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Original article

Estimation of heritability and genetic trend for herd life and productive life in Organic Holstein Cattle

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Abstract

This study aims to estimate the heritability and genetic trend for herd life (HL) and productive life (PL) on an organic dairy cattle farm in the Aegean Region of Turkey. The data from 1093 cows culled from the farm were evaluated. Ancestors were collected by going 6 generations back. Thus, the pedigree file consisted of 4212 animals. Variance components and breeding values were estimated using the MTDFREML package program. The heritability for both HL and PL was found to be equal and 0.16. Standard errors of the heritabilities were 0.06 and 0.08, respectively. Genetic progress per year for HL and PL was 1.60 and 0.60 days, respectively. Estimations for HL and PL were generally consistent with other studies. Heritabilities indicate that breeding for HL and PL is possible; however, response to selection would be slow. Despite the extended length of the selection process, genetic variation could be sufficient for a successful breeding. Indirect selection based on particular traits that have a strong relationship with HL and PL may be beneficial. Our study showed a phenotypic decline in HL and PL, confirming the fluctuation in genetic trends. Therefore, the importance of life traits in the selection index should be emphasised.

Keywords: breeding success, longevity, MTDFREML, organic dairy cattle

Introduction

The economic importance of life traits has been widely recognized and emphasized in many studies by animal breeders (Cassandro et al. 1999, Hu et al. 2021). Herd life (HL) is defined as the total number of days between birth and culling. Productive life (PL), also known as longevity, is defined as the total number of days between the first calving and culling (Zavadilová and Zink 2013), is considered one of the most critical functional traits in cattle breeding with high economic value but low heritability, and can also complement the breeding value of production traits (Hu et al. 2021).

PL is a trait that significantly impacts overall profitability and plays an important role in enhancing efficiency in terms of milk production (Cassandro et al. 1999, Martinez et al. 2004). Increased PL may lead to lower herd replacement rates, reduced rearing, veterinary, and insemination costs, a higher proportion of productive cows in the herd due to enhanced fertility and welfare, and higher voluntary culling rates, allowing cows to demonstrate their full potential, which is reached in the 3rd or 4th lactations, and raises the possibility of using individuals with higher potential among replacements in breeding.

PL has long been included in developed countries' selection indexes as an important breeding target. However, it has not been directly integrated into selection indexes in many developing countries. A survey conducted by ICAR in 23 countries in 2012 showed that genetic evaluations for breeding targets (involving up to 43 functional traits per country, including calving ease, fertility, longevity, foot and leg characteristics, and indirect health traits) are very common (Stock et al. 2012). It was stated that the decline in PL and cow fertility had led various countries to include these traits in breeding programs to achieve breeding success (Mirhabibi et al. 2018).

Milk yield and its components and type traits are part of the conventional cattle breeding program implemented in Turkey over the past few decades. HL and PL are not used directly or indirectly in the breeding program. The number of organic dairy farms is around 20. Since herd renewal costs are much higher in organic livestock, HL and PL are of greater importance. The aim of this study is to estimate heritability and the genetic trend of HL and PL for Holstein cattle raised under organic conditions in Turkey.

Materials and Methods

Environmental Conditions

The research was conducted on a private organic dairy cattle farm with a capacity of 500 Holstein cows, which is a member of the Cattle Breeders' Association, located in Aydın Province, Southwestern Turkey (37°46′48.81" N; 27°51′30.78" E). Aydın province is a coastal area bordering the Aegean Sea, under Mediterranean climatic conditions, with hot and dry summers and mild to cool, wet winters. The cows roamed freely inside semi-open free stalls and outside the cowshed. Total mixed ration (TMR) is served twice a day as roughage (consisting of maize silage, alfalfa grass and wheat straw) and concentrate feed with additives throughout the year. Feed is obtained by processing over 2000 hectares of land belonging to the farm under organic production conditions. The cows are milked three times a day using a 2×10 herringbone milking parlor system equipped with electronic devices that provide various data flow to the herd management system.

Animals

Lifetime records of 72 sires' 1093 daughters and 796 dams were evaluated for HL and PL, respectively. All cows under investigation were either culled or slaughtered, ensuring that each cow's precise HL and PL were determined. If female calves were culled before becoming heifers or cows, their lifespan was included in the calculation of HL. However, for PL calculation, only the lifespan of cows was considered.

Pedigree and data files

The pedigree file was generated by ordering the animals from oldest to youngest according to their birth dates. The 72 sires mentioned above have three or more offspring and are from USA (55), Turkey (6), Italy (4), Canada (3), Germany (3), and France (1). Pedigree information for the sires was acquired by going 6 generations back from the Lactanet (2021) website.

In this way, information for a total of 913 ancestors was added to the pedigree file. Consequently, the pedigree file consisted of 4212 animals. Alphanumeric codes assigned to the animals and their parents in the pedigree file were processed using the CFC package program (Sargolzaei et al. 2006), and the animals were given numeric codes by reordering them from oldest to youngest.

Data analysis

In the evaluation of the data, Microsoft Excel (2016), Minitab (2019), CFC (Sargolzaei et al. 2006), and MTDFREML (Boldman et al. 1995) programs were used. To determine the factors affecting the characteristics examined in the study, analysis of variance (ANOVA) was used.

Heritabilities were estimated using Multiple-Trait Derivative-Free Restricted Maximum Likelihood (MTDFREML) in a single-trait animal model (Boldman et al. 1995). The model included the year the cow was born as a fixed effect and the direct genetic animal effect as a random effect for both traits. As a result, variance components, including additive genetic variance (σ_p^2), residual variance (σ_p^2), and phenotypic variance (σ_p^2), were estimated. Using these variance components, heritability (h^2) was estimated for each trait. The convergence criterion was first set to 10^{-6} and later to 10^{-9}.

The mixed model used in the analysis for HL and PL is as follows: $Y = Xb + Za + e$

Here, Y is the vector containing observed values for each trait, X is the design matrix for fixed effect (year), Z is the design matrix for random effects, b is the vector

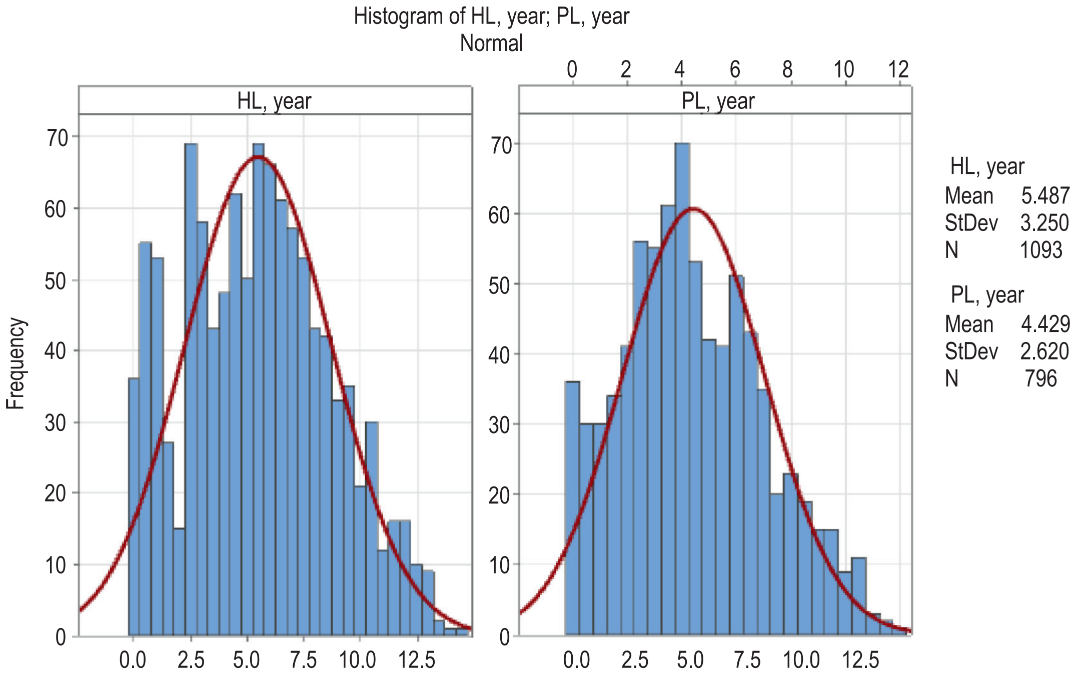

Fig. 1. Data histogram.
HL – Herd life, PL – Productive life

Table 1. Descriptive statistics for herd life (HL) and productive life (PL) in dairy cattle.

Trait	N	Mean	SEM	St Dev	CV	Minimum	Median	Maximum
HL, year	1093	5.49	0.10	3.25	59.2	0.02	5.43	14.48
PL, year	796	4.43	0.09	2.62	59.2	0.01	4.06	11.89

HL – Herd life, PL – Productive life. N – Number of data, SEM – Standart error of the mean, St Dev – Standard deviation, CV – Coefficient of variation

of fixed effects, *a* is the vector of random effects (breeding values), and *e* is the vector of error effects.

Genetic trend

The annual change in genetic value can be used to measure the success of a selection program applied for a certain period of generations in a population for a particular trait. This change observed in estimated breeding values (EBV) over the years is expressed as the genetic trend. Genetic trends give information on both the direction and the magnitude of the phenotypic trend and demonstrate whether or not the selection of ancestors of the next generations is successful. The genetic trend of the herd investigated in this study was determined by taking the EBVs' average according to the animals' birth years. Estimates of genetic change per year were determined using the regression of the EBV of the animals on their birth years according to the following model: $Y_{ij} = a + b_{yx}Xi + e_{ij}$

Here, Y_i is the predicted breeding value of the animal i, is the regression constant, b_{yx} is the genetic progress per year, X_i is the birth year of the animal i, e_{ij} is the term of error.

Results

Descriptive Statistics

Table 1 summarises the observations and descriptive statistics for HL and PL. The mean of HL and PL in cows are 5.49 and 4.43 years, respectively. PL indicates that heifer cows are culled from the herd after 4.43 years from the first calving. Considering the average calving interval in the herd, it can be calculated that 3.4 calves are born per cow in 4.43 years. To enhance the understanding of the data distribution, a histogram is presented as Fig. 1.

All female calves and cows that were culled were included in the calculation. This means that there could be cows that were culled in the herd one month after calving, as well as cows that stayed in the herd for up to 14 years, as seen from the maximum value. In other words, females were only culled from the herd for involuntary reasons. It is clearly seen from Fig. 2 that there has been a decline in herd life over the years. HL, which was 9.3 years in 2001, has gradually decreased and has been less than 3 years since 2015. The continuous decline of HL since 2001 is shown in Fig. 2.

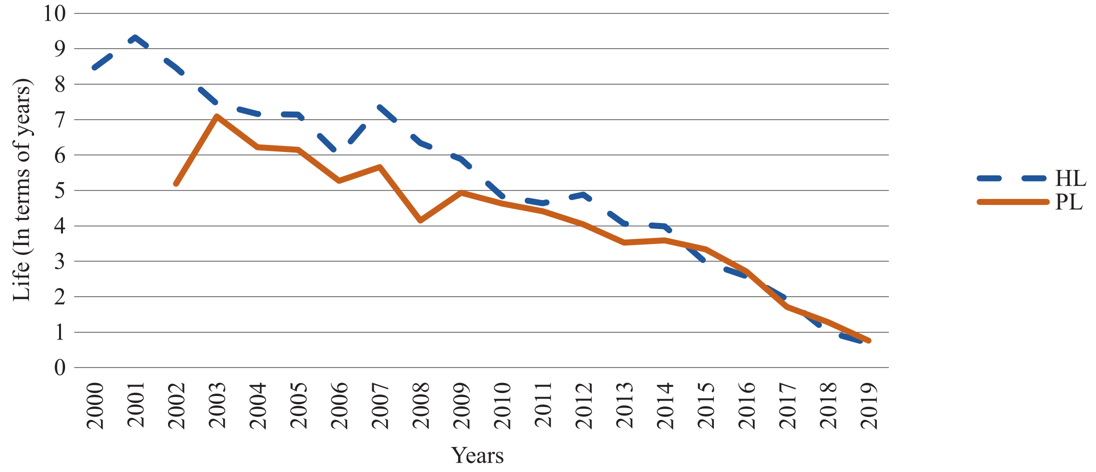

Fig. 2. The phenotypic trend for HL and PL.
HL – Herd life, PL– Productive life

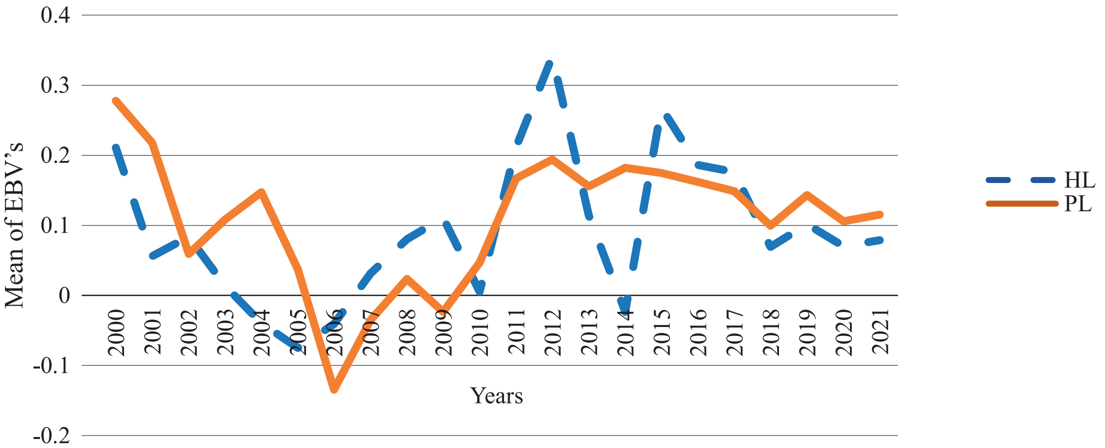

Fig. 3. Genetic trend of HL and PL.
EBV – Estimated breeding value, HL – True herd life, PL – Productive life

Table 2. Variance components and genetic parameter estimations for HL and PL.

Trait				h^2±SE	e^2±SE	-2LogL
HL, Year	0.98	5.16	6.14	0.16 ± 0.06	0.84 ± 0.06	3068.59
PL, Year	0.81	4.17	4.99	0.16 ± 0.08	0.84 ± 0.08	2074.25

HL – Herd life, PL – Productive life

Although this situation can be interpreted as deliberately rejuvenating the herd in recent years, it is also possible that the animals were involuntarily culled.

Heritabilities and genetic trend

The variance components and heritabilities for HL and PL are given in Table 2. Heritability estimation was as low as 0.16 for both HL and PL. Considering all the data presented, a general conclusion can be reached that traits related to HL and PL exhibit a low heritability, indicating their substantial susceptibility to environmental factors.

The genetic trends for HL and PL traits are given in Fig. 3.

Genetic progress per year for HL and PL is found to be 0.00438 and 0.00163 years or 1.60 and 0.60 days, respectively.

Discussion

The breeding target of dairy cattle has started to switch towards a more balanced breeding goal, considering lifetime, welfare, health, environmental sustainability, and milk quality. This switch is driven by the growing emphasis on breeding value, lifetime benefits and the impacts of climate change. HL and PL are highly desirable traits within dairy production that greatly influence the operations' overall profitability.

An extended PL may enhance profitability by reducing the annual expenses related to cow replacements and elevating voluntary culling rates while lowering involuntary culling rates (Martinez et al. 2004). The need for dairy farmers to provide cows with higher economic efficiency leads to the interest in placing HL and PL in the breeding program for the Turkish Holstein population. Cow replacement costs are very high, especially in organic milk production. The organic cattle market in Turkey is quite limited, and farmers usually have to meet the herd's cow renewal needs themselves. This is why cows that need to be culled cannot be culled in time, so breeders continue production with less efficiency and more cost. It is important to define what constitutes an organic herd, as organic producers often face restrictions on the use of antibiotics, even for sick animals. This can lead to involuntary culling to prevent animal suffering when treatment is not permissible, potentially impacting the PL differently compared to conventional herds. Selection for PL is especially attractive to reduce the involuntary culling rate, which has become a higher cost in Turkish dairy herds.

Evaluating the genetic potential of cattle in terms of HL and PL is of great importance as it allows animals to demonstrate their full genetic capabilities and encourages producers to review selection criteria, thus accelerating genetic advancements; such evaluation also allows an increase in voluntary culling and a decrease in involuntary culling (Imbayarwo-Chikosi et al. 2016). Another purpose of selection for PL is to give animals the opportunity to live longer (Martinez et al. 2004). However, selection for increasing lifetime is hindered due to low heritability and the length of time required to complete the cows' records. It is also expected to progress more slowly due to the low heritability levels and potentially lengthening of the generation interval (Martinez et al. 2004). Nevertheless, with increased lifetime, the herd's average production experiences an increase due to a larger share of the culling decision factor in production rates, while simultaneously increasing the proportion of mature cows, known for their higher milk yields compared to younger cows. This will enable older cows to reach their highest milk production potential based on age.

Some researchers have reported a negative relationship between milk yield and PL (Hare et al. 2006, Egger-Danner et al. 2015). The average 305 DMY from 1991 to 2011 increased from 7000 to 11000 kg, while PL from 1992 to 2007 decreased from 2000 to 1000 days, respectively (Mirhabibi et al. 2018). However, the correlation between HL and milk yield is not yet clear. Looking ahead, if HL and PL are going to be fully integrated into selection indexes, a comprehensive evaluation will be required to determine whether this integration will affect the milk yield of dairy cows or not (Hu et al. 2021).

In recent years, the dairy cattle industry in multiple countries has witnessed a decline in PL. There was a widespread negative genetic trend for PL in various countries until 2000, but positive genetic trends emerged later. These positive genetic trends signify a growing emphasis on PL within national selection indices (Mirhabibi et al. 2018). In the Netherlands, thr PL of Holstein dairy cattle declined from 4.5 years to 3.5 years between 1979 and 1986 (Vollema and Groen 1998). Also in the US, the PL of Holstein cattle decreased from 3.2 years to 2.8 years between 1980 and 1994 (Hare et al. 2006). The genetic trend for PL decreased in various countries from 1990 to 2000 in Holstein cattle. Afterwards, the genetic trend increased in a positive direction and exceeded the average value (Egger-Danner et al. 2015).

The decline in PL not only significantly impacts productivity but also limits the scope for selecting other desirable traits. It was reported that in traditional breeding, researchers in various countries have used different models and trait definitions to directly or indirectly select for HL and PL (Buenger et al. 2001, Hu et al. 2021). The accuracy of HL and PL evaluations could be improved with direct and indirect measures combining Multiple-Trait assessments (Miglior et al. 2017).

It was reported that there was a better genetic progress of 3.3 days per year (Cassandro et al. 1999) compared to 0.60 days of genetic progression for PL in this study. The HL average of 5.49 years in the present study is similar to 5.33 years (Alıç 2007), higher than the result of 4.69 years (Mirhabibi et al. 2018), but lower than the results of 5.64 years (Yaylak 2003), 6.10 years (Boğokaşayan and Bakır 2013) and 6.20 years (Koç 2017). However, the PL of 4.43 years is higher than 2.90 (Yaylak 2003), 3.39 (Boğokaşayan and Bakır 2013) and 2.61 (Mirhabibi et al. 2018).

The PL average of 4.43 years in the present study is higher than Holstein cows in Spain at 2.19 years and in Catalonia at 2.47 years (Chirinos et al. 2007), and also higher than the value of 2.39 years for Holstein Friesian in Turkey (Koç 2017). An analysis conducted on Holstein cows in Tunisia for PL reached 2.62 years (M'hamdi et al. 2004). In contrast, a longer PL value of 6.03 years was observed for PL for Holstein cows in Poland (Nienartowicz-Zdrojewska et al. 2009).

Heritability of HL and PL was found to be 0.16 and 0.16 respectively, higher than the values of 0.03 and 0.03 respectively (Boldman et al. 1992), 0.03 and 0.03 respectively (Short and Lawlor 1992), 0.07 for PL (Vollema and Groen 1998), 0.06 and 0.04 respectively (Cassandro et al. 1999), 0.04 and 0.03 respectively (Daliri et al. 2008), 0.06 for PL (Pritchard et al. 2013), 0.03 and 0.05 respectively (Zavadilová and Štípková 2012), 0.01 for PL (Zavadilová and Zink 2013), 0.03 and 0.03 respectively (Mirhabibi et al. 2018) and 0.06 for PL (Djedović et al. 2023) but similar to the value of 0.19 for PL (M'hamdi et al. 2004). Heritabilities in the present study are higher than most published values. This could be attributed to the analysis being confined to a single herd, which may reduce environmental noise and variability.

These heritabilities indicate that breeding for HL and PL is possible. However, response to selection would be slow, particularly when considering the antagonistic relationships between HL and PL and other traits, such as high milk production (Pritchard et al. 2013).

In this study, estimations for HL and PL were generally consistent with other studies, regardless of the different models used by the researchers. According to the results of this study, it can be said that despite the extended length of the selection process, genetic variation is sufficient to achieve successful breeding in terms of HL and PL. In addition, indirect selection may be beneficial when the heritabilities of indirect traits are greater than the heritability of HL or PL (Hu et al. 2021). Conformation traits have long been used as indirect selection criteria for an extended lifetime, and these traits can be assessed early in life and exhibit moderate to high genetic correlations in contrast to the low heritability of life traits (Short and Lawlor 1992, Zavadilová and Štípková 2012, Pritchard et al. 2013, Imbayarwo-Chikosi et al. 2016). In particular, the feet, legs and the mammary system, have a strong relationship with PL. Although the reasons for culling from the herd were not emphasized in the study, fertility, udder, and feet problems, as well as metabolic diseases, can be counted among the reasons for involuntary culling (Barański et al. 2021, Barański et al. 2023).

In conclusion, selection for HL and/or PL could be effective in a breeding program. However, it may proceed at a relatively slow pace, mainly due to low heritability levels and long generation intervals. Since dairy cattle are bred globally, it is vital to investigate the interaction between life traits and environmental variations across countries due to the low heritability and high environmental impact. There is no unity among countries in terms of definitions of life traits, and since all terms are used interchangeably, inconsistencies and ambiguities arise in the definitions (Brickell and Wathes 2011). Therefore, there is an urgent need to establish a standardized terminology for life traits, and researchers should be guided to select specific definitions appropriate to the goals of their own studies. Consequently, it becomes necessary to conduct comprehensive studies on the interactions between life traits and locally common environmental conditions that animals experience throughout their entire life. It can be stated that enhancing production and type traits, whether through genetic selection or improved management practices, would positively influence the lifetime of cows. Consequently, the judicious selection of appropriate type traits, especially related to functional traits, can effectively predict HL and PL. However, animal welfare and life traits can be ignored if the national breeding targets are focused on production efficiency and profit. Therefore, the future selection of dairy cattle for HL and PL will require the establishment of a fully integrated and balanced selection index. Although our study showed a phenotypic decline in HL and PL, it confirmed that the genetic trends fluctuate. By maintaining careful record-keeping practices, using suitable statistical models for genetic evaluation, and applying a well-balanced selection index, it is possible to achieve more significant improvements in HL and PL for the Turkish Holstein population in the future. Different models may be recommended accordingly. Therefore, developing a selection index that includes HL and PL in Turkey is important.

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