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# Validation of the evaluation of longevity by weighted analysis

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**Abstract:** We applied the Interbull validation methodology, a widely accepted method in animal breeding, to assess novel weighted and nonweighted repeatability models for the prediction of breeding values for longevity in Czech Holstein cattle. The population included in the estimation also contained 58 704 animals with genotypes. Performance records from 1 055 814 cows in the full dataset and from 831 995 cows in the trimmed dataset were used for evaluation. Both linear models included effects of herd-year-period, animal, permanent environment, and correction for milk production of individual cows in relation to herd average lactation curve, differing only in the use of weighs. The average reliability of the validation bulls increased in the full dataset from 0.85 without weight to 0.91 in the model with weight. This increase was also apparent in the trimmed dataset (from 0.42 to 0.50). Both models showed considerable inflation of genomic breeding values (GEBVs) by Interbull validation and did not manifest distinct benefits supporting their use in the routine evaluation of Czech Holstein cattle in the Czech Republic.

**Keywords:** cattle; genomic evaluation; linear model; repeatability model

Longevity is a very complex trait that includes culling due to milk production, the health of cows, farm and national policies, the cost of feeds and the cost of replacement heifers (Ferris et al. 2014; Grandl et al. 2016). Therefore, it is difficult to estimate the genetic basis of longevity in animals with accuracy. Promising new methods suggest the use of different linear models, such as the routine evaluation of Holstein cattle in the USA based on VanRaden et al. (2006) or in Germany based on Taubert et al. (2017). The most used definition of longevity is the "length of productive life", the period from first calving to culling or slaughter, given in days or months (Ducrocq 1988).

The breeding value for longevity has been published in the Czech Republic since 2008. We also use so-called censored data, which are live cow data that refine the breeding value estimate but do not provide any gain for the reliability of the breeding value estimate. Today, the single-trait sire–maternal grandsire model is used as the model for routine Czech evaluation by the methodology of Pachova et al. (2005), a single-trait paternal model that builds the relationship matrix using the sire and the dam's sire. It is a nonlinear model that uses hazard functions with a Weibull distribution. The evaluation is carried out by applying the Survival Kit software (v3.12) package

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developed by Meszaros et al. (2013), which can work with one-dimensional proportional hazard models. The predicted breeding value for direct longevity has not been published for Holstein bulls and cows since April 2017 because this approach overestimates the breeding values of young bulls, according to Sewalem et al. (2005), and by today's view, it does not include genomic information on animals. Thus, the officially published longevity estimated breeding value (EBV) was replaced by the "longevity index" where traits showing a greater degree of correlation with longevity traits are included to increase the precision of direct longevity EBV. The traits are udder depth, body depth, overall feet and legs, somatic cell score and the cow's conception. The direct longevity EBV of the sire is before inclusion to the index enhanced by genomic evaluation in so-called blending method, where the EBVs from conventional national evaluation and EBVs from international multiple Across Country Evaluation (MACE) evaluation are inputted as records into standard single-step genomic best linear unbiased prediction (GBLUP) (Misztal et al. 2009; Aguilar et al. 2010) where the model includes only fixed effect of source of EBV and random animal effect. The Interbull evaluation reflects foreign information and is available for bulls and recalculated on a Czech basis. The weight of supporting traits in the longevity index are proportional to the reliability of the individual direct longevity GEBV.

Cerna et al. (2023) introduced a novel approach where records of the survival of a cow are considered as repeated observations and, in one variant of the method, the weight equal to a number of subsequent periods without the cow's observation is assigned to a record in the period where the cow was culled. We tested this method for its usefulness in national evaluation and international evaluation by validation method of Interbull organisation for potential replacement of current domestic routine evaluation.

## MATERIAL AND METHODS

The data from the performance recordings were provided by Holstein cattle in the Czech Republic (with the consent of the Association of Holstein Cattle Breeders in the Czech Republic). We used genetic parameters and heritability 0.057, estimated by Cerna et al. (2023), because both studies evaluated the same current domestic population, and the evaluation models in the studies were identical. The BLUPF90 software package (v3.12) by Misztal et al. (2002) was used to test the models. The relative breeding values used in our validation study are the same as those used in the routine evaluation of longevity in the Czech Republic, i.e. defined as a mean value of 100 and a standard deviation of 12 for the base population, which is the population of cows in the longevity evaluation born in 2010.

Animals with recorded performance data in the model had a proportion of Holstein breed of at least 75% (Holstein breed and red Holstein variant were added together). Cows had to be born after 1991, and the date of their first calving was required to be after 1994. Six generations of parents of recorded cows were considered in the models. In addition to pedigree information, the genotypes were included in estimating breeding values for longevity. A total of 58 704 genotypes were used for the calculation, of which 5 380 were proven bulls and 53 324 were cows, heifers, and young bulls. The Immunogenetics Laboratory of the Czech Moravian Breeders Corporation in Hradistko, Czech Republic provided the cow, heifer and young bull genotypes. The following types of chips were included: BovineSNP50_v3_A1. with 53 218 single nucleotide polymorphisms (SNPs), Geneseek GGP 150 K with 138 974 SNPs, Euro G MD version 1 with 44 847 SNPs, Euro G MD version v2 with a supplied corporate cluster file created with 50 478 SNPs, Euro G MD version 2 with a custom cluster file created with 51 376 SNPs and EuroG_MDv3_HTS_2B0063939_1.bpm with 59 963 SNPs. Only those SNPs also present in the BovineSNP50_v2_A1 chip with 54 609 SNPs were included in the study; the minimum common number of SNPs for inclusion in the breeding value prediction was 25 000 SNPs.

The longevity observation was defined as status of cow in herd at the end of nine consecutive periods, three periods for each the first three lactations. If the cow survived, the record value had value one, if the cow died in given period, the value was two. Two models were chosen for the evaluation study, and they differed in whether or not weight was given to the lactation periods as defined by Cerna et al. (2023).

The equation of the first model, i.e. the model without weight for the lactation period, was as follows:

$$Y_{ijklm} = \text{HYS}_i + \text{period}_j + \text{animal}_k + \text{permanent environment}_l + \text{milk}_m + e_{ijklm} \quad (1)$$

where:

$Y_{ijklm}$ – a record of survival of the given period – takes only two values, namely, one if the cow survived the given period of lactation or two if it did not survive the period;

$\text{HYS}_i$ – fixed effect of interaction of herd, year and season;

$\text{Period}_j$ – fixed effect of the lactation period (1–9), a total of the first three lactations of a cow were evaluated, and each lactation was divided into three uneven periods according to the most common reasons for culling in the given time periods: In the 1st period, on days 1–49 days of lactation, the most common side effects are postpartum complications. In the 2nd period, on days 50–249 of lactation, the most common reason for culling is hoof disease or other difficult-to-treat diseases. In the 3rd period, on days 250–305 days of lactation, the most common reason for culling is failure to conceive;

$\text{Animal}_k$ – the random additive genetic effect of an individual with the relationships among animals included in $H^{-1}$ as defined in single-step GBLUP methodology;

$\text{Permanent environment}_l$ – A random effect of a permanent cow environment in survival records;

$\text{Milk}_m$ – the given effect had five classes, into which cows were divided on the basis of the deviation of their productivity from the average of the herd in the previous period of lactation;

e – random residual effect.

The deviation ($d$) of productivity of cow $j$ in herd-year season group $k$ was calculated as:

$$d_{jk} = \frac{\sum_{i=1}^{n} \text{mlk}_{ij} - \text{mlkhrd}_{ik}}{n} \quad (2)$$

where:

$\text{mlk}_{ij}$ – milk yield in days in milk $i$ of cow $j$;

$\text{mlkhrd}_{ik}$ – milk yield in days in milk $i$ of herd-year-season group $k$ calculated by quadratic function describing average phenotypic milk production curve.

The deviations of productivity were then divided into five production classes depending on rank of cow performance in given herd-year-season: best cows (top 20%), better cows (21–40%), average cows (41–60%), worse cows (61–80%) and worst cows (bottom 20%).

The equation of the second model, i.e. the model with weight ($v$) per lactation period:

$$Y_{ijklm} = \text{HYS}_i + \text{period}_j + \text{animal}_k + \text{permanent environment}_l + \text{milk}_m + e_{ijklm}/v \quad (3)$$

The difference in the evaluated models lies in the fact that the first model is evaluated without weight for a given period of lactation, and the second model has given weight for each period of lactation, i.e. weighted analysis. Each period has a weight of one if the cow survived all nine lactation periods. However, if the cow did not survive a period of lactation, the surviving periods are assigned a weight of one, and the period in which the cow did not survive is assigned a weight ($v$), as in Cerna et al. (2023):

$$v = 9 - \sum \text{survived period of lactation} \quad (4)$$

The missing records for the lactation period were not included in the data for the models.

Breeding values for longevity were predicted in both ways, with no weight per lactation period and with a weight per lactation period in which a cow did not survive. Data from 1 055 814 cows were entered into the models, and the observed lactation periods for these cows totalled 6 073 685 for breeding values in the full dataset containing phenotype records until the end of June 2023. For breeding values from data trimmed by four years (trimmed dataset), i.e. data until the end of June 2019 containing phenotype data from 831 995 cows were entered into the model, a total of 4 686 915 lactation period records were included. The number of records in consecutive periods were decreasing as the underperforming cows were continuously culled (Figure 1).

Subsequently, the breeding values were predicted *via* both methods from the trimmed and full dataset, and the resulting breeding values were compared.

The Interbull validation test method of predicted EBVs was used to test the suitability of the models. The method assesses the quality of national breeding value predictions for appropriateness to be included in international evaluation. The principle of this method consists of the fact that the phenotypic data, which are trimmed by the last four years, are then compared to EBVs from

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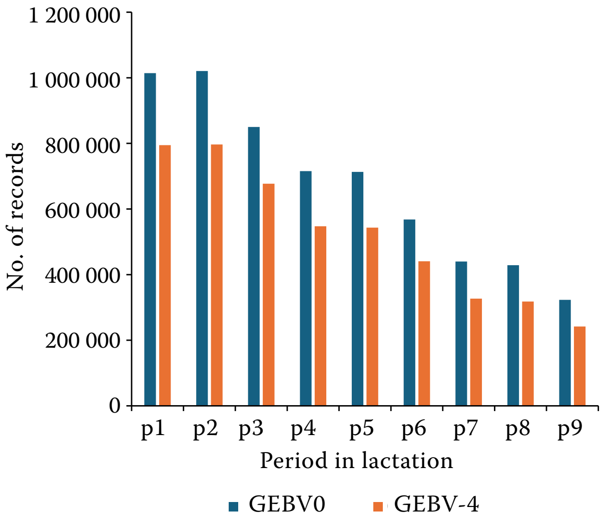

Figure 1. Number of measured records in individual periods of lactation

GEBV = genomic estimated breeding value

current data with full phenotypic information. The values from both datasets should present similar results for young bulls in the preliminary evaluation and when these bulls are proven in the full dataset. We used correlations between the resulting breeding values to assess the similarity of the estimated breeding values. The regression coefficients between the breeding values of the young bulls from the trimmed dataset and the breeding values from the full dataset were calculated by Mantysaari et al. (2010) procedure:

$$DRP_{\text{full}} = b_0 + b_1 \times \text{GEBV}_{\text{trimmed}} + e \qquad (5)$$

where:

$\text{DRP}_{\text{full}}$ – the deregressed proof of the GEBV estimated on the basis of the full dataset;

$b_0$ – the average bias;

$b_1$ – the prediction bias;

$\text{GEBV}_{\text{trimmed}}$ – the predicted genomic breeding value on the basis of the trimmed dataset, and the expected value of $b_0$ is 0 and of $b_1$ is 1 in the unbiased data;

$e$ – residuum.

If the regression coefficient $b_1 < 1$, young bulls are overestimated in the calculation. If $b_1 > 1$, young bulls are underestimated by the calculation. The deregressed proof was calculated as the GEBV resulting from evaluation of full dataset divided by its reliability.

Genotypes of 58 704 animals were included in the estimation of genomic breeding values from the full dataset (GEBV0) and GEBVs from the trimmed dataset (GEBV-4). The models were then evaluated on validation bulls, i.e. bulls with at least 20 daughters with performance records for milk production for GEBV estimation in 2023 and 0 daughters with performance for this trait four years before in 2019. Moreover, two different groups of animals were also checked: (*i*) Animals with a genotype – animals with a valid genotype for the calculation of breeding values, i.e. no disagreement was found in the pedigree by proof of genotypes, and the number of valid SNPs was greater than 25 000. (*ii*) For active bulls, bulls born after 1992, the proportion of Holstein cattle breed (including the red variant) was at least 75%, the registration date was no older than 48 months or had more than ten inseminations in the last 365 days, and it was not an active bull in natural breeding.

## RESULTS AND DISCUSSION

We used a novel approach introduced by Cerna et al. (2023) for longevity GEBV prediction *via* weighted analysis, where the weight is determined by the number of periods in which a cow did not survive, and the cows' productive life is recorded in 9 periods as repeated observations. Cerna et al. (2023) reported that the model with weight showed higher heritability, repeatability and standard deviations of breeding values of the whole evaluated population compared to the model without weight. We agree that the use of weight increases the reliability of predicted breeding values, as weight increases the effective number of records input into evaluation by the model, and our results show this as reliability is 0.86 in the model without and 0.91 in the model with weight in the full dataset (Table 1). This increase was also noticeable in the trimmed dataset (from 0.42 to 0.50; Table 2), and the minimal reliability of the GEBVs in the full dataset increased from 0.47 to 0.64 (Table 1). However, the effect of the increase in the standard deviation of GEBVs was not detected. This was despite the premise that increasing reliability should emphasise extremely positive and negative GEBVs. The reason for this may be that the validation bulls were preselected by farmers in 2019 based on their positive deviation from the mean EBV in the routine

Table 1. Descriptive statistics of 583 validation bull's GEBVs and their reliabilities from the full dataset in both models

| Descriptive statistic | GEBV0 without weight | $r^2$ without weight | GEBV0 with weight | $r^2$ with weight | Differences | |
|---|---|---|---|---|---|---|
| | | | | | GEBV0 | reliability |
| Mean | 106 | 0.86 | 106 | 0.91 | 1.96 | –0.048 |
| Standard deviation | 16.0 | 0.09 | 15.6 | 0.07 | 1.51 | 0.03 |
| Max-min difference | 114 | 0.52 | 106 | 0.35 | 7.6 | 0.17 |
| Minimum | 46 | 0.47 | 52.9 | 0.64 | 0 | –0.17 |
| Maximum | 160 | 0.99 | 158 | 0.99 | 7.6 | 0 |

GEBV0 = genomic breeding value from the full dataset; $r^2$ – reliability of the GEBV

Table 2. Descriptive statistics of 583 validation bull's GEBVs and their reliabilities from the trimmed dataset in both models

| Descriptive statistic | GEBV-4 without weight | $r^2$ without weight | GEBV-4 with weight | $r^2$ with weight | Differences | |
|---|---|---|---|---|---|---|
| | | | | | GEBV-4 | reliability |
| Mean | 92.2 | 0.42 | 82.6 | 0.50 | 10.5 | –0.08 |
| Standard deviation | 24.1 | 0.10 | 23.4 | 0.12 | 7.82 | 0.04 |
| Max-min difference | 162 | 0.70 | 149 | 0.86 | 43.1 | 0.27 |
| Minimum | 16.2 | 0.02 | 12.4 | 0.03 | 0 | –0.27 |
| Maximum | 179 | 0.72 | 161 | 0.09 | 0 | 0 |

GEBV0 = genomic breeding value from the full dataset; $r^2$ – reliability of the GEBV

evaluation of that year. Only the bulls that met this criterion were accepted as breeding bulls in the farmers' mating program and were permitted to sire daughters.These bulls are more similar in genetic quality to each other than to the whole bull population evaluated in 2019; thus, the validation bulls can have a lower standard deviation which can also in long-term reduce genetic gain as described by Vanavermaete et al. (2020). This factor can cause even smaller standard deviations in the model with weight, as the range of reliability of the validation bulls is reduced by increasing the reliability of the less accurately predicted GEBVs of the validation bulls with scarcer information in the input data (the range of reliability is 0.52 without *vs* 0.35 with weight in the full dataset). However, Jibrila et al. (2021) remark that bias caused by preselection can be prevented in ssGBLUP (single stap GBLUP) evaluation by the inclusion of genotypes and phenotypes of all animals in two previous generations of parents. In the Czech Republic, all bulls registered for breeding are mandatorily genotyped, and the project Fit Cow by the Holstein Cattle Breeders Association of Czech Republic promotes all-over genotyping of cows has been running since 2018 and therefore has a reduced effect on potential bias in evaluations. Farmers usually do not select intensively for longevity traits. Still, bulls with a genetic disposition for a longer productive life of daughters are selected indirectly by the selection of maternal fertility and somatic cell score. These traits have a high genetic correlation with longevity; specifically, maternal fertility has 0.42, and the somatic cell score with longevity has a correlation of 0.28 in the Czech Holstein population. Correlated traits are also included in the National Selection Index for Holstein cattle as defined by the Holstein Cattle Breeders Association of the Czech Republic in 2008. The high correlation of somatic cell score to mastitis (i.e. 0.84) was reported by Brand et al. (2009) in German Holstein cattle, and susceptibility to disease is one of the main factors of premature culling (Pant et al. 2011). Fertility as an important reason for mortality was already observed in Chinese Holstein cattle (Zhang et al. 2019) and Polish Holstein cattle (Adamczyk et al. 2021). Reproduction problems were also found to be one of the main reasons for economic wastage as low fertile cows are culled in New Zealand (Kerslake et al. 2018).

Even though the differences in GEBVs between the full dataset models without and with weight were low with maximum of 7.6 points and SD of 1.52 points of GEBVs (Table 1), the results from the trimmed dataset revealed distinct differences in predicted values of up to 43 GEBV points and a standard deviation of 7.83 points (Table 2), indicating important dissimilarity in early predictions, as these are values which will be used in praxis for the primary selection of breeding bulls by farmers. However, the correlation of GEBVs between the model without and with weight was 0.93 for the trimmed dataset and 0.99 for the full dataset, suggesting overall high similarity with individual exceptions (Figure 2). The average value of GEBVs in the trimmed dataset in the model without weight was significantly greater by 9.6 points (Table 2). Still, no apparent pattern was detected in validation bulls, with a large difference.

The validation test for both methods (i.e., without and with weight) resulted in similar values, as average biases were high ($b_0$ = 84.8 without, 85.2 with weight), and both prediction biases of the validation of the models showed low regression coefficients of GEBVs from the trimmed dataset to full dataset ($b_1$ = 0.445 without, 0.407 with weight), indicating high inflation of GEBVs by the methodology of Mantysaari et al. (2010). A difference in coefficients could be noticeable, preferring evaluation without weight. Still, the validation reliability was low in both validation models (0.157 without and 0.204 with weight in (Tables 3 and 4) even though the similar trend of GEBVs was apparent (Figures 3 and 4). Therefore, the results did not satisfactorily support a clear choice of a better model. Cerna et al. (2023) also reported that the model with weight showed higher heritability and better convergence. We used genetic parameters from their study, but

Table 3. Validation results and descriptive statistics for three groups of bulls from models without weight

| GEBV-4/GEBV0 without weight | Validation bulls | | Animals with genotype | | Active bulls | |
|---|---|---|---|---|---|---|
| No. of animals | 583 | | 58 661 | | 1 076 | |
| Correlation of GEBV-4 and GEBV0 | 0.463 | | 0.616 5 | | 0.610 3 | |
| Prediction bias ($b_1$) | 0.405 | | 0.854 | | 0.804 | |
| Validation reliability | 0.157 | | 0.224 | | 0.108 | |
| GEBV | GEBV-4 | GEBV0 | GEBV-4 | GEBV0 | GEBV-4 | GEBV0 |
| Mean | 92.23 | 106 | 99.54 | 112 | 88.4 | 106.6 |
| Standard deviation | 24.09 | 16.06 | 23.28 | 17.35 | 25.44 | 18.26 |
| Minimum | 16.2 | 46 | 0.3 | 32.7 | 1.4 | 41.6 |
| Maximum | 178 | 160 | 205 | 188 | 179 | 166 |
| Normal distribution | no | no | no | no | no | no |

GEBV0 = genomic breeding value from full dataset; GEBV-4 = genomic breeding value from trimmed dataset

Table 4. Validation results and descriptive statistics for three groups of bulls from models with weight

| GEBV-4/GEBV0 with weight | Validation bulls | | Animals with genotype | | Active bulls | |
|---|---|---|---|---|---|---|
| No. of animals | 583 | | 58 694 | | 1 077 | |
| Correlation of GEBV-4 and GEBV0 | 0.454 | | 0.604 | | 0.615 | |
| Prediction bias ($b_1$) | 0.407 | | 0.746 | | 0.689 | |
| Validation reliability | 0.204 | | 0.364 | | 0.108 | |
| GEBV | GEBV-4 | GEBV0 | GEBV-4 | GEBV0 | GEBV-4 | GEBV0 |
| Mean | 82.64 | 106 | 92.65 | 112 | 79.44 | 106 |
| Standard deviation | 23.45 | 15.66 | 21.37 | 16.98 | 23.78 | 18.08 |
| Minimum | 12.4 | 52.9 | 3.7 | 33.6 | 3.7 | 43.6 |
| Maximum | 161 | 159 | 195 | 187 | 164 | 165 |
| Normal distribution | no | no | no | no | no | no |

GEBV0 = genomic breeding value from full dataset; GEBV-4 = genomic breeding value from trimmed dataset

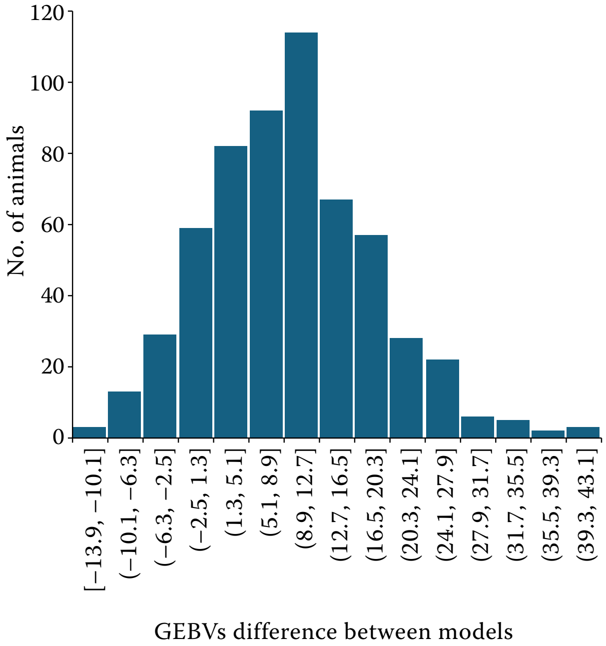

Figure 2. Differences in GEBVs in the trimmed dataset between models without and with weight

GEBV = genomic breeding value

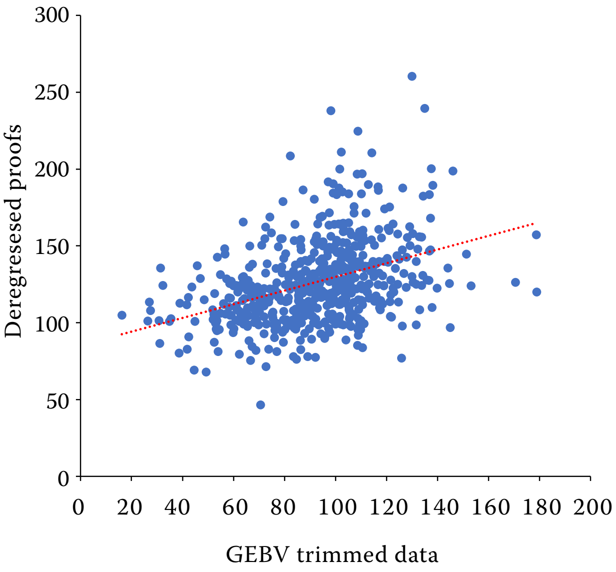

Figure 3. Regression of breeding values of the trimmed dataset to deregressed proofs from full data for validation bulls from the unweighted model

GEBV = genomic breeding value

we did not observe distinct better convergence in our prediction as a needed number of iterations for conversion value lower than E-12 in full data was 355 and 343 rounds in the model without and with weight, respectively.

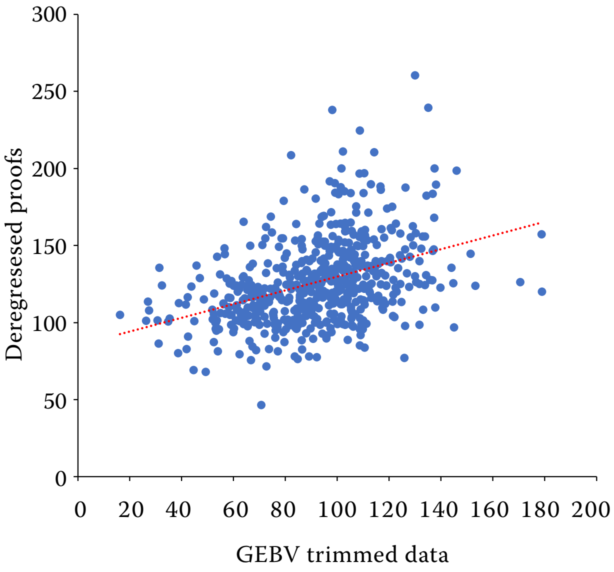

Figure 4. Regression of breeding values of the trimmed dataset to deregressed proofs from full data for validation bulls from a model with weight

GEBV = genomic breeding value

The evaluation of complex traits of longevity is usually difficult. A comparison with other models for evaluating longevity is not straightforward because of different definitions of analysed traits in other methods, such as the usual definition of production life. The productive life in linear models can be evaluated as a summation of days in the herd before culling, eventually with added credits for economic benefit according to VanRaden et al. (2006), or by dividing the first three lactations into nine periods, three in each lactation, due to different reasons for culling and solving a nine-trait model described by Taubert et al. (2017). The model described by Cerna et al. (2023) has a definition of a trait more obscured as it divides the productive life of a cow in a herd into nine periods according to different culling reasons but assumes that the trait is the same (i.e. survival or culling).

## CONCLUSION

Longevity is a very complex trait and difficult to analyse and finding an appropriate model to predict breeding value is very complicated. The weighted analysis to estimate breeding value for longevity is one possible way. The goal of our work was to verify if a novel approach to the evaluation of longevity by weighted and nonweighted repeatability models is applicable to routine evaluation of the Czech Republic for Holstein cattle. The weighted model increased the reliability of GEBVs by 0.05 on average compared to the nonweighted model. Neither of the models yielded convincing results, as documented in our study, and it seems that this is not the optimal method for our conditions, and the breeding values estimated by this model do not show adequate precision and stability. The method of validation is commonly used in the population genetics field and in the process of testing the results of national evaluation for inclusion into international evaluation by the Interbull organisation. The Interbull validation test results did not distinctly present the benefit of the weighted model in comparison to the nonweighted analysis of longevity. The validation of the novel method did not support the replacement of the current method in official routine evaluation in the Czech Republic for the purpose of better prediction of the genetic foundation of longevity in Czech Holstein cattle.

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## Conflict of interest

The authors declare no conflict of interest.

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