p, and p is the prevalence of survived cows at different lactations.

Phenotypic and genetic correlations

Phenotypic and genetic correlations were calculated with the following formula

$$r_{ij} = \frac{\sum covar_{ij}}{\sum \sqrt{\sigma^2_i * \sigma^2_j}}$$

where r_{ij} is the correlations between two traits, $\sum covar_{ij}$ is the sum of covariances of the random effects, and $\sigma^2_i * \sigma^2_j$ is the product of standard deviations of all traits. Those correlations were derived from bivariate models between stayability traits and the others, as stayability was a binary variable. This formula was applied to correlations between stayability traits and productive traits, type traits and AFC. It was applied to values obtained from each iteration of the Gibbs sampler, the posterior mean was used as estimate while the posterior standard deviation was used as error. In addition, the 95% highest probability density intervals were used to define significance, with $p<0.05$ when the value '0' was not included in the interval.

Breeding values estimation

Estimated breeding values (EBV) for all the animals in the initial dataset D-a were computed with MiX99 software (Lidauer et al. 2022). This software is highly optimized for large-scale national routine evaluations and was used to solve the mixed model equations using the variance components and the four animal models described previously. Bull's rank correlations among breeding values

obtained have been calculated with the Spearman method. Eventually, M2g was chosen out of the four proposed because it gave similar results while being more parsimonious, in terms of genetic variance, heritability, rank correlations, and easy use of routine application.

As all functional traits published by ANAFIBJ, EBVs of the M2g model were standardised to a mean of 100 and a standard deviation of 5. EBVs larger than 100 identify animals that are more likely to survive the fourth lactation. Bulls' daughter's stayability rate (DSR) to the fourth lactation was calculated as a phenotypic indicator; it was derived from the percentage of bull's alive daughters at the fourth lactation. After that, all bulls were categorised into three groups: low index bulls (EBV < 95), medium index bulls (95 ≤ EBV <105), and high index bulls (EBV ≥105). For those three categories, the average mean of the DSR was calculated; as a consequence, it was possible to quantify a phenotypic standard deviation for each group of breeding values. Thereby, breeders could better understand the relationship between bulls' EBVs and their live daughters.

Results

Descriptive statistics and phenotypic cow survival

The phenotypic stayability curve has a descending trend over parity, from the second lactation to the tenth; particularly, at the third lactation there is almost 50% of culled cows (Figure 1).

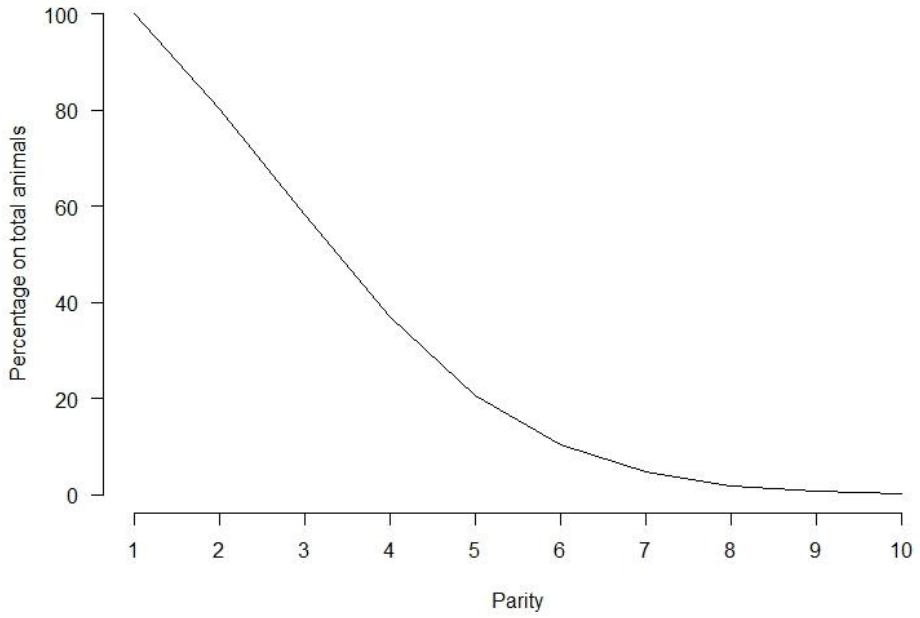

Figure 1 - Stayability rate across parities, assuming first parity to be a starting point for all the cow (100% survived).

In Table 1, these and other phenotypic information about stayability are presented. It can be seen that parity 2 and 3 were those with the highest percentage of culled cows. In addition, we calculated average herd life as the average number of lactations from 1st calving to culling, and replacement rate (annual percentage of herd replaced, assuming a calving interval of 365days). These results were respectively 3.05 and 31.8%.

Table 1 - Phenotypic survival information over parity. Lactations from 11th are aggregated in a single class.

Parity	Culled/parity[1], n.	Culled/parity[1], %	Survived[2], n	Survived[2], %
1	0	0	15569	100
2	3446	22.13	12123	77.87
3	3744	24.05	8379	53.82
4	3183	20.44	5196	33.37
5	2477	15.91	2719	17.46
6	1426	9.16	1293	8.30
7	736	4.73	557	3.58
8	349	2.24	208	1.34
9	137	0.88	71	0.46
10	48	0.31	23	0.15
11+	23	0.15	0	0

[1] Culled/parity: animals culled over the single lactations, considering both the number and the percentage of the total amount of the specific lactation.

[2]Survived: animals survived as a cumulated number of cows through lactations, considering both the number and the percentage of the total amount of animals.

Secondly, the trend across years of the average lactation number reached was examined. Considering the last year of calving as the replacement year, an average parity at culling was calculated, and it is shown in Figure 2. No meaningful variations can be seen in this analysis between 2006 and 2022: stayability averaged 2.65±1.62 lactations, and it was stable across years of replacement.

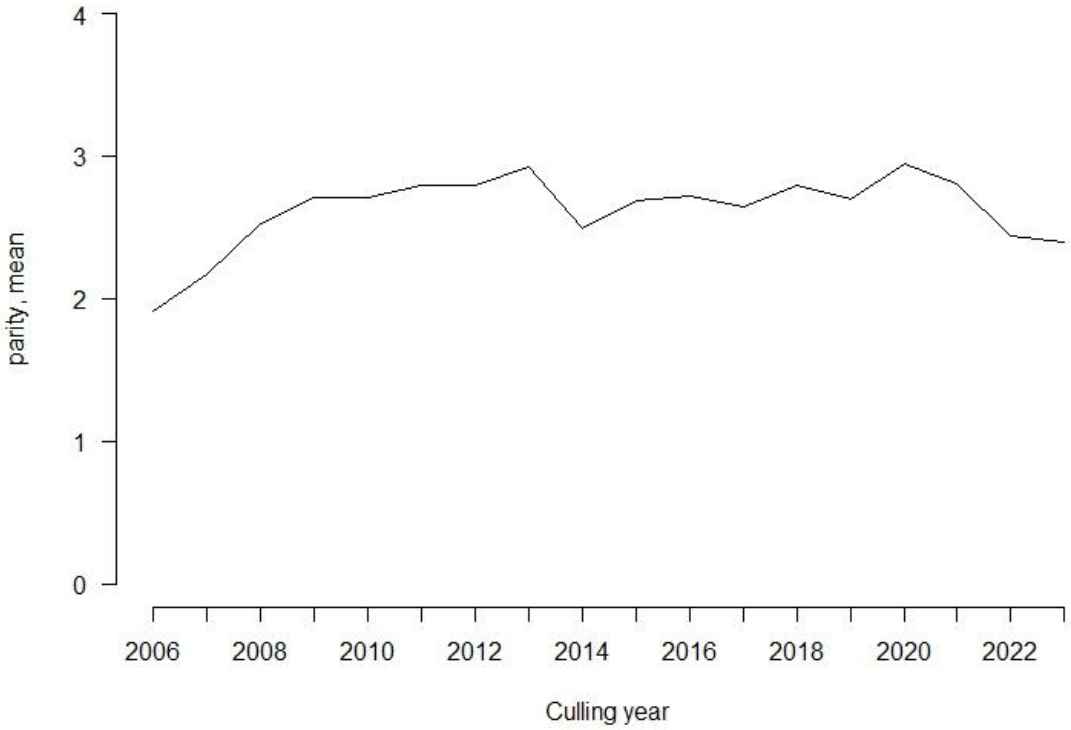

Figure 2 - Phenotypic trend of average lactations across year of disposal.

The second analysis was about descriptive statistics for all the traits, and they can be seen in Table 2. Regarding stayability traits, the average percentage of alive cows at 2nd, 3rd and 4th lactations were those reported in the stayability curve, with the corresponding values of 1 for alive animals and 0 for culled ones. On average, animals in the dataset had the first calving at 25.85months, with 28.46% of animals that calved before 23months. Approximately 50% of the cows calved for the first time

between 24 and 28months, and 21% of them calved after 29months. Moreover, 24months of AFC was the mode of distribution. At first lactation, cows produced 5634.89kg ± 1518.71kg of milk, with fat and protein levels of 4.97% and 3.91% respectively. Their type evaluation score for the traits reported in Table 2 were distributed in their possible range, from 1 to 50. In particular, the mean of each trait was close to the optimum for the character under investigation, that is 25 in linear score.

Table 2 - Statistical descriptive analysis for all the phenotypic traits.

trait	dataset	N	Mean[1]	SD	min	max
STAY2[a], %	D-vce	15,569	0.78	.	0	1
STAY3[a], %	D-vce	15,569	0.54	.	0	1
STAY4[a], %	D-vce	15,569	0.33	.	0	1
AFC[b], months	D-afc	15,550	25.85	3.52	17	36
milk, kg	D-p	14,534	5634.89	1518.71	24	9990
fat, %	D-p	14,534	4.97	0.63	2.25	8.97
fat, kg	D-p	14,534	276.59	74.35	6	656
protein, %	D-p	14,534	3.91	0.29	2.70	5.85
protein, kg	D-p	14,534	219.76	59.36	6	483
foot angle, linear score	D-m	9,706	25.09	6.32	2	46
fore udder attachment, linear score	D-m	9,706	24.37	6.65	1	47
rear udder height, linear score	D-m	9,706	27.72	6.09	2	49
udder support, linear score	D-m	9,706	27.97	6.75	1	50
udder depth, linear score	D-m	9,706	26.08	6.75	1	50

[1]: percentage of alive cows at each stayability trait, coded as 1 for alive and 0 for not alive; since SD was a measure related to an incidence, it could not be calculated.

[a]: stayability traits for parity 2, 3 and 4

[b]: age at first parity

Heritability and model comparison

Heritability and the phenotypic variance for each of the four animal models (M1g, M2g, M1t and M2t), with their standard deviations, are shown in Table 3 (see supplementary materials Table 3S for the entire table with lower and upper bounds of 95%). Comparing M1g vs M2g, heritability was found

higher in the latter compared to the former. Nevertheless, comparing M1t vs M2t, heritability was lower in the latter, whereas the sum of the variance components was higher in M2t. By nature, the categorical model gave on average higher heritability compared to the linear model, but also a higher phenotypic variance component; this is due to the different distributions of these scales (van Vleck 1972). This was confirmed in the present study. To avoid errors in interpreting the results, the heritability estimates from M1t and M2t were transformed to the observed scale. The results were very similar to those derived from M1g and M2g, with heritability for M1t of 0.058 for STAY2, and heritability for M2t of 0.026 for STAY2.

Table 3 - Heritability and standard deviation (SD) and phenotypic variation of contemporary group with standard deviation (SD) of the four different animal models, from stayability at 2nd to 4th lactation.

	Gaussian model				Threshold-liability model			
	M1g[1]		M2g[2]		M1t[3]		M2t[4]	
	h^2 (SD*)	herd effect (SD*)	h^2 (SD*)	herd_year effect (SD*)	h^2 (SD*)	herd effect (SD*)	h^2 (SD*)	herd_year effect (SD*)
STAY2[a]	0.051 (0.011)	0.050 (0.008)	0.094 (0.012)	0.041 (0.001)	0.112 (0.021)	0.097 (0.015)	0.051 (0.017)	0.231 (0.018)
STAY3[a]	0.099 (0.013)	0.081 (0.010)	0.101 (0.013)	0.123 (0.002)	0.159 (0.020)	0.137 (0.017)	0.084 (0.019)	0.264 (0.017)
STAY4[a]	0.128 (0.016)	0.079 (0.010)	0.110 (0.013)	0.152 (0.003)	0.208 (0.022)	0.150 (0.019)	0.116 (0.021)	0.294 (0.019)

M1g[1]: model with random effect of herd of first calving as contemporary group, Gaussian.

M2g[2]: model with random effect of herd_year of first calving as contemporary group, Gaussian.

M1t[3]: model with random effect of the herd of first calving as contemporary group, threshold-liability.

M2t[4]: model with random effect of herd_year of first calving as contemporary group, threshold-liability.

*: standard deviation

[a]: stayability traits for parity 2, 3 and 4

Afterwards, bull's rank correlations among breeding values obtained with the different models have been calculated with Spearman method (shown in Table 4). Almost all correlations were above 0.9, reaching the highest correlation at STAY4 among each comparison. Accounting for EBVs' reliability,

high correlations can be found in the same comparisons. Particularly, when increasing the stayability trait, the correlations become higher, reaching 0.994 in STAY4 (data not shown).

Table 4 - Bull's rank correlations between the four animal models.

	M1g[1] vs M1t[3]	M2g[2] vs M2t[4]	M1g[1] vs M2g[2]	M1t[3] vs M2t[4]
STAY2[a]	0.995	0.985	0.928	0.909
STAY3[a]	0.998	0.995	0.891	0.899
STAY4[a]	0.999	0.999	0.961	0.954

M1g[1]: model with random effect of herd of first calving as contemporary group, Gaussian.

M2g[2]: model with random effect of herd_year of first calving as contemporary group, Gaussian.

M1t[3]: model with random effect of the herd of first calving as contemporary group, threshold-liability.

M2t[4]: model with random effect of herd_year of first calving as contemporary group, threshold-liability.

[a]: stayability traits for parity 2, 3 and 4

Phenotypic and genetic correlations

Further, the phenotypic and genetic correlations between stayability traits and the other prementioned traits were investigated (Table 5). Looking at the dataset D-afc, the relationship between STAY and AFC was analysed. From a phenotypical point of view, correlations were quite stable over parities, remaining below −0.1; besides, genetic correlations had an average of −0.27, even though they did not result in significant values except for stayability in 4th lactation.

Table 5 - Phenotypic and genetic correlations, with their standard errors (SE), between age at first calving (AFC), productive traits, type traits and stayability traits.

	Phenotypic correlations			Genetic correlations*		
	STAY2[a] (SE)	STAY3[a] (SE)	STAY4[a] (SE)	STAY2[a] (SE)	STAY3[a] (SE)	STAY4[a] (SE)
AFC, months	-0.063 (0.008)	-0.069 (0.008)	-0.098 (0.010)	-0.252 (0.236)	-0.248 (0.109)	**-0.242** (0.063)
milk, kg	0.227 (0.014)	0.130 (0.010)	0.072 (0.011)	**0.722** (0.036)	0.129 (0.121)	-0.058 (0.098)
fat, %	-0.033 (0.013)	-0.011 (0.010)	0.007 (0.011)	**-0.919** (0.020)	-0.090 (0.112)	0.072 (0.091)
fat, kg	0.239 (0.013)	0.129 (0.011)	0.075 (0.011)	**0.139** (0.060)	0.174 (0.131)	0.002 (0.111)
protein, %	-0.033 (0.012)	-0.004 (0.010)	0.004 (0.010)	**-0.792** (0.030)	-0.197 (0.106)	0.052 (0.088)

protein, kg	0.243 (0.013)	0.134 (0.010)	0.075 (0.011)	**0.483** (0.051)	0.126 (0.125)	-0.027 (0.104)
foot angle	0.048 (0.010)	0.056 (0.010)	0.041 (0.010)	0.208 (0.165)	**0.309** (0.156)	0.277 (0.149)
fore udder attachment	0.059 (0.010)	0.080 (0.010)	0.056 (0.010)	**0.432** (0.142)	**0.499** (0.117)	**0.325** (0.119)
rear udder height	0.039 (0.010)	0.055 (0.010)	0.039 (0.011)	0.276 (0.167)	**0.461** (0.133)	0.104 (0.156)
udder support	0.036 (0.010)	0.055 (0.010)	0.041 (0.011)	0.253 (0.156)	**0.316** (0.135)	-0.010 (0.155)
udder depth	0.289 (0.240)	0.076 (0.010)	0.094 (0.014)	**0.426** (0.107)	**0.468** (0.093)	**0.409** (0.096)

*In bold significant genetic correlations that lie within the 95% probability density interval.

[a]: stayability traits for parity 2, 3 and 4

With regards to the dataset D-p with phenotypes for milk, fat and protein yield, fat and protein percentage, the genetic and phenotypic correlations between production at first lactation and stayability traits were calculated as previously described. Phenotypically, there was a medium-low correlation between milk and stay-n, which tended to decrease as parities progress; moreover, a very similar trend was followed by fat and protein kilogram content. However, fat and protein percentages had zero or very low correlation. These findings were partially supported by the genetic correlations: in STAY2 all correlations were strong and significant, while in STAY3 and STAY4 they weakened and lose importance.

Considering the dataset D-m for type traits, phenotypic values were not constant in the different stayability tests, varying from −0.04 to 0.29 according to the type trait. Fore udder attachment and udder depth were the highest positively correlated traits with stayability, while other traits presented weak correlations. On the contrary, genetic correlations presented some traits moderately correlated, i.e. fore udder attachment and udder depth for STAY2, foot angle, fore udder attachment, rear udder height, udder support and udder depth in STAY3, fore udder attachment and udder depth for STAY4. Overall, fore udder attachment and udder depth were the most strongly correlated traits with

stayability, with positive correlations between 0.325 and 0.499. The remaining traits did not show relevant correlations with stayability; thus, they were not reported in Table 5. For complete phenotypic and genetic correlations, with lower and upper bounds of all traits, include those not shown, consult Table 5S in supplementary materials.

Bulls' daughter's stayability rate

Regarding bulls' DSR, results for STAY4 of the M2g model were the following: for low EBVs' bulls, the DSR was 21.79%, for medium EBVs' bulls, the DSR was 34.94% and for high EBVs' bulls, the DSR was 45.50% (data not shown). Furthermore, the correlation between DSR and the bull's EBV at STAY4 was 0.67.

Discussion

Longevity in dairy cattle has been widely studied, but it is still under investigation since its great impact on farm economics (Langford and Stott, 2012) that can arrive at $2.50 of breeding costs per day (Hutchison et al., 2017). In Italy, Brandts et al. (1996) estimated an economic value for involuntary culling (IC) and herd life (HL) for Italian Holstein, showing 3.61 euro per one point of percentage of IC and 0.59 euro per day of HL. In the present study, we aim to investigate the aspects that may affect this economic incidence; however, we did not determine its real incidence for Jersey, but we did prepare the basis for a possible future study.

Stayability curve

Phenotypically, Italian Jersey showed a stayability rate that reached 50% of culled cows after the third lactation. These results were slightly different from those reported by Khansefid et al. (2021) for Australian Jersey, but similar to those of Hare et al. (2006) for American Jersey, which found, respectively, 53.2% of culled cows at the fourth lactation and 55.5% of culled cows at the third lactation. Moreover, the Italian average herd life resulted in 3.05 years compared to 4.11 of Australian Jersey, and an annual replacement rate of 31.8%. This information suggested that reaching the fourth lactation could be used as a breeding objective in our stayability approach. Furthermore, we found no

significant trend during the years according to average stayability age. This could be explained mostly by the fact that no selective pressure, based on breeding values, has been applied to this trait. Notably, this phenotypic stability occurred despite the increase in milk production levels over the last two decades. Although high milk yields are typically phenotypically antagonistic to survival traits, this potential negative impact was likely mitigated by continuous advancements in dairy nutrition, transition cow management, and overall animal welfare. Additionally, specific management factors characteristic of the Italian dairy sector must be considered. Even though officially recorded animals increased in the last years (7,025 cows in 2022, source AIA – Italian Breeders Association), the majority of multi-breed Italian farms have only a few Jersey cows compared to Holstein. Indeed, on average there are less than 9 cows/herd of Jersey breed and only a few farms are 100% Jersey. This structural setup can lead to preferential treatment in favour of Jersey cows; for instance, a Jersey cow may be retained in the herd under health or reproductive circumstances where a Holstein counterpart would otherwise be culled, effectively extending the phenotypic longevity of the breed over the years.

Heritability and correlations between stayability traits

Heritability for stayability was quite low, yet in line with those reported by other works (Schuster et al. 2020; Hardie et al., 2021, Khansefid et al., 2021; Nascimento et al., 2023), ranging from 0.02 to 0.20. Particularly, in our work, we found a heritability of 0.094 ± 0.001 for stayability at the second lactation, after second estimate with prior method. Consistently with the findings of Heise et al. (2016), we found increasing heritability from STAY2 to STAY4. Different methods can be used to analyse this trait since limited differences will be generated, as reported by Holtsmark et al. (2009). Here, linear and categorical models both gave similar results and had almost unity bulls rank correlations. Despite the different scales of Gaussian and threshold-liability models, bull's ranks were similar, and little re-ranking was observed. This implies that a linear multiple-trait model could be proposed for its ease of implementation. Furthermore, accounting for the contemporary group, the two models that included a time-linked effect (M2g and M2t) seemed preferable to avoid bias due to different years. The parameters estimated with the M2g model reflect true longevity rather than

functional longevity, as the model was not adjusted for production traits. In major dairy breeds, correcting for milk yield is standard practice; however, due to the limited number of Jersey cows per herd in Italy, contemporary groups were too small to support additional production-related fixed effects. Additionally, the approach of treating production as an alternative random effect was avoided, since the addition of a second random factor for production within such small cohorts would result in collinearity between the two random effects. Consequently, the decision to maintain the model in its original state provided the most reliable and computationally stable framework for the genetic parameters of this population. All that considered, M2g was eventually chosen for a national selection index, thus for all the following analysis.

Phenotypic and genetic correlations with other phenotypes

Despite different studies (Sherwin et al., 2016; Hutchison et al., 2017; Boothby et al., 2020; Pytlewski and Antkowiak, 2021; Hardie et al., 2021) found relevant genetic correlations between AFC and longevity traits in dairy cattle, in our study genetic correlations were not significant, excepted with STAY4. This could suggest that genetically other traits may affect the stayability of cows, but also that this trait is more likely to influence the length of productive life (not investigated in this study) instead of the stayability of a cow. These results could also mean that AFC influences only late stayability while is not relevant for cows during the first two or three lactations.

Genetic correlations found with milk yield were in line, or slightly higher, with those reported by Khansefid et al. (2021), while fat and protein percentages had a negative correlation with stayability. This could suggest that more productive animals are those who are likely to survive more, but those with higher milk solid components are more susceptible to early culling, probably due to a higher negative balance on lactation. Furthermore, this negative association became null when passing to STAY3 and STAY4; this can be explained by high requirements in the first lactation to which cows are not prepared. These results agreed also with culling causes described by Norman et al. (2022), who found low production to be one of the main reasons for culling Jersey cows.

Lastly, accounting for morphological traits, the most correlated traits with all the single stayability were fore udder attachment and udder depth; in addition, foot angle and rear udder height resulted significantly but less strongly correlated with STAY3. A variety of papers explore the relationship between type traits and longevity in dairy cattle (Setati et al., 2004; Sewalem et al., 2004; Caraviello et al., 2004; Williams et al., 2022; Khansefid et al., 2021; Nascimento et al., 2023), and all confirmed the positive association with longevity and some relevant type traits, specifically for udder attachment and udder depth. In our study, other traits had no significant correlation with longevity; this could derive from the low number of records considered after the editing.

Bulls' daughter's stayability rate

A high correspondence of 0.67 between daughters' stayability at STAY4 and sires' EBV was found; this implies that the genetic model used was quite strong and that selecting high genetic merit bulls will likely enhance population longevity. In addition, DSR for STAY4 in M2g was 45.5%; this means that, on average, 45.5% of the daughters of a high genetic merit bull survive to the 4th lactation while only the 21.79% of the daughters of low genetic merit bulls reach this goal. However, the correlation is not 1, thus further implementation in the future could lead to a better selection.

Conclusion

In conclusion, the stayability approach to evaluate a genetic selection routine for Italian Jersey longevity can be used. Despite the binary nature of this trait, EBVs can be calculated with linear model with almost the same performances but with less routinely efforts. National selection for longevity will be enhanced using this trait, resulting also in an indirect positive selection for milk production and for some morphological traits. Increasing cow longevity, but even more reducing involuntary culling, will decrease negative health impact, increase the profitability of the cow, improve animal welfare and farmer's wellbeing, contributing to the sustainability of the dairy sector. However, a forced increase in longevity, without adjustments to the health and structural management of farms, could lead to negative effects, such as increasing the incidence of diseases and the slowdown

of genetic progress. Consequently, production traits should also be taken into account when considering a genetic evaluation for longevity to avoid economic losses. Provided that, it is necessary to have a holistic and complete approach to all the social, environmental and economic components, evaluating them in one's own business reality, which is not necessarily the same for all farmers.

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Supplementary materials

Table 3S - Heritability and phenotypic variation of contemporary group, with their confidential intervals, of the four different models, from stayability at 2nd to 4th lactation.

	Gaussian model				Threshold-liability model			
	M1g[1]		M2g[2]		M1t[3]		M2t[4]	
	h^2 (C.I.)	herd effect (C.I.)	h^2 (C.I.)	herd_year effect (C.I.)	h^2 (C.I.)	herd effect (C.I.)	h^2 (C.I.)	herd_year effect (C.I.)
STAY2	0.051 (0.030; 0.071)	0.050 (0.033; 0.064)	0.094 (0.069; 0.116)	0.041 (0.040; 0.043)	0.112 (0.073; 0.152)	0.097 (0.070; 0.127)	0.051 (0.018; 0.083)	0.231 (0.195; 0.265)
STAY3	0.099 (0.074; 0.124)	0.081 (0.062; 0.102)	0.101 (0.077; 0.124)	0.123 (0.119; 0.127)	0.159 (0.118; 0.196)	0.137 (0.105; 0.169)	0.084 (0.046; 0.119)	0.264 (0.229; 0.296)
STAY4	0.128 (0.100; 0.160)	0.079 (0.058; 0.097)	0.110 (0.086; 0.134)	0.152 (0.148; 0.157)	0.208 (0.165; 0.250)	0.150 (0.112; 0.184)	0.116 (0.074; 0.156)	0.294 (0.254; 0.329)

M1g[1]: model with random effect of herd of first calving as contemporary group, Gaussian.

M2g[2]: model with random effect of herd_year of first calving as contemporary group, Gaussian.

M1t3: model with random effect of the herd of first calving as contemporary group, threshold-liability.

M2t4: model with random effect of herd_year of first calving as contemporary group, threshold-liability.

Table 5S - Phenotypic and genetic correlation, with their confidential intervals, between age at first calving (AFC), productive traits, type traits and stayability traits.

	Phenotypic correlations			Genetic correlations*		
	STAY2	STAY3	STAY4	STAY2	STAY3	STAY4
AFC, months	-0.063 (-0.079; -0.049)	-0.069 (-0.084; -0.054)	-0.098 (-0.199; -0.080)	-0.252 (-0.657; 0.232)	-0.248 (-0.466:-0.048)	**-0.242** (-0.366; -0.124)
milk, kg	0.227 (0.199; 0.252)	0.130 (0.110: 0.150)	0.072 (0.050; 0.091)	**0.722** (0.645; 0.790)	0.129 (-0.119; 0.349)	-0.058 (-0.242; 0.131)
fat, %	-0.033 (-0.057; -0.008)	-0.011 (-0.033; 0.008)	0.007 (-0.017; 0.026)	**-0.919** (-0.952; -0.877)	-0.090 (-0.308; 0.129)	0.072 (-0.107; 0.250)
fat, kg	0.239 (0.212; 0.263)	0.129 (0.108; 0.148)	0.075 (0.055; 0.096)	**0.139** (0.019; 0.258)	0.174 (-0.092; 0.423)	0.002 (-0.225; 0.207)
protein, %	-0.033 (-0.056; -0.010)	-0.004 (-0.024; 0.015)	0.004 (-0.016; 0.024)	**-0.792** (-0.845; -0.728)	-0.197 (-0.409; -0.001)	0.052 (-0.114; 0.221)
protein, kg	0.243 (0.219; 0.269)	0.134 (0.113; 0.153)	0.075 (0.054; 0.095)	**0.483** (0.376; 0.580)	0.126 (-0.118; 0.362)	-0.027 (-0.237; 0.168)
stature	0.008 (-0.014; 0.024)	0.018 (-0.002; 0.037)	-0.012 (-0.031; 0.007)	-0.025 (-0.405; 0.341)	0.239 (-0.052; 0.547)	-0.070 (-0.292: 0.164)
chest width	0.011 (-0.009; 0.029)	0.020 (0.001; 0.043)	-0.009 (-0.030; 0.013)	-0.034 (-0.383; 0.345)	0.253 (-0.075; 0.573)	-0.067 (-0.326; 0.189)
body depth	0.011 (-0.008; 0.030)	0.016 (-0.005; 0.037)	-0.012 (-0.032; 0.011)	-0.017 (-0.410; 0.344)	0.235 (-0.103; 0.571)	-0.091 (-0.368; 0.202)
angularity	0.030 (0.008; 0.047)	0.026 (0.003; 0.044)	-0.009 (-0.031; 0.012)	0.119 (-0.252; 0.481)	0.267 (-0.076; 0.573)	-0.126 (-0.438; 0.195)
rump angle	-0.004 (-0.024; 0.014)	-0.004 (-0.023; 0.015)	-0.015 (-0.034; 0.006)	0.028 (-0.416; 0.448)	0.163 (-0.122; 0.500)	-0.070 (-0.331; 0.177)
rump width	0.026 (.007; 0.044)	0.035 (0.013; 0.053)	0.014 (-0.005; 0.036)	0.116 (-0.292; 0.501)	0.324 (-0.034; 0.642)	0.202 (-0.112; 0.508)

rear leg, side view	-0.046 (-0.065; -0.029)	-0.045 (-0.065;-0.025)	-0.041 (-0.062; -0.021)	-0.132 (-0.447; 0.258)	-0.168 (-0.491; 0.166)	-0.097 (-0.399; 0.198)
foot angle	0.048 (0.027; 0.065)	0.056 (0.034; 0.074)	0.041 (0.020; 0.060)	0.208 (-0.118; 0.533)	**0.309** (0.011; 0.590)	0.277 (-0.043; 0.541)
fore udder attachment	0.059 (0.040; 0.077)	0.080 (0.060; 0.100)	0.056 (0.036; 0.076)	**0.432** (0.144; 0.679)	**0.499** (0.270; 0.717)	**0.325** (0.061; 0.528)
rear udder height	0.039 (0.019; 0.056)	0.055 (0.034; 0.073)	0.039 (0.019; 0.058)	0.276 (-0.044; 0.603)	**0.461** (0.209; 0.704)	0.104 (-0.205; 0.406)
rear udder width	0.031 (0.011; 0.047)	0.029 (0.010; 0.047)	-0.002 (-0.023; 0.015)	0.159 (-0.167; 0.516)	0.262 (-0.034; 0.516)	-0.064 (-0.372; 0.208)
udder support	0.036 (0.017; 0.054)	0.055 (0.033; 0.073)	0.041 (0.019; 0.060)	0.253 (-0.036; 0.567)	**0.316** (0.048; 0.579)	-0.010 (-0.332; 0.286)
teat placement	0.027 (0.006; 0.044)	0.035 (0.014; 0.053)	0.041 (0.020; 0.062)	0.240 (-0.062; 0.553)	0.163 (-0.130; 0.421)	0.099 (-0.206; 0.354)
udder depth	0.289 (-0.255; 0.638)	0.076 (0.054; 0.094)	0.094 (0.066; 0.121)	**0.426** (0.214; 0.624)	**0.468** (0.287; 0.640)	**0.409** (0.207; 0.584)

*In bold significant genetic correlations that lie within the 95% probability density interval.

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Chapter 3:
Genetic parameter estimations for different stayability approaches in the Italian Holstein cattle population

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Introduction

The aim of the paper presented in this chapter was to evaluate different approaches for longevity selection by estimating genetic parameters for stayability in the Italian Holstein population. The investigation conducted served as baseline for the review of the genetic model in use at the moment of the writing. Indeed, the genetic evaluation in question employs a statistical methodology that has been described by Ducrocq (1988), who developed a Survival Analysis approach. Despite the advantages of this approach, the application of survival analysis in the era of genomics and large-scale data processing faces severe limitations. The implementation of survival models, particularly those attempting to incorporate a full animal model, requires substantial computational resources. Secondly, as suggested by different authors, genetic trends from a Weibull survival model seemed to be overestimated for young sires with a high amount of censored daughter information (Sewalem et al., 2005; Heise et al., 2016). Moreover, the software in question had not been in-house developed, and thus might be considered a black box. Consequently, a need to renovate the genetic evaluation and the genetic parameters estimation was identified. In this context, we focused on comparing different longevity selection approaches to determine which could better fit the needs of extending a cow's life.

Abstract

The debate on the optimal herd life for dairy cows involves balancing the need to maximise herd life while sustaining genetic progress. Since cows typically reach their economic 'break-even point' only after their second or third lactation, adequate longevity is fundamental to farm sustainability. As selection for longevity can be challenging in the context of dairy breeding programs, the objective of this study is to evaluate different approaches for longevity selection by estimating genetic parameters for stayability in the Italian Holstein population. The investigation was conducted into four different modelling approaches, with eighter single-trait or multi-trait analyses, and both using Gaussian or threshold-liability models. The present study investigated three traits: stayability from first to second,

from second to third, and from third to fourth calving. Phenotypically, longevity showed an average of 2.8 lactations and a 35.99% replacement rate; moreover, at the beginning of the third lactation, less than 50% of the cows were still alive. The heritability estimates ranged from 0.024 ± 0.02 to 0.172 ± 0.08, depending on the approach and the model used. Genetic correlations between traits were strong, underlying the relevant relationship between those traits. Furthermore, sire rank correlations across models and approaches were computed: correlations between linear and threshold approaches ranged between 0.941 and 0.995, while those between single and multiple trait evaluations ranged from 0.644 to 0.879. Our findings indicate that the statistical model to be preferably adopted involves adjusting for voluntary culling, that is for low production, in combination with a multi-trait evaluation that considers genetic correlations. At the same time, Gaussian or threshold-liability approach can be utilised with equal efficacy.

Material and Methods

Data and edits

For this study, records on the Italian Holstein population were provided by the Italian Holstein, Brown Swiss and Jersey Association (ANAFIBJ, Cremona, Italy). We considered only Holstein cows born in Italy after the year 1984, for which the first calving was recorded. To ensure the continuity of lactation data, cows that changed their herd or with non-consecutive lactation histories were removed from the dataset. Furthermore, only cows showing their first test day until 60 days after calving and with their first calving before 37 months of age were retrieved. Moreover, cows with more than 11 test days between two calvings were discarded. As the standard test day recording is conducted on a five-week basis, and the August recording is frequently absent, this condition was necessary to ensure the absence of missing calving recordings. Cows showing an ongoing lactation at the time of data extraction were flagged as censored for that lactation number.

Calving records were used to determine different stayability traits. Stayability traits were labelled as STAY12, STAY23, STAY34, respectively for first to second calving, second to third calving, third to fourth calving. Considering that stayability is a binary trait, it was coded as ‘1’ to indicate animals

that showed survival success, and '0' otherwise.

The statistical models included two fixed effects: herd size change (**HSC**) and the difference in milk production deviation (**DM**). The HSC was calculated as the percentage difference between the number of animals in the current calving year compared with the previous year. The DM was calculated for each cow as the standardized deviation from its contemporary group (CG) average, expressed in standard deviation units. The CG itself, defined as the combination of herd and year of calving, was included in the model as a random effect.

The HSC effect was defined in 7 classes. On one side, the total number of cows (**n_cows**) for each contemporary group was calculated; on the other, the average number of cows (**m_cows**) and the number of consecutive calving years in the history of each herd (**n_years**) were defined. Herds with less than 4 consecutive calving years (n_years) and less than 6 animals on average (m_cows) were discarded. This information was merged to achieve a dataset where n_cows, m_cows and n_years were available. A progressive number was then given to each herd beginning on its first activity year. After that, we compared n_cows in a specific contemporary group with that of the same herd in the previous year, to assess whether there were differences in the number of cows (**d_cows**); for herds with a progressive number equal to 1, d_cows was set to 0 because no difference could be calculated with the previous year. Finally, **diff** was calculated as the percentage ratio between d_cows and n_cows for each CG. Classes of herd size change were coded as follows: for herds that did not fulfil the initial editing requirements, that is at least 4 n_years and 6 m_cows, class 1 was assigned. Class 2 was assigned for herds with no prior records to compare; classes 3 to 7 were given according to the degree of the percentage change, where 3 stood for a big negative percentage and 7 for a big positive percentage. Specifically, classes had the following thresholds: diff lower than -50% for class 3, diff between -50% and -15% for class 4, diff between -15% and +15% for class 5, diff between +15% and +50% for class 6, diff greater than +50% for class 7. As final editing, all herds that failed to have valid data in consecutive years were deleted.

The DM effect was partitioned into 10 discrete classes based on the animal's standardized milk

production deviation (**devm**) from its CG mean, expressed in phenotypic standard deviation units. Herds with fewer than 2 animals (**n_cows**) were discarded. Consequently, class 1 was assigned as a missing-data category for animals that lacked a valid CG within their herd, preventing their exclusion from the wider dataset. The remaining animals were assigned to classes 2 through 10 according to their devm thresholds: class 2 for devm lower than -1.5, class 3 for devm between -1.5 and -1, class 4 for devm between -1 and -0.6, class 5 for devm between -0.6 and -0.3, class 6 for devm between -0.3 and < +0.3, class 7 for devm between +0.3 and +0.6, class 8 for devm between +0.6 and +1, class 9 for devm between +1 and +1.5, and class 10 for devm greater than +1.5. Class 1 was assigned to the animals that had no CG in their herd and had consequently been excluded from previous allocations.

These edits generated the first dataset, which has been used to estimate the breeding values for the population, referred to as **D-1**. Descriptive statistics were generated on this dataset, including a survival curve, the proportion of culled animals across parity, the survival rate for each lactation as the average percentage of survived cows, the average herd life (the average number of lactations from first calving to culling), and replacement rate (the annual percentage of herd replaced, assuming a calving interval of 365 days).

For Variance Components Estimation step (**VCE**), an additional editing was applied, generating a smaller dataset referred to as **D-2**. In this case, we considered only cows that presented valid records for type traits, body condition score (**BCS**), test days with somatic cell count (**SCC**), and milk production (**MY**). All these traits were recorded during routine national data collection under the test-day model. MY was considered as the conventional 305-d production, and it referred to the first lactation only. Ensuring data completeness for production, health, and morphology guaranteed that only cows from herds integrated into official national herd-testing programs were retained, thereby ensuring a highly reliable and stable data baseline for stayability estimation. Additionally, all classes with a frequency of fewer than 100 observations were combined with the most closely class related to them. Particularly, for HSC, classes 2 and 3 have been grouped with class 4 for all stayability traits;

for DM, class 1 was grouped with class 6, as they both express a measure of lack of difference from the mean. Each class of the two effects showed the probability of survival for animals in that class affected by the specific effect, taking HSC1 as the reference value.

Furthermore, to optimize genetic connectedness and ensure computational feasibility for the VCE step, an iterative data-filtering procedure was applied to the dataset. The thresholds utilized in this process refer to the cumulative number of animals across the entire historical timeframe of the dataset. The final data structure was achieved through successive filtering cycles, which restricted the sub-dataset to sires with at least 228 daughters and herds with at least 500 cows, ultimately yielding a subset containing fewer than 500 sires overall. Additionally, only cows that were born after 2004 and that were uncensored in their career were considered; in particular, cows included were those born before 2019 for STAY12, before 2018 for STAY23 and before 2017 for STAY34. As a result, for the VCE step, we retrieved the following data: 303,315 cows, 343 sires, and 238 herds for STAY12; 247,551 cows, 340 sires, and 230 herds for STAY23; and 153,393 animals, 335 sires, and 221 herds for STAY34. The pedigree obtained was of 640,251 for STAY12, 564,455 for STAY23 and 414,837 for STAY34.

For the forward-in-time validation, two ancillary datasets were generated. First, only records from cows reporting the first three lactations as complete were retained. Editing dataset D-2, the newly generated dataset was name **D-3** and included cows born before 2019 for STAY12, before 2018 for STAY23 and before 2017 for STAY34. Additionally, a further editing implied removing records with calving events occurred after 2012, defining dataset **D-4**. Therefore, cows with calving following this 2012 were designated as group B, and cows with previous calvings were designated as group A. Consequently, three groups of sires were identified: **bulls A**, which consist of bulls with only daughters in group A; **bulls B**, which consist of bulls with only daughters in group B; and **bulls AB**, which consist of bulls with daughters both before and after the threshold year 2012. The data set D-3 included 3,113 bulls and 550,398 cows in group A, 2,067 bulls and 724,951 cows in group B, and 2,924 bulls and 3,034,045 cows in group AB.

Statistical analysis

The estimates for variance components for four different models were obtained with single-trait analyses using the **D-2** dataset. Gaussian and threshold models were implemented as follows:

$$[1]\ \mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_p p + \mathbf{Z}_a a + e$$

and

$$[2]\ \boldsymbol{\lambda} = \mathbf{X}\beta + \mathbf{Z}_p p + \mathbf{Z}_a a + e,$$

where y is the linear vector of STAY traits and λ is the unobserved liability for STAY in threshold models; β is the vector associated to the fixed effects (specific to each class of traits); p is the vector of random effects for the CG, following as $p \sim N(0,\mathbf{I}\sigma^2_p)$; a is the vector of solutions for the animal additive genetic effect, assumed as $a \sim N(0,\mathbf{A}\sigma^2_a)$, where **A** is the pedigree-based relationship matrix and σ^2_a the additive genetic variance; e is the vector of residual error values, assumed as $e \sim N(0,\mathbf{I}\sigma^2_e)$, where ***I*** is the identity matrix and σ^2_e is their variance. $\mathbf{X}$, $\mathbf{Z}_p$, $\mathbf{Z}_a$ are the respective incidence matrices for the fixed and random effects.

To identify the models, the following notation was defined. The designation M1 was used for the models that did not include any fixed effect; M2 for models that included HSC as fixed effect t; M3 for models that included DM as fixed effect; M4 was used for models that included both HSC and DM. Additionally, the designation Mg was used for the Gaussian approach, while Mt was used for the threshold-liability approach. Thus, the models were labelled M1g (M1, Gaussian), M1t (M1, threshold-liability), M2g (M2, Gaussian), M2t (M2, threshold-liability), M3g (M3, Gaussian), M3t (M3, threshold-liability), M4g (M4, Gaussian), M4t (M4, threshold-liability).

Because multi-trait models facilitate the simultaneity of analysis of multiple correlated traits, genetic correlations between stayability traits were estimated. Accordingly, two-trait models, with the same fixed and random effects as described above, were used to fit (co)variance components. Indeed, the Gibbs sampling was implemented in a Bayesian framework, with the assumptions of null means and normal univariate or bivariate prior distributions for CG, additive genetics and residual effects. Since CG was defined as trait-specific, covariances for this effect couldn't be estimated. Here, the matrix

notation applied was:

$$\mathbf{G} = \begin{vmatrix} \sigma^2_{a1} & \sigma_{a1a2} \\ \sigma_{a2a1} & \sigma^2_{a2} \end{vmatrix};\ \mathbf{P} = \begin{vmatrix} \sigma^2_{p1} & 0 \\ 0 & \sigma^2_{p2} \end{vmatrix};\ \mathbf{R} = \begin{vmatrix} \sigma^2_{e1} & 0 \\ 0 & \sigma^2_{e2} \end{vmatrix}$$

where **G** is the matrix of additive genetic (co)variances σ^2_{a1}, σ^2_{a2} and σ^2_{a1a2} of traits one and two, **P** is the matrix of (co)variances of the CG random effect σ^2_{p1}, σ^2_{p2} and σ^2_{p1p2} of traits one and two, and **R** is the matrix of residual (co)variances σ^2_{e1} and σ^2_{e2} of traits one and two. Residual covariances were fixed to '0' for inherent difficulties in their estimation. Since all records with '0' for a STAY trait in a given parity order will have missing values for the STAY trait in the following parity order, covariance at the level of the statistical unit cannot be calculated. For instance, all records (cows) with '0' values for STAY12 will have missing values for STAY23.

Variance Components and Fixed Effects Estimation

The pedigree of cows with phenotypes was traced back to at least 4 generations. Unknown parents were assigned to phantom parent groups based on animal origin and year of birth (142 genetic groups), as described by Famula et al. (1983). The analysis followed a two-step procedure using the THRGIBBS1F90 software (Misztal et al., 2014). First, variance components were estimated with 130,000 iterations, a burn-in of 30,000 and a thinning interval of 20. Subsequently, to obtain the fixed effect solutions, a separate analysis was implemented in THRGIBBS1F90 by fixing the variance components to the posterior means obtained from the estimation step. The post-Gibbs analysis was performed with the software POSTGIBBSF90 (Misztal et al., 2014). Convergence was assessed by visual inspection of the trace plots. The software uses flat priors for the variance components by default. An animal model was used; the additive genetic effect of the animal was fitted to the pedigree-based relationship matrix, and it was included as a random effect. The formula was applied to values obtained from each iteration of the Gibbs sampler, the posterior mean was used as an estimate, while the posterior standard deviation was used as an error.

Heritability (h^2) was calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_p^2 + \sigma_e^2} \quad [3]$$

Where σ_a^2 is the additive genetic variance, σ_p^2 is the CG effect variance and σ_e^2 is the residual variance. For h^2 estimated with the threshold models, a transformation from the underlying to the observed scale was made to make the results comparable. The formula used is the one from Dempster and Lerner (1950):

$$h_{obs}^2 = \frac{h_{und}^2 \; x \; z_{ord}^2}{p \; x \; (1-p)} \quad [4]$$

Where h_{obs}^2 is the heritability after the transformation on the observed scale, h_{und}^2 is the heritability on the underlying scale, z_{ord}^2 is the ordinate height of the normal distribution at the threshold point corresponding to p, and *p* is the prevalence of survived cows at different lactations.

Genetic correlations

Multiple-trait analysis permitted the estimation of the genetic correlation between traits through the implementation of two-trait models, as described in the "*Statistical analysis*" section. The genetic correlations followed the formula:

$$r_{a,ij} = \frac{\sigma_{a,ij}}{\sqrt{\sigma_{a,i}^2 * \sigma_{a,j}^2}}$$

where $\sigma_{a,ij}$ is the genetic covariance between the two considered traits in the bivariate analysis, and $\sigma_{a,i}^2$ and $\sigma_{a,j}^2$ are the additive genetic variances, respectively. In addition, the 95% highest probability density intervals were used to define significance, declaring $P<0.05$ when the value '0' was not included in the interval.

Bull's rank correlations among the solutions obtained in the different analyses have been calculated with the Spearman method, to assess the re-rank of animals.

Breeding values estimation and validation

The forward-in-time validation was carried out by comparing estimated breeding values (EBVs) produced by the Gaussian multi-trait models, using datasets D-3 (full data) and D-4 (partial data) for the three groups of bulls. The D-3 dataset was utilized to estimate the EBVs of 5,180 bulls and their

daughters. This estimation was performed using the GIBBSF90+ software (version 3.23; Misztal et al., 2002). The convergence of the iterative process was achieved after a number of iterations that ranged between 1,023 and 2,381, with final residuals ranging between 9.25 x 10^{-13} and 9.97 x 10^{-13}. With regard to the D-4 dataset for the same bulls but with partially masked phenotypes, it was found that convergence was achieved with 1,569-6,160 iterations, with final residuals ranging between 0.96 x 10^{-12} and 0.99 x 10^{-12}. To perform the validation, the EBVs obtained from the masked dataset (D-4) were compared against those from the full phenotypic dataset (D-3) using Pearson correlation coefficients. It should be noted that while simple Pearson correlations provide a reference point for conventional pedigree-based evaluations, they do not account for selection bias or the statistical shrinkage of low-accuracy sires toward the parent average. Although modern validation alternatives, such as the LR method or deregression techniques (VanRaden et al., 2009), are generally preferred in genomic validation frameworks, this classic forward-in-time correlation approach was considered sufficient to evaluate the operational consistency of the conventional routine.

Results

Phenotypic cow survival

The phenotypic stayability curve for the total population had a descending trend over parity, from the second lactation to the tenth, as shown in Figure 1. Particularly, at the beginning of the third lactation, there was less than 50% of the population that had survived. The averages incidence of alive cows at 2nd, 3rd, and 4th lactations were those reported in the stayability curve, calculated based on the corresponding values of 1 for alive animals and 0 for the non-alive ones (0.74, 0.48 and 0.27, respectively); since survival was a measure related to incidence, the standard deviation could not be calculated.

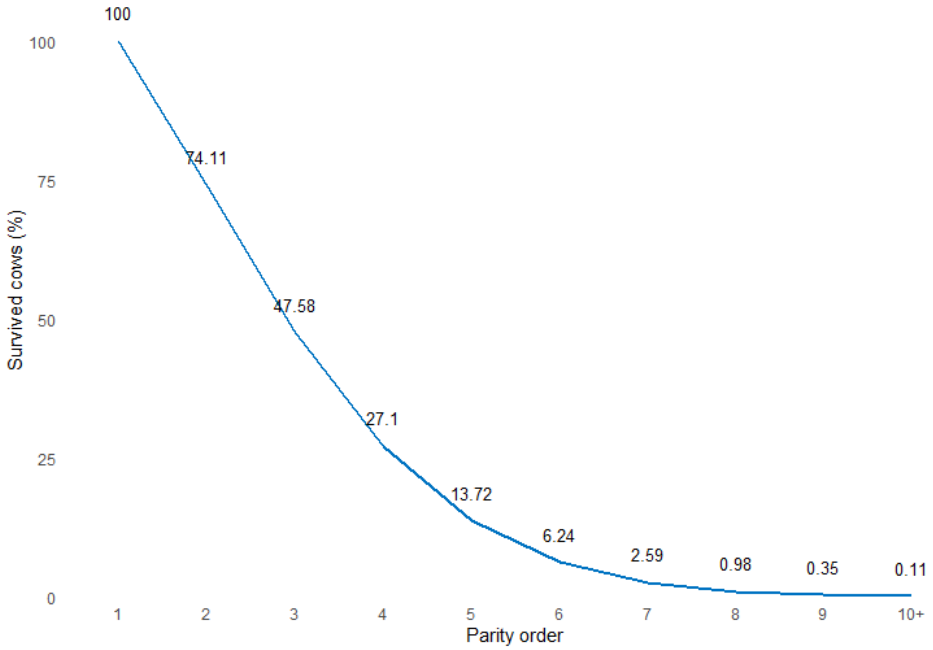

Figure 1 - Phenotypic survival curve for the Italian Holstein population, according to parity order; lactations greater than 10 are grouped (10+).

In addition, we calculated average herd life, as the average number of lactations from the first calving to culling, and the annual replacement rate (percentage of herd replaced, assuming a calving interval of 365 days), according to the culling year. The trend is shown in Figure 2: the average parity order reached was quite stable across years, with a small increase in the last years, reaching 2.85 in 2024. The mean results for herd life and replacement rate were 2.78 years and 35.99%, respectively.

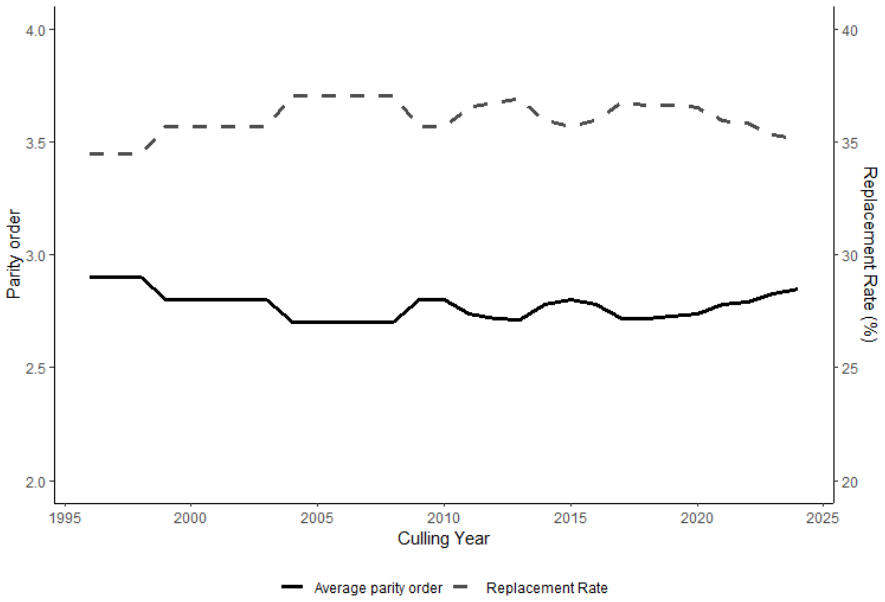

Figure 2 - Phenotypic average herd life, expressed as average parity order, and replacement rate for the Italian Holstein population, according to the culling year.

Fixed effects estimation

Accounting for fixed effects included in the statistical models, solutions estimated for HSC and DM are reported in Figures 3 and 4, respectively. The solutions reported were all estimated with the M4t model, on consideration of the binary nature of the trait, and are expressed on the probability scale. The number of observations for HSC effect varied from 246 for the least numerous class to 255,345 for the most numerous class (data shown in Table S1 of Supplementary Materials).

On the other hand, for the DM effect, the number of observations varied from 2,467 for the least numerous class to 98,550 for the most numerous (data shown in Table S2 of Supplementary Materials). For HSC, the smallest impact was observed in STAY12, while for DM, the least affected trait was STAY34. Indeed, STAY12 for HSC and STAY34 for DM had the highest probability of survival, with values higher than 0.98 for the former and values between 0.546 and 0.985 for the latter.

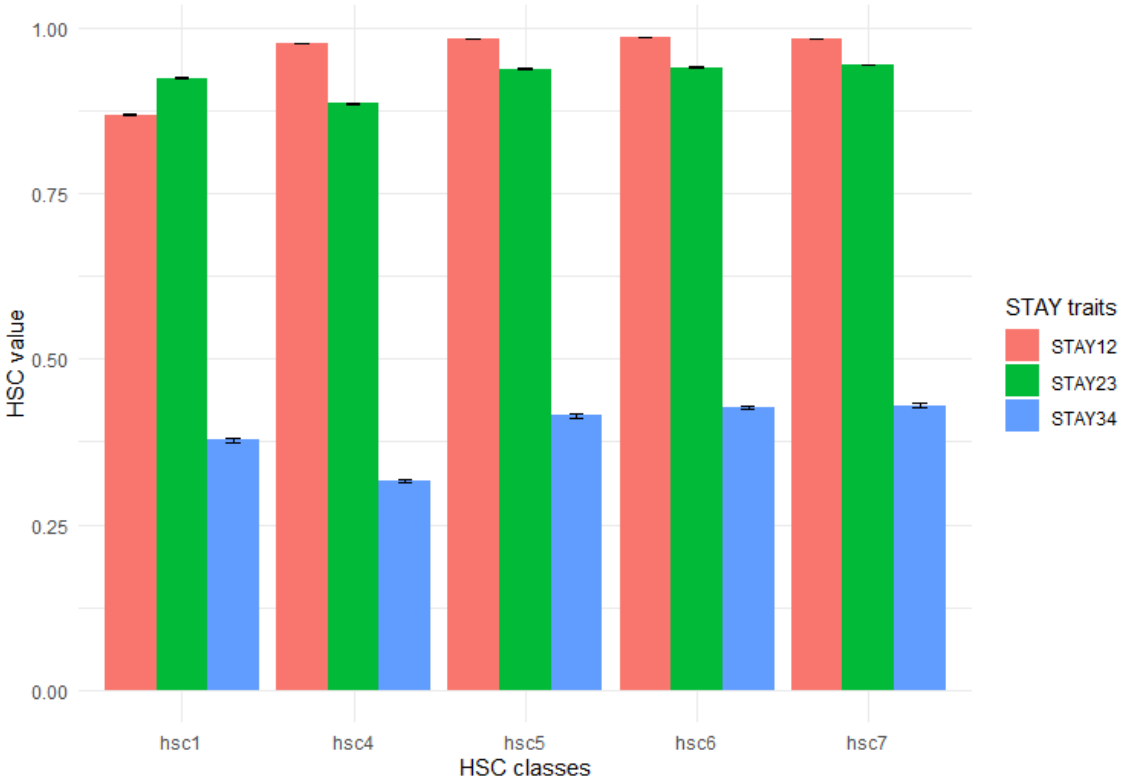

Figure 3 - Mean and confidential intervals (C.I.) for the 5 classes of herd size change (HSC), for the three stayability traits; classes 2-3 were grouped with class 4 due to low number of records.

Furthermore, the probability of a cow surviving shows a linear trend, with lower classes indicating a

lower probability of survival, with the most affected classes being those from 3 to 5 of DM for STAY23 and class 3 of DM in STAY12. The solutions for the HSC effect classes of STAY12 always demonstrated significance, while for STAY23 and STAY34, two distinct groupings were observed. Specifically, for STAY23, classes 3 and 6 exhibited no significantly different effects, while for STAY34, classes 3 and 6, and then 6 and 7, showed overlapping confidential intervals. Moreover, the DM effect exhibited a statistically significant increase in the probability of stayability, particularly for classes 2 to 6. In the case of STAY12, a partial overlap was identified between classes 7-10 and 9-10. Additionally, a larger number of intersecting categories was identified in all the higher classes for STAY23, leading to a greater number of overlaps between class 7 and 10. Similarly, the overlapping test for DM in STAY34 concluded that there were no significant differences in higher classes (from 7 to 10), while for the others, some differences were found.

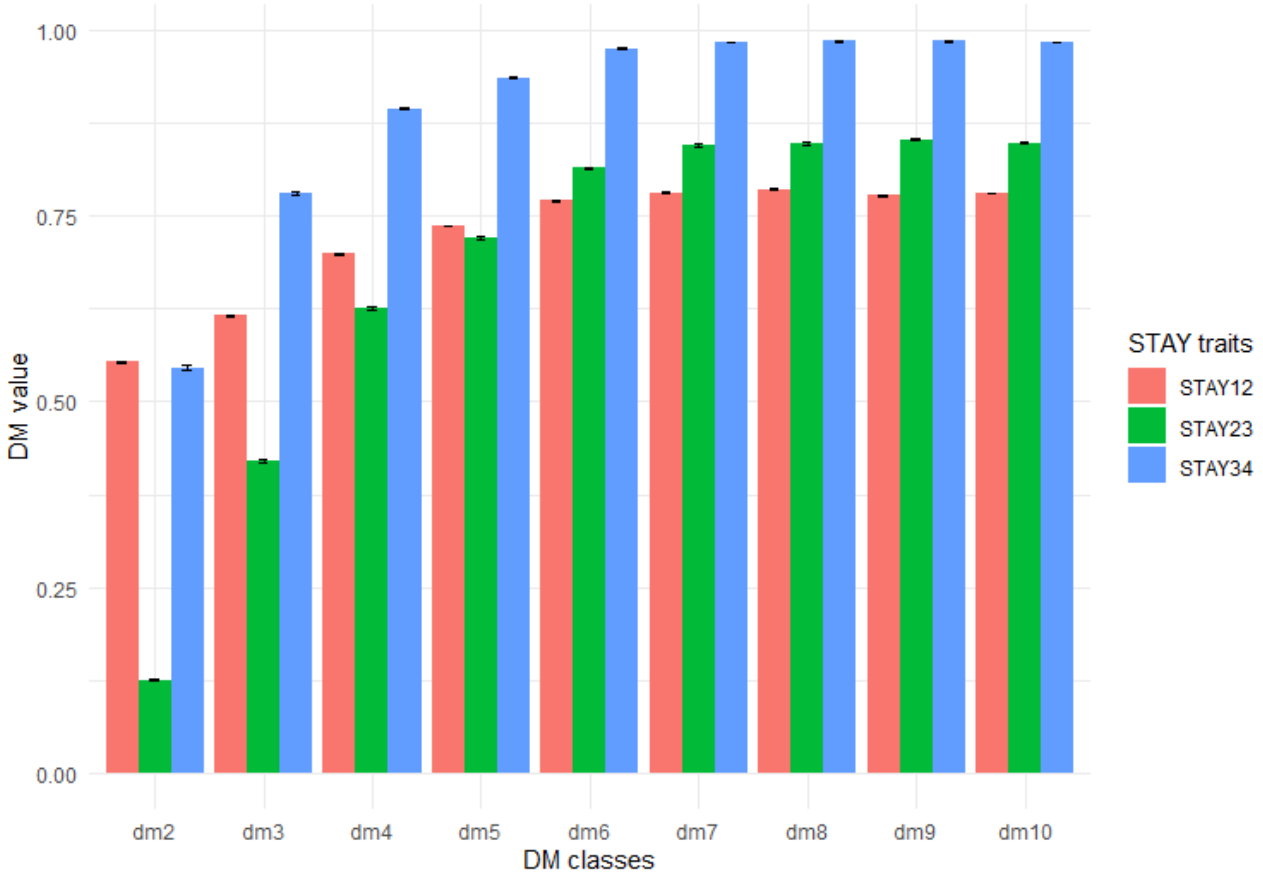

Figure 4 - Mean and confidential intervals (C.I.) for the 9 classes of difference of milk production (DM), for the three stayability traits; class 1 has been grouped with class 6, as they both express a measure of lack of difference from the mean.

Variance Components Estimation and heritability

Table 1 presents the heritability and variance proportions for the contemporary group across all models, including both Gaussian and threshold-liability approaches, for single-trait analysis. Within Gaussian or threshold-liability approaches, heritability increases from STAY12 to STAY34 in all the models, even though with different magnitudes. Between the Gaussian approaches, the highest heritability was found in M1 STAY34, and it was 0.044; similarly, in the threshold-liability approach, the highest heritability was also found in M1 and it was 0.064. Considering that categorical models gave on average higher heritability compared to linear models, due to the different distributions of these scales (van Vleck, 1972), the heritability estimates from threshold-liability models were transformed to the observed scale with the formula previously described [4]. This was computed to avoid errors in interpreting the results. In the Supplementary Materials, Tables S3 and S4, the transformed results are reported, for both single and multi-trait analyses. Comparing the observed heritability of Gaussian models and the transformed heritability of threshold-liability models, the differences lessened; however, threshold-liability models maintained a higher heritability for all traits, except for STAY34 in M1 and M2, where the transformed h^2 for threshold is lower than the observed for Gaussian. Accounting for the herd-year variance proportion, it increased from STAY12 to STAY34 in all the traits. Moreover, generally it was smaller than the genetic proportion in all the models, except for STAY23 and STAY34 in M3g, for STAY23 in M4g, and for STAY23 in M3t and M4t.

Partially similar results were found for the multi-trait models, which are presented in Table 2. All the models showed a higher heritability for STAY34 compared to STAY12 and STAY23, with values of 0.094 for M4g and 0.172 for M4t. Additionally, for the herd-year variance proportions, it increased from STAY12 to STAY34 in all the estimations, and it was always smaller than the genetic proportion. Comparing the observed heritability for Gaussian models and the transformed one for the threshold-liability models, little differences were observed, except for STAY12 in M2, all traits in

M3 and STAY12 in M4 (Table S4 in Supplementary Materials). Furthermore, for STAY34 in M2 and M3, the observed heritability of threshold models is lower than the Gaussian model.

Table 1 - Heritability with standard deviation (SD), and variance proportions of the contemporary group with standard deviation (SD) of models 1, 2, 3 and 4, from stayability at 2nd to 4th lactation, for single-trait evaluation.

	Gaussian model								Threshold-liability model							
	M1g[1]		M2g[2]		M3g[3]		M4g[4]		M1t[5]		M2t[5]		M3t[7]		M4t[8]	
	h^2 (SD)	herd_year effect (SD)	h^2 (SD)	herd_year effect (SD)	h^2 (SD)	herd_year effect (SD)	h^2 (SD)	herd_year effect (SD)	h^2 (SD)	herd_year effect (SD)	h^2 (SD)	herd_year effect (SD)	h^2 (SD)	herd_year effect (SD)	h^2 (SD)	herd_year effect (SD)
STAY12	0.025 (0.003)	0.019 (0.001)	0.024 (0.002)	0.018 (0.001)	0.026 (0.003)	0.020 (0.001)	0.025 (0.002)	0.019 (0.001)	0.049 (0.004)	0.035 (0.001)	0.054 (0.004)	0.035 (0.002)	0.056 (0.006)	0.038 (0.002)	0.053 (0.004)	0.037 (0.001)
STAY23	0.036 (0.003)	0.029 (0.001)	0.037 (0.004)	0.029 (0.001)	0.030 (0.003)	0.033 (0.001)	0.032 (0.004)	0.032 (0.001)	0.058 (0.004)	0.043 (0.002)	0.061 (0.005)	0.043 (0.002)	0.056 (0.005)	0.056 (0.002)	0.054 (0.005)	0.055 (0.002)
STAY34	0.044 (0.005)	0.029 (0.001)	0.039 (0.004)	0.029 (0.001)	0.031 (0.004)	0.034 (0.001)	0.035 (0.003)	0.033 (0.001)	0.064 (0.004)	0.043 (0.002)	0.062 (0.005)	0.042 (0.002)	0.062 (0.006)	0.059 (0.002)	0.062 (0.006)	0.058 (0.002)

M1g[1]: model with no fixed effects, Gaussian.

M2g[2]: model with HSC as a fixed effect, Gaussian.

M3g[3]: model with DM as a fixed effect, Gaussian.

M4g[4]: model with HSC and DM as fixed effects, Gaussian.

M1t[5]: model with no fixed effects, threshold-liability.

M2t[6]: model with HSC as a fixed effect, threshold-liability.

M3t[7]: model with DM as a fixed effect, threshold-liability.

M4t[8]: model with HSC and DM as fixed effects, threshold-liability.

Table 2 - Heritability with standard deviation (SD), and variance proportions of the contemporary group with standard deviation (SD) of models 1, 2, 3 and 4, from stayability at 2nd to 4th lactation, for multi-trait evaluation.

	Gaussian model								Threshold-liability model							
	M1g[1]		M2g[2]		M3g[3]		M4g[4]		M1t[5]		M2t[6]		M3t[7]		M4t[8]	
	h² (SD)	herd_year effect (SD)	h² (SD)	herd_year effect (SD)	h² (SD)	herd_year effect (SD)	h² (SD)	herd_year effect (SD)	h² (SD)	herd_year effect (SD)	h² (SD)	herd_year effect (SD)	h² (SD)	herd_year effect (SD)	h² (SD)	herd_year effect (SD)
STAY12	0.031 (0.004)	0.018 (0.001)	0.030 (0.002)	0.018 (0.001)	0.050 (0.003)	0.018 (0.001)	0.043 (0.003)	0.020 (0.001)	0.063 (0.004)	0.034 (0.001)	0.071 (0.004)	0.033 (0.001)	0.101 (0.006)	0.036 (0.001)	0.089 (0.005)	0.039 (0.002)
STAY23	0.047 (0.003)	0.028 (0.001)	0.046 (0.003)	0.028 (0.001)	0.068 (0.004)	0.031 (0.001)	0.075 (0.004)	0.039 (0.001)	0.077 (0.005)	0.042 (0.002)	0.072 (0.004)	0.042 (0.002)	0.117 (0.008)	0.052 (0.002)	0.121 (0.005)	0.068 (0.002)
STAY34	0.049 (0.002)	0.029 (0.001)	0.051 (0.003)	0.029 (0.001)	0.072 (0.005)	0.034 (0.001)	0.094 (0.005)	0.041 (0.002)	0.092 (0.006)	0.043 (0.002)	0.090 (0.004)	0.042 (0.002)	0.133 (0.009)	0.057 (0.002)	0.172 (0.008)	0.074 (0.003)

M1g[1]: model with no fixed effects, Gaussian.

M2g[2]: model with HSC as a fixed effect, Gaussian.

M3g[3]: model with DM as a fixed effect, Gaussian.

M4g[4]: model with HSC and DM as fixed effects, Gaussian.

M1t[5]: model with no fixed effects, threshold-liability.

M2t[6]: model with HSC as a fixed effect, threshold-liability.

M3t[7]: model with DM as a fixed effect, threshold-liability.

M4t[8]: model with HSC and DM as fixed effects, threshold-liability.

Subsequently, a comparison was made between single-trait and multi-trait analyses within models. In all the investigated traits, multi-trait analyses gave higher heritability compared to the single-trait estimations; at the same time, herd-year variance proportion remained comparable in all the traits, except for STAY23 and STAY34 of M4t, which resulted in higher variance in the multi-trait estimation.

Genetic correlations

Genetic correlations for stayability traits were estimated using the multi-trait equations, with the threshold-liability approach. In Figure 5, the genetic correlations for all models are reported. The correlations varied according to the model and the traits compared, and they ranged between 0.886 and 0.973. Nevertheless, a similar pattern was observed within the different comparisons: correlations between STAY12 and STAY34 were the lowest in all the models, while the highest was found between STAY23 and STAY34. Specifically, correlations between STAY12 and STAY23 were 0.929, 0.962, 0.953 and 0.941 for models M1t, M2t, M3t and M4t respectively; between STAY12 and STAY34, correlations found were 0.893, 0.886, 0.902 and 0.887 for the same models; correlations between STAY23 and STAY34 were 0.939 for M1t, 0.962 for M2t, 0.955 for M3t and 0.973 for M4t.

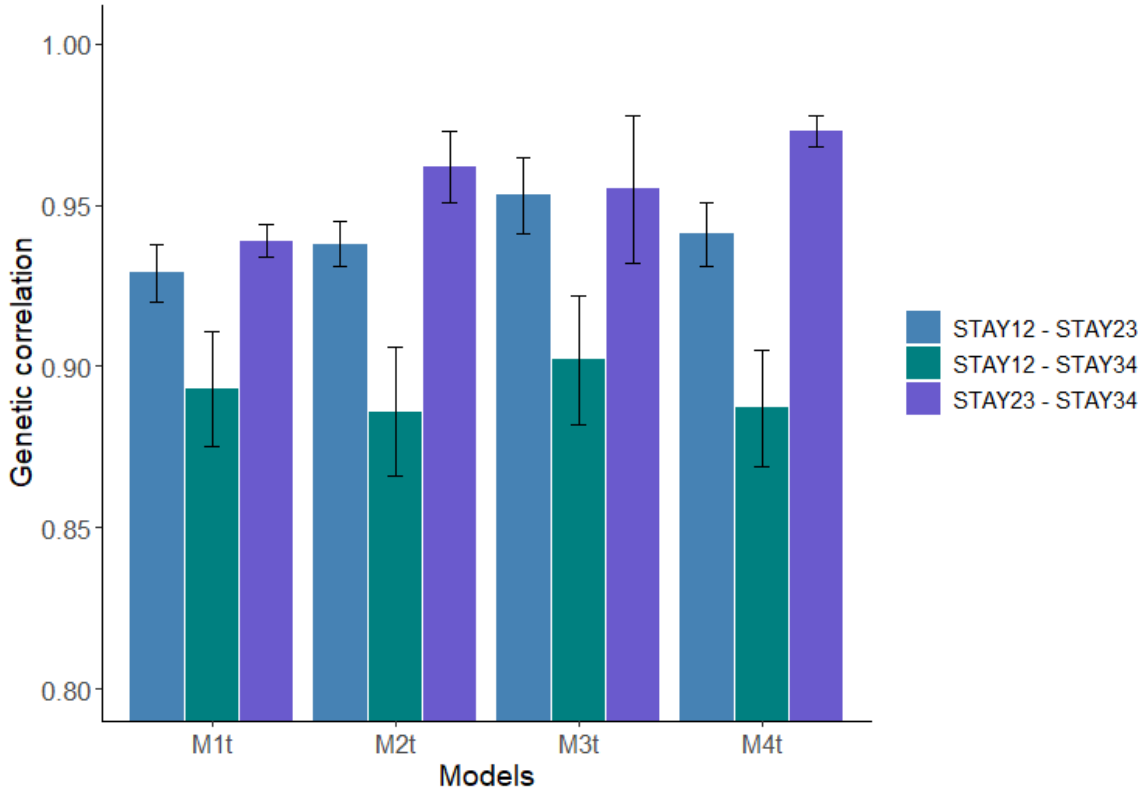

Figure 5 - Genetic correlations, with their standard errors, for stayability traits in M1t, M2t, M3t and M4t.

Sires' rank correlations

A comprehensive comparison between models is presented in the Figures 6-7. Models were tested for different pairings, and Spearman's rank correlations were calculated to evaluate bulls' rank.

As showed in Figure 6, the rank of the bulls exhibited robust positive correlations between the Gaussian and threshold-liability approaches, for both single-trait and multi-trait evaluations. In particular, the highest values were observed in model M4, with all correlations approximating 0.99. In contrast, the correlations observed in model M1 were the lowest, ranging from 0.941 to 0.991. Within the models, STAY23 displayed the highest correlations between Gaussian and threshold-liability approaches in nearly all models, except for M3 multi-trait, where the highest value was observed in STAY12.

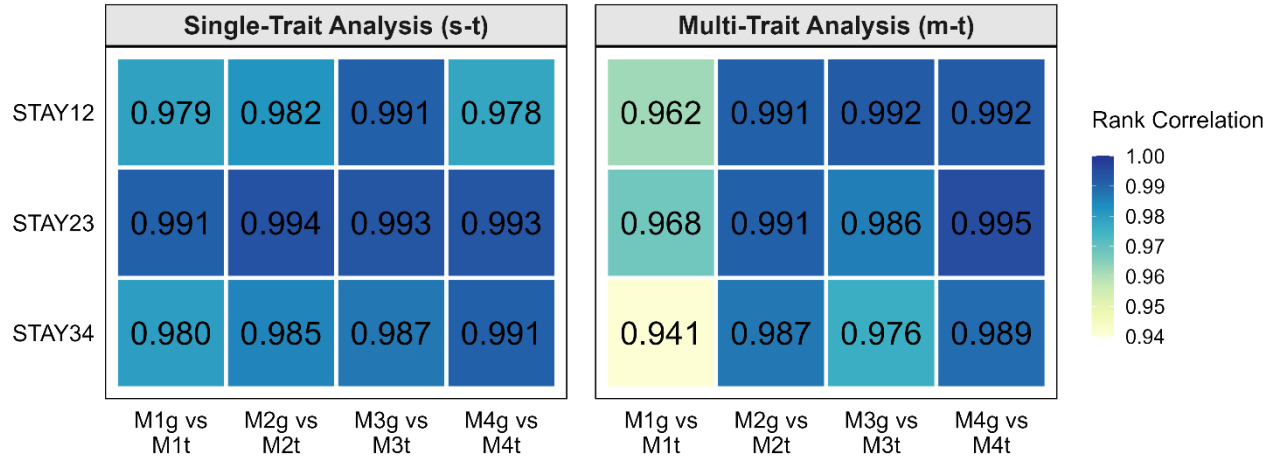

Figure 6 - Bulls' rank correlations for stayability traits, Gaussian (g) vs Threshold-liability (t) approach, in a single-trait (s-t) or multi-trait (m-t) analysis, for M1, M2, M3 and M4.

Regarding the performance of single-trait evaluation compared to multi-trait evaluations (Figure 7), Spearman's correlations were generally of medium intensity, ranging from 0.644 to 0.879. Stay23 showed the lowest re-ranking across the traits, with correlations between 0.733 in M4g and 0.879 in M1g.

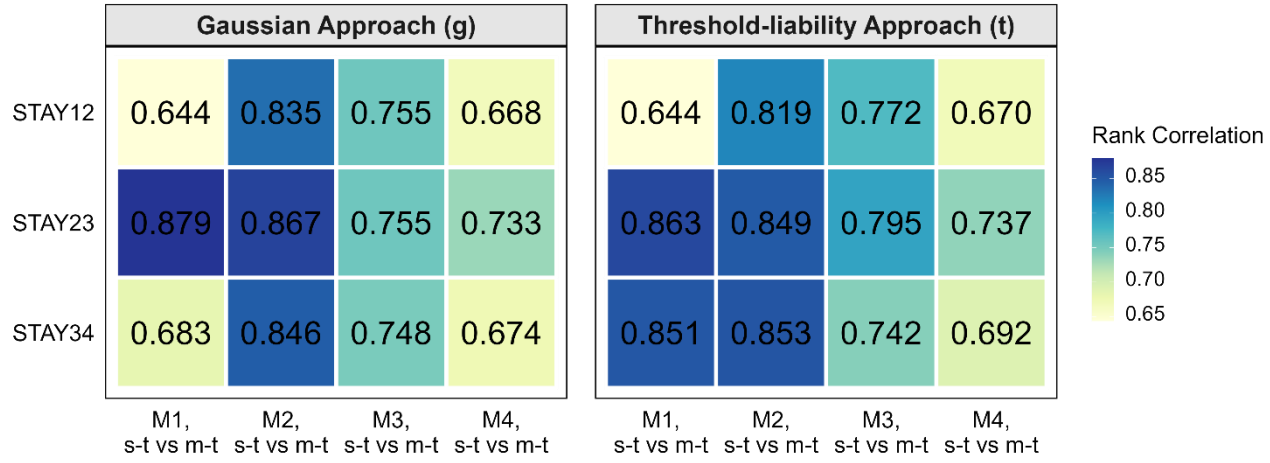

Figure 7 - Bulls' rank correlations for stayability traits, single-trait (s-t) vs multi-trait (m-t) analysis, in a Gaussian (g) vs Threshold-liability (t) approach, for M1, M2, M3 and M4.

Accounting for the correlations for each stayability trait across the four models, some differences could be observed in Figures 8 and 9. The greatest re-ranking was found in STAY12 for multi-trait analysis (Figure 9): in particular, this trait had the weakest correlations between models, ranging from 0.632 to 0.701 in Gaussian evaluation. Conversely, the same trait had a low re-rank when considering the single-trait analysis (Figure 8). Predominantly, single-trait evaluations had the lowest re-rank for

all the traits, while multi-trait evaluations showed higher differences between models for the same trait.

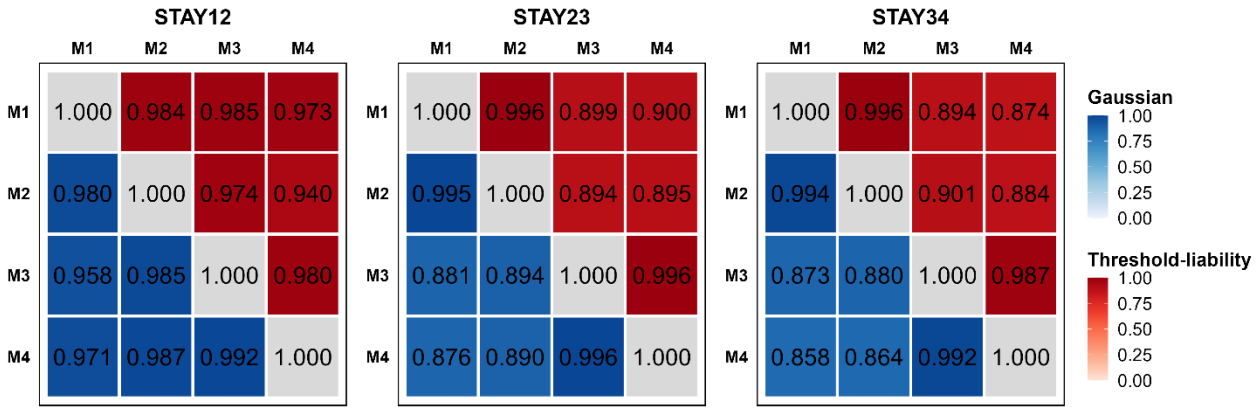

Figure 8 - Bulls' rank correlations between Gaussian (below the diagonal) and Threshold-liability (above the diagonal) approaches for stayability traits in M1, M2, M3 and M4, single-trait evaluations.

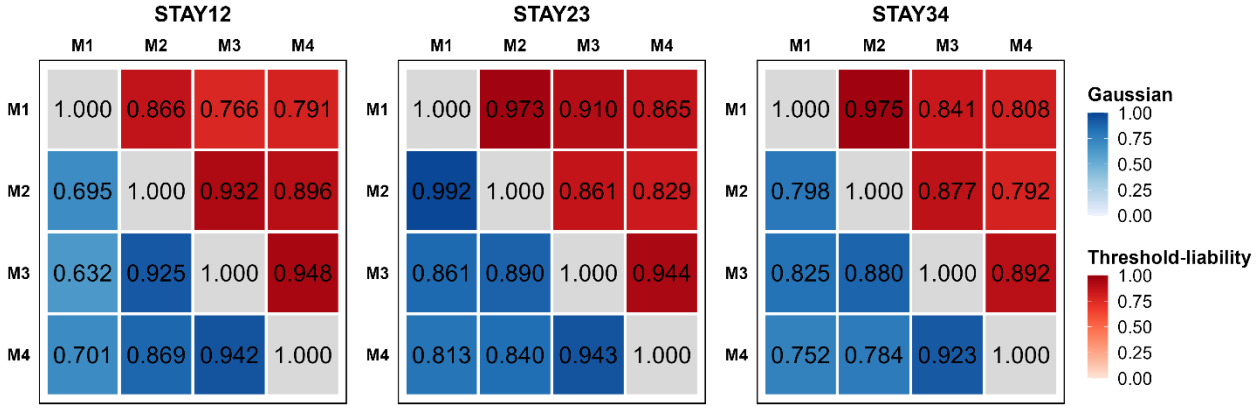

Figure 9 - Bulls' rank correlations between Gaussian (below the diagonal) and Threshold-liability (above the diagonal) approaches for stayability traits in M1, M2, M3 and M4, multi-trait evaluations.

Forward-in-time validation

In order to validate the results obtained, a forward-in-time validation was set up. In particular, an investigation was conducted into the correlation between sires' breeding values obtained without the use of daughters' phenotypes and their breeding values obtained when daughters' phenotypes were present, using a time-split approach. The results are presented in Table 3.

Table 3 - Pearson (Spearman) correlations between official bulls' EBVs (D-3) and masked bulls' EBVs (D-4), for the three stayability traits. Correlations refer to Gaussian models, for multi-trait evaluation. P-values are not reported as they were all < 0.001.

	M1g[1]	M2g[2]	M3g[3]	M4g[4]

	Bulls A[a]	Bulls B[b]	Bulls AB[c]	Bulls A[a]	Bulls B[b]	Bulls AB[c]	Bulls A[a]	Bulls B[b]	Bulls AB[c]	Bulls A[a]	Bulls B[b]	Bulls AB[c]
STAY12	0.994 (0.994)	0.489 (0.468)	0.878 (0.868)	0.995 (0.994)	0.457 (0.435)	0.878 (0.867)	0.994 (0.993)	0.415 (0.387)	0.886 (0.872)	0.994 (0.994)	0.421 (0.394)	0.888 (0.874)
STAY23	0.993 (0.993)	0.442 (0.421)	0.844 (0.833)	0.993 (0.993)	0.365 (0.340)	0.854 (0.842)	0.993 (0.993)	0.375 (0.349)	0.864 (0.849)	0.992 (0.992)	0.343 (0.318)	0.855 (0.839)
STAY34	0.991 (0.991)	0.444 (0.424)	0.808 (0.794)	0.992 (0.991)	0.370 (0.347)	0.821 (0.806)	0.992 (0.991)	0.378 (0.354)	0.834 (0.814)	0.991 (0.991)	0.330 (0.307)	0.824 (0.803)

M1g[1]: model with no fixed effects, Gaussian.

M2g[2]: model with HSC as a fixed effect, Gaussian.

M3g[3]: model with DM as a fixed effect, Gaussian.

M4g[4]: model with HSC and DM as fixed effects, Gaussian.

[a]: bulls with daughters that calved only before 2012, thus real phenotypes in both official and masked datasets

[b]: bulls with daughters that calved only after 2012, thus real phenotypes in the official dataset and masked phenotypes in the masked dataset

[c]: bulls with daughters that calved before and after 2012, thus real phenotypes in the official dataset and both real or masked phenotypes in the masked dataset

The correlation coefficient for the A groups was found to be close to 1 for all the models investigated, even when analysing rank correlation with the Spearman method for all the evaluated stayability traits. Conversely, for groups B, the correlations drastically decreased to 0.33-0.49 according to stayability trait and model, with the worst effect in STAY34 of M4g. The results for groups AB exhibited an intermediate pattern, with a range from 0.808 to 0.888, and the most favourable result was observed in STAY12 of M4g. Furthermore, it was found that the correlation in STAY34 was systematically lower than that observed for STAY12. To achieve a more profound understanding of the AB group performance, a second analysis was performed (with the results shown only for M4g).

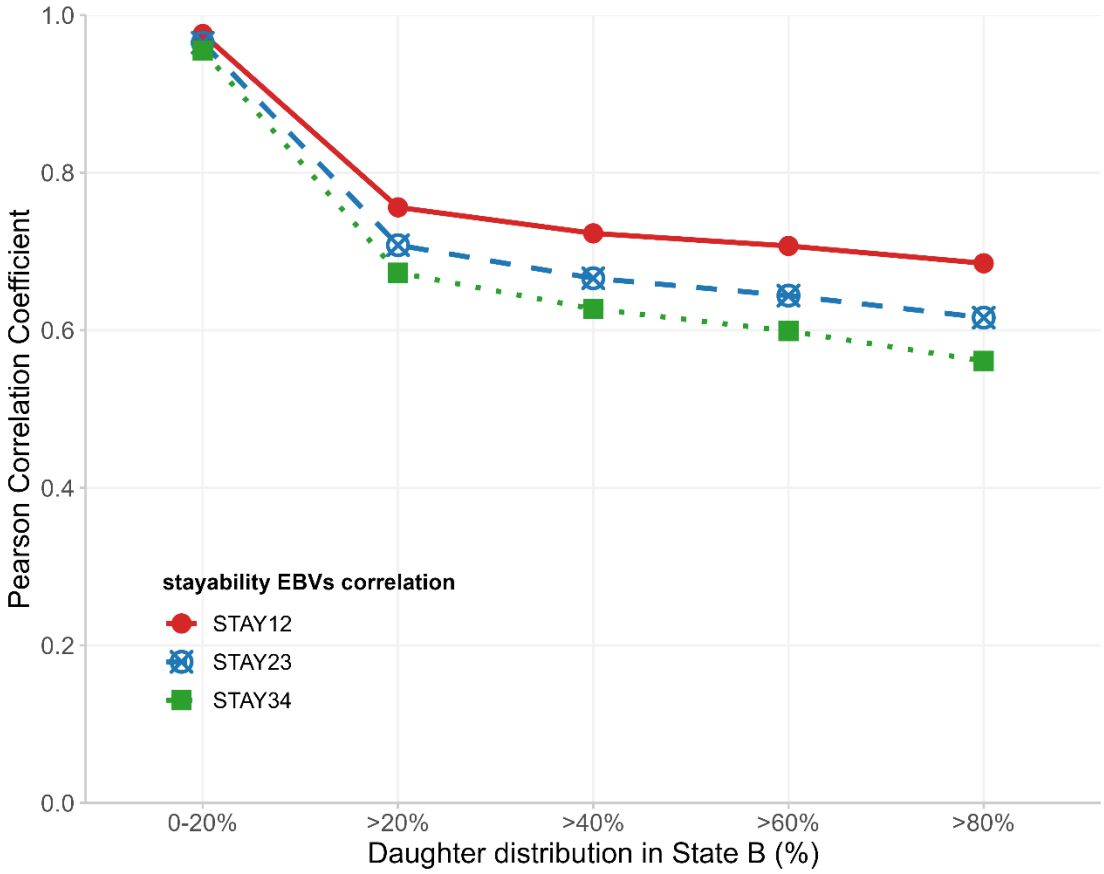

Figure 10 - Bulls' EBVs correlations used as estimation of the forward-in-time validation, according their percentage of daughters that calved after 2012 (B daughters), for the analysed stayability traits.

As illustrated in Figure 10, the AB bulls were grouped according to the percentage of daughters that gave birth prior to or subsequent to 2012. The number of bulls for each class varied, with 1987 recorded for B-daughters ranging from 0-20%, 277 for the range of 21-40%, 219 for the range of 41-60%, 149 for the range of 61-80%, and 292 for bulls with more than 81% B-daughters. The correlation pattern for the three stayability traits is analogous: the maximum correlation is observed when the number of daughters with masked phenotypes is minimal, and it decreases as the proportion of daughters with masked phenotypes increases. This trend is more evident in stay34, where the correlation at 80% of B daughters is 0.561, compared to STAY12 where the correlation is 0.685. With respect to the convergence of breeding value estimations, it was observed that the models M1 and M4 required fewer iterations in both D-3 and D-4.

Discussion

Increasing importance is being given to cows' longevity by the dairy cattle sector, both for social

acceptance of dairy herds and for economic significance to breeders. In this context, genetic selection can support farmers in extending the lives of their animals, complementing their current efforts in feeding and management. In this study, we examined the genetic differences among four statistical models to assess the longevity of cows in the Italian Holstein herds. Stayability analysis was conducted starting from the first calving event; thus, stayability on heifers was not evaluated in this study. This choice was made because stayability for heifers could be considered a different trait, as stated by different authors (Pritchard et al., 2013; Khansefid et al., 2023).

The comparisons made had several aims: first, to compare the performances of the Gaussian versus threshold-liability models; second, to assess to what extent solutions for single-trait models differ from multi-trait models; third, to compare the differences between definitions of longevity as defined by the impact of herd and production effects on longevity itself.

Phenotypic survival curve

Phenotypically, the survival rate of the Italian Holstein population decreases sharply when increasing the number of lactations, with less than 50% of the population surviving at the beginning of the third lactation. These results were aligned to other Holstein populations (Hare et al., 2006; Heins et al., 2012; Brickell et al., 2011; Horváth et al., 2017). However, they showed some differences with those reported by other studies: Khansefid et al. (2023) in Australian Holstein found that 64.4% of cows were culled at the third lactation; also, Heise (2016) found a percentage of 54.4 of alive cows at the end of the second lactation. Regarding herd life and replacement rate, the literature values vary according to breed, rearing system and country. Herd life in dairy cows typically ranges from 2.5 to 4 years (De Vries et Marcondes, 2020), and replacement rate varies from 27.8% to 38% (USDA, 2018; De Vries et Marcondes, 2020). Italian Holstein data are thus aligned with the reported information. However, those values are not always in the optimal range to obtain a profitable herd; indeed, the optimal replacement rate appears to be between 23% to 30% (De Vries, 2017).

Fixed effects solutions

Longevity, especially in dairy cattle farms, is influenced by a variety of elements. They can be related

to the cow itself, or to the environment and the historical period where the cow is raised. In the present study, two factors were investigated, one extrinsic as the variation of the herd size, and one intrinsic, that is the milk production.

The impact of the HSC effect was investigated. In both shrinking and expanding scenarios (HSC4 and HSC6-7, respectively), the greatest impact was found for STAY34, suggesting that voluntary culling due to shrinking herd size affects older animals rather than younger ones. This outcome was expected given that the greater parity orders can only be reached by mature cows, which have been shown to be more productive but also more likely to have health problems (Schneider et al., 2007; Pinedo et al., 2010; Brickell et al., 2011; Pinedo et al., 2014; Owusu-Sekyere et al., 2023). Furthermore, they are frequently linked to inferior genetic merit in comparison to more recent generations within a population under genetic selection (De Vries, 2017). Furthermore, the rearing cost of younger cows may not yet have been reimbursed (Lactanet, 2019; Gambonini et al., 2022). Taking all the aforementioned factors into consideration, it could be concluded that the disposal of young animals by farmers could result in economic loss. In the present study, these factors affecting culling decisions are reflected in the drastically lower probability of survival of an older cow compared to the previous stages of life. However, in the expanding herd scenario (HSC6-7), the probability of not being culled of a cow is greater than the lower classes, even for STAY34; this finding is corroborated by Owusu-Sekyere et al. (2023), which indicates that even older cows are retained within expanding herds. Similar results were also found by Miller et al. (2008), with a decrease in culling while herd size increases. Oppositely, in STAY12 and STAY23 the impact of this effect is weak, enabling more than 88% of the cows to survive despite the differences in herd size from the previous year.

Many authors suggest that the link between the milk production strongly affects the longevity of the cows (Hudson and Van Vleck, 1981; Miller et al., 2008; Pinedo et al., 2010; Pinedo et al., 2014; De Vries et al., 2020; Dallago et al., 2021), and low milk production is assumed to be the major source of voluntary culling (van Pelt et al., 2017). To investigate this aspect, Italian Holstein longevity has

been evaluated with two statistical models that account for the milk production of the cow compared to the average of its contemporaries, yielding EBV for functional longevity. Nowadays, this procedure is quite common when evaluating national selection indexes, as reported in the study by Forabosco et al. (2009), because there is a need to evaluate only the improvement that is genetically independent from milk yield (Meuwissen et al., 2002). As found in some papers (Hudson and Van Vleck, 1981; Heise et al., 2016; Norman et al., 2022), the negative influence of poor milk production in stayability is greater in early stages of life, such as STAY12 in the present case, probably due to the greater production of older cows compared to the primiparous cows. This result was found in our study as well: the DM effect always has a higher impact in STAY12 compared to STAY34, for the same DM classes, stating that STAY12 is more susceptible to the impact of this effect; the only exception is class 2. Indeed, looking at the class DM6, which represents no significant differences in milk production from the average of the herd, the probability of a cow to survive is 0.771 compared to 0.976 for the same class in STAY34. This pattern is particularly true for the greater DM classes, which are from 6 to 10, but some differences are seen in the "production under the average" classes. In fact, in classes 2 to 5, the highest impact of milk production is seen in STAY23, with the probability of survival in the lower classes that ranges from 0.125 in DM2 to 0.627 in DM4. This can be explained partially by the fact that a cow repays her rearing cost between her first and second lactations; consequently, if a cow is sensibly less productive than her contemporaries, a farmer can decide to dispose of her prematurely.

Heritability estimation and genetic correlations

Heritabilities found in the present study are aligned with those found in the literature, which ranged from 0.016 to 0.173 according to different types of breeds and models used (Cassandro et al., 1999; Forabosco et al., 2009; Heise et al., 2016; Hardie et al., 2021; Khansefid et al., 2023; Interbull database, 2025). In our study, heritabilities for Gaussian models ranged from 0.024 to 0.094, and for the threshold models from 0.049 to 0.172. Nevertheless, heritability estimates of binary traits from linear models are frequency dependent and cannot be compared directly (Holtsmark et al., 2009);

therefore, a transformation on the same scale is required. Here, a transformation to the observed scale has been done, following the formula [4]. When comparing the observed and the transformed heritabilities, those from threshold-liability models are frequently higher, implying that for this trait, a categorical approach should be preferred to properly handle the genetic variation. However, differences are often minimal, especially in M1 and M4; therefore, Gaussian approaches could be used as well. The fact that in STAY34 for M1 and M2 heritability for categorical traits is lower than the linear can be explained by two aspects. On one side, the more extreme the frequency of the phenotype, the more difficult it is to correctly estimate the values (Dempster and Lerner, 1950). On the other, M1 and M2 are models where a correction for milk production is not included; this means that the correction for milk could enhance the selection for longevity and better estimate the real genetic potential of the cow. This is corroborated by the findings previously analysed in this study. One other key aspect to consider is the always higher heritability in multiple-trait analysis compared to single-trait analysis. This can be attributed to the high genetic correlations between traits, which strengthen and increase the genetic variance of the estimations in all the models, leaving the phenotypic variation unchanged. Regarding genetic correlations, those obtained using linear models were similar to the categorical ones, except for some traits with slightly lower results (not shown in the manuscript). However, given the binary nature of the traits and the findings by Gates et al. (1999) and Stock et al. (2005), we report here only the genetic correlations obtained through multiple trait analyses in the categorical models. This is because those studies showed that linear genetic correlations underestimate the real genetic correlations between categorical traits, even though in our case this was not always the rule. The correlations within threshold models in the present work show high values, demonstrating the strong relationship between the traits. Indeed, a cow can show the third parity only if she survived the previous.

Sires' rank correlations

Accounting for bulls' rank correlations, when linear and categorical models are compared, both gave similar results and had almost unity correlations in the ranks of bulls. Indeed, regardless of the

different outcome scales, only a little re-ranking was observed. Contrarily, when comparing single-trait and multi-trait evaluations for the same model, Spearman's correlations have a greater variation, implying that the use of the genetic correlations between traits significantly affects the evaluation. These results indicate that, for a routine genetic evaluation, a Gaussian multiple-trait model could be used in spite of the binary nature of this trait. In a national context, the same conclusions were found by Fabris et al. (2025) for Italian Jersey.

Forward-in-time validation

In general, masking phenotypic records (D-4) has been demonstrated to have a detrimental effect on the outcomes, with the most unfavourable results being observed in cases where all EBVs are pedigree-based (group B). Earlier studies have demonstrated that predictions based exclusively on pedigree information exhibit modest reliability for young bulls, particularly for low-heritability functional traits such as fertility and longevity (VanRaden et al., 1995; Samuelson et al., 1995). Furthermore, a recent study by Strabel (2025) in a Holstein population has confirmed that pedigree index reliabilities seldom exceed approximately 0.30 in the absence of a very large number of daughters and herds. In the present study, when the analysis was focused on the AB group of M4g, these outcomes became more evident. Indeed, the general correlation between full-data-based (D-3) and partial-data-based (D-4) EBVs demonstrates a high degree of consistency. However, an examination of the group's progeny distribution reveals a critical limitation: sires with a low number of phenotypic records undergo heavy statistical shrinkage, pulling their EBVs closer to the population mean. This shrinkage effect can artificially distort or inflate the general correlation if not properly accounted for, explaining the decline in consistency observed in groups with limited progeny. The nature of these findings is further reinforced by the existing literature on similar studies. Brito et al. (2020) found a 0.50 correspondence between original and under-test BLUP breeding values of Nellore cattle; similarly, Legarra et al. (2018) found a correlation in the range of 0.66-0.81 between predicted and original breeding values, when fitting 50% of missing phenotypes. As expected, the group exhibiting no masked phenotypes showed no reduction in consistency, maintaining a

correlation near 1.00. This finding indicates that, regardless of the model applied, traditional validation metrics are highly sensitive to data availability when a limited number of phenotypes are utilised; further, it identifies a potential issue that could be addressed through the utilisation of a genomic approach, as stated by VanRaden et al. (2009).

Conclusion

The present study aimed to characterise Italian Holstein longevity with different evaluation methods. In this work, we analysed the average herd life in Holstein herds and investigated different outcomes of various stayability evaluation methods to extend cows' lives. Extending the cow's ability to survive will increase not only the farmer's profitability, but also the social acceptance of dairy herds and the animals' welfare. Despite the binary nature of this trait, results show that a Gaussian approach can be used with almost the same performance of the threshold-liability. Furthermore, a multiple-trait evaluation is to be favoured, given the strong genetic correlation between the investigated traits. With regard to the statistical model that was employed, it was found that the rank correlations were more sensitive to the definitions of stayability (given by the model specification) than to the approach (Gaussian vs. threshold). Indeed, the results suggested that a functional, production adjusted approach is to be preferred to avoid bias in the estimation of genetic variance due to voluntary culling of the animals. As demonstrated in the extant literature, this is further corroborated by the most frequently employed method in routine evaluation. However, this approach identified suboptimal outcomes in younger animals and requires a sufficient number of phenotypes to ensure reliable results. The present study established the foundations for a more detailed evaluation, with a focus on functional stayability for Holstein, and a more reliable basis to estimate breeding values for candidate bulls in a future genomic evaluation.

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Chapter 4:
Assessing stayability in Italian Holstein cattle: type traits and somatic cell count as early predictors for traditional and genomic estimated breeding values

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Abstract

The debate on the optimal herd life for dairy cows involves balancing the need to maximize herd life while sustaining genetic progress. In the dairy industry, the primary objective for a farmer is to ensure that a cow remains in the milking herd for a sufficient period to generate a profit that will cover her rearing costs. In addition, the longevity of dairy cows is intrinsically linked to animal welfare and societal acceptance. In this context, the objectives of this study are as follows: firstly, to identify potential phenotypic predictors for stayability; secondly, to compare traditional breeding values with those obtained from single step evaluation, in order to overcome the difficulties of estimating a late-life phenotype. This study investigated nine traits representing stayability across the first three lactations, each of which was divided into three sub-periods. The statistical linear model applied included a fixed effect of herd-year of calving, a fixed effect for the correction of milk production in the third period of each lactation, and the random effect of the animal. The heritability estimates ranged from 0.004 ± 0.001 to 0.055 ± 0.005, depending on the trait. The genetic correlations between traits ranged between 0.58 and 0.94, indicating a significant relationship between them. The second part of the study evaluated the predictivity of stayability traits from type traits and somatic cells, to use the derived stayability predicted as covariate trait in estimating breeding values. The stayability breeding values estimated as bivariate traits were found to be more informative compared to the single trait values, with a reliability ranging from 0.453 to 0.462 for type traits and between 0.297-0.381 for somatic cell count based traits. Finally, pedigree-based EBV and single-step genomic EBV were estimated. The Pearson correlations between the datasets were high, with a general increased in the accuracy of estimation when genotype information were added. These findings confirm that, especially for low heritability traits, using conformation or animal health indicators could improve the genetic selection, but the best results are obtained with genomic information.

Introduction

The productive lifespan of modern dairy cows is a topic of increasing concern, linking economic

efficiency, environmental sustainability, and animal welfare. Although the biological life expectancy of a dairy cow is approximately 20 years, the average time spent in the lactating herd ranges between 2.5 and 4 years (De Vries and Marcondes, 2020; Schuster et al., 2020). Premature removal from the herd is predominantly driven by involuntary culling due to health and reproductive failures, and this association has been found in a variety of papers (Roxström et al., 2001; Samorè et al., 2003; Langford & Stott, 2012; De Vries and Marcondes, 2020; Dallago et al., 2021; Owusu-Sekyere et al., 2023). Thus, dairy cow longevity is intrinsically linked to animal welfare and societal acceptance. The length of a cow's life is not merely an economic parameter; it serves as a global indicator of the herd's welfare status (Dallago et al., 2021). Consequently, improving functional longevity, considered as the ability of a cow to avoid involuntary culling, is essential to address both ethical concerns and the social acceptability of dairy farming, as suggested in the works of Bell (2011) and Rushen and de Passillé (2013). Because the true phenotype for longevity is only available at the end of a cow's life, identifying early predictors is crucial for a rapid genetic selection and herd management. Researches consistently highlights somatic cell count (SCC) and morphological conformation as primary determinants of a cow's stayability and overall resilience. Subclinical and clinical mastitis, indicated by elevated SCC, are among the most frequent and costly health disorders leading to involuntary culling. High SCC is strongly associated with an increased risk of culling across multiple lactations, reflecting chronic inflammation that negatively impacts both production and cow comfort (Samorè et al., 2003; Pritchard et al., 2013; Hardie et al., 2021; Rostellato et al., 2021). Simultaneously, linear type traits related to the mammary system, body capacity, and feet and legs serve as valuable early-life indicators of long-term survival. Morphological soundness, particularly udder depth and attachment, protects against injuries and mastitis, directly influencing a cow's ability to remain productive. Pryce et al. (2000) highlighted that physical conformation is phenotypically and genetically correlated with various health disorders. All the results suggest that animals with optimal conformation scores and consistently low SCC demonstrate greater genetic and phenotypic resilience, effectively delaying culling. Therefore, integrating morphology and udder health parameters into

breeding indices not only enhances herd profitability but also prioritizes animal welfare by promoting structurally sound and disease-resistant cows (Zavadilova et al., 2012; Shabalina et al., 2020; William et al., 2022; Hu et al., 2025). In this context, this study had different objectives: firstly, to identify potential phenotypic predictors for stayability; secondly, to compare traditional breeding values with those obtained from single step evaluation, in order to overcome the difficulties of estimating a late-life phenotype.

Material and Methods

Data editing and preparation

For this study, records from the Italian Holstein population were provided by the Italian Holstein, Brown Swiss and Jersey Association (ANAFIBJ, Cremona, Italy). Only Holstein cows, born in Italy after the year 1984, and with at least the first calving record were included. Cows with non-consecutive lactation histories, or with more than 14 test days between two consecutive calvings, were removed from the dataset. As the standard test day recording is conducted on a five-week basis, and the August recording is frequently absent, this condition was necessary to ensure the absence of missing calving recordings. This choice provides a more conservative threshold than our previous study, ensuring better coverage in case of longer lactations. We also right censored all cows that showed ongoing lactation at the time of data extraction.

The first three lactations were used in the definition of stayability for this study. The breeding objective in the Italian national context was defined as the ability to survive the 3rd lactation. Based on the paper of Heise et al. (2016), each lactation was divided into three sub-periods: period **A** from calving to 49 days in milk (**DIM**), period **B** from 50 to 249 DIM, period **C** from 250 DIM to the next calving, when available. Considering that stayability is a binary trait, the phenotype was coded as '1' indicating animals that survived the period, and '0' when the animal was culled. Moreover, before assign the phenotype, a waiting period was allowed. This period has been called "opportunity window", and it is period-specific: for periods A and B, it is 100 DIM and 300 DIM respectively; for period C, the end could occur with the next calving event or, if not available, at 600 DIM. If the

opportunity window was not concluded, the phenotype was set as missing for that period. This generated nine different stayability traits. For survival from first to second calving: **STAY12A**, **STAY12B**, **STAY12C**; for survival from second to third calving: **STAY23A**, **STAY23B**, **STAY23C**; for survival from third to fourth calving: **STAY34A**, **STAY34B**, **STAY34C**; where A, B, C refer to the lactation stages as reported above. They will generally be referred to as observed stayability (**STAY$_{obs}$**), representing the raw binary outcomes derived directly from herd culling events. Furthermore, the definition of stayability was different whether considered withing or across lactations. Within lactation, the definition had a cumulative approach: when a cow showed '0' in a given lactation stage, the following stages of the same lactation showed '0' as well. Across lactations, missing values were assigned to cows that showed '0' in any of the previous lactations, i.e. did not calve.

Below is a schematic representation of the possible survival outcomes. The encoding process is exemplified by four scenarios: cow A was culled during the first lactation, resulting in a 0 for STAY12C and missing records (NA) for subsequent periods. Cow B survived the first lactation but was culled during the second, thus being recorded as 1 for STAY12A-B-C and for STAY23A, but 0 for STAY23B-C. Cow C has a similar pattern of cow B but with also STAY23A recorder as culled, while Cow D represents a censored record, where the cow is currently alive but has not yet reached the end of the third observation period.

Cow	Status	STAY 12A	STAY 12B	STAY 12C	STAY 23A	STAY 23B	STAY 23C	STAY 34A	STAY 34B	STAY 34C
A	Culled during 1st lactation	1	1	0	NA	NA	NA	NA	NA	NA
B	Culled during 2nd lactation	1	1	1	1	0	0	NA	NA	NA
C	Culled during 3rd lactation	1	1	1	0	0	0	NA	NA	NA

D	Alive (ongoing lactation)	1	1	1	1	NA	NA	NA	NA	NA

Contemporary groups were defined as the combination of herd and year of calving. A production indicator was generated and assigned to each lactation, that is the difference in milk production deviation (**DM**), for each cow compared to the average of her contemporary group. Milk records used were derived from the national routine test day recording, and it was expressed as 305-d conventional production. The DM effect was categorized in 10 classes. Herds with less than 2 animals (**n_cows**) were discarded. The milk production of each animal was calculated as a standard deviation from the mean of its contemporary group (**devm**). Classes of difference in milk production have been coded with numbers from 2 to 10 as follows: class 2 for devm lower than -1.5, class 3 for devm between -1.5 and -1, class 4 for devm between -1 and -0.6, class 5 for devm between -0.6 and -0.3, class 6 for devm between -0.3 and < +0.3, class 7 for devm between +0.3 and +0.6, class 8 for devm between +0.6 and +1, class 9 for devm between +1 and +1.5, and class 10 for devm greater than +1.5. Class 1 was assigned to the animals that had no contemporary group in their herd and had consequently been excluded from previous allocations. This effect could be implemented only in the period C of each lactation, as it used milk predicted with the information from all the lactation.

Information regarding type traits, body condition score (**BCS**) and somatic cell count (**SCC**) were included. Normally, type traits and BCS in Italy are registered once in a cow's life, during her first parity, by a classifier; SCC are instead recorded during routine national test days. All this information merged, led to the dataset **D-total**, with a total amount of 9,383,533 cows.

For type traits and BCS, the traits were transformed from the linear score into a binary code 0-1 generating binary variable that indicated the desired '1' versus the undesired '0' score. For type traits, the classification applied in Italy goes from 1 to 50, while for BCS the score goes from 1 to 5. For some traits the score given by the classifier has a linear increase, that goes from 1 to 50, that is from

the lowest possible value the auspicial value to have. In our study, this was the case of conformation, stature, chest width, body depth, angularity, rump width, foot angle, feet and leg functionality, rear leg set rear view, locomotion, fore udder attachment, rear udder height, udder support, rear udder width and udder depth. For these traits, scores 1-24 were grouped to the '0' (undesirable) value, while 25-50 were grouped to the '1' (desirable). For some of these traits though, the value 50 is considered negative, thus the code changed into '0' (undesirable); this was implemented for stature, chest width, body depth, foot angle, rear leg set rear view, and udder depth. Lastly, for traits with an intermediate biological optimum, the original scale was partitioned into three binary variables: 'low', 'intermediate', and 'high' (e.g., *trait_low*, *trait_interm*, and *trait_high*, where 'trait' represents the specific morphological feature). For each record, a value of 1 was assigned to the variable corresponding to the animal's phenotype, while the other two variables were set to 0. Specifically, *trait_interm* was set to 1 if the original score fell within the optimal range, whereas *trait_low* or *trait_high* was set to 1 if the score fell below or above this range, respectively. This encoding was implemented for BCS, rump angle, rear leg set side view, front teat placement, teat length, and rear teat placement.

Regarding SCC, we derived 2 traits for each lactation, the arithmetic mean of the SCC in the specific lactation and the harmonic mean. For the harmonic mean, we considered the ratio between the number of test days for each period and the sum of the inverse of the SCC found in each period.

For Variance Components Estimation (**VCE**), a restricted dataset was generated by further editing. We considered only cows that presented a known sire and with a first calving event between 2005 and 2015. We retained only sires with more than 300 daughters, classifiers with at least 9 cows evaluated, and contemporary groups with at least 17 cows. Furthermore, all DM classes with a frequency of less than 100 observations were combined with the most closely class related to them. No censored cows were included. As a result, for the VCE step, we retrieved data for 598,877 cows, daughters of 512 bulls. This dataset was referred to as **D-vce**. This stringent filtering was necessary to ensure computational feasibility during the variance component estimation and to establish robust genetic ties across contemporary groups, thereby minimizing confounding between sire and herd

effects.

Following the VCE step, the estimated variance components were utilized in a single-step GBLUP (**ssGBLUP**) framework to evaluate a broader population. Genotypic information from 7,977 Holstein bulls was utilized to estimate genomic breeding values. This integration captures genetic relationships across a wider population, including young bulls and ancestors without direct progeny, maximizing the accuracy of genomic predictions without imposing the computational constraints inherent to the VCE step. The animals were genotyped using a 70k SNP panel (70,012 markers) and the quality control protocol was implemented with the PREGSF90 software (version 1.26, Aguilar et al., 2010). Markers were excluded if they were monomorphic, had a minor allele frequency (MAF) < 0.05, or showed a call rate < 0.90, resulting in 65,736 effective SNPs retained. Numerical stability was ensured by blending the genomic relationship matrix G with 5% of the pedigree-based relationship matrix A_{22}, following the weighting procedure described by VanRaden (2008). This blending prevents the matrix from being singular or near-singular, which is critical for the stability of the single-step genomic BLUP (ssGBLUP) equations. The final genomic-derived block $G^{-1} - A_{22}^{-1}$ was then integrated into the relationship matrix H^{-1} to compute the final GEBVs, as described by Legarra et al., 2014.

Stayability prediction

To asses if the use of morphological and somatic cell counts information could enhance the genetic selection for longevity, the first analysis performed was to predict the stayability traits from several predictors. With the D-vce data set, two diverse groups of predictions were computed to predict STAY12C, STAY23C and STAY34C: the first was the prediction with morphological traits, while the second predicts STAY12C, STAY23C and STAY34C from SCC indicators. Below is a schematic representation of the combinations:

Stayability traits predicted	Morphological traits predictors	SCC predictors	
STAY12C	Type traits at 1st lactation	Mean SCC 1st lactation	Harmonic SCC 1st lactation

STAY23C	Type traits at 1st lactation	Mean SCC 2nd lactation	Harmonic SCC 2nd lactation
STAY34C	Type traits at 1st lactation	Mean SCC 3rd lactation	Harmonic SCC 3rd lactation

All fitted analyses were performed in the R (version 4.2.2) using the **BGLR** (Bayesian Generalized Linear Regression) package (version 4.2.3, Perez and de los Campos, 2014). The BGLR function was utilized to fit various parametric Bayesian regressions to estimate animal stayability across different production stages. Stayability phenotypes STAY12C, STAY23C and STAY34C were modelled as the response vector y, and their predicted values will be referred to as **STAY12Cm, STAY12Cs**, **STAY23Cm, STAY23Cs, STAY34Cm** and **STAY34Cs** according to the stay-trait and the original predictor (m for morphology and s for SCC). Given the nature of the predictors, Bayesian Ridge Regression (**BRR**) was implemented for all final analyses. The BRR model specifies a linear predictor where regression coefficients β are assigned a Gaussian prior with a common variance. This approach ensures that all type and SCC traits contributed to the final estimate through Bayesian shrinkage; by shrinking less informative, the BRR provides a more stable and comprehensive phenotypic index. The model parameter estimates were obtained using a Gibbs sampler, with 15,000 iterations, a burn-in of 5,000 and a thinning rate of 5. The linear analyses were performed using the following regression:

$$y_i = \mu + \sum_{j=1}^{p} X_{ij}\beta_j + e_i$$

where: y_i is the vector of the stayability phenotypes of the i^{th} animal; μ is the overall mean of the trait; p is the number of predictors included in the model (33 morphological traits; 2 for SCC for the current analyses); Xi_j is the incidence vector for the j^{th} predictor; β_j is the regression coefficient for the j^{th} predictor; e_i is the vector of random residuals. The BRR model assumes that all predictors have an effect on the trait, distributed from a common Gaussian. In this study, the regression coefficients

β_j were assigned a prior distribution of $\beta_j \sim N(0,\boldsymbol{\sigma}^2_\beta)$, where $\boldsymbol{\sigma}^2_\beta$ is a common variance estimated from the data. The residuals (e_i) were also assumed to follow the Gaussian distribution $e_i \sim N(0,\boldsymbol{\sigma}^2_e)$. Both variance components σ^2_b and σ^2_e were assigned scaled inverse-chi squared priors.

To evaluate the goodness of fit of the implemented models, the correlation between the observed binary phenotypes and the predicted values was calculated. Since the evaluation was performed on the full dataset without a cross-validation, this metric represents the model fit, indicating how well the morphological phenotypes or the SCC explain the observed variability in stayability (as described by Jamrozik et al., 2013).

Statistical analysis

The estimates for variance components regarding the stayability model was obtained with two set of analyses. The first regarded the single-trait estimation for $STAY_{obs}$ for D-vce dataset, while the predicted stayability traits from BGLR analysis and their corresponding original observed stayability phenotypes (STAY12C, STAY23C, and STAY34C) were jointly analyzed as correlated traits in a series of bivariate models. They will generally be referred to as fitted stayability (**$STAY_{fit}$**).

The analyses were performed using the following sire model:

$$\boldsymbol{y} = \boldsymbol{X}b + \boldsymbol{Z}_s s + e$$

where y is the linear vector of STAY traits at each period; b is the vector associated to the fixed effects (including the contemporary group and the DM effects for STAY12C, STAY23C, STAY34C); s is the vector of random genetic effects for the sires of the cows; e is the vector of random residuals; $\boldsymbol{X}$ and $\boldsymbol{Z}_s$ are the incidence matrices related to fixed and sire effects, respectively. The solutions for sire genetic effects were assumed as $s \sim N(0,\mathbf{A}\boldsymbol{\sigma}^2_s)$, where **A** is the pedigree-based relationship matrix among the sires and $\boldsymbol{\sigma}^2_s$ the sire variance, and the residual error values are assumed as $e \sim N(0,\mathbf{I}\boldsymbol{\sigma}^2_e)$, where $\boldsymbol{I}$ is the identity matrix and $\boldsymbol{\sigma}^2_e$ is their variance.

Bivariate models, with the same fixed and random effects as described above, were used to estimate (co)variance components of $STAY_{obs}$. For all statistical models, the contemporary group (defined as herd-year of calving) was modeled as a fixed effect to completely account for macro-environmental differences among herds without the shrinkage constraints of random modeling, and the DM effect was applied for traits in period C. Preliminary analyses treating the contemporary group as random or using a finer granularity (e.g., herd-year-season) resulted in non-convergence in the Gibbs sampler due to the cumulative nature of the trait and the discrete distribution of the observations. Consequently, the fixed herd-year framework was maintained to ensure numerical stability and model convergence, avoiding data fragmentation and confounding with the random sire effect.

Here, the matrix notation applied was:

$$\mathbf{G} = \begin{vmatrix} \boldsymbol{\sigma}^2_{s1} & \boldsymbol{\sigma}_{s12} \\ \boldsymbol{\sigma}_{s21} & \boldsymbol{\sigma}^2_{s2} \end{vmatrix}; \ \mathbf{R} = \begin{vmatrix} \boldsymbol{\sigma}^2_{e1} & 0 \\ 0 & \boldsymbol{\sigma}^2_{e2} \end{vmatrix}$$

where **G** is the matrix of sires additive genetic (co)variances $\boldsymbol{\sigma}^2_{s1}$, $\boldsymbol{\sigma}^2_{s2}$ and $\boldsymbol{\sigma}^2_{s12}$ of traits one and two, and **R** is the matrix of residual (co)variances $\boldsymbol{\sigma}^2_{e1}$ and $\boldsymbol{\sigma}^2_{e2}$ of traits one and two.

Variance components were estimated using the Gibbs sampler THRGIBBS1F90 (Misztal et al., 2014, ver. software 2.118), in its linear model configuration (via OPTION cat 0), with 300,000 iterations, a burn-in of 250,000 and a thinning rate of 20, and the post-Gibbs analysis was performed with the software POSTGIBBSF90 (Misztal et al., 2014, ver. software 3.15). The formula was applied to values obtained from each iteration of the Gibbs sampler, the posterior mean was used as an estimate, while the posterior standard deviation was used as an error. Heritability (h^2) was calculated as

$$h^2 = \frac{4\sigma^2_s}{(\sigma^2_s + \sigma^2_e)}$$

where σ_s^2 is the sire additive genetic variance and σ_e^2 is the residual variance. The genetic correlations followed the formula:

$$r_g = \frac{\sigma_{s,12}}{\sqrt{\sigma_{s,1}^2 * \sigma_{s,2}^2}}$$

In addition, the 95% highest probability density intervals were used to define significance, with $P<0.05$ when the value '0' was not included in the interval.

The prediction accuracy of the estimated breeding values was computed as

$$acc = \sqrt{1 - \frac{SE^2}{\sigma_s^2}}$$

Where SE^2 represents the standard error of prediction extracted from the model, and σ_s^2 is the estimated additive genetic variance of the sire.

Breeding value estimation

Once genetic parameters were estimated, the estimated breeding values were computed following the same statistical model as previously described in the VCE section. Pedigree-based Estimated Breeding Values (**EBVs**) and Genomic EBVs (**GEBVs**) were estimated using BLUPF90+ (Misztal et al., 2002, ver. software 2.57). For the genomic component, a single-step Genomic BLUP (ssGBLUP) approach was implemented. The convergence criterion for all evaluations was set at 10^{-12}.

Results and Discussion

The dairy cattle sector is increasingly recognizing the importance of cows' longevity, both in terms of social acceptance of dairy herds and economic significance to breeders. In this context, genetic

selection can support farmers in extending the lives of their animals in the best way possible, complementing their current efforts in feeding and management. In this study, we developed a new model for routine genetic evaluation of longevity and defined some useful predictors to obtain earlier results rather than waiting for the animal to die. Furthermore, we compared pedigree-based EBVs and single-step GEBVs to assess the reliability of traditional evaluation when genotyping is unavailable.

Stayability prediction

To asses to what extent some morphological and somatic cell counts predictors count in the environmental context, a phenotypic prediction of stayability was conducted. Valid information used for the three lactations were: 598,877 for STAY12, 462,989 for STAY23 and 308,547 for STAY34. Regarding the type traits and somatic cell score, the valid records used were 598,877 as for STAY12. All investigated models yielded 95% credibility intervals that did not overlap with zero, and are reported in Table 1.

Table 1 - Model fit and regression coefficients of type traits (top-three traits) and somatic cell count (SCC) on cow stayability.

Predictive indicator	Trait predicted	Model fit [a]
Body depth	STAY12C	0.198
Angularity_interm (optimum intermediate)	STAY12C	0.194
Stature	STAY12C	0.186
Udder depth	STAY23C	0.044
Fore udder attachment	STAY23C	0.036
BCS_interm (optimum intermediate)	STAY23C	0.025
Udder depth	STAY34C	0.042
Fore udder attachment	STAY34C	0.030
BCS_low (undesirable values)	STAY34C	0.019
Mean SCC 1st lactation	STAY12C	0.120
Harmonic mean SCC 1st lactation	STAY12C	0.098
Mean SCC 2nd lactation	STAY23C	0.127
Harmonic mean SCC 2nd lactation	STAY23C	0.102
Mean SCC 3rd lactation	STAY34C	0.132
Harmonic mean SCC 3rd lactation	STAY34C	0.113

[a] Model fit represents a goodness of fit coefficient between observed and fitted values within the same dataset.

Morphological conformation served as a primary predictor of early survival (STAY12C), with a general model incorporating all 33 type traits yielding a goodness-of-fit of 0.244. Individually, body depth and an intermediate optimum for angularity (angularity_interm) reached the highest fits of approximately 0.20. These results are consistent with studies showing that extreme conformations impair survival (Zavadilová et al., 2011; Nascimento et al., 2023). However, morphological predictive power dropped significantly in later stages, resulting in a model fit for STAY23C and STAY34C of 0.068.

Unlike morphological traits, udder health demonstrated a consistent negative influence on survival probability across all lactations. The model fit for the arithmetic mean ranged from 0.120 to 0.132, while the values for the harmonic mean ranged from 0.098 to 0.113, with the highest values consistently found in the latest stages (STAY34Cm and STAY34Cs). These results are corroborated by the existing literature (Pinedo et al., 2010; Pritchard et al., 2013; Mohd Nor et al., 2014; Rostellato et al., 2021). Indeed, previous studies confirm that deteriorated udder health systematically compromises the ability of cows to remain in the productive herd over time, emphasizing the critical need for robust somatic cell count (SCC) management to extend dairy cow longevity.

Heritability estimation

Estimated heritabilities for $STAY_{obs}$ were generally low across all evaluated traits, ranging from 0.004 (0.003-0.006) to 0.055 (0.044-0.063), and are reported in Figure 1, on the diagonal. These findings are consistent with the existing literature on fitness and survival traits in dairy cattle, where the additive genetic variance is often masked by a large proportion of environmental variance, primarily driven by herd management and voluntary culling decisions (Miller et al., 2008; Nascimento et al., 2023). Indeed, literature findings for this trait ranges between 0.01 and 0.10 (Forabosco et al., 2009;

Hu et al., 2021; Nazari-Ghadikolaei et al., 2025; Hu et al., 2025). In our study, the definition and modeling of the contemporary group (CG) as a fixed effect of herd-year of calving may have also contributed to the large proportion of residual variance. Alternative models fitting the CG as a random effect to allow for finer seasonal granularity were initially tested but discarded, as they led to complete lack of convergence within the Bayesian Gibbs sampling framework (THRGIBBSF90). Therefore, maintaining herd-year as a fixed effect with a large average group size represented the most robust approach to guarantee model convergence and to completely eliminate the environmental variation among herds, even though any intra-year environmental or seasonal variation was inevitably captured by the residual variance.

	STAY12A	STAY12B	STAY12C	STAY23A	STAY23B	STAY23C	STAY34A	STAY34B	STAY34C
STAY12A	0.005	0.819	0.744	0.723	0.643	0.697	0.648	0.579	0.700
STAY12B	0.420	0.018	0.858	0.781	0.779	0.796	0.672	0.736	0.804
STAY12C	0.220	0.520	0.036	0.694	0.714	0.916	0.636	0.678	0.908
STAY23A				0.004	0.715	0.665	0.688	0.653	0.670
STAY23B				0.360	0.021	0.755	0.608	0.783	0.747
STAY23C				0.190	0.520	0.051	0.615	0.682	0.936
STAY34A							0.006	0.657	0.644
STAY34B							0.380	0.030	0.743
STAY34C							0.200	0.540	0.055

Figure 1 - Heritability estimates on diagonal, genetic correlations above and phenotypic below, between stayability traits, estimated with bivariate sire models.

As was demonstrated in the present study, the residual variance was found to be consistently greater than the additive genetic variance (results in Table 2). Of particular interest was the increasing trend

in heritability that was observed as the stayability of the subjects advanced. Traits measured in later periods exhibited higher heritability estimates compared to early-life survival (e.g., STAY12A = 0.005 vs. STAY34C = 0.055), and it is consistent with recent literature (Heise et al., 2016). This suggests that the genetic ability to remain in the herd is more clearly expressed in older animals, giving them a greater opportunity to express their true genetic variation (Nascimento et al., 2023). Furthermore, survival to later parities is likely to be driven by true genetic superiority, such as structural robustness and good health, whereas early-life survival is often heavily influenced by random factors and voluntary, production-driven culling by farmers (van Pelt et al., 2015; Khansefid et al., 2023).

Table 2 – Sire and residual variance, and heritability, with their posterior standard deviations (SD), from single traits variance components estimation, for the nine stayability traits.

	sire variance (SD)	residual variance (SD)	heritability (SD)
STAY12A	0.010 (0.002)	8.427 (0.015)	0.005 (0.001)
STAY12B	0.186 (0.018)	41.588 (0.076)	0.018 (0.002)
STAY1C	0.747 (0.060)	82.954 (0.152)	0.036 (0.003)
STAY23A	0.011 (0.002)	10.308 (0.022)	0.004 (0.001)
STAY23B	0.344 (0.034)	63.910 (0.133)	0.021 (0.002)
STAY23C	1.379 (0.114)	106.790 (0.221)	0.051 (0.004)
STAY34A	0.024 (0.005)	16.710 (0.044)	0.006 (0.001)
STAY34B	0.623 (0.063)	83.650 (0.217)	0.030 (0.003)
STAY34C	1.585 (0.142)	114.669 (0.310)	0.055 (0.005)

Phenotypic and Genetic correlations

Phenotypic and genetic correlations (r_g) estimated via bivariate models for $STAY_{obs}$ are shown in Figure 1. Genetic correlations were all positive and ranged from 0.579 to 0.936, while phenotypic correlations ranged from 0.190 to 0.540. The strongest genetic relationships were observed among the final stages of the evaluated period (0.936 for both STAY12C-STAY23C and STAY23C-STAY34C). This strong association suggests a pleiotropic effect, implying that a largely overlapping set of genes controls the ability to survive through the later stages of productive life, regardless of the starting point of the evaluated period (Holtsmark et al., 2009; Heise, 2017; Zhang et al., 2021). Conversely, the lowest genetic correlations, although still favorable, were found between early and late survival traits (r_g = 0.579 between STAY12A and STAY34B). This inverse relationship between correlation strength and the time interval separating the parities is widely supported by recent literature. For instance, Hu et al. (2025) reported genetic correlations among stayability traits measured at different months ranging from 0.382 to 0.975, with the lowest values observed between the most distant periods. Similarly, Williams et al. (2022) observed correlations ranging from 0.42 between first and ninth parity to 1.00 between adjacent later parities. Khansefid et al. (2023) confirmed this by estimating a genetic correlation of approximately 0.77 between early (first to second lactation) and late survival in both Holstein and Jersey cattle. This pattern highlights that the genetic background required to survive the initial phases (often related to first-calving or early-lactation issues) is not entirely identical to the genetic makeup necessary for long-term longevity (Holtsmark et al., 2009; Pritchard et al., 2013; Heise et al., 2016). From a phenotypic perspective, stayability traits are considerably less stable, particularly when comparing early and later stages of productive life, confirming the strong impact of the environment and management in the animal performance. This phenomenon has been documented in literature, showing that phenotypic correlations among stayability traits are consistently lower than their genetic counterparts (Jamrozik et al., 2023; Hu et al., 2025). This finding suggests that, while the genetic predisposition to survival

exhibits a high degree of correlation across lactations, the phenotypic manifestation of longevity is significantly influenced and diluted by the environmental context experienced by the cow throughout its lifetime.

Building upon these relationships, the inclusion of early-life predictors in bivariate models revealed distinct genetic patterns over time, and are shown in Figure 2. Specifically, the genetic correlations between $STAY_{obs}$ and stayability predicted by somatic cell counts were moderate, but consistently decreased as lactations progressed, diminishing from 0.381 in the first lactation (STAY12C) to 0.297 in the latest lactation (STAY34C). This decreasing predictive power aligns with the findings of Hu et al. (2025), who reported that the negative genetic correlation between stayability and somatic cell score significantly decreased with extended survival time. Cows genetically predisposed to high somatic cell counts and mastitis susceptibility are typically culled early in their productive life; leaving a pre-selected, healthier cohort in later parities. However, this trend varies across all dairy populations; for instance, Khansefid et al. (2023) and Shabalina et al. (2020) observed stronger genetic correlations between survival and udder health indicators in later lactations, highlighting that the impact of somatic cells on the genetics of survival is sensitive to the specific management strategies.

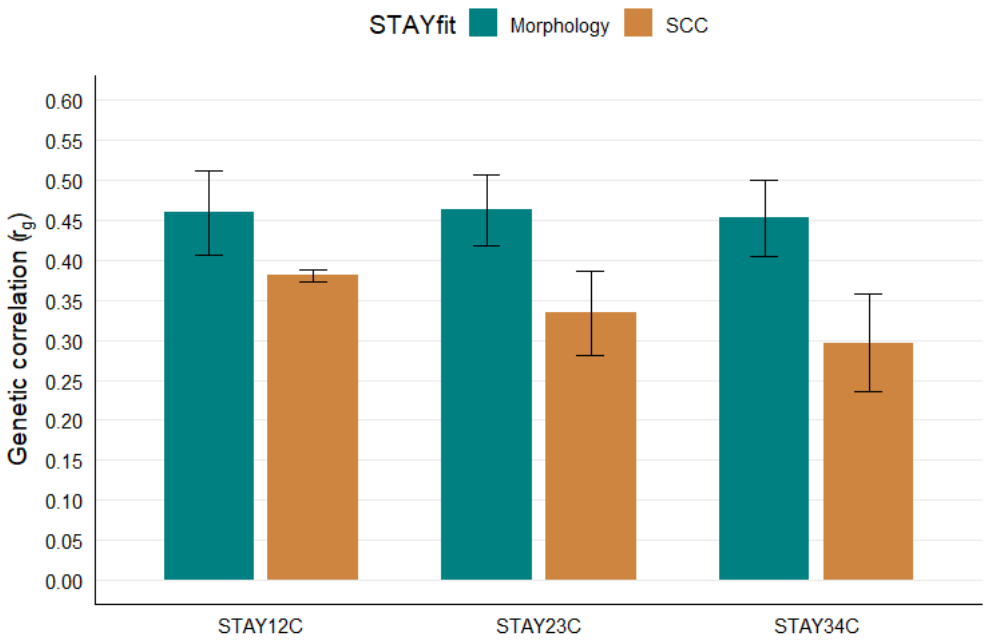

Figure 2 - Genetic correlations (r_g) with standard errors between observed stayability ($STAY_{obs}$, i.e. STAY12C, STAY23C, STAY34C) and fitted stayability ($STAY_{fit}$), both for morphology predictors (teal bars) and SCC predictors (orange bars).

In contrast, the genetic correlation between $STAY_{obs}$ and survival predicted by morphological traits remained stable and moderate-to-high across all evaluated stages (0.459, 0.462, and 0.453 for STAY12C, STAY23C, and STAY34C, respectively). The present findings are consistent with those of Williams et al. (2022), who described that while genetic correlations between survival and body size traits (e.g., body depth and stature) diminish with advancing parity, the predictive power of udder-related traits concurrently strengthens. Consequently, a comprehensive morphological index can capture the different influences, providing a robust, age-independent indicator of cow stayability.

Breeding value estimations

The low heritability estimates confirm the challenges of improving stayability through traditional phenotypic and pedigree-based selection. Given their low heritability and late-in-life expression, stayability traits are ideal candidates for genomic selection, particularly using the single-step Genomic BLUP (ssGBLUP) approach (Aguilar et al., 2010; Christensen and Lund, 2010; Legarra et al., 2014). The integration of genomic information into genetic evaluations could enhances the accuracy of genomic estimated breeding values (GEBVs) for young genotyped animals, overcoming

the limitations of the weak fragile signal captured by traditional pedigree-based models (VanRaden et al., 2009; Hayes et al., 2009). This is the case of our study as well. Indeed, the comparison of pedigree-based EBVs and GEBVs for genotyped bulls in the D-vce dataset, revealed strong correlations, generally ranging from 0.80 to 0.93 (with the exception of 0.58 for STAY12B). The strongest associations were observed in later survival stages, specifically for STAY12C (0.93), STAY23C (0.91), and STAY34C (0.90). Other correlations were 0.86 for STAY12A, 0.80 for STAY23A, 0.87 for STAY23B, 0.80 for STAY34A, and 0.86 for STAY34B.

Furthermore, Table 3 presents the results regarding the prediction accuracy between single-trait stayability evaluations and bivariate models (incorporating type traits and SCC as predictors) for both pedigree-based EBVs and GEBVs. Due to a lack of convergence in the traditional bivariate evaluations for the latest stage (STAY34Cm), this specific EBV results was excluded from the comparison; however, the corresponding genomic model converged successfully and was retained.

Table 3 - Comparison of prediction accuracy between single-trait and bivariate models for traditional (EBV) and genomic (GEBV) evaluations of stayability traits.

Analysis	Comparison a	Acc. single-trait[b]	Acc. multiple-trait[c]	Delta accuracy[d]
EBV	STAY12C vs STAY12Cm	0.708	0.940	0.232
EBV	STAY12C vs STAY12Cs	0.708	0.940	0.232
EBV	STAY23C vs STAY23Cm	0.650	0.968	0.317
EBV	STAY23C vs STAY23Cs	0.650	0.953	0.303
EBV	STAY34C vs STAY34Cm	0.722	-	-
EBV	STAY34C vs STAY34Cs	0.722	0.730	0.009
GEBV	STAY12C vs STAY12Cm	0.932	0.938	0.006
GEBV	STAY12C vs STAY12Cs	0.932	0.938	0.006
GEBV	STAY23C vs STAY23Cm	0.935	0.940	0.005
GEBV	STAY23C vs STAY23Cs	0.935	0.940	0.005
GEBV	STAY34C vs STAY34Cm	0.929	0.934	0.005
GEBV	STAY34C vs STAY34Cs	0.929	0.935	0.006

[a] Evaluated comparison comparing single-trait stayability models with bivariate models that incorporate either morphological traits or somatic cell count (SCC) as correlated predictors.

[b] Prediction accuracy of the stayability trait estimated using a single-trait model.

[c] Prediction accuracy of the stayability trait estimated using a bivariate model.

[d] Absolute gain in accuracy achieved by the bivariate model compared with the single-trait model.

For traditional pedigree-based evaluations, the inclusion of correlated phenotypic predictors resulted in a substantial increase in accuracy. The baseline single-trait EBV accuracies for STAY12C, STAY23C and STAY34C were 0.708, 0.650 and 0.722, respectively. Incorporating morphological traits or SCC as correlated predictors in a bivariate framework substantially raised these accuracies, yielding absolute gains ranging from 0.009 to 0.317. This demonstrates the power of multi-trait evaluations for lowly heritable and late-expressed traits when relying solely on pedigree and phenotypic data, as these predictors provide early and reliable information on the animal's genetic merit for survival (Weigel et al., 1998; Khansefid et al., 2021). However, this benefit was less pronounced for the latest survival stage (STAY34Cs), where the gain in prediction accuracy was near zero. Despite the massive gain in accuracy for the earlier stages, the Spearman rank correlations between single-trait and bivariate EBVs were always greater than 0.99 (data not shown). This indicates that the inclusion of predictors significantly reduces the uncertainty of the estimates without altering the ranking of the top sires, in accordance to the correlation of 0.98 of Samoré et al. (2003). Conversely, when genomic information was included (GEBV), the single-trait accuracy for the bulls were already high, ranging from 0.929 to 0.935 across all stayability stages. As a result, the integration of morphological or SCC predictors in the bivariate genomic models yielded only marginal improvements in reliability, with absolute gains of approximately 0.005 to 0.009. The high level of accuracy suggests that the dense marker data in the ssGBLUP model already captures the shared genetic variation between survival and early-life predictors. Consequently, while bivariate models could be recommended for traditional pedigree-based evaluations to accelerate genetic progress, the single-trait genomic approach is sufficient to reach near-maximum reliability for proven bulls. Focusing only on the single trait evaluations applied to the entire dataset D-total, genomic information substantially increased prediction accuracy, especially for bulls with low number of daughters. Figure 3 illustrates these results for STAY34C, the defined breeding objective, across all genotyped bulls (Figure 3A) and a subset of young bulls with fewer than 150 daughters (Figure 3B). For this trait, GEBVs raised the minimum accuracy levels from approximately 0.63 of EBVs to over 0.78 across

all bulls (part A), while for the subset of young bulls, mean accuracy rises from 0.58 of EBVS to 0.74 of GEBVs. This confirms that for low-heritability and late-expressed traits like stayability, phenotypic validation alone requires excessively long waiting periods, whereas genomics allows for medium to high reliability selection early in life (García-Ruiz et al., 2016). Figures 4A and 4B corroborate this benefit: GEBVs achieve high accuracy even with very few phenotyped daughters, whereas the added value of genomics is almost irrelevant for heavily proven bulls. This pattern confirms that genomic selection is essential for young animals with limited records, a finding consistent with studies on other lowly heritable traits (Meuwissen et al., 2001; Dhakal et al., 2015).

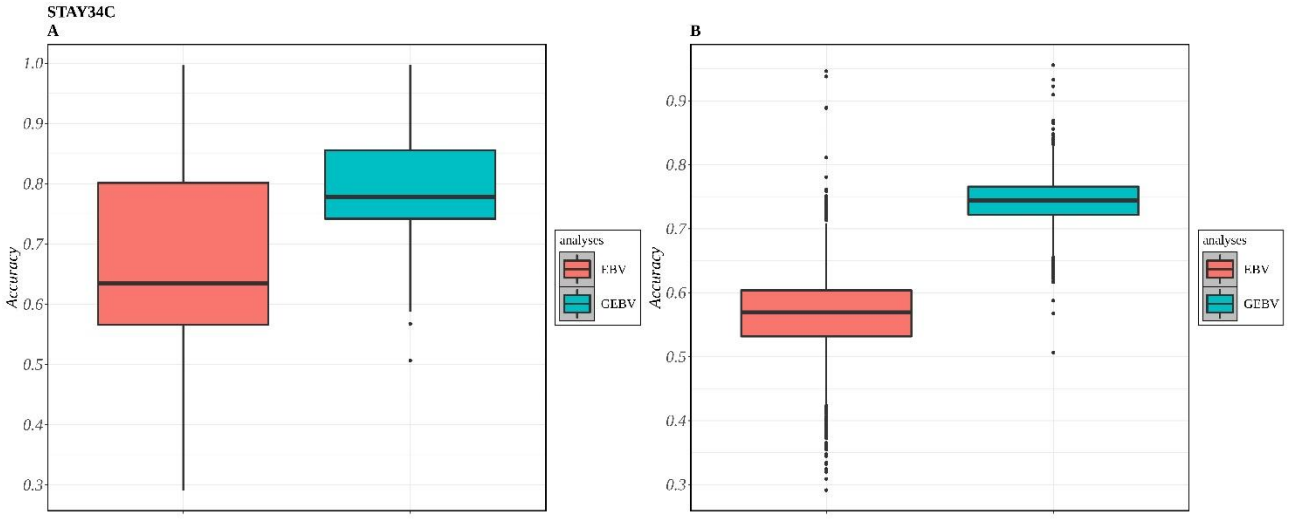

Figure 3 – Difference in prediction accuracy for pedigree-based EBVs and single-step GEBVs for STAY34C in the total dataset (A), and for bulls with less than 150 daughters (B).

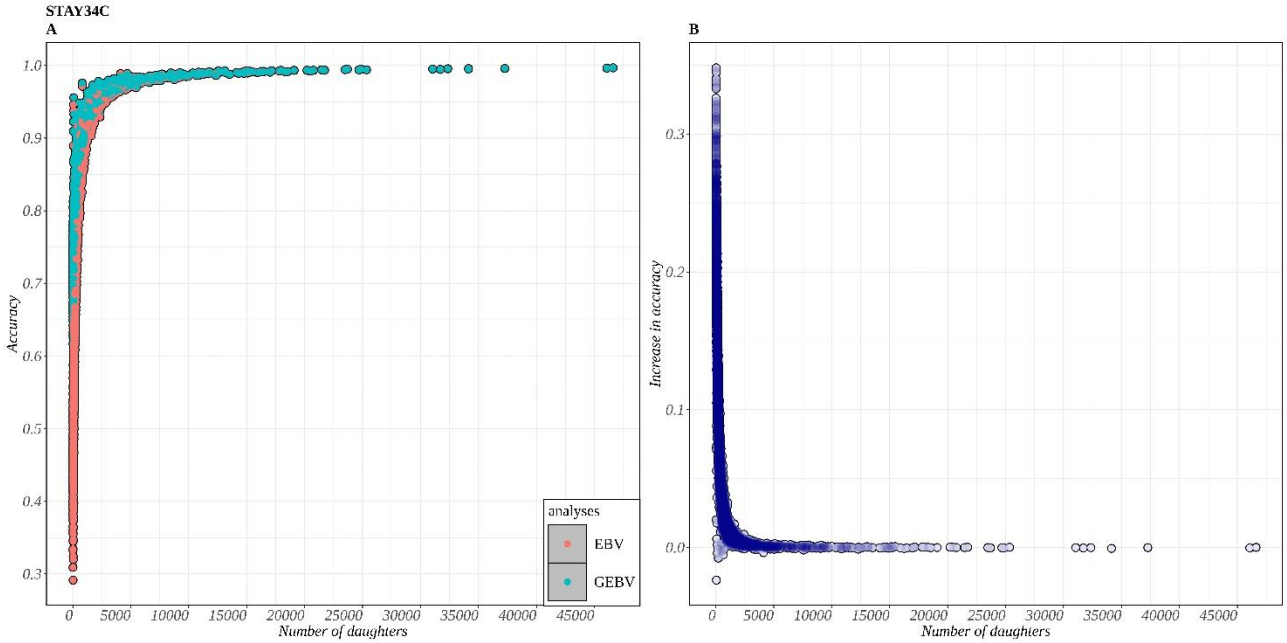

Figure 4 - Accuracies of EBV and GEBV models across daughter counts (A) and the absolute accuracy gain of GEBV relative to EBV (B) for the STAY34C trait.

Conclusion

The present study aimed to define a new approach for longevity evaluation in the Italian Holstein population. Extending the cow's ability to survive increases not only the farmer's profitability but also the social acceptance of dairy production and overall animal welfare. Despite the low heritability of this trait, our results demonstrate that a robust genetic evaluation can be established, achieving high prediction accuracies and yielding reliable breeding values. In particular, the use of genomic information effectively overcomes the limitations of late-in-life phenotypic recording. This is essential for young bulls with few or no daughters at all. Furthermore, this study proved that morphological traits and somatic cell count serve as early predictors of stayability. Their inclusion in bivariate models significantly enhances the prediction accuracy when no genotype information is available. Conversely, for genotyped animals, the dense marker data already captures this shared genetic variation, making the added benefit of a multi-trait model only marginal. Consequently, genomic evaluation emerges as the most efficient and definitive strategy to accelerate genetic progress for longevity, optimizing both computational resources and predictive power in modern breeding programs.

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Chapter 5:
General conclusions

This thesis aimed to define a novel and accurate approach for the genetic evaluation of longevity in the Italian Jersey and Holstein population.

The extension of the productive lifespan of dairy cows is of fundamental importance to the contemporary dairy industry. Enhanced longevity not only improves farm profitability by reducing replacement costs, but it also addresses the growing societal demands for improved animal welfare and the overall sustainability of dairy production. Although survival traits are inherently characterized by low heritability and late-in-life phenotypic expression, our findings demonstrate that a highly accurate genetic evaluation can be successfully implemented.

Moreover, phenotypic analyses highlighted the stage-dependent impact of different early-life predictors on cow survival. Although specific disposal codes were not available for the Jersey population, data from the Holstein breed is aligned with international trends: longevity in dairy cattle is heavily influenced by both management practices and health factors. The three most common causes of culling were determined to be low production, infertility, and mastitis. While these primary reasons drive culling decisions across all parity orders, suggesting that health status has a strong combined genetic and management component, their relative proportions vary significantly with the age of the cow. Specifically, primiparous cows are mostly affected by low production and early-lactation health issues, whereas multiparous cows are more frequently removed due to infertility or mid-lactation mastitis.

This dynamic is strongly corroborated by the prediction analysis used in the stayability evaluation for Holsteins: morphological traits, specifically body depth and an intermediate optimum for angularity,

proved to be good predictors of early survival. However, the predictive power of these conformation traits diminishes over time, reflecting a selection bottleneck where animals with poor conformation are culled early in their productive life. Conversely, udder health indicators have been demonstrated to negatively impact survival across all lactations, confirming their role as a primary driver of long-term involuntary culling. Consistent with these findings, the genetic framework applied to the Jersey breed revealed moderate-to-high genetic correlations between longevity and several morphological traits, further validating their use as effective early predictors of stayability.

In terms of the practicality of this approach, the consistently high correlations in bulls' rank indicate that a less effort in the operations can be applied both in Jersey and in Holstein. It is therefore possible to adopt a linear animal model in place of the threshold model, despite the binary nature of this trait.

From a quantitative genetic perspective, the integration of the early predictors in Holstein evaluation into bivariate models yielded contrasting benefits depending on the availability of genomic information. In traditional pedigree-based evaluations (EBVs), the inclusion of morphological traits and SCC in a multi-trait framework substantially increased prediction accuracy for young bulls, providing a highly recommended strategy for populations lacking genotype data. Conversely, the implementation of single-step genomic models (ssGBLUP) revealed that the dense marker data capture the shared genetic variation and pleiotropic effects between survival and early-life predictors. Consequently, for population with a large proportion of genotyped animals, such as the Holstein population, genomic evaluations (GEBVs) are sufficient to achieve near-maximum reliability, rendering the added computational complexity of bivariate models largely redundant. This outcome confirms that genomic information effectively overcomes the historical limitations associated with late-in-life phenotypic recording, likewise for stayability.

The study done culminates in a notable outcome for Jersey, as from April 2025, the Italian Jersey breed has established a national and international genetic evaluation. As a results, Italian farmers will

benefit not only from national evaluations but also from the effective use of imported bulls that have been evaluated with the adaption to the national context.

These implementations will result in a breeding scheme that will yield cows that are more resilient, healthier, and longer-living, thereby optimising both the economic efficiency and the social acceptability of the dairy sector. Increasing cow longevity, but even more reducing involuntary culling, will decrease negative health impact, increase the profitability of the cow, improve animal welfare and farmer's wellbeing, contributing to the sustainability of the dairy sector.

However, a potential trade-off of extending cow longevity is the reduction in the annual rate of genetic progress due to a slower herd replacement rate. Indeed, a lower culling rate decreases the need for replacement heifers, which consequently increases the generation interval and the genetic lag between the older cows in the herd and the genetically improved younger animals. Therefore, a forced increase in longevity, without appropriate adjustments to the structural and reproductive management of the farm, such as the targeted use of sexed and beef semen to generate selective replacements, may unintentionally decelerate overall genetic progress. Consequently, defining the optimal productive lifespan requires a holistic approach that simultaneously integrates the social, environmental, and economic components of the dairy sector. It is important to recognise that achieving the right balance between longevity and genetic progress can vary greatly between farms. This is due to the unique business reality and management conditions of each individual farmer. It is therefore essential that this evaluation is carefully tailored to suit the specific needs of each farmer.

List of abbreviations

AFC: age at first calving

AIA: Italian associations of breeders

ANAFIBJ: national breeders association of Italian Holstein, Brown and Jersey dairy cattle

BCS: body condition score

BGLR**:** bayesian generalized linear regression

BHB: beta-hydroxybutyrate

BLUP: best linear unbiased prediction

BRR: bayesian ridge regression

CG: contemporary group

DFS: Denmark, Finland, Sweden

DIM: days in milk

DM: difference in milk production deviation

DRP: deregressed proofs

DSR: bulls' daughter's stayability rate

EAAP: European association for animal production

EBVs: estimated breeding values

EDC: effective daughter contribution

EURC: European union reference centre

GEBVs: genomic estimated breeding values

GMACE: genomic multiple-trait across country evaluation

GxE: genotype by environment interactions

h^2: heritability

HL: herd life

HSC: herd size change

ICAR: international committee for animal recording

IDF: international dairy federation

LM-MT-AM-BLUP: linear multiple-trait BLUP animal model

MACE: multiple-trait across country evaluation

MAF: minor allele frequency

PDO: protected designation of origin

PFT, IES, and ICS-PR: Italian national selection indexes; Production, Functionality, Type (PFT); Health and Economic Index (IES); Cheese-making and Sustainability Index (ICS-PR)

SCC: somatic cell counts

SNPs: single-nucleotide polymorphism

ssGBLUP: single-step genomic estimated breeding values

ST S-MGS SA: single-trait sire-maternal grandsire survival analysis

STAY: stayability traits

ST-RR-BLUP-AM: single-trait random regression BLUP animal model

VCE: variance components estimation

List of scientific contributions

Peer-reviewed publication

Fabris A., Tiezzi F., Finocchiaro R., Marusi M., Cassandro M., 2025. *Genetic evaluation of longevity in Italian Jersey.* Italian Journal of Animal Science, 24(1):68-77. https://doi.org/10.1080/1828051X.2024.2440124

Under review publications

Fabris A., Tiezzi F., Panetto J.C.C., Finocchiaro R., Marusi M., Cassandro M. – *Genetic parameter estimations for different stayability approaches in the Italian Holstein cattle population*. Submitted to Journal of Animal Breeding and Genetics, currently under review.

Fabris A., Tiezzi F., Callegaro S., Finocchiaro R., Marusi M., Cassandro M. - *Assessing stayability in Italian Holstein cattle: type traits and somatic cell count as early predictors for traditional and genomic estimated breeding values.* Currently under internal peer-review, to be submitted.

Conferences

Fabris, A., Tiezzi, F., Finocchiaro, R., Marusi, M., Cassandro, M., 2023. *Preliminary genetic analysis for survival in Italian Jersey*. Book of Abstracts of the XXV National Congress of the Animal Science and Production Association (ASPA), June, Bari, Italy. Oral presentation.

Fabris, A., Tiezzi, F., Finocchiaro, R., Marusi, M., Cassandro, 2024. *Implementation of longevity genetic index in Italian Jersey*. Book of Abstracts of the 75th Annual Meeting of the European Federation of Animal Science (EAAP), 1 September – 5 September, Firenze, Italy. Poster presentation.

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Co-author publications

S. Magro, M. De Marchi, M. Cassandro, R. Finocchiaro, A. Fabris, M. Marusi, and A. Costa, 2025. Blood parameters predicted from milk spectra are candidate indicator traits of hyperketonemia - a retrospective study in the Italian Holstein population. Journal of Dairy Science, 108(3):2683-2696. https://doi.org/10.3168/jds.2024-25170

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