

## Analysis of longevity in the Slovak Pinzgau population – extension to the animal model

G. MÉSZÁROS<sup>1</sup>, O. KADLEČÍK<sup>2</sup>, R. KASARDA<sup>2</sup>, J. SÖLKNER<sup>1</sup>

<sup>1</sup>Division of Livestock Sciences, University of Natural Resources and Life Sciences, Vienna, Austria

<sup>2</sup>Department of Animal Breeding and Genetics, Faculty of Agrobiological and Food Resources, Slovak University of Agriculture in Nitra, Nitra, Slovakia

**ABSTRACT:** Breeding values for length of productive life in Slovak Pinzgau cattle were estimated using survival analysis. As the results were corrected for milk production, the final breeding values represented the ability of cows to avoid culling from reasons other than milk production. In addition to the relative milk yield, the risk of culling was also studied in connection with the herd and year of calving, parity and stage of lactation, herd size change and age at the first calving. Among the fixed effects, the low milk production, high age at the first calving, and decreasing herd size were associated with increased risk of culling. The risk was non-linear for parity  $\times$  stage of lactation classes, decreasing within the first parity and increasing during later parities. Two genetic random effects were considered in separate models: the sire of the cow and the animal itself, both with the corresponding pedigree records up to the third generation. The genetic effects were estimated in separate runs, but the rest of the model remained unchanged. Heritability was  $h^2 = 0.08$  for sire model, confirming the results of an earlier study in the Slovak Pinzgau population. The computational feasibility of the animal model for estimation of breeding values for cows was confirmed in this study. The new breeding values could be computed for each cow, accounting for all relationships within the population. The estimated heritability for the animal model was  $h^2 = 0.11$ , which should be used later on for animal breeding purposes.

**Keywords:** Pinzgau cattle; survival analysis; breeding value; genetic variability; reliability; heritability

Longevity is often said to be the most important functional trait (Essl, 1998). Each animal is a considerable investment of time, fodder, and money already at the time of its birth. It is very undesirable when an animal fails to reach productive age or dies during the first lactations, as it brings about not only economic loss (in future meat and milk production, replacement animal for the herd or direct sale), but also loss of potential genetic gain in the population. The economic importance of longevity in central European context was stressed by Krupa et al. (2006) and Wolfová et al. (2007).

Survival analysis methodology is often used to analyze longevity, as it utilizes all available information including incomplete, i.e. right censored (Ducrocq, 1994) or left truncated (Vukasinovic

et al., 2001) records, and it also accounts for the nonlinear characteristics of lifetime data (Ducrocq, 1997). Cox (Cox, 1972) and Weibull models are used to study factors influencing culling decisions (Ojango et al., 2005; Zavadilová et al., 2011). The Weibull model is used more often in national scale evaluations (e.g. Ducrocq, 1999), due to its computational feasibility. Papers dealing with longevity in dairy cows are reviewed in Essl (1998). Longevity studies in cattle are focusing on the length of productive life (LPL) which is defined as the time interval between the first calving to death, culling or censoring (Ducrocq, 1994). When the production is not taken into account in the model, the genetic effects reflect the so called “true” longevity, i.e. all reasons for culling are considered together.

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As the milk production is greatly influencing the decisions of the farmer about culling a particular animal, the milk production is often included into the model, resulting into “functional” length of productive life (Ducrocq et al., 1988; Ducrocq, 1999). Similarly to cattle, the milk production in goats (Mellado et al., 1991), litter size in sheep (Pollott and Gootwine, 2004) and pigs (Irgang et al., 1994; Mészáros et al., 2010) were used to assess the functional longevity.

The length of productive life in Pinzgau cattle was analyzed by Fuerst and Egger-Danner (2002), providing the methodology of the national evaluation for longevity of cattle in Austria. In Slovakia, effects influencing the length of productive life were explored by Mészáros et al. (2008a). The initial study was further extended to include the sire effect in Mészáros et al. (2008b), resulting into breeding values for sires. This work is an expansion of our previous study to an animal model, which would provide information about the genetic background of each animal, which can be further utilized in selection of sires and dams.

The aim of this study was to estimate the heritability and compare reliability of breeding values for functional length of production life in Slovak Pinzgau cattle using animal and sire models.

## MATERIAL AND METHODS

### Data

Herd book data for Slovak Pinzgau cows were provided by the Slovak Breeding Services for the time span January 1<sup>st</sup>, 1993–October 31<sup>st</sup>, 2011. For each cow the dates of calving, date of culling, and milk production records had to be known, as these were essential for assessment of functional length of productive life. Animals aging at first calving less than 540 days (18 months) or more than 1800 days (60 months) were removed. Cows from small herds with less than 20 calvings per year or from small half sib families (less than 9 daughters per bull) were not considered. Animals alive at the time of data collection, withdrawn from the milk recording due to breeders’ decision and those from herds decreasing in size by more than 50% between subsequent years were right censored. After data editing, 40 397 cows, daughters of 334 sires, remained in the dataset out of which 8055 animals (19.9%) were right censored.

### The model

The general setup of the Weibull proportional hazards model was based on our previous work on the sire model (Mészáros et al., 2008b). Altering the genetic effect in the model we estimated the genetic variance using an animal model with the corresponding relationship matrix between all animals. The structure of the model was:

$$\lambda(t) = \lambda_0(t) \exp(hy_i + rp_j + ps_k + hs_l + afc_m + g_n)$$

where:

$\lambda(t)$  = hazard function of an animal at time  $t$

$\lambda_0(t)$  = Weibull baseline hazard function

$hy_i$  = random time dependent effect of herd  $\times$  year of calving

$rp_j$  = fixed time dependent effect of relative milk production

$ps_k$  = fixed time dependent effect of parity  $\times$  stage of lactation

$hs_l$  = fixed time dependent effect of annual herd size change

$afc_m$  = fixed time independent effect of age at first calving

$g_n$  = random genetic effect of sire or animal

The results for the fixed effects were expressed in risk ratios, which can be interpreted as the risk of culling for an animal in a certain class compared to a reference class with a risk ratio of 1.

The milk yield was included into the model by comparing the production of each animal with the herd average. The lactations lasting less than 240 days were extended to standard length using the Wood curve (Wood, 1967). In further steps, similarly to Mészáros et al. (2010), the lactation yields were weighed using the average production of the first lactation. This was needed to even out the biological tendency of increased production in later lactations. The average and standard deviation of milk production was calculated for each herd, which was used as a reference for individual production level for each cow on each lactation. In the final step, the differences from the herd average were expressed as standard deviations from the mean (Mészáros et al., 2010). The limits of the nine classes were  $-1.5$ ,  $-1.0$ ,  $-0.5$ ,  $-0.2$ ,  $+0.2$ ,  $+0.5$ ,  $+1.0$ ,  $+1.5$  standard deviations. The animals with the worst production (1.5 standard deviations below the herd average) were in class 1, whereas average production animals (standard deviations oscillating  $\pm 0.2$  around the mean) were in class 5.

The effect of parity and stage of lactation was considered as a combined time dependent effect, with three stages changing at the beginning, at day 61, and at day 181 of each lactation. The only exception was the first lactation with only two stages with breaking point of 180 days.

The changes in herd size were taken into account by comparing the number of calvings per herd in subsequent years. The herds were divided into those rapidly decreasing their size, with decrease over 50% within one year, herds decreasing by 20–50%, stable herds with less than 20% increase or decrease, herds with 20–50% and more than 50% increase. Animals from herds rapidly decreasing in size were right censored as this rapid decrease was likely associated with an extraordinary event (e.g. disease outbreak), which led to mass culling, irrespective of the ability of the cow to cope with the environment.

Two model types were explored in the current study. The first one was a sire model based on the 334 sires with pedigree information about their sires and maternal grandsires. The other one was an animal model using the 40 397 cows (daughters of the 334 sires) and their entire known pedigree up to the third generation, with the total of 79 435 animals. In this case the pedigree file consisted of the animal, its sire, and dam.

### Heritability and reliability

Survival Kit v6 (Ducrocq et al., 2010; Mészáros et al., 2013) was used to estimate the influence of fixed and random effects on the length of productive life.

The heritability was computed as:

$$h^2 = \frac{\sigma_g^2}{1/p + \sigma_{hy}^2 + \sigma_g^2} \quad (1)$$

where:

$h^2$  = heritability

$\sigma_g^2$  = genetic variance

$\sigma_{hy}^2$  = herd × year variance

$p$  = proportion of uncensored records

In animal model the genetic variance was equal to animal variance. In the case of the sire model the numerator was equal to 4-fold sire variance and the denominator was equal to sire variance, similarly to Yazdi et al. (2002).

The reliabilities for the sire effect were computed using the method of Ducrocq (2005):

$$R = \frac{n \times h^2}{(n - 1) h^2 + 4} \quad (2)$$

where:

$R$  = reliability of breeding value

$n$  = number of daughters per sire

$h^2$  = heritability for functional length of productive life

In the case of the animal model the reliability was based on the prediction error variance for each estimate as:

$$R = 1 - \frac{PEV}{\sigma_a^2} \quad (3)$$

where:

$R$  = reliability of breeding value

$PEV$  = prediction error variance

$\sigma_a^2$  = genetic variance

The prediction error variance was calculated as the square of the standard error for each estimate from the Survival Kit.

### RESULTS AND DISCUSSION

The results for the fixed effects are presented in Figures 1–4. The fixed effects are shown only once, as the general tendencies were very similar between the two model types.

The risk of culling was the highest for animals with the lowest milk production compared to the mean within the herd (Figure 1). When the animals were producing under the 1.5 standard deviation threshold within the herd, they were 6 times more likely to be culled than an average animal. The risk decreased sharply with increasing milk production with only 23% risk increase for animals slightly under average (0.5–0.2 standard deviation under average). The risk was decreasing further for animals with increasing milk production indicating that cows with higher production remain in the herd for a longer time. The difference between the extremely good and average animals was not as big as between the extremely bad and average animals. Animals with the highest milk production were only twice less likely to be culled. This might indicate that the breeders put more emphasis on culling the low producing animals in comparison to keeping the ones with the highest production.

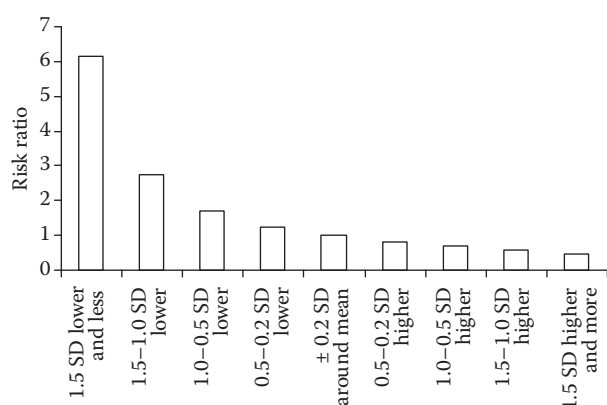


Figure 1. Risk of culling for classes of relative milk production

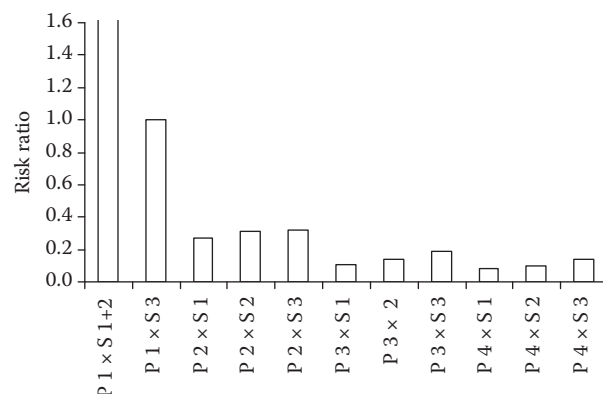


Figure 2. Risk of culling for parity and stage of lactation  
P = parity, S = stage: 1 = 0–60 days, 2 = 61–180 days, 3 = 181–305 days

The classification of animals according to production might differ from study to study, but tendencies in the risk ratios are very common. Several studies showed that animals with low milk production are culled more often compared to average or high producing herd mates. Ducrocq (1999) found 13 times higher risk for the worst animals compared to those with average production. According to Vukasinovic et al. (2001) the cows producing on the level of 80% herd average were culled 3–4 times more often than the average animals. Páchová et al. (2005) found five times higher risk in the worst compared to the best animals. The risk has doubled for cows producing one standard deviation below average in Egger-Danner et al. (2005).

The pattern for risk of culling is different for subsequent lactations (Figure 2). Whereas in the first parity the risk is the highest at the beginning of lactation, in later parities it is low at the beginning and increases towards the end. This pattern was also reported by Vukasinovic (1999) and Egger-

Danner et al. (2005), who found increased risk of culling at the beginning of the first lactation. The reason of the high risk could be unfavourable energetic balance and higher requirements on cow's metabolism, as reported by Wall et al. (2007). The differences can be also explained by the preferences of the breeders, also described in Vukasinovic et al. (2001). In the first lactation they decide as soon as they get enough information on the cow. In this case the reason behind the culling is mostly based on production, as they get rid of animals which are not worth investing in. In later parities however the culling takes place mostly at the end of lactation. The reason could be the failure of the cow to conceive. In majority of cases though, the farmers tend to milk the animals, even if they know that they will be culled, to get as much revenue as possible.

The fluctuation of the herd size between years was also influencing the risk of culling as shown in Figure 3. The risk was increased by 44% for herds

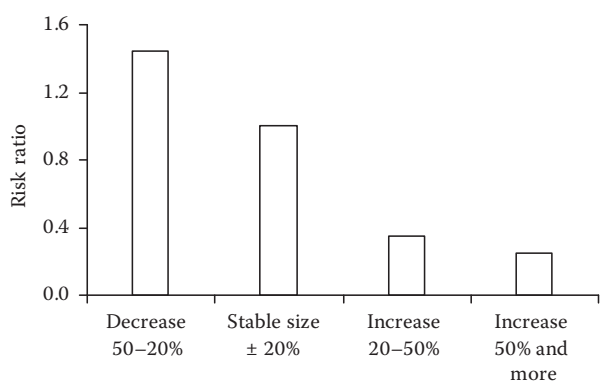


Figure 3. Risk of culling for classes of herd size change

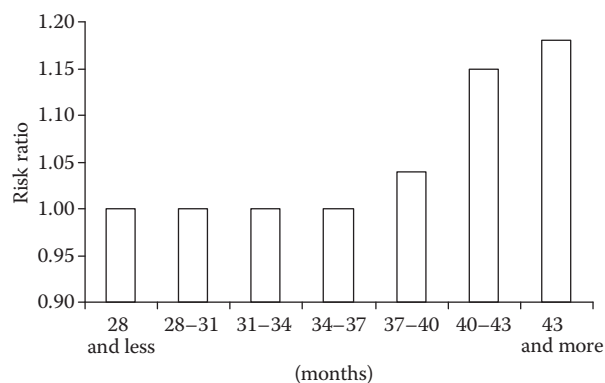


Figure 4. Risk of culling for classes of age at the first calving



moderately decreasing their size (by 20–50%). All animals from herds with more than 50% decrease in size between years were treated as censored, based on suggestion of Ducrocq (1999). The reason behind this approach was that such a rapid decrease might be caused by a major non genetic factor, such as disease outbreak or economic difficulties on the farm, leading to culling the animals. This might result into extensive culling also for animals which would otherwise remain in the herd. Animals from herds increasing in size had a lower risk of culling compared to stable herds, as expected. The same tendency was described in earlier publications. Vollema et al. (2000) found a 1.64 times higher risk of culling for herds decreasing their size by 30%, for herds increasing their size the risk was by 15% lower compared to a stable herd size. Egger-Danner et al. (2005) found 1.4 times higher risk of culling for herds decreasing their size by more than 50%.

The risk was practically unchanged for animals below 40 months of age at the first calving (Figure 4), and for older animals it slightly increased. These results were in line with previous findings of Páchová et al. (2005), Chirinos et al. (2007), Strapák et al. (2010) and others, who also found only a minor influence of age at the first calving on longevity. We could hypothesize that the reasons which led to the late first calving (e.g. reproductive problems) were influencing the length of productive life of these cows.

The sire variance in the sire model was 0.032, which resulted into heritability of 0.08 taking into account the almost 20% censoring rate and the herd  $\times$  year variance of 0.38. The heritability is somewhat higher as found in an earlier study by Mészáros et al. (2008b) for Slovak Pinzgau cattle (increase from 0.05 to 0.08), which can be explained by an improved data structure including all foreign bulls with known identity. In general, the heritability is comparable with that found in other studies using sire model in cattle in the Czech Republic (Páchová et al., 2005), France (Ducrocq, 2005), Hungary (Van der Linde et al., 2006), and Spain (Chirinos et al., 2007). According to Egger-Danner et al. (2005) the heritability was higher in Austrian Pinzgau ( $h^2 = 0.12$ ) and according to Potočník et al. (2011) in Slovenian Holstein cattle ( $h^2 = 0.14$ ).

The genetic variance in the animal model was 0.21 resulting into heritability of 0.11. Although the same data set and the same model structure

were used for both the sire and animal models, the heritability was slightly different. Mészáros et al. (2010) also observed differences in genetic variances when comparing survival analysis models. They noted that the sire model assumes that mates are non-related, non-inbred, non-selected, and that each dam has one recorded progeny only, whereas the animal model accounts for all relationships in the population. In their case the heritability from the animal model was consistently lower compared to heritability from the sire model. Interestingly, the animal variance was about 6 times higher than the sire variance instead of the expected 4 times higher value. This might suggest that the animal model might capture some non-genetic variation.

The reliabilities for the sire model were calculated using equation (2), those for animal model were calculated with equation (3). The standard error of each estimate provided by the Survival Kit can be interpreted as the standard deviation, which was squared to get the prediction error variance. Although both methods of computation were able to identify highly reliable breeding values, one has to be careful with direct comparison of the results. The two models are conceptually not equivalent, when the sire model puts  $\frac{3}{4}$  of the genetic variance into the residual and the animal model is accounting for the full genetic variance.

The animal model is particularly important, as it is possible to get breeding values for each animal. It was implemented in dairy cattle evaluations a long time ago (Wiggans et al., 1988). The emphasis was put on the possibility of simultaneous genetic evaluation of male and female animals with all relationships included. Ducrocq (2001) sees the main restriction of the sire-maternal grandsire models in the ignorance of relationships between females. He developed a procedure to get estimates for all animal model solutions to be used in genetic evaluations of length of productive life. The approximation of the estimate was needed due to the fact that the whole data set was too large to run an animal model. In our case the population of the Pinzgau cattle was not so extensive, thus the estimation covering all animals was feasible.

Ducrocq et al. (2001) envisaged the utilization of animal EBVs to approximate a multiple trait BLUP animal model evaluation on production and functional traits. Miesenberger (1997) assigned 22.3% of the total merit index in the Austrian Pinzgau cattle as the second most important trait after milk protein content. Kasarda et al. (2007)

suggested creating a total merit index to reflect the dual purpose nature of Slovak Pinzgau cattle. The result of our study could be further utilized as the main functional trait in the upcoming index.

## CONCLUSION

Length of productive life was analyzed in the population of Slovak Pinzgau cattle using the survival analysis methods. The risk of culling was studied in connection with the herd and year of calving, relative milk production, parity and stage of lactation, herd size change, age at the first calving. The results for fixed effects in both models were similar to those published in earlier studies. In separate models two genetic effects were considered: the sire of the cow and the animal itself with the corresponding pedigree records. The heritabilities resulting from the two models were different:  $h^2 = 0.08$  for the sire model and  $h^2 = 0.11$  for the animal model. As the animal model accounts for all relationships in the population, including those between cows, it is the favourable alternative for a genetic evaluation. It is also a pre-requisite for a potential total merit index for Slovak Pinzgau cattle, where breeding values for functional length of productive life could play a decisive role when accounting for the functional traits.

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*Corresponding Author*

Doc. Ing. Radovan Kasarda, Ph.D., Slovak University of Agriculture in Nitra, Department of Animal Genetics and Breeding Biology, Tr. A. Hlinku 2, 949 76 Nitra, Slovakia  
Tel. +421 376 415 522, e-mail: radovan.kasarda@uniag.sk

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