Genetic parameters of longevity for improving profitability of beef cattle¹

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ABSTRACT: The objective of this study was to estimate genetic parameters for longevity and assess the suitability of using these selection criteria to improve the genetic merit of the beef cattle population of the Czech Republic. The performance record database, which contains records of 363,000 beef cattle animals of 19 breeds and their crosses, was used. The populations of Charolais and Aberdeen Angus were large enough that the genetic parameter estimations and all analyses were done for these breeds separately. Two similar approaches of longevity definition based on probabilities were considered as follows: productive longevity (PL), which is the number of calvings at target ages of 78, 90, 150, and 160 mo, and longevity (L), which is based on the probabilities of cow reappearance

in the next parity. A multibreed single-trait animal model for L and a multitrait animal model for combinations of 78/150 and 90/160 mo for PL were used. Specific combinations of months were established based on the analysis and represented the critical culling rates in the studied population. The high genetic correlations (0.88–0.95) of the combination 90/160 suggested that the PL at 160 mo of age can be predicted on the basis of the value at 90 mo, which will make earlier selection possible. Combination 78/150 is less efficient in the Czech population of beef cattle due to the lower correlations (0.79–0.93) between traits. The estimated heritabilities were low for both traits (below 0.14), but the additive genetic variance was sufficient for identifying animals with high genetic merit.

Key words: cattle, genetic parameters, productive life, reproductive traits, selection criteria

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INTRODUCTION

Longevity, the period from first to the last calving is an economically important trait. An improvement in longevity reduces the annual production costs associated with raising replacement heifers, reduces the number of involuntarily culled cows, and increases the number of high producing mature cows (Rogers, et al. 2004). True longevity is

not known until the end of a cow's life, but when the cow is still alive, longevity can be predicted. In recent decades, many statistical methods for longevity evaluation have been proposed. One of the most frequently used methods is survival analysis, which models longevity through a hazard function and describes the limiting probability that a cow will die or be culled at a specific time, given that she was alive in the same herd at a previous time (Jenko et al., 2013). The genetic evaluation of longevity has been implemented in many countries, and breeding values have been predicted (van Pelt et al., 2015). During genetic evaluation, many cows are still alive (censored data), so only part of their eventual productive life is known (Raguž et al., 2014). Pool et al. (2005) and Brotherstone et al. (1997) solved the problems

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of a large fraction of censored data by including reappearances in their analysis. Longevity for censored data was predicted from the known number of lactations and the expected additional lifespan, which was calculated based on the probability of reappearances in the next parities. Neves et al. (2012) considered the number of calvings at 53 mo to be an alternative selection criterion for productive longevity (PL) and used both single-trait linear and threshold models. Venot et al. (2013) predicted longevity based on the high genetic correlations between measures of production at different ages. The objective of this study was to estimate the genetic parameters for longevity and assess the suitability of using these selection criteria to improve the genetic merit of the beef cattle population of the Czech Republic.

MATERIALS AND METHODS

Animal Care and Use Committee approval was not obtained for this study because the data were obtained from an existing database supplied by the Czech Beef Cattle Association (Czech Republic).

Data

Genetic evaluation of beef cattle was performed on the database of performance testing, which is routinely collected by Czech Beef Cattle Association. Data recorded between 1991 and 2015 were used. The dataset was used for the genetic evaluation of

growth traits of beef cattle in the Czech Republic and contained the animals' birth dates and numbers of calves per cow. The database includes records of 363,000 calves and information about 64,000 females of 19 beef breeds (Table 1) and their crosses, which were used for longevity analysis. Crosses with dairy and dual-purpose breeds were also included in the original database because such cows were used in a program that aimed to upgrade the purebred beef population in the Czech Republic.

Definition of Traits

Two similar approaches were applied as follows: The first approach was inspired by Brotherstone et al. (1997). Longevity (L) was defined as the number of parity the cow achieved. In cases where the cow was still alive and the last number of parity was not yet known (censored data), longevity was predicted by the following formula according to Brotherstone et al. (1997):

$$L = n + \left(\sum_{i=1}^{LC} \prod_{k=1}^i p_{n+k-1} \right)$$

where n is the number of completed parities the cow achieved, LC is the last observed calving in the population, and p_i is the probability of survival from the i th calving to the next. Probabilities were established on the basis of uncensored data of the total beef cattle population.

Table 1. Number and percentage distribution (%) of cows in the base dataset before editing (N) and after editing (N_E)

<i>i</i>	Breed	N	%	N _E	%
1	Charolais	17,607	27.70	5,459	24.93
2	Beef Simmental	11,717	18.43	4,154	18.97
3	Aberdeen Angus	11,659	18.34	4,534	20.71
4	Hereford	8,907	14.01	4,045	18.47
5	Limousine	5,554	8.74	1,587	7.25
6	Blonde d'Aquitaine	2,427	3.82	628	2.87
7	Piemontese	1,814	2.85	266	1.21
8	Gasconne	1,426	2.24	515	2.35
9	Galloway	1,168	1.84	409	1.87
10	Highland	832	1.31	233	1.06
11	Salers	258	0.41	65	0.30
12	Aubrac	60	0.09		
13	Parthenaise	44	0.07		
14	Belgian Blue	43	0.07		
15	Shorthorn	17	0.03		
16	Bazadais	12	0.02		
17	Vosgienne	9	0.01		
18	Bruna d'Andorra	6	0.01		
19	Rouge des Prés	5	0.01		
	Sum	63,565	100%	21,895	100%

The second approach was inspired by Venot et al. (2013) and Neves et al. (2012). Productive longevity was defined as the number of calvings that a cow had achieved at a target age. As target ages, 78 and 150 mo were used, following Venot et al. (2013), and 90 and 160 mo were used, according to the analysis of our dataset. These points (78, 90, 150, and 160 mo) represent critical points at which the culling rates increase in the beef cattle population in the Czech Republic (Figure 1). The combinations 78/150 and 90/160 were chosen due to the possibility of predicting a cow's longevity later in life (at 150 or 160 mo) based on knowledge of the cow's longevity at an earlier age (78 or 90 mo) because there is an assumption of a high correlation between combinations. Venot et al. (2013) defined these terms according to the idea that a short term, 78 mo, generally corresponds to the probability for a cow to reach 4 calvings at a given age if the first calving is 3 yr, and a long term, 150 mo, generally corresponds to the opportunity for a cow to reach 10 calvings. The second short term, 90 mo, corresponds to the opportunity to reach 5 calvings if the first calving occurs at an age of 3 yr, which is the average age for a first calving in the Czech beef population. The second long term gives an opportunity for a cow to reach 11 calvings. If the cow had not yet reached a target age (censored data), PL was predicted by these 2 following formulas:

Expected number of calvings was calculated as follows:

$$EPL = (c - d) / CI$$

where EPL is the expected number of calvings at a target age (78, 90, 150, or 160 mo), c is the target

age in days, d is the age of a cow in days at the last recorded calving, and CI is the average calving interval for a particular calving.

The predicted PL (number of calvings) was calculated as follows:

$$PL = n + \left(\sum_{i=1}^{EPL} \prod_{k=1}^i p_{n+k-1} \right)$$

where n is the number of the last observed calving for a given cow and p_i is the probability of survival from the i th calving to the next one. Probabilities were established on the basis of uncensored data of the total beef cattle population.

Data Editing

Outliers and unreliable data were removed from the database for variance component estimation. Some edits were done. Crosses with dairy and dual-purpose breeds were removed from the database. Animals with an age at first calving that was not between 500 and 2,000 d were removed. Cows with an age at first calving under 500 d were excluded due to biological impossibility and the typical ages in the breeding system. The minimum calving interval length was set to 290 d. Embryo transfer calves and cows were also excluded from the genetic evaluation. The date of a cow's culling was known or unknown. For cows with an unknown date of culling, the upper limit of the last calving interval was restricted to 1,100 d. If the period from the last calving exceeded 1,100 d (3 yr), the cow was considered culled. The third group consisted of animals that had not yet been culled from the herd; their date of culling was not known, and the period from

Figure 1. Graphical representation of the probabilities of survival to the next parity based on uncensored data (represented by average age of cows for a given parity) in beef cattle in the whole population and the populations of Charolais (CH) and Aberdeen Angus (AA).

last calving did not exceed 1,100 d. Coefficients of heterosis were calculated as functions of the degree of heterozygosity of animals using the following formula from [Hickey et al. \(2007\)](#):

$$\text{Heterozygosity} = Pd(1 - Ps) + Ps(1 - Pd),$$

where Ps and Pd are the proportions of genes of the primary breed in the sire and dam, respectively. The breed that is most prevalent across each sire and dam pairing is considered the primary breed for the parental pair, but few crossbreeds were present in the database.

When estimating the genetic parameters, it was necessary to ensure sufficient data connectedness in the database. For this reason, the composite HYS (herd–year–season effect) of the cows' last calving was determined. The year was divided into 3 seasons: January to April, May to August, and September to December. The HYS effect included at least 5 cows with a minimum of 3 sires. When estimating the genetic parameters for individual breeds separately, these requirements were moderated to provide a sufficient number of animals: each HYS included at least 4 cows, and these cows were required to be progeny minimally after 2 sires. After these edits, many animals were removed: the database initially contained 363,000 beef cattle animals, including approximately 64,000 dams. After editing without the HYS conditions, information about 2,000 cows was removed. After editing with the HYS conditions, the final dataset contained only 21,895 dams ([Table 1](#)).

Four generations of ancestors were included in the pedigree. If one or both parents were unknown, phantom parent groups were used ([Quaas, 1988](#)). Phantom parent groups were constructed based on breed, which meant that all unknown animals of a known breed were joined into a specific genetic group and then added to the pedigree. Finally, the additive genetic relationship matrix for all breeds together contained 64,319 animals for the genetic analysis of longevity. For Charolais and Aberdeen Angus, the matrix contained 17,857 and 10,703 animals, respectively.

Statistical Methods

The significant environmental fixed effects were determined using the GLM procedure in SAS 9.4. The fixed effects tested were HYS of birth, HYS of last calving, year of birth, year of last calving, heterosis of dam, breed of dam, and average calving difficulty. Fixed effects were tested for significance ($P < 0.05$), but effects that were biologically important

were included in the model, regardless of the level of significance. Nevertheless, all of the effects that were included in the model equation were significant, except for the effect of dam heterosis. The effects of animal and HYS of last calving were treated as random effects. HYS of last calving was chosen because this effect includes the impact of environmental conditions during the last calving before culling.

The variance components were estimated by residual maximum likelihood using the AIREMLF90 program ([Misztal et al., 2002](#)). The general linear model includes random effects in matrix notation as follows:

$$y = Xb + Zu + e,$$

where y is the vector of observations for longevity or the combination of 2 traits in PL, X and Z are the matrices of explanatory variables assigning performance records to fixed and random effects, respectively, b and u are the estimated unknown vectors of fixed and random effects, respectively, and e is a vector of random residual effects.

In the single and multitrait models, we assume that the random effects show a normal random distribution with zero average and variances:

$$\text{Var} \begin{Bmatrix} u1 \\ u2 \\ e \end{Bmatrix} = \begin{Bmatrix} I \otimes P & 0 & 0 \\ 0 & A \otimes G & 0 \\ 0 & 0 & I \otimes E \end{Bmatrix},$$

where $u1$ is the vector of random permanent environment effects of animals with records, $u2$ is the vector of additive genetic effects, I is an identity matrix, P is the (co)variance matrix for permanent environmental effects, A is the numerator relationship matrix, G is the (co)variance matrix for additive genetic effects, and E is the diagonal matrix of residual variances.

The suitability of the models was tested by variance component estimation, heritability estimation, and the Akaike information criterion (AIC) ([Bozgodan, 2000](#)), which is defined as

$$AIC = -2\log L(\theta) + 2d,$$

where $\log L(\theta)$ is the logarithm of the value of likelihood function and d is the number of free parameters in the model.

Finally, this model equation for single and multitrait models was used as follows:

$$y_{ijklmno} = HYS_i + het_j + year_k + CD_l + AFC_m + AFC_m^2 + Anim_n + e_{ijklmno},$$

where $y_{ijklmno}$ is longevity and productive lifespan at 78 and 150 or at 90 and 160 d; HYS_i is random

effect of the i th contemporary group (HYS) of the last calving of a cow; het_j is linear regression on heterozygosis of a cow (fixed effect); $year_k$ is the fixed effect of cow's year of birth; CD_l is the linear regression of average calving difficulty during cow's productive life; AFC_m is the linear regression of age at first calving; AFC_m^2 is the quadratic regression of age at first calving; $Anim_n$ is random animal additive genetic effect on the o th animal (4 generations are included); and $e_{ijklmno}$ is random residual error.

Longevity (L) was estimated by a single-trait animal model. A multitrait animal model was used for 2 combinations of PL: PL78/150 and PL90/160. These estimations were carried out for the whole population and then separately for the 2 most common breeds in the Czech Republic: Charolais and Aberdeen Angus. Only Charolais and Aberdeen Angus individuals that were 88% to 100% purebred were chosen for the genetic parameter estimation.

RESULTS AND DISCUSSION

Table 2 shows descriptive characteristics of the whole population—both uncensored and all data included the breeds Charolais and Aberdeen Angus, and both selected breeds, Charolais and Aberdeen Angus, were also considered separately.

The databases adjusted in this way were subsequently used to estimate the genetic parameters. The Charolais and Aberdeen Angus breeds accounted for 34% of all of the data in the database, which is a substantial part of the beef cattle population in the Czech Republic. Therefore, after separating them out to estimate the genetic parameters, there were only some moderate deviations in the descriptive statistics of these 2 breeds compared with the whole population (including these breeds), especially in longevity at older age (150 and 160 mo), which were reflected mainly in lower values for the whole population's mean and maximum. The reason for such a change was apparently the removal of the very numerous Aberdeen Angus population, which typically have good fertility and longevity.

For the censored data, longevity (L) was computed according to [Brotherstone et al. \(1997\)](#), based on the probability of transition to the next parity. These probabilities were computed from the whole population of animals with a known date of culling ($n = 36,426$) and are shown in [Table 3](#). [Pool et al. \(2005\)](#) evaluated longevity using the probability that the cow will survive until the next parity. For the time interval from parity 1 to 4, [Pool et al. \(2005\)](#) used the following probabilities: 0.73, 0.8, 0.84, and 0.80. The probability that the cow would reach

Table 2. Descriptive statistics for longevity traits for the estimation of genetic parameters after data editing

Uncensored population (all breeds)					
	Number	Mean	SD	Min	Max
L	13,732	3.32	2.384	1	15.00
PL78	13,732	2.52	1.266	1	6.00
PL90	13,732	2.80	1.546	1	7.00
PL150	13,732	3.29	2.294	1	11.00
PL160	13,732	3.30	2.332	1	12.00
Whole population (all breeds)					
L	21,895	4.15	2.513	1	15.00
PL78	21,895	2.98	1.315	1	6.00
PL90	21,895	3.26	1.582	1	7.23
PL150	21,895	5.15	3.410	1	11.70
PL160	21,895	5.37	3.689	1	12.45
Charolais					
L	6,224	4.50	2.383	1	13.00
PL78	6,224	3.00	1.144	1	5.41
PL90	6,224	3.56	1.482	1	6.47
PL150	6,224	5.72	3.250	1	11.33
PL160	6,224	6.02	3.550	1	12.06
Aberdeen Angus					
L	5,104	5.50	2.969	1	15.00
PL78	5,104	3.50	1.383	1	6.00
PL90	5,104	4.11	1.736	1	6.88
PL150	5,104	6.49	3.590	1	11.51
PL160	5,104	6.82	3.905	1	12.30

L = longevity; PL78, PL90, PL150, and PL160 = productive longevity in 78, 90, 150, or 160 mo; SD = standard deviation.

Table 3. Probabilities of survival (reappearance) to the next parity

<i>i</i>	age _{<i>i</i>}	Whole population (n = 36,426)		Charolais (n = 7,556)		Aberdeen Angus (n = 4,963)	
		N	p _{<i>i</i>}	N	p _{<i>iCH</i>}	N	p _{<i>iAA</i>}
1	36.54	8,803	0.73	1,745	0.74	1,014	0.68
2	51.77	6,441	0.79	1,287	0.84	686	0.87
3	66.22	5,061	0.81	1,081	0.82	596	0.90
4	78.83	4,095	0.87	890	0.87	537	0.91
5	91.63	3,546	0.77	771	0.81	488	0.87
6	103.38	2,727	0.75	621	0.76	423	0.84
7	115.81	2,043	0.72	475	0.61	352	0.85
8	126.07	1,463	0.69	291	0.64	297	0.79
9	136.14	1,006	0.59	187	0.63	232	0.58
10	147.87	593	0.57	118	0.47	133	0.69
11	157.75	338	0.58	55	0.44	91	0.72
12	166.41	197	0.37	24	0.42	65	0.44
13	180.13	72	0.43	10	0.1	28	0.5
14	188.71	31	0.29	1	0	14	0.43
15	200.40	9	0.11	0	0	6	0.17
16	203.34	1	0.00	0	0	1	0

i = transition from *i* to the *i*th + 1 calving; age_{*i*} = average age of cows in months for *i*th + 1 calving; N = number of cow from *i* to the *i*th + 1 calving; p_{*i*} = average probability of survival to the next calving; p_{*iCH*} = average probability of survival to the next calving in Charolais; p_{*iAA*} = average probability of survival to the next calving in Aberdeen Angus.

parities 2 and 3 estimated in our study was almost the same, 0.73 and 0.79, respectively. The probabilities increased to 0.81 and 0.87 until parity 4, after which there was a sharp decrease to 0.77. The trend in the Irish population described by Pool et al. (2005) was similar; however, the probability gradually increased until parity 3, and the first decrease was recorded after parity 3. These differences may be caused by the different management practices for herds in particular countries, different population structures, different reproductive and genetic levels of the breeds kept, etc. Van der Westhuizen et al. (2001) reported percentage of dams retained and culled at stayability levels at 36, 48, 60, 72, and 84 mo and the found probabilities of survival to be 0.76, 0.8, 0.78, 0.8, and 0.79, respectively. In our dataset, the estimated probabilities were 0.73, 0.79, 0.81, 0.87, and 0.77 at 35, 52, 66, 79, and 91 mo, respectively. A similar trend can be observed. The probability of survival from the second to the third calving is higher than that observed from the first to the second calving. Additionally, the probability of survival from the fourth to the fifth calving reached the highest level and then started to decrease. Van der Westhuizen et al. (2001) claimed that culling was mainly done due to a failure to calve in the previous year. At the age of 24, 22% of the cows were removed for this reason. In our dataset, the reasons for culling were not known.

The probabilities computed for a specific breed may differ from the values obtained for the whole

population. Separate evaluation and probability computation could be done only for the 2 most numerous breeds: Charolais and Aberdeen Angus (Table 3). In the other, less numerous breeds, the values were biased because the probability was computed from a small group of animals, in which even a small change can considerably influence and distort the results, particularly in further parities with a decreasing number of records.

A comparison of probabilities of Charolais and Aberdeen Angus breeds shows that Aberdeen Angus, a breed that matures early and is long-lived, reaches a lower culling rate than does the whole population; this trend is apparent until the end of animal culling from breeding (Figure 1). In contrast, the late matured French breed Charolais, which is a breed intended for intensive production and fattening, generally reaches lower probabilities of transition to the next category of parity than Aberdeen Angus does. The values of survival remain on the same level or often a higher level than that of the whole population, which indicates the very good reproduction of the Czech population of Charolais. Venot et al. (2013) published probabilities for the French population of Charolais, and the published values were mostly lower. A difference between the populations is obvious until parity 6; thereafter, the culling rates are almost the same. The culls of animals in the population of the Czech Republic are higher after parities 7 and 9. However, the shape of the curve may be influenced by the number of

included animals, whereas the curve for Charolais in France has a smooth shape, for the population in the Czech Republic, the shape is “jagged.” The reason is mainly the number of animals included in the computation. In our study, 7,556 cows were used for the probability computation, whereas in France, this number was more than one million. The probabilities of transition to the next parity for the whole population including and/or excluding Charolais and Aberdeen Angus breeds rather resemble the probabilities found in the Charolais breed. [Brigham et al. \(2007\)](#) published the percentage of dams with successful stayability in red Angus breed at 3, 4, 5, and 6 yr. The probability of stayability to reach 4 yr of age from 3 yr of age was 0.67. Almost the same value was found according to our dataset (0.68), but the percentage of stayability decreased for every year of the cow’s age, leading to probabilities of 0.58 and 0.50 to reach 5 and 6 yr, respectively.

The main objective of PL evaluation is to increase the probability that the cows will produce rentability number of calves, which will ensure the return of expenditure on their management and costs ([Maiwashe et al., 2009](#); [Neves et al., 2012](#)). [Silva et al. \(2003\)](#) claimed that financial losses are considered when a cow at an advanced age does not produce one calf per year after the first calving. [Maiwashe et al. \(2009\)](#) worked with stayability, which is defined as the probability that a cow remains in the herd until a specific age, given that she was a dam and had an opportunity to reach that age. Stayability was evaluated at 5 specific age categories (4, 5, 6, 7, 8 yr and older). A cow that was in the herd until the specific age was assigned “1”; otherwise, it was assigned “0.” [Martinez et al. \(2004\)](#) concluded that the prediction of PL could be made in early life, thanks to a high genetic correlation between lifetime productivity and different ages of the cow. [Venot et al. \(2013\)](#) evaluated PL as the number of calvings reached at a target age. As mentioned in the MATERIALS AND METHODS section, the target age of 78 mo was chosen as a short period, which roughly corresponds to a cow’s ability to deliver a calf 4 times if the age of first calving is 3 yr. The target age of 150 mo was chosen as an advantageous period in the long run, which, on average, corresponds to the cow’s potential to achieve 10 calvings. [Neves et al. \(2012\)](#) described the genetic evaluation of PL in the Nellore cattle breed using a similar principle. The number of calvings until 53 and 89 mo of age was taken as an evaluated trait. The value at 53 mo is considered optimal for primiparous cows in relation to the selection of new animals for herd replacement,

with the possibility of an earlier genetic evaluation of individuals ([Geary, 2003](#); [Neves et al., 2012](#)). It is preferable that the computation gives an advantage to the cows that managed to calve within 53 mo over those who only survived until the target age but did not have a calf. In Brazil, grazing management for cows is used, and under this system, all heifers theoretically have the same chance of conceiving and delivering a calf once, twice, or not at all. The analysis of our data indicated that for the current Czech population of beef cattle, the use of the number of calvings at 90 and 160 mo of age seemed to be the most suitable because this period is considered critical due to the increased culling rates ([Figure 1](#)).

[Table 4](#) shows estimated genetic parameters for the whole population (censored and all data), for the Charolais population and Aberdeen Angus population. Estimates of heritability coefficients were higher in the uncensored population compared with the whole population (uncensored and censored data together). The estimated genetic parameters for the whole population are consistent with those of other authors ([Pool et al., 2005](#); [Roughsedge et al., 2005](#); [Neves et al., 2012](#); [Venot et al., 2013](#)). [Sneeling et al. \(1995\)](#) published heritability estimates ranging from 0.019 to 0.195 by using an animal model. Heritabilities of 0.56, 0.38, and 0.27 for stayability at 4, 5, and 6 yr, respectively, were reported by [Van der Westhuizen et al. \(2001\)](#). Stayability at 6 yr corresponds to approximately 78 mo. Our estimated heritability was lower, but the heritabilities reported by [Van der Westhuizen et al. \(2001\)](#) were estimated by a threshold model, which results in higher heritabilities than obtained by using linear models; thus, only a single herd was used in the analysis.

The estimation of genetic parameters for individual breeds was done only in Charolais and Aberdeen Angus breeds because the population of the other breeds was not large enough. The results are shown in [Table 4](#). Heritability coefficients estimated by [Venot et al. \(2013\)](#) for Charolais were similar. We assume that higher heritability coefficients result from a higher variability of additive genetic variance because in previous studies, Canadian Charolais was used in the Czech population, which could increase the within-breed variability. However, the heritability coefficient that we estimated for PL150 is lower because, unlike the study of [Venot et al. \(2013\)](#), the number of older animals was lower, and it was assumed that their genetic variability was also low. Genetic parameters for PL90 and PL160 were similar, and for the

Table 4. Variance components and genetic parameters for the whole population (uncensored data, all data) and population of Charolais and Aberdeen Angus

Whole population (only uncensored data)									
Trait	σ_a^2	σ_a	σ_{HYS}^2	σ_{HYS}	σ_e^2	σ_e	h^2	SE	AIC
L	1.029	0.476	8.688	0.054	0.969	0.042	0.096	0.001	70804
PL78	0.325	0.015	1.751	0.099	0.360	0.015	0.134	0.011	97216
PL90	0.464	0.026	3.172	0.176	0.449	0.020	0.114	0.005	102991
PL150	0.949	0.037	8.365	0.456	0.814	0.037	0.094	0.007	97216
PL160	0.987	0.051	8.556	0.467	0.860	0.039	0.095	0.006	102991
Whole population (all data)									
L	0.684	0.037	16.750	0.729	1.149	0.030	0.037	0.002	70804
PL78	0.233	0.014	2.002	0.093	0.493	0.012	0.085	0.005	179481
PL90	0.356	0.021	3.900	0.177	0.704	0.017	0.072	0.004	199020
PL150	0.989	0.066	16.212	0.727	2.434	0.056	0.050	0.003	179481
PL160	1.128	0.076	17.995	0.809	2.843	0.065	0.051	0.003	199020
Charolais									
L	0.653	0.107	5.502	0.500	1.750	0.094	0.083	0.013	28387
PL78	0.111	0.061	0.673	0.022	0.660	0.021	0.076	0.039	55088
PL90	0.191	0.035	1.406	0.122	1.028	0.034	0.073	0.012	62214
PL150	0.549	0.129	9.943	0.718	5.023	0.131	0.035	0.008	55088
PL160	0.515	0.146	8.611	0.830	4.237	0.152	0.039	0.011	62214
Aberdeen Angus									
L	0.918	0.122	10.490	0.875	2.440	0.101	0.066	0.008	27910
PL78	0.270	0.038	0.891	0.084	0.710	0.031	0.144	0.018	42217
PL90	0.445	0.058	1.692	0.154	1.038	0.046	0.140	0.016	46683
PL150	1.337	0.189	9.778	0.845	3.733	0.156	0.090	0.011	42217
PL160	1.473	0.214	11.091	0.960	4.397	0.179	0.087	0.012	46683

L = longevity; PL78, PL90, PL150, and PL160 = productive longevity at 78, 90, 150, and 160 mo; σ_a^2 = additive genetic variance; σ_a = standard deviation of additive genetic variance; σ_{HYS}^2 = Herd–Year–Season variance; σ_{HYS} = standard deviation of Herd–Year–Season effect; σ_e^2 = residual variance; σ_e = standard deviation of residual variance; $h^2 = (\sigma_a^2 / \sigma_p^2)$ = heritability; SE = standard error of heritability coefficient; AIC = Akaike information criterion.

L trait, they were also comparable. Another reason why PL90 is preferable to PL78 is that the heritability coefficient was not statistically significant; the standard error of the heritability coefficient was high (in Charolais breed), so its use for this population did not make sense.

With the exception of L trait, heritability coefficients for Aberdeen Angus (Table 4) reached a higher ratio of additive genetic variance than all previously tested populations. This breed is well known for its good reproductive traits, earliness, and longevity, and it is expected that its variability in this field would be higher than in other breeds. For Aberdeen Angus, a higher heritability coefficient (0.13) was also published by Roughsedge et al. (2005) by comparison with breeds Limousine (0.08) and Simmental (0.03). Additive genetic variability of Charolais was smaller than that of Aberdeen Angus. We assumed that the higher additive genetic variance of Aberdeen Angus can be caused by long-time direct selection for higher longevity and fertility, but unfortunately, no results for comparison of additive genetic variance in Aberdeen Angus with

Charolais were found in the literature. Maiwashe et al. (2009) presented higher heritabilities (0.18 to 0.30) for Aberdeen Angus's stayability in 5 categories (4 to 8 yr) by using a threshold sire and animal model. Stayability at 6 and 7 yr corresponds to approximately 78 and 90 mo. For stayability in the categories 6 yr and older and 7 yr and older, the estimated heritabilities using the sire threshold were 0.30 and 0.24, respectively. Lower heritabilities were estimated by an animal threshold model (0.18 to 0.20). Martinez et al. (2004) reported lower heritabilities estimated by a linear model (0.05 to 0.19) compared with a threshold model (0.09 to 0.30). A heritability in the range of 0.23 to 0.24 for stayability at 3 yr of age in Canadian Angus was found by Rasali et al. (2005) using a mixed linear model. Brigham et al. (2007) estimated heritability coefficients (0.17, 0.18, 0.16, and 0.15) for stayability in the Red Angus breed using a threshold model for 3, 4, 5, and 6 yr, respectively.

Genetic and environmental correlations between traits were high (Table 5). The correlations between the PL90 and PL160 traits showed higher

Table 5. Comparison of genetic and environmental correlations between the combinations PL78/150 and PL90/160, calculated based on the whole dataset (uncensored and censored data together) and uncensored data only

Dataset	Genetic correlations		Environmental correlations	
	PL78/150	PL90/160	PL78/150	PL90/160
Uncensored	0.817	0.882	0.956	0.973
All dataset	0.789	0.847	0.966	0.977
Charolais	0.829	0.881	0.956	0.973
Aberdeen Angus	0.933	0.951	0.947	0.965

PL78, PL90, PL150, and PL160 = productive longevity at 78, 90, 150, and 160 mo.

values. Venot et al. (2013) published higher genetic correlations between number of calvings at 78 and 150 mo: 0.95 for Charolais and 0.92 for Aubrac. The high genetic correlation suggests that the PL at 160 mo of age can be predicted on the basis of the value at 90 mo, which will make earlier selection possible. Selection for the PL value at 78 mo would be less efficient in terms of the lower correlations with PL150, so this combination is less suitable for predicting PL at an older age. For this reason, based on estimated genetic correlations, efficient selection is preferable at an older age (PL90). Venot et al. (2013) and Neves et al. (2012) stated that if the genetic correlation between traits is close to 1, selection for productive efficiency at an early age is comparable with selection for productive efficiency at a later age. This finding implies that the trait can be measured in cows earlier and that a lower amount of censored data is required for the computation. Phenotypic correlations between traits are shown in Supplementary material.

Although the genetic and environmental correlations are high (0.79 and higher), the probabilities of survival are still decreasing. We assumed that the genetic potential of cows would be higher than it was. The culling criteria can differ between producers. Sanders et al. (2012) reported that the most common culling criteria are reproductive performance, udder problems, poor body condition, tooth wear, eye problems, leg problems, death of calf, age of cow, and light calf at or before weaning. They also reported that in some herds, especially commercial herds, it may be feasible to cull many remaining cows at a given age because of the average, if there is a higher probability of losing the next calf, weaning light calves or being too thin to have adequate values as a cull cow. Some other reasons can be a reduction in herd size due to pasture capacity because the farmer would prefer to keep

young animals. We assumed that the probabilities of survival in our study are influenced by combinations of all these factors, but unfortunately, the reasons for culling were not known.

The genetic parameters for longevity and PL were estimated. The idea of PL seems to be better because it includes economically determining the number of calves, not just the cow's longevity. However, additive genetic variance of both traits is sufficient to ensure the success of consistent breeding. Heritabilities were low, but improving longevity is possible by selecting animals with high genetic merit in terms of longevity and PL. The target age adjustment should be based on the population analysis and breeding goals for each population. For the current Czech population, the most suitable is the number of calvings at 90 and 160 mo because of the high culling rates at this age; moreover, high genetic correlations between these ages enables the earlier selection of individuals with the highest genetic potential.

SUPPLEMENTARY DATA

Supplementary data are available at *Journal of Animal Science* online.

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