

Proceedings, Applied Reproductive Strategies in Beef Cattle

December 2 and 3, 2008, Fort Collins, CO

GENETIC IMPROVEMENT OF HEIFER PREGNANCY AND PERFORMANCE IN BEEF CATTLE

D. H. Crews, Jr. and R. M. Enns

Center for Genetic Evaluation of Livestock

Department of Animal Sciences, Colorado State University, Fort Collins 80523

Introduction

Current genetic improvement programs should place more emphasis on improving profitability than on one or a small group of traits, under the framework of economic relevance (Golden et al., 2000). When profit is defined generally as revenue minus cost, true economically relevant traits (ERT) have a direct impact on either income or expenses, whereas indicator traits provide a means to increase accuracy of evaluation through their genetic correlation with ERT but are not directly economic (Enns and Crews, 2008). It is important, therefore, to distinguish between ERT and their indicators in the design and implementation of genetic evaluation and improvement programs for beef cattle. Traits related to fertility and maternal productivity are certainly a key component of improving the profitability of beef production. In fact, fertility traits are typically ranked as having a greater impact on revenue in beef production than other groups of traits such as growth performance and carcass merit (Melton, 1995). Enns and Crews (2008) identified traits such as calving ease, heifer pregnancy, bull fertility, health status, stayability or productive longevity, milk production, and calf and cull cow sale weights as likely ERT for the large cow-calf sector of the North American beef industry.

National Cattle Evaluation

For more than 25 years, breeding values or expected progeny differences (EPD) predicted using mixed model methods have been used by beef breed association members and other producers as selection tools. The most commonly evaluated traits such as weight and growth rate have shown significantly positive genetic trend over the same period (Crews et al., 2008). Those EPD, along with accuracy values, are the most common tool used in the seedstock sector for effective, additive, and permanent genetic improvement of cattle. Current national cattle evaluations (NCE) are generally conducted on a within-breed basis, and each breed program includes a wide range of EPD for both ERT and indicator traits. Golden (2001) stated that evaluations for more than 60 traits were routinely conducted worldwide. The challenge in NCE development remains increasing the accuracy with which cattle are evaluated with respect to economic relevance, in order to increase genetic trend for profitability.

New trait development takes on many forms as current NCE programs are expanded and improved. In one case, novel traits are identified and can be added to existing NCE programs through the usual process of field data collection, model development,

parameter estimation, and genetic evaluation information packaging. In fact, most EPD now published were developed in this way. In the future, it will be less likely that this traditional approach will result in significant economic gains, at least in terms of adding novel traits due to limitations on current field data collection schemes. There will be opportunities to improve the economic relevance of existing evaluations, and increase the accuracy thereof using existing field databases. A second approach is to prototype NCE systems in research or experimental populations that would eventually lead to field data collection and NCE implementation. Carcass traits such as tenderness, and efficiency traits such as feed intake have followed this development approach. However, field data collection for such traits is nearly cost-prohibitive, resulting in very low data density at the population level and low accuracy evaluations on most animals. In this case, the use of indicator traits to improve evaluation accuracy can provide some benefit. When prototype NCE exist, but are infeasible because of lack of phenotypic data on large numbers of animals, genomics tools could provide increases in evaluation accuracy (Pollak, 2008) although appropriate methodology for combining polygenic and genomic data is still in development. The long-term potential for use of gene-assisted evaluation remains very high (Crews, 2008). Lastly, multiple trait selection index methods are increasingly used to combine genetic evaluation and economic information under the selection objective of increasing profit or net revenue. Along with appropriate decision support, multiple trait and profit indexes can be useful genetic evaluation tools.

Evaluation of Fertility Traits

Within the framework of economic relevance, traits related to fertility are mainly revenue related that ultimately increase outputs such as live calves. Although their importance is clear, few large scale NCE have been implemented for these traits. Examples of fertility and maternal productivity NCE include stayability (Snelling et al., 1995), productive survival (e.g., Mwansa et al., 2000), heifer pregnancy (Evans et al., 1999), and cow maintenance requirement (Enns and Crews, 2008). Genetic improvement of fertility remains largely relegated to evaluation and selection for indicator traits such as scrotal circumference (Crews and Enns, 2008) and in some cases, growth traits that may be genetically correlated to fertility.

As an indicator trait, scrotal circumference (SC) is known to be favorably correlated with bull fertility and age at puberty in female relatives (Brinks et al., 1978; Toelle and Robison, 1985). Also, SC in yearling bulls is at least moderately heritable (e.g., Koots et al., 1994a), and is considered to be relatively easy to measure in field populations. Increasing selection for yearling SC EPD is expected to result in moderate rates of genetic change, given a sufficiency of field data. Several beef breed associations conduct SC evaluations (BIF, 2002) in which SC breeding values are typically estimated with multiple trait models that include growth rate and(or) weight traits. Numerous studies (e.g., Bourdon and Brinks, 1986; Keeton et al., 1996; Crews and Porteous, 2003; Crews and Enns, 2008) have reported significantly positive genetic correlations of SC with birth, weaning and yearling weights. From these estimates (and from the meta-analysis of Koots et al., 1994b), increasing selection for SC and growth rate up to yearling age are expected to be concomitant. That is, simultaneous selection for increased growth and increased yearling scrotal size leads to correlated responses in both traits, and may not

follow expectation because of their moderate to high positive genetic correlation. Under the framework of economic relevance, an alternative measure of SC, more closely describing its indication of genetic merit for fertility, is needed.

Red Angus Heifer Pregnancy NCE

The Red Angus Association of America (RAAA) currently publishes a large suite of EPD in their twice-annual NCE which is conducted by the Center for Genetic Evaluation of Livestock (CGEL) at Colorado State University. In addition to EPD for weight (birth, weaning, and yearling), carcass traits, maintenance energy, and calving ease (CED, CEM), CGEL also performs evaluations for heifer pregnancy (HP) and stayability (ST). Heifer pregnancy is defined as the probability that a heifer will become pregnant by the end of her first breeding season whereas stayability is defined as the probability that a female will remain in the herd until she is 6 years of age. Genetic trends for reproductive traits in the RAAA NCE program are shown in Figure 1.

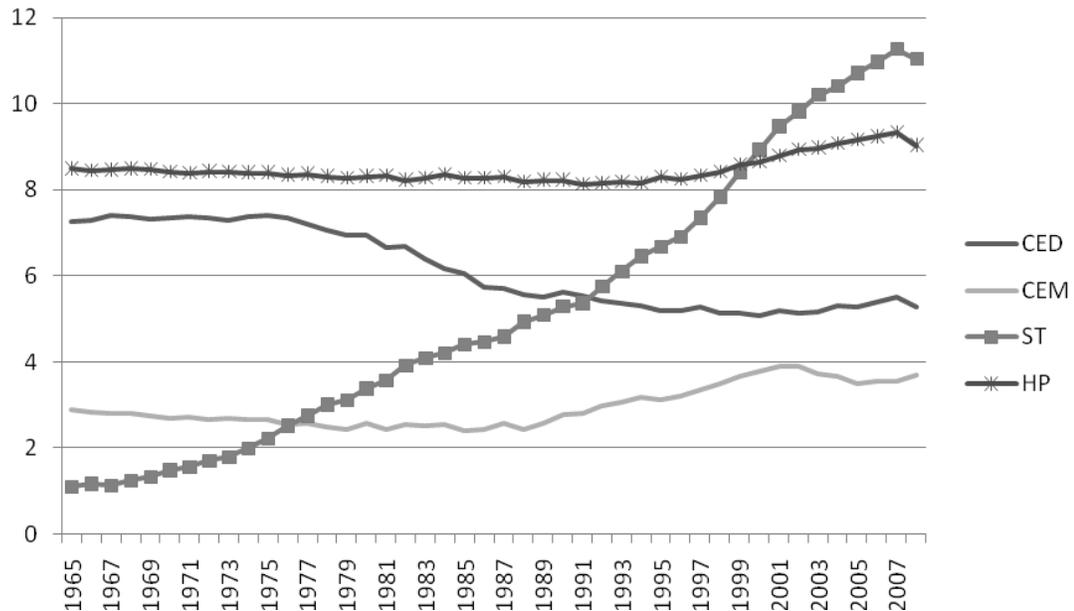


Figure 1. Genetic trend (1965-2008) for reproductive traits in Red Angus. Obtained and used with permission (www.redangus.org).

As is shown, although an increasing trend has been realized in Red Angus for stayability, although no appreciable trend has been realized for heifer pregnancy rate. As an ERT, heifer pregnancy has not shown a significant improvement, and the genetic trend has largely been flat.

Increasing the positive genetic trend for HP in Red Angus, like for any NCE trait, requires several key components. First, data must be available in suitable quantity and quality in order to evaluate the sires that are selected for use in breeding, and the heifers selected as replacements. Secondly, the EPD for HP must be included in the selection decision process. Lastly, to make optimal selection decisions, those HP EPD likely need

to have accuracy values above 0.60 or higher. Even though HP exhibits binary phenotypic expression (i.e., heifers are either pregnant or not) and is considered a “threshold” trait, research suggests that the underlying continuous distribution of genetic effects account for a significant portion of HP expression. That is, heritability of HP on the “underlying scale” is similar to that observed for most early-life growth traits (0.24 in Red Angus; S. Speidel, personal communication). Currently, less than 300 Red Angus bulls have HP accuracy of at least 0.50. With these parameters, and a general lack of data to predict EPD, it is not altogether surprising that very little genetic trend has been observed for HP. The problem remains to increase accuracy of evaluation for ERT like HP while considering the challenges specific to NCE for threshold traits. A major limitation with HP (similar to stayability) is that heifers must reach the age of their yearling breeding season and become pregnant before they have a non-missing record, which implies that bulls must be at least 3 – 4 years of age before he has any daughters with HP records. Furthermore, in a typical HP evaluation, all calves and all males have HP observations that are missing.

Red Angus Scrotal Circumference

Crews and Enns (2008) developed a traditional NCE model for yearling scrotal circumference (YSC) in Red Angus, including recommended age of dam and age at measurement adjustment factors. Table 1 summarizes the variance components and parameter estimates obtained in those analyses, as well as genetic correlations with birth, direct and maternal weaning weights, and postweaning gain.

Table 1. Summary statistics, heritability and genetic correlations for yearling scrotal circumference (YSC) with growth traits in Red Angus (n = 40,865)^a

YSC parameter ^b	Estimate	SE
Phenotypic variance, cm ²	5.12	
Heritability ^c	0.51	0.02
<u>Genetic correlations</u>		
Direct birth weight	0.10	0.03
Maternal birth weight	0.05	0.05
Direct weaning weight	0.13	0.04
Maternal weaning weight	0.35	0.04
Direct postweaning gain	0.13	0.03

^a Adapted from Tables 2 and 4 (Crews and Enns, 2008).

^b Single and multiple trait analyses included animals with data plus a minimum of three ancestral generations (total n = 100,261).

^c Heritability was from a model including only direct genetic effects on YSC.

Genetic correlations have not been estimated in Red Angus for YSC with HP. Even though RAAA has not officially published EPD for YSC, the results above were used to estimate a positive genetic trend for YSC over the past 25 years. In fact, YSC breeding value has been increasing in Red Angus by approximately 0.02 cm per year. It is safe to

conclude that this trend is predominantly the result of correlated response to growth selection, which has been positive in Red Angus for the past 40 years.

Given that sufficient YSC data exists in the RAAA database, accuracy of HP evaluation may be increased by including YSC in that evaluation as a correlated indicator trait. The question remains of how might YSC be modeled or adjusted to better reflect its value as a fertility indicator and therefore increase the genetic correlation with other fertility traits including HP. Considerable evidence has been shown suggesting that a portion of YSC variance is attributable to growth rate, however, the YSC variance not related to growth may be more related to fertility. To test this hypothesis, consider the following conceptual model:

$$\text{YSC} = f(\text{growth}) + f(\text{fertility})$$

where $f(\text{growth})$ is that portion of YSC that is correlated with, and can be predicted by, growth rate. The remainder, $f(\text{fertility})$ is that portion of YSC that is independent of growth rate but is potentially closely related to fertility. Using the matrix representation of multiple linear regression, define

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{e}$$

where YSC (\mathbf{y}) is a function ($\boldsymbol{\beta}$) of multiple growth trait measurements (\mathbf{X}), and \mathbf{e} is a residual portion that is independent of growth. In other words, \mathbf{e} is the residual component of YSC that is not correlated with weight or growth rate. It is straightforward to show that under the normal multiple linear regression model that $\text{cov}(\mathbf{X}_i, \mathbf{e}) = 0$ (Searle, 1982). Using the same data as in Crews and Enns (2008), Table 2 summarizes sample statistics and variance components for the growth-independent residual portion of YSC.

Table 2. Summary statistics and parameters for residual scrotal (RSC) compared to YSC

Parameter	YSC	RSC
n	40,865	29,661
Mean, cm	35.0	0.0
Minimum, cm	20.8	-11.5
Maximum, cm	47.2	12.5
Phenotypic variance, cm ²	5.124	3.936
Heritability	0.51 ± 0.02	0.35 ± 0.02

The difference in numbers of records available for YSC and RSC is due to the need for complete growth records to compute RSC. Again, basic linear regression dictates that $E(\text{RSC}) = E(\mathbf{e}) = 0$. Also, the phenotypic variance of RSC must be less than for YSC because RSC is defined as a component of YSC. It is important to note that RSC here is defined as the residual from phenotypic regression of YSC on weights recorded up to yearling age. This forces RSC to be uncorrelated with birth and weaning weights, and with postweaning gain. This regression could also be conducted at the genetic level, which would ensure that RSC is genetically uncorrelated with weight traits. In terms of selection, the genetic regression approach is appealing because of the forced genetic

independence, but for purposes of illustration, phenotypic and genetic RSC show similar results. A typical NCE for either RSC or YSC would produce very similar animal rankings (Genetic correlation (R_g) = 0.94 ± 0.04), although RSC may be a more useful data point in the development of multiple trait NCE for fertility. As was stated earlier, correlated response to growth selection has resulted in a positive genetic trend for YSC of about 0.02 cm per year. Conversely, the genetic trend for RSC (compared with YSC) is shown in Figure 2. The slope of the linear trend line for RSC was 0.0015 ($P > 0.10$), and the R^2 (0.15) confirms no linear trend in RSC. Therefore, when considering that no trend has been observed for either HP (Figure 1) or RSC (Figure 2), one might hypothesize that the value of scrotal size as an indicator of fertility may lie in that portion not related to growth.

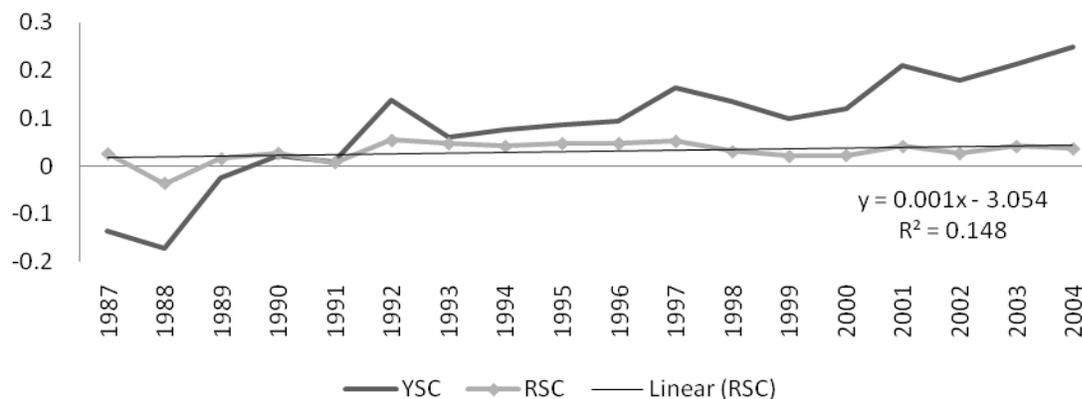


Figure 2. Genetic trend (1987-2004) for yearling scrotal (YSC) and residual scrotal (RSC, linear trend line included). Data protected: Red Angus Association of America/CGEL.

In terms of information packaging, an NCE for RSC is a straightforward extension of traditional YSC evaluation. And, considering that RAAA doesn't currently (as of 2008) publish a scrotal NCE, RSC may be a desirable alternative regardless of its added value in evaluation of HP. That is, RSC may be a favorable measure of general male fertility (similar to YSC) which can be used by producers for genetic improvement of fertility in both males and females. Its value in improving HP or other measures of fertility will depend on those genetic correlations.

Future Directions

Systems for genetic evaluation of fertility continues to develop in terms of defining the optimal economically relevant trait set, and increasing the accuracy with which animals are evaluated relative to those ERT. However, prediction of EPD is not an end unto itself. Implementation of fertility evaluations relies heavily on producer acceptance which leads to realized genetic improvement. Traditionally, fertility traits have been a challenge in large scale genetic prediction, mostly because of low data density and the threshold or binomial nature of the most easily recorded phenotypes. The combination of multiple trait approaches to modeling, increasing accuracy with indicator traits, and the potential

of marker assisted or phenomic selection will result in more optimal genetic improvement in beef cattle fertility.

References

- Beef Improvement Federation (BIF). 2002. Guidelines for Uniform Beef Improvement Programs, 8th ed. Beef Improvement Federation (www.beefimprovement.org).
- Bourdon, R. M. and J. S. Brinks. 1986. Scrotal circumference in yearling Hereford bulls: Adjustment factors, heritabilities and genetic, environmental and phenotypic relationships with growth traits. *J. Anim. Sci.* 62:958-969.
- Brinks, J. S., J. M. McInerney, and P. J. Chenoweth. 1978. Relationships of age at puberty in heifers to reproductive traits in young bulls. *Proc. West. Sec. Amer. Soc. Anim. Sci.* 29:28-32.
- Crews, D. H., Jr. and D. J. Porteous. 2003. Age of dam and age at measurement adjustments and genetic parameters for scrotal circumference of Canadian Hereford bulls. *Can. J. Anim. Sci.* 83:183-189.
- Crews, D. H., Jr. 2008. Developing optimal marker assisted evaluation systems for beef cattle. *Proc. 2008 Alberta Bovine Genome Program, Banff, Alberta.* pp. 22-23.
- Crews, D. H., Jr. and R. M. Enns. 2008. Models for genetic evaluation of scrotal circumference in Red Angus. *Prof. Anim. Sci.* 24:128-135.
- Crews, D. H., Jr., S. S. Moore and R. M. Enns. 2008. Optimizing traditional and marker assisted evaluation in beef cattle. *Proc. 40th Beef Improvement Federation Research Symposium and Annual Meeting, Calgary, Alberta.* pp. 44-49.
- Enns, R. M. and D. H. Crews, Jr. 2008. New trait development and economic relevance in national cattle evaluation. *Proc. 40th Beef Improvement Federation Research Symposium and Annual Meeting, Calgary, Alberta.* pp. 40-43.
- Enns, R. M. 2008. Hot topics in genetic evaluation: CSU cattle health project. *Proc. 2008 National Beef Cattle Evaluation Consortium Brown Bagger Series.* www.ansci.cornell.edu/nbcec/, October 29, 2008.
- Evans, J. L., B. L. Golden, R. M. Bourdon, and K. L. Long. 1999. Additive genetic relationships between heifer pregnancy and scrotal circumference in Hereford cattle. *J. Anim. Sci.* 77:2621-2628.
- Golden, B. L. 2001. Genetic prediction for time to finish end points in beef cattle. *J. Anim. Sci.* 79 (Suppl. 1):99 (Abstr.).
- Golden, B. L., D. J. Garrick, S. Newman and R. M. Enns. 2000. A framework for the next generation of EPD. *Proc. 32nd Beef Improvement Federation Research Symposium and Annual Meeting, Wichita, Kansas.* pp. 2-13.
- Keeton, L. L., R. D. Green, B. L. Golden, and K. J. Anderson. 1996. Estimation of variance components and prediction of breeding values for scrotal circumference and weaning weight in Limousin cattle. *J. Anim. Sci.* 74:31-40.
- Koots, K. R., J. P. Gibson, C. Smith, and J. W. Wilton. 1994a. Analyses of published genetic parameter estimates for beef production traits. 1. Heritability. *Anim. Breed. Abstr.* 62:309-328.

- Koots, K. R., J. P. Gibson and J.W. Wilton. 1994b. Analyses of published genetic parameter estimates for beef production traits. 2. Phenotypic and genetic correlations. *Anim. Breed. Abstr.* 62:825-853.
- Melton, B. E. 1995. Profiting from change in the U.S. beef industry: Genetic balance for economic gains. Technical Report of the National Cattlemen's Association, Englewood, Colorado.
- Mwansa, P. B., D. H. Crews, Jr., J. W. Wilton, and R. A. Kemp. 2002. *J. Anim. Breed. Genet.* 119:391-399.
- Pollak, E. J. 2008. Practical aspects and current status of genome-assisted genetic evaluation of beef cattle. *Proc. 2008 Alberta Bovine Genome Program, Banff, Alberta.* pp. 12-13.
- Searle, S. R. 1982. *Matrix Algebra Useful for Statistics.* John Wiley and Sons, New York.
- Snelling, W. M., B. L. Golden, and R. M. Bourdon. 1995. Within-herd genetic analysis of stayability of beef females. *J. Anim. Sci.* 73:993-1002.
- Toelle, V. D., and O. W. Robison. 1985. Estimates of genetic correlations between testicular measurements and female reproductive traits in cattle. *J. Anim. Sci.* 60:89-97.