

## Single-step evaluation for milking cow survival in Poland

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### Abstract

In Poland, the current genetic evaluation of dairy cow survival is performed using Survival Kit with sire model. Genomic evaluation is implemented using a two-step approach. The Centre for Genetics of Polish Federation of Cattle Breeders and Dairy Farmers together with National Research Institute of Animal Production in Balice are currently undertaking the review of the Polish genetic evaluation system for all traits to implement single-step genomic evaluations using BLUPF90 family of programs. The goal of this research was to develop single-step evaluation of cow survival. The following approaches to defining cow survival phenotype were considered: 1) length of productive life in months from first calving to culling (with and without dry period included, continuous); 2) survival from one calving to the next (binary) implemented as either four-trait model (survival from 1<sup>st</sup> to 2<sup>nd</sup>, 2<sup>nd</sup> to 3<sup>rd</sup>, 3<sup>rd</sup> to 4<sup>th</sup> and 4<sup>th</sup> to 5<sup>th</sup> calving) or as a repeated records model (up to ten parities included); 3) survival to a given day in milk during lactation (binary) with lactations divided into three parts based on when most culling for specific reasons occurs (1-74, 75-250, and >250 to next calving days in milk). This approach was implemented using a nine-trait model (first 3 lactations split into 3 periods each) or a three-trait repeated records model (each part of lactation as separate repeated records trait in up to ten parities); 4) random regression model with survival defined per month from first calving up to 72 months; 5) number of completed lactations (categorical treated as continuous); 6) number of days survived within each lactation (continuous). Variance components were estimated for all phenotypes, and alternative modeling approaches were tested, with a primary focus on assessing the feasibility of correcting for levels of milk production in the model. Next, the list of phenotypes of interest was narrowed down to options 1-3 listed above. For those phenotypes, both conventional pedigree-based evaluations and single-step evaluations were performed using BLUPF90 with the APY approach. Formal validation was carried out for all runs, including the Interbull trend test and Mendelian sampling test. This paper will present the results of the validation work which leads to the choice of the cow survival phenotype for single-step implementation.

**Key words:** dairy, genetic evaluation, genetic parameters, single-step evaluation, survival

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### Introduction

In Poland, the current genetic evaluation of dairy cow survival is performed using Survival Kit with sire model (Ducrocq, 2005; Morek-Kopec and Zarnecki, 2012). Genomic evaluation is implemented using a two-step approach. The Centre for Genetics of Polish

Federation of Cattle Breeders and Dairy Farmers (PFHBiPM, CGEN) together with National Research Institute of Animal Production in Balice are currently undertaking the review of the Polish genetic evaluation system for all traits to implement single-step genomic evaluations using BLUPF90 family of programs (Aguilar, *et al.*, 2018). Although

survival hazard model might be statistically superior for genetic evaluation (GE) of cow survival, its implementation in single step methodology is problematic and not available in BLUPF90 software. The goal of this research was therefore to develop and implement a single step evaluation of milking cow survival for Polish Holstein-Friesian population using BLUPF90 software.

## Materials and Methods

### *Phenotypic data*

Phenotypic records were obtained from national database maintained by PFHBiPM. Data from 1995 were included for Holstein-Friesian and Holstein-Friesian Red cows. Many versions of possible survival phenotype definitions were tested. In this paper the focus is on the five most promising options used in final testing and validation runs.

### *Trait definitions*

Option 1 – Length of productive life defined as time in days from first calving to culling. It was modeled as linear trait. Pros of this option are that it is simple single trait model, the phenotype would be the closest to the currently evaluated one, heritability is reasonable. Cons: phenotype is only available after cow's death. Abbreviation: *prodlife*.

Options 2-5 use binary phenotypes modeled on an observable scale.

Option 2 – Nine-trait model (MT-ML). Survival to a given DIM during lactation. Data from the first three lactations is used and each is split into periods of time representing culling for different reasons. Time periods were decided based on DIM at culling typical for main culling reasons (1-74, 75-249, 250-next calving). Dry period was included in the last period. This model was very similar to the one implemented in Germany (Taubert, *et al.*, 2017). Abbreviation: *surv9*.

Option 3 – Four-trait model. Phenotype is defined as survival from one parity to the next (one calving to next calving), parities 1-2, 2-3,

3-4, and 4-5 are considered. Abbreviation: *surv15*.

Option 4 – Repeated records variation of Option 2. Each parity is split to the same three periods as in Option 2, but each period is modeled as repeated records. It results in a three-trait repeated records model. Up to ten parities are included. Abbreviation: *prep*.

Option 5 – Repeated records variation of Option 3. Survival from one parity to the next is modeled as repeated records. It is a single trait model with up to ten parities included. Abbreviation: *rep*.

### *Models*

In all the options phenotypes were modeled on the observable scale. Fixed effects included age at first or previous calving, contemporary group (herd-year-season of first/previous calving) and lactation number for repeated records model. Additional effects like the level of milk production were tested in earlier stages of the project but discarded.

### *Variance components data*

For variance components estimation a subset of herds with larger size and data of higher and consistent quality was used. The dataset used included over 300,000 records for over 100,000 cows from 160 herds collected across 10 years. Pedigree included over 250,000 individuals. Variance components were estimated using ASReml software (Gilmour *et al.*, 2015).

### *Genetic evaluation data*

Genetic evaluation runs were performed using all available data from 1995. Contemporary groups with less than 5 observations and no variation in phenotypes were excluded from the analysis. For Option 1 there were 2.2M records with phenotypic average of 35 months of productive life. For Options 2&3 there were 2.4M of cows with records available. Phenotypic averages are presented in Table 1.

For Options 4&5 there were 3.6M of cows with records. Phenotypic averages are presented in Table 2.

Table 1. Phenotypic averages for survival (to the next stage) phenotypes for Option 2&amp;3.

Parity	Option 2			Option 3
	DIM1-74	DIM75-249	DIM250+	
1	0.92	0.90	0.82	0.76
2	0.93	0.87	0.76	0.68
3	0.89	0.83	0.71	0.61
4	---	---	---	0.55

Table 2. Phenotypic averages for survival (to the next parity) phenotypes for Option 4&amp;5.

Parity	Option 4			Option 5
	DIM1-74	DIM75-249	DIM250+	
1	0.95	0.93	0.85	0.79
2	0.95	0.90	0.78	0.72
3	0.93	0.87	0.74	0.64
4	0.91	0.83	0.69	0.59
5	0.89	0.80	0.65	0.53
6	0.89	0.76	0.62	0.50
7	0.89	0.73	0.58	0.46
8	0.86	0.69	0.59	0.43
9	0.84	0.65	0.52	0.39
10	0.83	0.62	0.48	0.35

All genetic evaluation runs were performed using BLUPF90 family of programs (Aguilar, *et al.*, 2018). Pedigree based (conventional; PBLUP) evaluations were performed on all models as well as single step evaluations (SSBLUP) using APY approach (Misztal, *et al.*, 2014).

### Combining EBVs

The EBVs from multiple trait models were combined into one EBV using the following weights: 1) Option 2 (nine-trait model) – 0.06, 0.09, 0.15, 0.05, 0.075, 0.125, 0.09, 0.135, 0.225; 2) Option 3 (four-trait model) – 0.3, 0.25, 0.2, 0.25; 3) Option 4 (three-trait repeatability model) – 0.2, 0.3, 0.5.

### Validation methods

In order to validate the five options, records from the last four years were removed from the validation datasets (2018-2022), while keeping the pedigree unchanged. The results from the truncated runs were used for three types of validation. 1) Legarra and Reverter (LR) validation method as described by Legarra and Reverter (2018); 2) Quintile analysis, where validation cows are classified into quintiles (5

groups of equal size) based on EBVs from truncated runs. Validation phenotypes are then fit as dependent variables in model including quintile groups. Least square means solutions for those quintile groups are obtained. The differences between best and worse quintile groups are used to compare predictive abilities of the models with assumption that higher value of the difference means better prediction; 3) Interbull trend test III and Mendelian Sampling test.

There were three focal groups used in LR validation. 1) “Young Sires” – bulls with no daughters in truncated data and minimum 25 daughters in full data (N=679); 2) “Proven Sires” – bulls with 5-25 daughters in truncated data and minimum twice as many daughters in full data (N=196); 3) “Cows” – females with good quality phenotypes from large herds that calved first time in 2018 with phenotypes removed from truncated data (N=21,977). Only the “Cows” focal group was used for Quintile validation.

Correlations between EBVs from the current official survival evaluation and tested approaches were also assessed as well as genetic trends.

## Results and Discussion

### Variance components

The Heritability for Option 1 was estimated to be 0.12. Variance components obtained for Option 2 are presented in Table 3 (last page). Heritabilities for the nine-trait model were lower than for other options, but results in general align with those obtain in Germany for similar model (Taubert, *et al.*, 2017). Variance components obtained for Option 3 are presented in Table 4. Heritabilities for the four-trait model were substantially higher than for nine-trait model.

Heritabilities, genetic and residual correlations obtained for three-trait model (Option 4) are presented in Table 5. Permanent environmental variances were estimated to be very close to

Table 4. Heritabilities (diagonal) genetic correlations (above diagonal) and residual correlations (below diagonal) obtained for Option 3.

Trait	Surv12	Surv23	Surv34	Surv45
Surv12	0.034	0.74	0.69	0.64
Surv23	-0.09	0.046	0.78	0.71
Surv34	-0.07	-0.12	0.040	0.79
Surv45	-0.04	-0.09	-0.09	0.038

Table 5. Heritabilities (diagonal) genetic correlations (above diagonal) and residual correlations (below diagonal) obtained for Option 4.

Trait	DIM1-74	DIM75-249	DIM250+
DIM1-74	0.012	0.84	0.79
DIM75-249	0.07	0.013	0.74
DIM250+	0.05	0.06	0.026

zero, therefore permanent environmental effects were excluded from genetic evaluation models and repeatabilities are not presented for repeated records models (Options 4&5).

Also here, heritabilities for model where lactation is being split into parts are lower, especially for DIM 1-74 and DIM75-249. This might be due to the fact that most culling occurs in the last part of the lactation.

The heritability for single trait repeatability model (Option 5) was estimated to be 0.040.

**Current vs new EBVs**

The correlations between EBVs from 5 options tested and current official EBVs published for longevity for chosen groups of focal cows and bulls are presented in Table 6 (last page).

Single and three-trait repeatability models (Options 4&5) had the highest correlations with current official EBVs for longevity.

**Genetic trends**

Genetic trends for current official evaluation and for the five tested alternatives for bulls and cows are presented in Figure 1. As with correlations, single and three-trait repeatability models (Options 4&5) had the closest genetic trends to the current official EBVs for longevity.

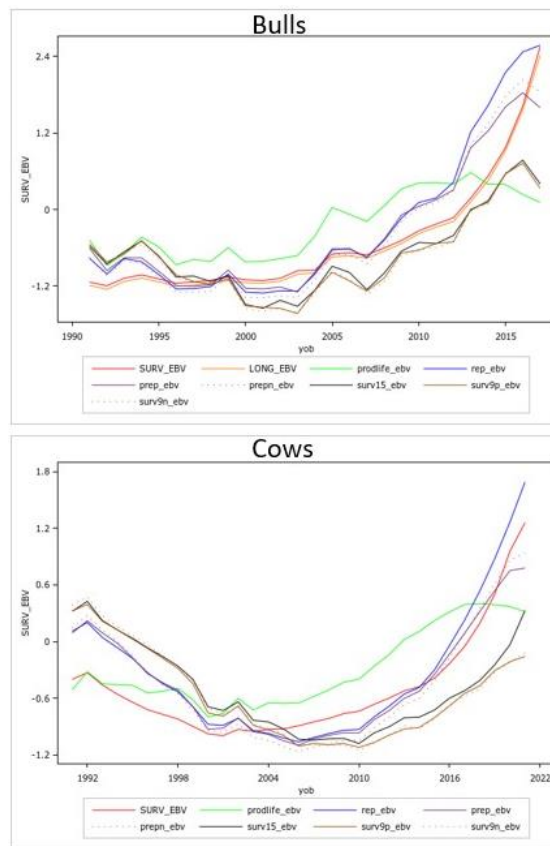


Figure 1. Genetic trends for current official EBVs (SURV\_EBV & LONG\_EBV) and for tested alternative Options 1-5 (prodlife\_ebv, surv9\_ebv, surv15\_ebv, prep\_ebv, rep\_ebv) for bulls and cows.

**LR validation**

The results of the validation performed using the method of Legarra and Reverter are presented in Table 7. The values obtained for bias, slopes and accuracy are presented. All results are standardized to the same standard deviation of 1. Bias is the difference between mean EBVs obtained for full and truncated runs. The expectation of it is zero. A positive value means that animals with partial information are over evaluated. Slope is a linear regression of full on truncated EBVs. The expected value is one. Values lower than one mean that selected candidates are overestimated. Accuracy is calculated as correlation between EBVs from full and truncated runs. Values close to one indicate that truncated evaluation was as accurate as whole evaluation, but both evaluations could have low accuracy.

Table 7. Results for LR validation for pedigree based (PBLUP) and single step (SSBLUP) models for Option 1-5 for young sires (YoungS), proven sires (ProvenS) and cows.

Group	PBLUP			SSBLUP		
	bias	slope	acc	bias	slope	acc
surv9_ebv (Option 2)						
YoungS	-0.012	1.011	0.606	0.163	0.819	0.814
ProvenS	0.025	0.920	0.757	0.094	0.893	0.865
Cows	0.029	0.953	0.782	0.095	0.907	0.846
surv15_ebv (Option 3)						
YoungS	0.061	0.892	0.570	0.181	0.783	0.806
ProvenS	0.041	0.867	0.740	0.087	0.849	0.858
Cows	0.038	0.909	0.759	0.087	0.887	0.834
prep_ebv (Option 4)						
YoungS	-0.161	1.113	0.658	0.187	0.831	0.820
ProvenS	0.149	1.028	0.738	0.285	0.905	0.838
Cows	0.132	1.023	0.768	0.262	0.930	0.843
rep_ebv (Option 5)						
YoungS	0.271	1.017	0.631	0.004	0.852	0.818
ProvenS	0.554	0.933	0.727	0.105	0.860	0.829
Cows	0.535	0.930	0.751	0.078	0.896	0.831
prodlife_ebv (Option1)						
YoungS	0.263	0.397	0.468	0.518	0.449	0.828
ProvenS	0.056	0.671	0.789	0.218	0.594	0.847
Cows	0.069	0.719	0.768	0.233	0.643	0.820

For pedigree based (conventional) models, bias was the lowest in nine-trait model (Option 2), slopes were closest to one in three-trait repeatability model (Option 3), accuracy was the highest for Option 2 again.

For single step models, bias was the lowest in single trait repeatability model (Option 5), slopes were closest to one in three-trait repeatability model (Option 3), accuracy was the highest for Option 2.

The single trait model had slightly higher bias and slopes further from one than PBLUP models. However, all SSBLUP models resulted in higher accuracy than PBLUP models. With differences being largest for young sires, which is desired outcome.

It is worth noticing that differences between models were not big and all models from Options 2-4 performed very well in this validation.

**Quintile validation**

In quintile style validation many different phenotypes (N=35) were evaluated. The advantage of this approach is that any phenotype can be used as dependent variable, also one that is completely independent from the phenotypes used to derive EBVs. Here only one example is presented (Figure 2) for probability of surviving from first to fourth calving. This phenotype was not used to derive any of the EBVs validated.

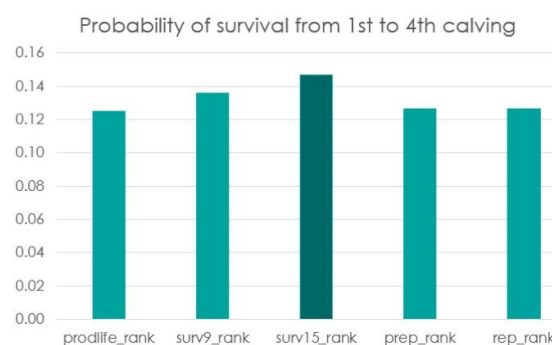


Figure 2. Example result from quintile validation for Options 1-5. Probability of surviving from first to fourth calving.

For this phenotype (as well as for many others, results not presented), the four-trait model (Option 3) showed the highest predictive ability. Validation shows substantial differences between the best and the worse EBV animals, for example difference between top and bottom 20% of cows based on surv15 (Option 3) combined EBV for probability of survival from first to fourth calving is 14.7%.

In general, the differences between models were relatively small (for phenotype above, best EBV predictions differ by 14.7%, the worst differ by 12.5%) and satisfactory results were obtained for all tested options. Overall, the four-trait model (Option 3) performed best, followed by nine-trait models (Option 2) and three-trait repeatability model (Option 4).

**Interbull test**

All models except Option 4 (three-trait repeatability model) passed the Interbull trend test III. Number of bulls available for this test varied between traits from 142 to 215. All models except Option 5 (single trait repeatability model) failed Mendelian sampling test (Table 8). Options 2-4 failed for bulls only, while Option 1 failed by a significantly higher margin for both sexes.

Table 8. The results of Interbull Mendelian sampling test.

Option	Bulls	Cows
1 (prodlife)	-13.4	-12.3
2 (surv9)	-5.9	1.0
3 (surv15)	-4.6	1.2
4 (prep)	-5.3	-1.2
5 (rep)	0.0	2.0

**Run times**

Consideration was also given to the time it takes to run each model. Single trait models (Options 1 & 5) took around 10 minutes for PBLUP and 30-40 minutes for SSBLUP. Three- and four-trait models needed less than one hour for PBLUP and almost 2 hours for SSBLUP. Nine-trait model took the longest, over five hours for PBLUP and almost nine hours for SSBLUP. While differences in run times between different options are substantial, for none of the models they would be considered problematic for implementation.

**Conclusion**

Based on the presented results no one model was a clear winner. The only clear “no” would be Option 1 – Length of productive life. Although this was the only phenotype with normal distribution and heritability >0.1, the phenotype itself has more disadvantages. It takes the longest to collect phenotypes, because as long as cow remains in a herd her phenotype would be missing. The resulting EBVs from this option has the lowest correlation with current official evaluation for longevity and genetic trends deviated the most from current ones.

Additionally, this model resulted in the poorest results for Interbull Mendelian sampling test and LR validation (especially slopes).

For Options 2-5:

- Based on comparisons with current official proofs for longevity, both correlations and genetic trends, both repeatability models performed better than Options 2 & 3.
- Based on LR validation a nine-trait model (Option 2) looked slightly better but followed closely by three-trait repeatability model (Option 4) and four-trait model (Option 3).
- Based on quintile validation, the four-trait model performed best across many validated phenotypes.
- Based on Interbull tests Option 4 (three-trait repeatability mode) should be discarded as it did not pass trend test III. Additionally, only the single trait repeatability model (Option 5) passed Mendelian sampling test for both sexes.

Based on the results presented in this paper no clear winner has been identified. However, based on further analysis and industry consultations, Option 3 – the four-trait model has been chosen as preferred for implementation for Polish dairy population.

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Table 3. Heritabilities (diagonal) genetic correlations (above diagonal) and residual correlations (below diagonal) obtained for Option 2.

Trait	Lactation 1			Lactation 2			Lactation 3		
	DIM1-74	DIM75-294	DIM250+	DIM1-74	DIM75-294	DIM250+	DIM1-74	DIM75-294	DIM250+
	1	2	3	4	5	6	7	8	9
1	0.014	0.91	0.58	0.68	0.67	0.58	0.68	0.61	0.52
2	0.05	0.010	0.75	0.75	0.75	0.63	0.65	0.65	0.68
3	0.03	0.05	0.029	0.66	0.65	0.72	0.50	0.65	0.64
4	-0.01	-0.01	-0.13	0.016	0.88	0.59	0.67	0.67	0.58
5	-0.17	-0.13	-0.08	0.00	0.009	0.80	0.75	0.75	0.63
6	-0.02	-0.04	-0.19	-0.04	0.02	0.026	0.65	0.64	0.72
7	0.00	-0.02	-0.10	-0.10	-0.06	-0.10	0.010	0.88	0.69
8	-0.14	-0.11	0.01	-0.10	-0.09	-0.04	-0.05	0.006	0.80
9	0.02	-0.02	-0.14	-0.03	-0.05	-0.13	0.03	0.07	0.022

Table 6. Correlations between current official EBVs and the five tested Options.

Evaluation type	All bulls		Available (young) bulls		Cows
	Domestic	MACE	Domestic	MACE	Domestic
Number of animals	19,568	36,099	621	777	2,490,297
Average reliability	0.60	0.45	0.45	0.50	0.30
prodlife (Option 1)	0.46	0.34	-0.15	-0.14	0.54
surv9 (Option 2)	0.58	0.47	0.34	0.44	0.59
surv15 (Option 3)	0.58	0.48	0.32	0.42	0.59
prep (Option 4)	0.72	0.60	0.43	0.52	0.77
rep (Option 5)	0.73	0.64	0.49	0.57	0.78