

## STAYABILITY TO CONSECUTIVE CALVINGS AS A MEASURE OF LONGEVITY IN CANADIAN SIMMENTALS

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### SUMMARY

Calving performance and culling data on Canadian Simmentals were used to determine whether a cow stayed in a herd for her 2<sup>nd</sup> and later (up to the 8<sup>th</sup>) calvings, given that she had calved as a 2 yr old. Estimates of heritability for stayability to consecutive calvings from linear random regression model were moderate (from 0.12 to 0.36) and they decreased in time. Variance due to cow's permanent environmental effect constituted the largest part of the total variance for all longitudinal points, followed by genetic and contemporary group components. Genetic effects of stayability to different calvings were highly correlated and the magnitude of correlation decreased with the increased time span between calvings. Stayability evaluations were favourably associated with estimated progeny differences for female fertility traits, direct and maternal growth and calving ease for bulls and cows. Scrotal circumference was not significantly correlated with estimates of genetic merit for stayability.

### INTRODUCTION

Stayability is a measure of whether or not an animal remains in the herd until a specified point in time. It is a trait with significant economic value. Stayability in beef cattle is traditionally defined as a probability that a cow remains in the herd until 6 yr of age given she has calved once (Brigham *et al.*, 2007). The main problem with such defined stayability is the lag between accurate prediction of stayability and the need for young replacement sires. Estimates of expected progeny differences (**EPD**) for stayability based on survival to 6 yr of age are currently being generated for Red Angus, Limousin and Simmental bulls in the USA (Garrick, 2011).

Martinez *et al.* (2005) considered 3 different approaches to defining beef cattle stayability: stayability to a specific age (whether a cow survived to a specific age given she was in the herd as 2 yr old), stayability to calving (whether a cow has a second, or later, calf given she had a calf as a 2 yr old), and stayability to weaning (whether a cow weans a second, or later, calf given she weaned the first calf). Brigham *et al.* (2007) estimated correlations among EPD for sires at different age definition for stayability (from 3 to 6 yr) ranging from 0.18 to 0.47, indicating that the expression of genetic merit of bulls changes depending on the age definition for stayability. Earlier measures of stayability, however, could serve as indicator traits of stayability to 6 yr (Martinez *et al.*, 2005).

Different statistical models have been used to analyze stayability. Random regression (**RR**) model is a longitudinal generalization of the multiple-trait model. Binary observations can be assigned to each discrete time in the cow's lifetime and EPD for stayability can be generated for

each point on the trajectory. Time dependent environmental effects are easy to implement in the RR model. Veerkamp *et al.* (2001) showed that the RR model is relatively robust to censoring.

The Canadian Simmental Association has been collecting calving performance data since the early 1970's. The Total Herd Reporting system providing culling information on cows has been in place since 2000. These two sources of data can easily be used to create stayability phenotypes for the population. The objective of this study was to estimate genetic parameters for stayability to consecutive calvings for Canadian Simmentals using a linear RR model and to compare stayability with other economically important traits in terms of associations among EPD for bulls and cows.

## MATERIAL AND METHODS

**Data.** Stayability to calving was selected as a measure of animal's longevity. Each cow was assigned up to 7 binary records (**S2**, **S3**, ..., **S8**) corresponding to stayability to 2<sup>nd</sup>, 3<sup>rd</sup>, and up to the 8<sup>th</sup> calving, given that she calved as a 2 yr old. Phenotypes for a given calving event were 1 (= cow calved, she was still present in the herd) or 0 (= no calving record, meaning that she was culled prior to that particular calving). Stayability records were generated by merging calving and culling data. The data file included 1,164,319 binary records on 188,579 cows. More than 62% cows had all 7 stayability records. Number of cows increased with a degree of completeness for a stayability history. Almost 70% of cows that calved as heifers stayed in the herd until their 2<sup>nd</sup> calving. Proportion of culled cows increased with the calving number: from 37% for S3 to 87% for S8.

**Model.** Random regression linear animal model was fitted to the stayability binary data. The model was:

$$y_{ijkmt} = YS_{it} + age_{jt} + \sum_{n=0}^p \beta_{ikn} z_{nt} + \sum_{n=0}^p \alpha_{mn} z_{nt} + \sum_{n=0}^p \rho_{mn} z_{nt} + e_{ijkmt} ,$$

where  $y_{ijkmt}$  is the stayability observation (S2, ..., S8) on cow  $m$  for calving  $t$ ;  $YS_{it}$  is fixed effect of year of birth by season of birth for calving  $t$ ;  $age_{jt}$  is fixed effect of age at first calving class for calving  $t$ ;  $\beta_{ikn}$  are random regression coefficients specific to  $k$ -th contemporary group (**CG**) defined as herd within  $i$ -th year by season;  $\alpha_{mn}$  are random additive genetic coefficients specific to cow  $m$ ;  $\rho_{mn}$  are random permanent environmental (**PE**) coefficients specific for cow  $m$ ;  $e_{ijkmt}$  is the random residual effect for each observation, and  $z_{nt}$  are covariates. Orthogonal Legendre polynomials of order 3 were used for all fixed and random regressions.

Censored records were treated as missing data in the model. The CG effect comprised 72,986 levels. The pedigree file (5 generations back) included 282,775 animals.

In matrix notation the model can be written as:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{U}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\alpha} + \mathbf{W}\boldsymbol{\rho} + \mathbf{e},$$

where  $\mathbf{y}$  was a vector of observations;  $\mathbf{b}$  was a vector of fixed effects,  $\boldsymbol{\beta}$  was a vector of random CG effects,  $\boldsymbol{\alpha}$  was a vector of animal additive effects,  $\boldsymbol{\rho}$  was a vector of cow PE effects,  $\mathbf{e}$  was a vector of residuals;  $\mathbf{X}$ ,  $\mathbf{U}$ ,  $\mathbf{Z}$  and  $\mathbf{W}$  denoted respective incidence matrices. Conditional distribution of the data (sorted by calving number) was assumed to be:  $\mathbf{y} \mid \mathbf{b}, \boldsymbol{\alpha}, \boldsymbol{\beta}, \boldsymbol{\rho}, \mathbf{R} \sim N[\mathbf{X}\mathbf{b} + \mathbf{U}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\alpha} + \mathbf{W}\boldsymbol{\rho}, \mathbf{R}]$ ; with  $\mathbf{R} = \sum_{i=2}^{+8} \mathbf{I}_{n_i} \sigma_i^2$  and  $\mathbf{I}$  denoting an identity matrix.

**Methods.** Bayesian methods with Gibbs sampling were used for fitting the model. Prior distributions for the parameters were:  $\boldsymbol{\beta} \mid \mathbf{C} \sim N(\mathbf{0}, \mathbf{I} \otimes \mathbf{C})$ , where  $\mathbf{C}$  is the covariance matrix for the CG effect;  $\boldsymbol{\alpha} \mid \mathbf{G} \sim N(\mathbf{0}, \mathbf{A} \otimes \mathbf{G})$ , where  $\mathbf{A}$  is an additive genetic relationship matrix between individuals, and  $\mathbf{G}$  is the additive genetic covariance matrix between elements of  $\boldsymbol{\alpha}$ ;  $\boldsymbol{\rho} \mid \mathbf{P} \sim N(\mathbf{0}, \mathbf{I} \otimes \mathbf{P})$ , where  $\mathbf{P}$  is the covariance matrix for the PE effect;  $p(\mathbf{b}) = N[0, p\mathbf{I}]$ , with  $p = 10000$  for all

levels of all fixed effects;  $\sigma_k^2 | v_k, s_k^2 \sim \text{SIC} [v_k, v_k s_k^2]$ ,  $k = 2, \dots, 8$ ;  $\mathbf{C} | v_c, \mathbf{C}_0 \sim \text{IW} [v_c, v_c \mathbf{C}_0]$ ;  $\mathbf{G} | v_g, \mathbf{G}_0 \sim \text{IW} [v_g, v_g \mathbf{G}_0]$ ;  $\mathbf{P} | v_p, \mathbf{P}_0 \sim \text{IW} [v_p, v_p \mathbf{P}_0]$ ; where  $v_k$  and  $s_k^2$  are parameters of independent inverted chi-square distributions,  $v_c$  ( $v_a, v_p$ ) and  $\mathbf{C}_0$  ( $\mathbf{G}_0, \mathbf{P}_0$ ) are hyper-parameters of the inverted Wishart distributions. Minimal number of prior degrees of freedom was assumed for all co-variance components. Scale parameters for inverted Wishart were uncorrelated; prior values were equal to 0.01 and 0.0 for all variances and co-variances, respectively. All conditional distributions were of a closed form and Gibbs sampling scheme followed standard procedure for Gaussian linear models. Sampling was performed for 250,000 iterations where 50,000 constituted burn-in for each model. Convergence was monitored by visual inspection of trace-plots for selected co-variance components. Estimates of variance components, genetic parameters and EPD were calculated as posterior means of respective samples after burn-in.

Estimates of genetic merit for different stayability traits were subsequently correlated with EPD for other available traits in Canadian Simmentals. The traits were: growth (birth weight, weaning weight, post-weaning gain, yearling weight), calving ease, carcass (marbling, fat thickness, rib-eye area, carcass weight), female fertility (calving to first insemination, days to calving) and scrotal circumference. Correlations were estimated separately for bulls (with at least 10 daughters in the stayability model) and cows (with phenotypes for stayability).

**RESULTS AND DISCUSSION**

The largest contribution to the variance on the longitudinal scale was due to the PE effects, with an increasing impact along the time scale (from 40 to 80%), followed by genetic and CG components. Both genetic and CG relative contribution to the phenotypic variance decreased linearly with consecutive calvings. Residual variance constituted from 0.4% to 22% of the total variance, indicating relatively good fit of the model.

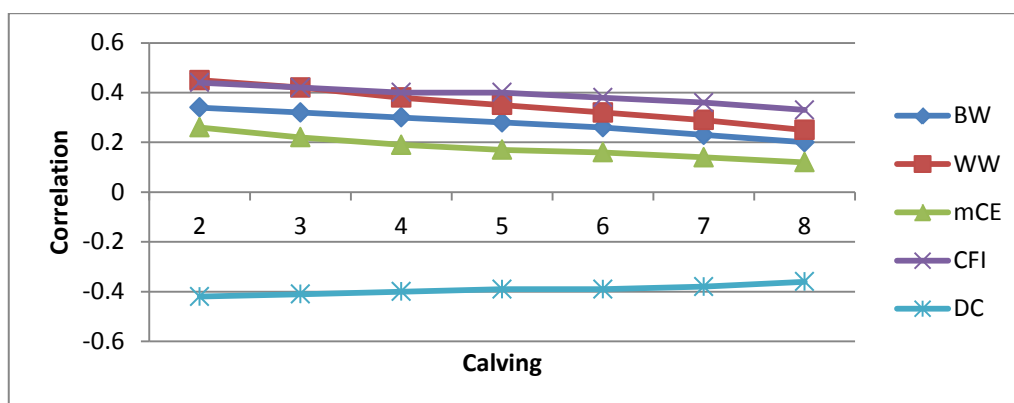
**Table 1. Heritabilities (diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations for stayabilities to consecutive calvings (posterior SD are in brackets)**

Calving number	2	3	4	5	6	7	8
2	<b>0.36</b> ( <b>0.006</b> )	0.96 (0.002)	0.89 (0.006)	0.83 (0.008)	0.77 (0.010)	0.71 (0.011)	0.61 (0.013)
3	0.84 (0.001)	<b>0.23</b> ( <b>0.004</b> )	0.98 (0.001)	0.94 (0.003)	0.87 (0.006)	0.81 (0.009)	0.74 (0.010)
4	0.67 (0.002)	0.96 (0.001)	<b>0.19</b> ( <b>0.004</b> )	0.98 (0.001)	0.94 (0.003)	0.89 (0.006)	0.81 (0.008)
5	0.56 (0.003)	0.87 (0.001)	0.97 (0.001)	<b>0.16</b> ( <b>0.004</b> )	0.98 (0.001)	0.95 (0.003)	0.86 (0.006)
6	0.47 (0.003)	0.71 (0.002)	0.85 (0.001)	0.96 (0.001)	<b>0.15</b> ( <b>0.004</b> )	0.99 (0.001)	0.89 (0.005)
7	0.40 (0.003)	0.55 (0.002)	0.69 (0.002)	0.85 (0.001)	0.96 (0.001)	<b>0.13</b> ( <b>0.004</b> )	0.94 (0.003)
8	0.31 (0.003)	0.44 (0.002)	0.53 (0.002)	0.64 (0.002)	0.75 (0.001)	0.88 (0.001)	<b>0.12</b> ( <b>0.003</b> )

Heritabilities of stayability to different calvings (Table 1) showed decreasing trend in time; S2 had the largest value of heritability. Stayability to the last calving (S8) still showed a reasonable

level of heritability. Heritability estimates are comparable with results from other studies. Martinez *et al.* (2005) reported heritability for stayability to calvings (from second to sixth in Hereford cows) between 0.18 to 0.25 from linear models. Estimates of phenotypic and genetic correlations among different stayability to calving traits are in Table 1. Not totally perfect correlations indicated, in general, that stayabilities to different calvings are different traits from both a phenotypic and genetic perspective. The magnitude of correlations decreased with the increasing distance between calving events on the longitudinal scale. Stayability to 2<sup>nd</sup> calving (S2) would still, however, be a relatively good indicator of stayability to later calvings. Estimates of correlations among CG (PE) effects for different stayability traits exhibited, in general, similar patterns as phenotypic and genetic correlations.

Estimates of correlations between sires EPD for stayability and other traits available for Canadian Simmentals were smaller in magnitude than corresponding values for cows. Cows' correlations for selected trait are in Figure 1. Stayability was favourably associated ( $P < 0.001$ ) with female fertility traits (calving to first insemination and days to calving) for bulls and cows. Cows with better genetic potential for direct and maternal growth, calving ease, carcass marbling and adult cow weight tended to exhibit better stayability. Only maternal calving ease in sires influenced stayability, and the strength of associations decreased in time. Growth traits in bulls also showed positive correlations with stayability, although the magnitude of correlation coefficients was smaller than for cow's EPD. Sire's EPD for carcass traits did not show significant association with stayability. Similarly, scrotal circumference EPD were not significantly correlated with EPD for stayability for bulls and cows



<sup>1</sup>BW = direct birth weight, WW = direct weaning weight, mCE = maternal calving ease, CFI = calving to first insemination (heifers), DC = days to calving (mature cows)

**Figure 1: Correlations among EPD for stayability and other selected traits<sup>1</sup> for cows with phenotypes for stayability**

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