Genetic evaluation for longevity of dairy cattle in the Netherlands

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Abstract

Longevity of dairy cattle is an important trait from an economic and welfare perspective, as well as from a societal and government perspective. For a farmer it is beneficial to keep older cows, as it will reduce costs of rearing. The Dutch government aims to reduce the environmental impact of livestock, and for that it is also beneficial to keep older cows. Older cows produce more on average, and feed is converted more efficiently. In the Dutch-Flemish genetic evaluation of functional longevity a random regression animal model with a fifth order Legendre polynomial is used, where within-herd production level is fitted as an explanatory effect. Published breeding values for longevity are partially based on predictor traits. The breeding values for milk production, as well as udder health, claw health and locomotion are added as predictor traits through selection index theory. In this paper the impact of the introduction of genetic evaluation of longevity is assessed. Over the past 25 years all statistics on longevity metrics have been favorable. Productive life increased with 337 days to 1,445 days for cows culled in 2024. Together with a reduced amount of youngstock, the rearing period reduced 40 days to 763 days. The mean number of calvings increased by 0.8 to 3.9 calvings. Lifetime production increased in 25 years by 14,329 kg to 38,283 kg of milk (with 4.40% fat and 3.58% protein), resulting in 1,684 kg fat and 1,369 kg protein. Production per day of life increased by 4.8 kg to 17.1 kg of milk. Longevity is a result of management (e.g. feeding, housing and culling decisions), environment, and genetics. Genetically, longevity increased by 600 days, which suggests that the full genetic potential is not yet utilized. The strong increase of the genetic trend for longevity was supported by selection on udder health, claw health and feet & legs. Culling decisions can also be affected by governmental changes in regulations. The genetic trend is more consistent over the years than the phenotypic trend. Long-term trends show that all these factors together resulted in significant improvements for longevity and lifetime production. With the continuing improvement of production and health traits further improvement of longevity is expected.

Key words: longevity, genetic evaluation, trends

Introduction

Longevity of dairy cattle is an important trait from an economic and welfare perspective, as well as from a societal and government perspective. For a farmer it is beneficial to keep older cows, as it will reduce costs of rearing. The Dutch government aims to reduce the environmental impact of livestock, and for that it is also beneficial to keep older cows. Older cows produce more on average, and feed is converted more efficiently.

The genetic evaluation for longevity was introduced in 1999 based on a proportional hazard model and the published breeding value was for functional longevity, where functional longevity is longevity corrected for within-herd production level. The published breeding value changed in 2008 to true longevity, meaning that the adjustment for production was removed from the statistical model. In 2018 the statistical model was revised and changed to a random regression animal model, and true longevity is published.

Since the introduction of the breeding value of longevity it has not been investigated how lifetime performance of Dutch and Flemish cattle has evolved, and in this paper the impact of genetics on lifetime performance is assessed.

Genetic evaluation

Data

Length of productive life is defined as the time from first calving to the last test date for milk production, before the animal died or was culled for slaughter; this also included dry periods. The analysed period is length of productive life until 72 mo after first calving. The data set is constructed from records of pedigree, lactations and movements of cows in the Netherlands and Flanders. Herdbook-registered cows from a dairy breed with a test-day record on or after January 1, 1988 are included for Dutch data, and on or after January 1, 2006 for Flemish data. Data up to February 14, 2025 are included in the most recent genetic evaluation of April 2025. Cows are required to have an age at first calving between 20 and 40 mo. If the first calving of a cow took place before the starting date of the study, the record is considered to be left-truncated. Records of cows that are still alive at the time of data collection are considered to be right-censored. Records of cows that moved to another milking herd are also considered to be right-censored, if this herd is not participating in a milk recording scheme.

Records are constructed for each month a cow is present in a herd, from first calving up to the month the cow is culled, or 72 mo, or when the cow is censored. A cow culled in month j has j – 1 records with score 100 (alive), and record j with score 0 (culled). Monthly records are treated as missing after culling.

Additional selection criteria included: 1) data of a cow is used after a waiting period of 120 days after first calving; 2) Culled heifers without a milk testing, mostly culled before the first milk test, present in a herd with milk recording, are included; 3) Herd-year-months need to have a survival rate of at least 70%; 4) Herd-year-months with 5 or more culled animals need to have a survival rate that is higher than the mean survival rate of the past 12 months minus three times the standard deviation of survival of the past 12 months.

Statistical model

The genetic evaluation for the Netherlands and Flanders is a random regression animal model where survival per month is analysed:

$$
\begin{aligned}
Y_{ijklmno} = {} & HYS\_LS_i + YSAM\_LS_j + HSC_k \\
& + het_l + rec_m \\
& + \sum_{q=0}^{5} animal_{nq}\, leg_{oq} \\
& + error_{ijklmno}
\end{aligned}
$$

where

$Y_{ijklmno}$: observation for survival in month o after first calving; mo 1 – 72;

HYS_LS_i : fixed effect for herd-year-season x lactation-stage i; year-season observation, lactation split in 1, 2, 3+, stage of lactation split in mo 1-2, 3-9, 10+ and dry period;

$YSAM\_LS_j$: fixed effect for year-season x AFC x within-herd production level x lactation-stage j; year-season of observation, AFC in months 20, 21, …, 34, 35+, within-herd production level is defined per 3 years and is divided in 5 classes of 20% each for predicted or realised age-corrected 305-day yield of kg fat and protein;

HSC_k : fixed effect for herd size change k; HSC is calculated by comparing the number of cows present in a herd in a year with the number of cows in the same herd one year later. Seven classes are distinguished: shrinkage between 90 and 50%, shrinkage between 50 and 30%, shrinkage between 30 and 10%, neither shrinkage nor growth over 10%, growth between 10 and 30%, growth over 30%, and herds that were terminated (more than 90% shrinkage).

het_l : covariable for heterosis l of animal n;

rec_m : covariable for recombination m of animal n;

$animal_{nq}$: additive genetic random regression coefficient of animal n corresponding to polynomial q;

leg_{oq} : covariates of order q Legendre polynomial for month o;
$rest_{ijklmno}$: random residual effect of $Y_{ijklmno}$.

Within-herd production level is fitted to correct for culling due to low production, which is assumed to be the major source of voluntary culling yielding EBV for functional longevity.

Breeding values

In the direct breeding value estimation breeding values for functional longevity are estimated, because survival per month is adjusted for within-herd production level in the statistical model. Bull owners and farmers are used to using the breeding value for true longevity. With a selection index true longevity is derived from functional longevity and the production traits kg milk, kg fat, and kg protein.

Indirect information is used next to the direct information for longevity to increase the reliability of the breeding value longevity for young animals, as little direct information is available. Traits that are early available in life are preferred to increase the reliability, and for this the breeding values for subclinical mastitis, claw health and locomotion are used in a selection index.

Results & Discussion

The total data set for the routine genetic evaluation of longevity of April 2025 comprised 481,058,418 records from 14,292,149 animals in 44,328 herds. The pedigree included 16,834,548 animals including 226 phantom groups.

Genetic trend

The genetic trend for longevity for black & white Holstein cows is shown in figure 1. Since 2000 the genetic level increased by 615 days. Up to 2010 the average increase per year was 17 days, and since 2010 the increase per year increased to 37 days.

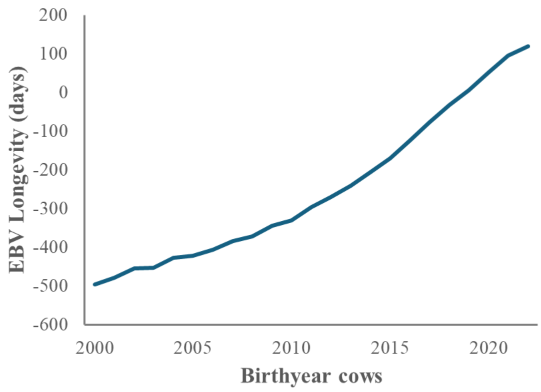

Figure 1. Genetic trend for black and white Holstein cows in the Netherlands.

Phenotypic trend

The phenotypic trend for productive life for culled herdbook cows in the Netherlands is shown in figure 2. From 2000 to 2024 the productive life increased by 337 days from 1,108 days to 1,445 days. This increase fluctuates over these 25 years. From 2000 to 2008 every year there was an increase in productive life. After 2008 productive life stabilized until 2016. From 2017 to 2019 the productive life declined because of culling excess cows related to national phosphate regulation. Since 2019 the productive life shows a sharp increase of 200 days in just four years. In the last two years, 2023 and 2024, the increase in productive life leveled off, likely due to more culling due to blue tongue infections.

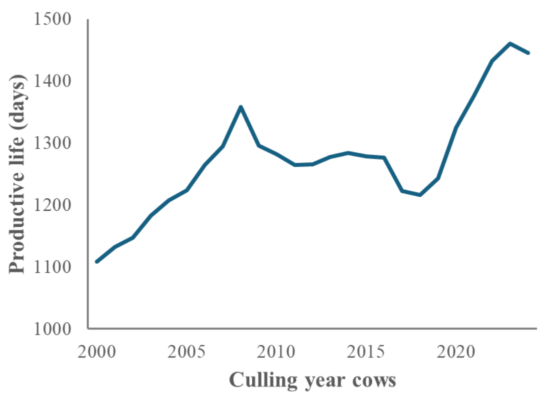

Figure 2. Phenotypic trend for productive life for culled herdbook cows in the Netherlands.

Genetic vs. phenotypic trend

The genetic trend and phenotypic trend both showed an increase since 2000. However, the phenotypic progress was 337 days, and the genetic progress was 615 days. Genetically the cows have the potential to get older than what is currently achieved.

The genetic trend for longevity shows a steady yearly increase with an acceleration since 2010 due to the introduction of genomics. The phenotypic trend shows more fluctuations, where especially the decline in the years 2017 to 2019 showed that national regulations can have significant effect. Also, the increase in productive leveled off in 2023 and 2024 showed that the environment in the form of disease pressure (blue tongue infections) has a marked effect.

The sharp increase in productive life since 2019 is the result of a change in replacement strategy of farmers. The incentive in change in replacement strategy is that it is more profitable to have a larger proportion of dairy cows compared to replacements. Genetically the cows are able to produce longer, and the sharp increase in productive life showed that cows are able to show their genetic potential.

Figure 3 shows the realized extra days for productive life for the daughters of black & white Holstein bulls born in 2012. The bulls are divided in four EBV classes. The daughters of the bulls with a breeding value longevity between -250 and 0 days had 1266 productive days after their first calving. Compared to the lowest EBV class these daughters have on average 112 days longer productive life. The daughters of bulls in the highest EBV class had 1484 productive days. The achieved productive life corresponds well with the breeding value of the EBV class. The difference between the productive life of the daughters of the best and the lowest scoring bulls for longevity is 330 days, and the difference in EBV is with 719 days. The expected difference is half of the EBV when mated on average cows, and the phenotypic difference is close to half of the genetic difference.

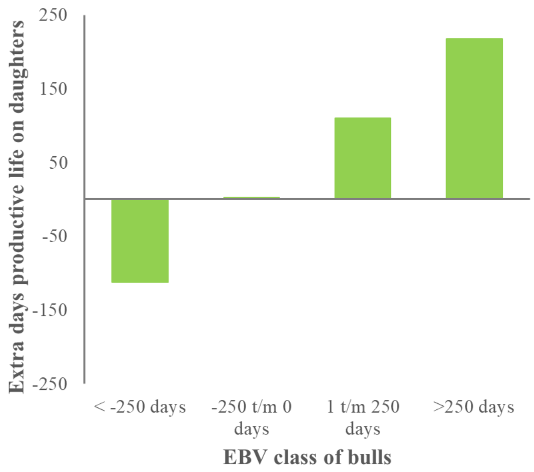

Figure 3. Realised extra days for productive life for daughters of black & white Holstein bulls born in 2012 divided in four EBV classes.

Change over time

Previous research showed that longevity changed over time. Van Pelt *et al.* (2016b) showed that the culling for low production reduced phenotypically. To compare animals genetically over time it is preferred to account for within-herd production level (Van Pelt *et al.*, 2016a), as genetically functional longevity showed less or no bias over years. For this reason, the genetic evaluation is analysing functional longevity.

The genetic parameters used in the genetic evaluation are based on phenotypic data from 1988 up to 2015. From the parameters genetic part-whole correlations can be derived as described in Van Pelt *et al.* (2015). The genetic parameters were re-estimated on a more recent data set with phenotypic data from 2008 up to 2023. In figure 4 the part-whole correlations for functional longevity are shown for the current parameters and the re-estimated parameters. With the current parameters the genetic correlation of cumulative survival up to 6 months after first calving with 72 months after first calving is 0.81, and then gradually increases. This shows that survival in early life is genetically different from survival later in life. With the re-estimated parameters based on more recent years the genetic correlations up to 24 months after first calving with total survival up to 72 months are lower than with the current parameters, and as low as 0.75. Over the years, survival in early life is genetically more different from survival in later life.

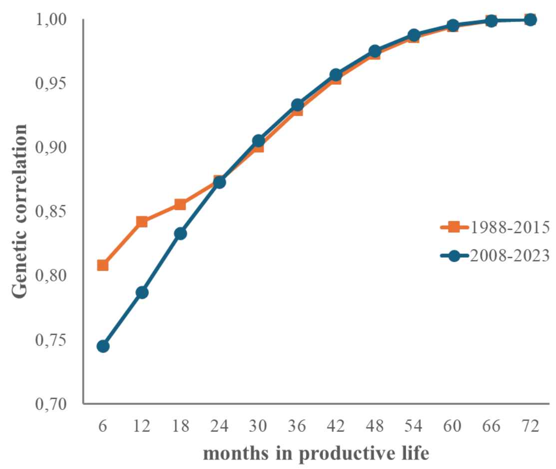

Figure 4. Genetic part-whole correlations for functional longevity based on phenotypic data from 1988 up to 2015 and from 2008 up to 2023.

Lifetime performance statistics

Over the past 25 years all statistics (CRV, 2024) on longevity metrics have been favorable (Table 1). Productive life increased with 337 days to 1,445 days for cows culled in 2024. Together with a reduced amount of youngstock, the rearing period reduced 40 days to 763 days. The mean number of calvings increased by 0.8 to 3.9 calvings. Lifetime production increased in 25 years by 14,329 kg to 38,283 kg of milk (with 4.40% fat and 3.58% protein), resulting in 1,684 kg fat and 1,369 kg protein. Production per day of life increased by 4.8 kg to 17.1 kg of milk. The highest relative change of 61% was achieved for lifetime production kg fat + protein. This is a result of the underlying traits; the rearing period reduced (-5%), production days increased (+34%), and kg m/day increased (+19%).

Longevity is a result of management (e.g. feeding, housing and culling decisions), environment, and genetics, as shown by the genetic and phenotypic trends. The genetic trend is also a result of the genetic response achieved by selecting on the Dutch/Flemish total merit index NVI.

Table 1. Lifetime performance statistics of culled herdbook cows in the Netherlands in 2000 and 2024.

	Culling year		Change	
	2000	2024	Abs.	Rel.
Calvings (nr)	3.1	3.9	0.8	26%
Production days	967	1,291	324	34%
Herdlife (d)	1,957	2,238	281	14%
kg m/day[1]	24.9	29.7	4.8	19%
LTP kg f+p[2,3]	1,895	3,053	1,158	61%
LTP kg m	24,044	38,283	14,239	58%
Productive life(d)	1,108	1,445	337	30%
Rearing period(d)	803	763	-40	-5%
kg m/day of life	12.3	17.1	4.8	39%
kg f+p/day of life	0.97	1.36	0.40	41%

[1]kg m : kg milk, [2]LTP: lifetime production, [3]kg f+p : kg fat + protein

The breeding goal has evolved over time from only including production traits, followed by including and put more emphasis on longevity and health traits. All traits in the NVI have favorable genetic correlations with longevity, resulting in the highest genetic response for longevity from all breeding goal traits.

Conclusions

Phenotypically, longevity increased by 337 days since 2000. Genetically, longevity increased by 600 days, which suggests that the full genetic potential is not yet utilized. The strong increase of the genetic trend for longevity was supported by selection on udder health, claw health and feet & legs. Culling decisions can also be affected by governmental changes in regulations. The genetic trend is more consistent over the years than the phenotypic trend. Long-term trends show that all these factors together resulted in significant improvements for longevity and lifetime production. With the continuing improvement of production and health traits further improvement of longevity is expected.

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