A Simple And Efficient Random Regression Model To Evaluate Fertility As A Reproductive Profile

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Introduction

Fertility behaves as a multi-faceted phenomenon on which information accrues along the productive lifetime of livestock. Phenotypes measured late in life are of limited use for breeding value estimation of the recorded animal as it approaches end of service, but are useful for evaluation of young relatives. For a review on fertility traits see Rust and Groeneveld (2001). Certain measures of fertility rely on data about service and calving, but most recording schemes fail to reliably provide both of these, especially when AI rates are not high (Robinson, 2007). Calving intervals (CI) are the lapses between two successive calvings, and provide a repeated measure of fertility during the productive lifetime that does not require service records but the quality of those records may be degraded by discrepancy in recording miscarriages, and CI does not provide either early records or information on life span. Estimated heritabilities in the literature range from 0.01 to 0.07. Precocity as age at first calving displays a low heritability (0.07 as estimated by Bourdon & Brinks, 1982).

Calving ages constitute a time series and thus may be regarded as a profile of reproductive life that reflects events from its onset, and the decline of fertility in older animals is seen as a departure from linearity. Inspection of reproduction records shows great differences in age at each calving, and that dispersion may be explored to identify individuals with the most precocious and clustered set of calving records.

The objective of this study was to present a simple and efficient calving age-based random regression model to evaluate reproductive performance in breeding schemes. We present results for Asturiana de los Valles beef cattle but the methodology is valid for other breeds and species as well.

Material and methods

Data. Records from the Asturiana de los Valles beef cattle breeders' (ASEAVA) herdbook database were used for this report. The choice of breed was due to their extremely long productive life (134 instances of 15th calvings in the edited data set). Data on 185,338 records were edited for missing birth dates, calvings higher than 15, and farms with less than 15 valid records for a final set of 140,217 calving ages from 46,373 purebred animals born between 1997 and 2004. An individual animal pedigree was constructed that included 69,354 identities, and 4,105 sires.

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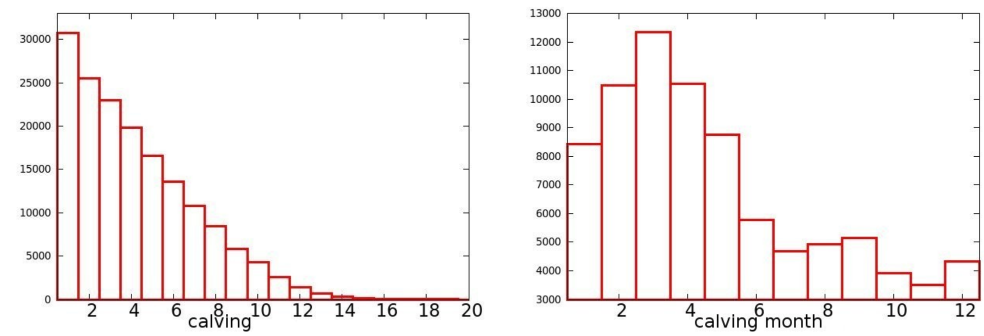

Figure 1: Distribution of calving numbers and calving months

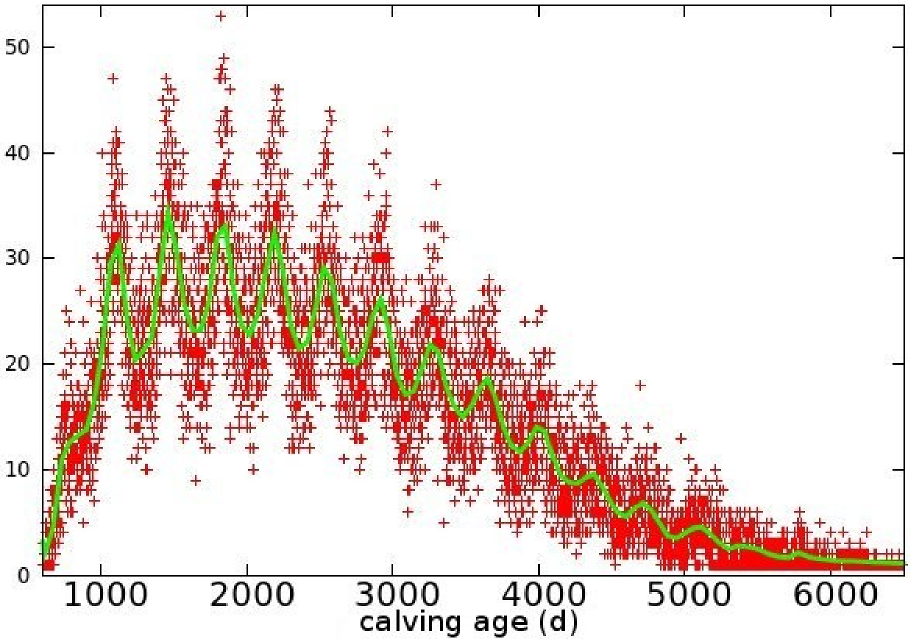

Figure 2: Distribution of calving ages measured in days.

Statistical analyses. (Co)variance components for calving ages were analysed using restricted maximum likelihood (REML) methodology by means of the AIREMLF90 program (Misztal et al., 2002). The single-trait animal model was:

$$y_{ijklm} = S_k + M_l + H_{mn}(C_{ij})^n + I_{jo}(C_{ij})^o + e_{ijklm}$$

where y_{ijkt} is the *i*th calving of animal *j*, S_k and M_l are the fixed effects of management system *k* and calving month *l*, H_{mn} is the *n*th random regression coefficient of herd *m*, I_{oj} is the *o*th random regression coefficient of individual *j*, and C_{ij} is calving age.

Results and discussion

Additive genetics of precocity accounted for 1% of the phenotypic variance of calving ages, fertility accounted for 29%, herd-related precocity accounted for 60% and herd-related fertility for 10%. Correlation between herd and additive genetic precocity was very high and negative (-.98) while correlation between herd and additive fertility was -.23.

Table 1: Estimates of model parameters

Traits	Intercept (precocity)	Slope (fertility)
Additive genetics	29%	1%
Herd environment	60%	10%
correlation	-0,98	-0,23

These estimates reflect the fact that herd management practices play the most important role in a cow's calving dates, mainly through calving seasonality. Still, the value of additive genetics is much higher than estimates for days-to-calving from Meyer et al. (1990), defined as days between the first service and the next calving. Additive genetics is thus similar to the slope of the calving-to-service interval, which reflects calving difficulty.

This model for calving age data incorporates classical fixed terms for productive system and for calving month. There are two random regression terms that take calving number as their regressor, and are nested within cow identity and herd code, respectively. The intercept of these may be interpreted as an estimate of age at first calving and thus a measure of precocity, while the slopes yield a measure of fertility in the sense of an average calving interval. It behaves as an aggregate trait in the sense of Rust and Groeneveld (2001), much like calving rate. The benefit is clear as the breeding goal usually involves getting the greatest number of calvings within a lifetime. There may be a large impact of management decisions on the calving dates, especially in the more extensive conditions. It reflects seasonality as illustrated in the calving month distribution on figure 1 and the large, herd-related variance components of table 1.

Conclusion

Figure 2 illustrates the multimodality of calving ages, which in turn reflects the underlying calving numbers. There is substantial variability in calving ages that may be exploited to identify the individuals with the most precocious and clustered set of calvings. Management related seasonality (depicted in figure 1b) has a large effect on calving intervals and this is probably due to seasonal differencies in oestrus detection efficiency.

The parameter estimates suggest that random regression terms for calving ages behave better than direct criteria for precocity such as time to first oestrus and age at first calving (Rust and Groeneveld, 2001), and slightly worse for fertility criteria such as gestation length, calving intervals, days to calving, and calving rates.

References

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