

Comparison between Methods for Estimation of Breeding Values for Longevity in Slovenian Holstein Population

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Abstract

Longevity or herd life is a highly desirable trait that has a great impact on economy of dairy production. Herd life can be measured in several ways, as survival in defined age or in days from first calving to culling. Breeding values (EBV) used for selection can be estimated for direct herd life (DHL) or indirect herd life (IHL). For Slovene Holstein population we compared different models for DHL: the proportional hazards (PH) model, multi trait sire (SM) models and multi trait animal (AM) models (for the last two dependent variables was defined as survival in particular period or days from first calving to culling). We estimated genetic parameters, correlations between various EBVs for DHL and correlations between DHL EBVs and EBVs for other traits in routine genetic evaluation. Heritability estimated using the PH was 0.179, for AM and SM between 0.08 - 0.19 and 0.05 - 0.17, respectively. Correlation coefficients between AM and SM EBVs were 0.70 - 0.88. Estimated correlation coefficients between EBVs for DHL using the PH and EBV of other traits are relatively low, as expected: milk yield (- 0.44), somatic cell count (0.21), rear teat position (- 0.25), rear teat placement (- 0.21), front teat placement (- 0.20) and muscling (0.22). Due too the low correlation between DHL EBVs from PH and MT models, correlations between various trait and all five DHL EBVs are similar.

Keywords: longevity, breeding value estimation, survival kit, multitrait animal model

1 Introduction

The longevity or herd life has great impact on economy of dairy production (Charffeddine *et al.*, 1996; Strandberg and Sölkner, 1996). Until survival analysis was applied, several linear models (especial sire models) were used for the prediction of BVs for DHL. In last ten years several countries introduced longevity in routine genetic evaluations. Most of them use the proportional hazard (PH) models (Interbull-centre, 2008). The main reason for using the PH model is possibility to properly account for censored data and time-dependent effects in the evaluation.

The purpose of our study was the comparison of different methods for the estimation of breeding values (BV) for longevity in Slovenian Holstein population.

2 Material and methods

The data was processed by SAS software package (SAS Institute, 2000). Survival Kit (Ducrocq and Sölkner, 1998) was used for the estimation of parameters in the PH model, while VCE (Kovač *et al.*, 2002) was used for sire (SM) and animal (AM).

2.1 Material

The data was obtained from the national data base, which is maintained at the Agricultural institute of Slovenia. Complete lactations of Slovenian Holstein cows used in first national evaluation of BV in the year 2008. We used all lactations for PH model and reduced material for SM and AM (only the first 3 lactations were considered, we also excluded cows with migrations and incomplete series of lactations).

The numbers of observed data were presented in the Table 1. Distribution of the whole data used with PH model was described in Figure 1.

We used the maternal grandsire relationship for PH model, father grandsire relationship (two levels) for SM model and whole pedigree for AM model.

Table 1. Data description for different models.

Data \ Model	PH	SM	AM
Lactations	264 885	184 039	184 039
Cows with obs.	87 668	79 162	79 162
Bulls	1 916	639	1 876
Pedigree	1 916	639	104 441
Censored data	29 844	19 223	19 223

Table 2. Percentage of different type of data per traits for SM and AM models.

Trait	1 st	2 nd	3 rd	4 th	5 th
0		3.08	8.91	17.83	24.28
1	95.80	89.77	76.23	53.39	33.68
2	4.20	7.15	14.86	28.77	42.04

0-censored; 1-survived; 2-culled

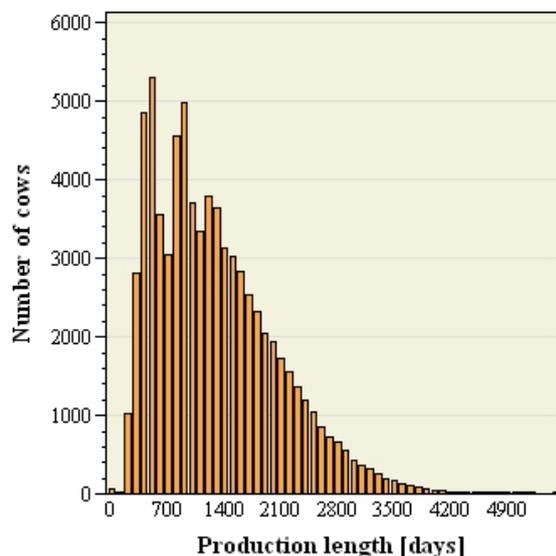


Figure 1. Distribution of data for PH model.

Traits for MT SM and AM were defined as proposed by Sewalem *et al.* (2006). The first of five traits was defined as survival (stayability) from the day of 1st calving to 120 days in milk (DIM), the second as survival from 120 DIM to 240 DIM, the third from 240 DIM to 2nd calving, the fourth from 2nd to 3rd calving, and

the fifth trait is defined as survival from 3rd to 4th calving.

The longevity for cows was described as stayability: 1 - the cow survived from 1st calving to the end of that time period; 2 - the cow was culled during that time period; or missing in case of censored data. The other definition of traits was number of days from 1st calving to the end of each time period. If the cow was alive in the defined time period we coded the trait as missing.

2.2 Methods

The following PH model was used,

$$h(t) = h_0(t) \exp \left\{ l_{jn}(t) + \sum_k f_k(t) + s_{sire} + 0.5s_{mgs} \right\}$$

where $h_0(t)$ is the Weibull baseline hazard function. t is the time in days from first calving to the end of the production life. $l_{jn}(t)$ is fixed time dependent effect of stage of lactation within lactation. $f_k(t)$ represents other fixed and random effects. The *herd* is a random time dependent effect assumed to follow a log gamma distribution. The *year* is a fixed time dependent effect. The *age at first calving* is a fixed time independent effect. The *milk* is a fixed time dependent effect. The *sire* is a random time independent genetic effect assumed to follow a multivariate normal distribution. We used sire-mgs model.

The following MT linear models were used,

$$y = Xb + Z_h h + Z_a a + e$$

where y was an observation for herd life (stayability or days). *Age at first calving* and *milk in first lactation* were fixed effects, *herd* was a random effect. The same multi trait model was defined as sire model and as animal model.

3 Results

In this chapter we present estimates for genetic parameters and correlations between EBVs with different models.

3.1 Genetic parameters

Estimated parameters for the PH model are high. Herd variance was estimated at 0.28 and sire variance at 0.06. For this model the heritability is 0.179.

Estimated heritabilities (Table 3) for SM were in the range from 0.06 to 0.10 for stayability, while the range for survival expressed in days was from 0.05 to 0.17. Heritabilities from AM were in range from 0.11 to 0.15 and from 0.08 to 0.19 for traits defined as stayability and as survival in days, respectively.

Table 3. Estimated heritabilities for SM and AM in two different trait definitions.

Model \ Trait	1 st	2 nd	3 rd	4 th	5 th
SM stayability	0.06	0.08	0.07	0.08	0.10
SM days	0.05	0.08	0.13	0.14	0.17
AM stayability	0.11	0.15	0.10	0.11	0.13
AM days	0.08	0.13	0.15	0.16	0.19

3.2 Correlations between different EBV of longevity

Estimated correlation coefficients between EBVs predicted with different MT models were high (Table 4; Figure 4). Exception was the correlation between EBVs for AM for days and SM for stayability. Comparison of EBVs between PH and MT models showed low correlation coefficients (Table 4; Figures 2 and 3).

Table 4. Estimated correlation coefficients between EBVs predicted with different models.

Model	SM *	SM days	AM *	AM days
PH	0.24	-0.15	0.39	-0.17
SM *		-0.70	0.88	-0.20
SM days			-0.58	0.78
AM *				-0.80

*stayability

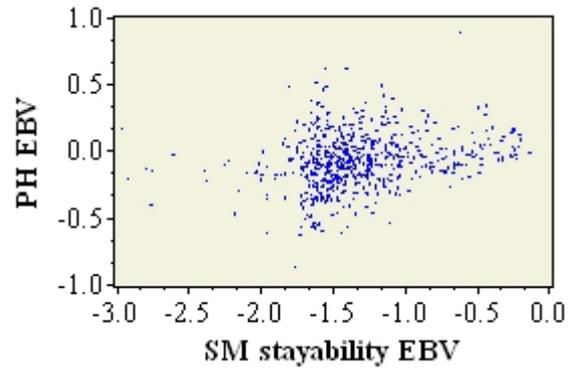


Figure 2. Correlation between EBVs from PH and SM stayability model.

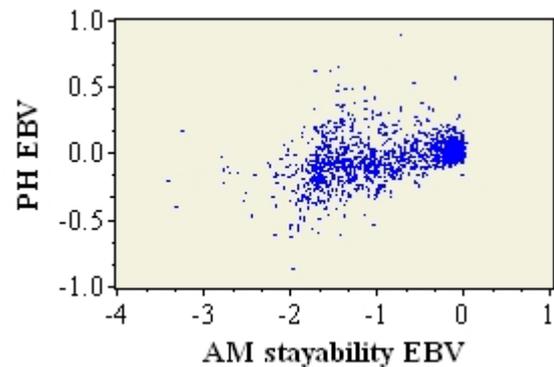


Figure 3. Correlation between EBVs from PH and AM stayability model.

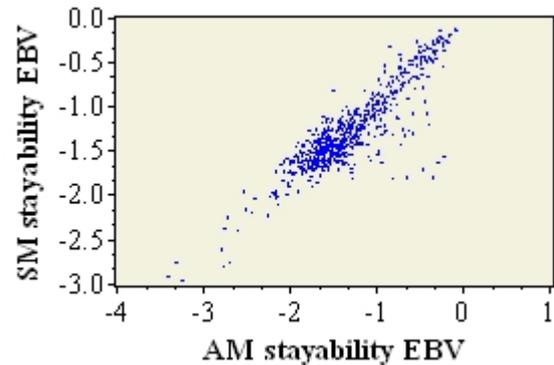


Figure 4. Correlation between EBVs from SM stayability and AM stayability.

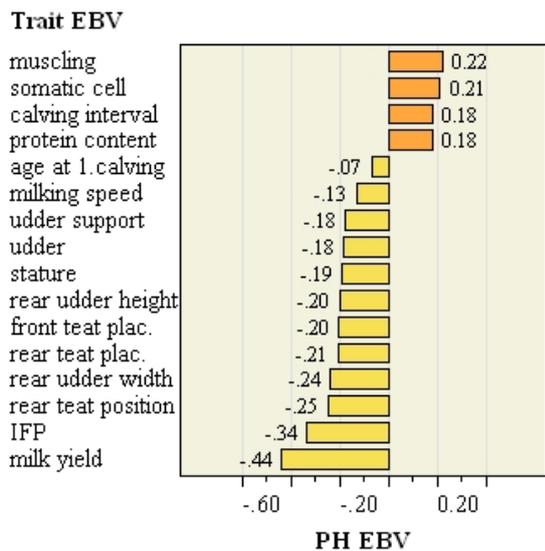


Figure 5. Correlation between EBVs from PH model and other traits from routine evaluation.

3.3 Correlations between direct herd life and other traits

Before calculating the correlation coefficients between EBVs for different traits we multiplied with -1 BVs for traits where positive number present undesirable expression of trait.

Correlation coefficients between EBVs for DHL from the PH model and EBVs of other traits (included in the routine genetic evaluation) were as expected relatively low. We show the highest and the most interesting relationships (Figure 5). The positive correlations with DHL were estimated for muscling, somatic cell count, calving interval and protein content. Negative correlations were obtained for milk yield, index for fat and protein yield, rear teat position, rear udder width, rear teat placement, front teat placement, rear udder height, stature and udder. Interesting were also EBV correlations with milking speed (-0.13), udder support (-0.18) and age at first calving (-0.07).

4 Discussion

Comparison of heritabilities between our study and those used by Interbull member countries (Interbull-centre, 2008) show that heritability estimated from the PH model is practically the same as reported in Germany and Switzerland.

Other countries reported lower heritabilities for prediction of breeding values for direct herd life in Holstein populations. Only four countries used multi-trait animal or sire model for prediction of breeding values in 2nd international evaluation for longevity in 2008. Our heritability estimates are high in comparison with heritabilities for these four countries.

Comparison of breeding values from different models shows that correlation between the PH and multi trait models are very low. In this case a lot of re-rankings occurred. Correlations between EBVs for SM and AM are relative high for both trait definitions. Because the data was obtained from the same source we expected higher correlations between all models and only a few re-rankings. Possible explanation for the differences between PH and linear models is different treatment of censored data and time-dependent effects.

Breeding values from the PH model were positively correlated with breeding values for SCC, muscling, calving interval and protein content. Correlations were a bit lower as reported in the literature, but have the same direction. On the other hand negative correlations were found with BVs for milk yield, some teat and udder traits, stature and age at first calving. These results are reasonable, because a lot of culling were done due to udder and/or teat defectiveness. Cows with too high stature or first calved too young are more frequently culled as average cows regarding to stature and age at first calving.

5 Conclusion

The results of our study show considerable differences between used methods. From theoretical point of view survival analysis is the method of choice. Nevertheless, it is always beneficial to corroborate the results with other methods that are well known and widely applied for other traits.

Based on our results and the literature we can conclude that PH method and proposed model for predicting of breeding values for direct herd life is suitable for routine breeding value prediction.

For estimation of indirect herd life or indirect longevity we can recommend using type traits as teat placement, muscularity, somatic cell count, and teat length.

6 References

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