

Dairy longevity trait group report

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Introduction

Longevity trait is one of the crucial traits in dairy cattle. The trait is considered as a supplemental trait to the production traits' breeding values (EBVs) in relation to the herd time and life time of milk yield of dairy cattle. In dairy cattle, longevity is considered as the period from the first calving to the time of leaving the herd when the cow becomes inefficient for productivity (Kerslake et al. 2018). The production life of dairy cows is usually less than 3–4.5 years (Kerslake et al. 2018) .

The heritability of the longevity trait is low in the range of 0.01 and 0.3 depending on the models used (Hu et al. 2021). There are different terms and definitions for longevity in different countries and based on the different breeding goals and selection indices (Hu et al. 2021). Many factors that can affect longevity, including inherent to the animal itself (such as lactation, conformation, health and fertility related traits) and external factors (milk price, management, nutrition, replacement heifer etc.) (Ferris et al. 2014). Thus, longevity is a very important trait in terms of the economic aspect for the dairy herds as if the cow stays longer in the herd the more profit would be for the given dairy herd (Amirpour Najafabadi et al. 2016). Moreover, there are different traits that are evaluated together with the longevity including conformation, production, fertility and some diseases related traits.

This report deals with longevity traits in dairy cattle within 17 European countries, and the trait definition between European countries will be compared. In addition to the trait definition, method of measurement and models used by European countries have been compared too. The data was obtained from the “Longevity” electronic form available on Performance Recording, Evaluation and Publication database (PREPdb) (Interbull Centre 2025). Gathering and comparing such information is important to identify needs for standardization and harmonization of such trait across countries.

Breeds evaluated for the longevity traits

Longevity evaluation is conducted in all dairy breeds, including Holstein (HOL), Red dairy cattle (RDC), Jersey (JER), Brown Swiss (BSW), Guernsey (GUE) and Simmental (SIM) in several European countries (Table 1). Holstein (HOL) appears to be the breed where such genetic evaluation is mostly applied in 13 European countries including Belgium (BEL), Switzerland (CHE), Czech Republic (CZE), Germany-Austria-Luxemburg (DEU), Spain (ESP), Denmark-Finland-Sweden (DFS), Hungary (HUN), Ireland (IRL), Italy (ITA), the Netherlands (NLD), Poland (POL), Slovenia (SVN) and the United Kingdom (GBR-Non-EU country) which is presented in Table 1. Other breeds evaluated in different countries for longevity traits are shown in Table 1.

Trait definition and method of measurement /recording

Longevity among the European countries is classified into different categories as: direct, indirect and combined (direct and indirect) longevity. Direct longevity estimation has been provided from all European countries as it is essential to be included in the Interbull international evaluation. Combined or indirect longevity is not evaluated at the Interbull international level, but ONLY at the countries' national level.

The trait definition for direct longevity can vary from country to country and depends mostly on the breeding goals and schemes they use in their national breeding decisions and indices. The most common definition among European countries was “length of productive life (LPL)” applied by CHE, Germany-Austria (DEA), France (FRA), POL and SVN. Survival across lactations or different years of longevity was the second most common definition applied by BEL, DEU, DFS, IRL, NLD and GBR and Norway (NOR) as non-EU countries. Functional herd life is the definition applied by CZE while Risk of involuntarily culling during a cow's lifetime was also another definition provided by both HUN and ITA (Both BSW and HOL breeds).

Different countries included various traits in their multi-trait evaluation. For example, using selection index theory, CHE combines direct longevity proofs with five indicator traits: somatic cell score, udder depth, overall feet and leg, non-return rate (NRR) daughters and days to first service. In DEA, the EBV for direct longevity is combined with six predictive conformation traits (overall feet and leg, overall udder score, real leg rear view, udder depth, teat length and

suspensory ligament) using selection index theory. In ESP, the selection index is based on somatic cell count, udder depth and feet and legs. FRA, includes Functional (somatic cell count, fertility, longevity), dairy (milk yield and protein content), Milking Speed and five type traits. In HUN, they evaluate the longevity combined with five predictive traits in a selection index: stature, rump angle, udder depth, overall udder and log of somatic cell count. IRL includes some fertility and production traits, including calving interval across lactation 1 to 6, calving to 1st service for each lactation of 1 to 6, number of services across lactation 1-3 and 305-day milk yield (kg) for lactation 1-5.

Regarding the method of recording, most countries collect the data from the milk recording system (Table 1). The number of days between the first calving and the last test date was the most common method of trait measurement by CHE, ESP, FRA, HUN, ITA and NLD (Table 1). Moreover, CZE and DEU recorded the longevity as the number of days between the first calving and culling or the first calving and actual date and the number of days between the first calving and censoring date adjusted for milk yield respectively. DFS recorded data on calving dates, date of disposal and reason for disposal. NOR as a non-EU country, also collected the same data as DFS, including birth dates. GBR, as a non-EU country, recorded the information of number of lactation and somatic cell counts from the milk records.

Table 1. Country, breeds, longevity traits included in the national evaluation, trait definition and method of recording/measurement for longevity trait in European countries.

Country	Breed(s)	Traits in national evaluation	trait definition	Traits in combined longevity trait	Method of measurement /recording
BEL	All dairy and dual purpose	Direct longevity	Survival over successive lactations	–	Data from the milk recording system
CHE*	BSW	Direct and combined	Productive life span of cow,	Somatic cell score, udder depth, overall feet & legs, NRR daughters, days to first service	Data from the milk recording system - calculated as: number of days between the first calving and the last test date
	HOL	Direct longevity	Productive life span of cow,	–	
CZE	HOL, SIM	Direct longevity	Functional herd life	–	Data from the milk recording system - number

					of days between first calving and culling or first calving and actual date – censored data
DEA	BSW	Direct and combined	Functional length of productive life	overall feet and leg, overall udder score, real leg rear view, udder depth, teat length and suspensory ligament	Data from the milk recording system , time between first calving and culling or between first calving and censoring date) adjusted for milk yield
DEU	HOL, RDC, JER	Direct longevity	Functional survival of 9 consecutive periods between 1 st and 4 th calving.	–	Data from the milk recording system, calving dates, culling dates and reasons, last observed date of milk recording, date of data cut-off
DFS	HOL, RDC, JER	Direct longevity	Number of days survived across 5 years of longevity as:	1 year to 5 year longevity	Data from the milk recording system, Calving dates, date of disposal and reason for disposal
ESP	HOL	Direct and combined	Combined longevity, It is estimated from Direct Functional Longevity, obtained from Productive Life Span of cows, and indirect Functional Longevity,	Somatic cell count, udder depth and feet and legs	Length of productive life span: days from first calving to the last known recording date.

			predicted from other traits		
FRA	HOL, SIM FRM, Normande, SIM FRA, BSW, Abondance, Tarentaise	Direct and combined	Length of productive life (LPL)	SCC, Mastitis occurrence, fertility traits, some type traits	Data from the milk recording system, number of days between first calving and last known test date
GBR*	HOL, SHO, AYR (RDC), JER, GUE, BSW & SIM all breeds and crossbreds	Direct longevity	Lifespan score computed from number of lactations completed up to the 5 th lactation.	–	Number of lactations and somatic cell counts taken from milk records from by ICAR approved recording organisations (NMR & HUK).
HUN	HOL	Direct and combined	Risk of involuntary culling during a cow's lifetime.	Stature, rump angle, udder depth, overall udder and log scc	Data from the milk recording system, number of days between first calving and last known test date
IRL	HOL, JER	Direct and combined longevity	Re appearance-Survival to the next lactation	calving interval across lactation 1 to 6, calving to 1st service for each lactation 1-6, number of services for lactation 1-3, 305-day milk yield (kg) for lactation 1-5	Cows still milking in current lactation are censored for that lactation and culled when the interval between last test date and last herd date known is > 140 days
ITA	BSW	Direct longevity	Protection from involuntary culling during a cow's lifetime	–	number of days between first calving and last known test date
ITA	HOL	Direct longevity	Risk of involuntary culling during a cow's lifetime	–	Data from the milk recording system, number of days between first

					calving and last known test date
NLD	ALL	Direct longevity	Survival from month 1 up to 72 after first calving.	–	Data from the milk recording system, number of days between first calving and last known test date, Culling and herd movement data are collected from the national Identification and Registration database
NOR*	RDC	Direct longevity	Survival days up to the certain days of lactation across lactation 1-3	–	Data from the Norwegian Dairy Herd Recording System: Calving dates, date of disposal and birth dates
POL	HOL	Direct longevity	Functional Direct longevity expressed as length of productive life (LPL) corrected for production.	–	Data from the milk recording system Symlek
SVN	HOL,BSW,SIM	Direct longevity	Length of productive life (LPL)	–	Data from the milk recording system

*= non-EU countries

Statistical models and parity/lactation recordings

There are different parametric, semi parametric and non-parametric survival analysis (SA) models to estimate longevity breeding values (Smith and Westgarth 1957). Among parametric models/methods, Weibull regression is the most popular method which is a multi-factor analysis model and is based on the Weibull distribution. The weight of each factor can be obtained with the change of time in production life of a cow. The Weibull model is more flexible to adaptation to

the censoring, covariates changes with time, and the screening process is more intuitively. Therefore, Weibull regression is more accurate than the Cox proportional hazard model (semi-parametric), but it is also more complicated (Hu et al. 2021).

Direct longevity has been evaluated using single-trait (ST) approach across various European countries including CHE, CZE, DEA, ESP, FRA, HUN, ITA (HOL and BSW), NLD, POL and SVN (Shown in Table 2). DFS and DEU used a multiple-trait longevity over five years, each as a separate trait to be included in the MT model.

Survival analysis (Weibull) model was the most common model used by 10 European countries for the Direct longevity presented in Table 2. As mentioned above, for indirect or combined longevity, countries have mostly used the MT trait approach and best linear unbiased prediction (BLUP) animal model, as shown in Table 2.

Regarding the parity/lactation of the animal used in the model, it also varied among countries. For example, CHE, IRL and SVN have been used lactation 1-6, while CZE, DEA, ITA and POL used animals from all parity. Moreover, HUN used animals from parity 1 to 10 (which can also be considered as all parities) and DEU and ESP included animals from parity 1-3 plus Norway as a non-EU country which is assigned to this category (Table 2).

Table 2. Country, breeds, statistical methods and parity/lactation of animals for longevity trait in European countries

Country	Breed	Statistical method/model used for Longevity ^a	Parity/lactation
BEL	All dairy and dual purpose	RR lactation survival- AM	All
CHE *	BSW	Direct longevity: ST S-MGS SA model, applying a proportional hazards model with a piecewise Weibull baseline hazard distribution, stratified according to lactation stage within lactation number (1 to 6). Combined longevity: direct proofs are combined with 5 indicator traits (SCS, udder depth, overall feet & legs, NRR daughters, days to first service) using selection index theory.	Parities 1-6
	HOL	Direct longevity: ST S-MGS SA model, applying a proportional hazards model with a piecewise Weibull	Parities 1 -6

		baseline hazard distribution, stratified according to lactation stage (4 stages: 0-50, 51-240, 241-340 and >340 days after calving) within lactation number (1 to 6).	
CZE	HOL, SIM	ST S-MGS SA model (Weibull)	All
DEA	BSW	Direct longevity: ST sire-mgs SA (Weibull model). Combined longevity: the EBV for direct longevity is combined with 6 predictive conformation traits using selection index theory	All
DEU	HOL, RDC, JER	LM-MT-AM-BLUP	Lactation 1 -3
DFS	HOL, RDC, JER	AM-MT including 5 traits (1y-, 2y-, 3y-, 4y- and 5y-longevity)	Lactation 1 -5
ESP	HOL	Direct Longevity: ST – S-MGS SA Model on lactation basis (Weibull model). Estimation of Risk of culling of sires.	Parity 1-3
		Indirect Longevity: Selection index based on SCC, Udder Depth and Feet and Legs.(Weigel et al. 1998).	Parity 1 -3
		Combined Longevity: Weighted mean of direct and indirect functional longevity.(Weigel et al. 1998).	Parity 1-3
FRA	HOL, SIM FRM, Normande, SIM FRA, BSW, Abondance, Tarentaise HOL, SHO, AYR (RDC), JER, GUE, BSW & SIM all breeds and crossbreds	Direct longevity: ST S-MGS SA model, applying a proportional hazard model with a stratified, piecewise Weibull, baseline hazard distribution.	All parities (up to 6th calving)
		Combined longevity is computed using an approximate MT BLUP AM based on pre-corrected records for Functional (SCC, Fertility, Longevity), dairy (Milk Yield and Protein content), Milking Speed and 5 type traits.	All parities (up to 6th calving)
GBR *	HOL, SHO, AYR (RDC), JER, GUE, BSW & SIM and crossbreds	BLUP Bivariate AM	Lactation 1-5
HUN	HOL	S-MGS SA, applying a proportional hazard function following a Weibull distribution.	Parity 1 - 10

IRL	HOL,JER	MT AM BLUP	Parity 1 - 6
ITA	BSW	Direct longevity: SA- sire model using a proportional hazard model following a Weibull distribution for the baseline hazard function. Cows that change herd after first calving are considered censored at date of changing herd	All lactations
ITA	HOL	Direct longevity is estimated directly from the data with a ST S-MGS SA, applying a proportional hazard function following a Weibull distribution.	All lactations
NLD	ALL	ST-RR-BLUP-AM	All animals with information up to 72 months after first calving
NOR *	RDC	ML-AM	Lactation 1-3
POL	HOL	Direct longevity : ST Sire model SA, Weibull model	All parity
SVN	HOL,BSW,SIM	Direct longevity : ST S-MGS SA model, applying a proportional hazard model with Weibull baseline hazard distribution	Parity 1-6

*= non-EU countries

^a=Abbreviations: RR = random regression, AM= animal model, ST= single traits, MT= multi trait, S-MGS= sire – maternal grand sire, LM= linear model, BLUP= best linear unbiased prediction, SA= survival analysis, ML= multi lactation

Conclusion:

Longevity is a complex and hard to select trait with different definitions in different countries. This can make the longevity trait more challenging in terms of harmonizing and standardizing the definition of the trait. In addition to direct longevity there are indirect indicators to assess longevity from conformation, fertility traits to some disease-related traits such as metabolic diseases. As the heritability for longevity is relatively low (0.01-0.3), genomic selection could help to speed up the improvement in such traits with lower heritability, although the genetic variation is still high enough to improve the trait using conventional genetic selection.

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