Genetic Parameter Estimates for Female Fertility and Post Weaning Growth and Efficiency Traits In Beef Cattle

by

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Master of Science

in

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The purpose of this thesis was to estimate genetic correlations between female fertility and feed efficiency measurements. Fertility data were collected from two Ontario beef herds and feed efficiency data were collected from one station with animals that originally came from five Ontario beef herds. Genetic parameters were estimated for female fertility traits (first-service conception rate, pregnancy rate, number of services per conception, gestation length and days-to-calving) and feed efficiency traits (feed conversion ratio, residual feed intake, average daily dry matter intake, average daily gain and metabolic mid-test body weight). Heritabilities for fertility traits were low to moderate and feed efficiency traits were moderate to highly heritable. Both traits need to be evaluated and considered in selection programs. Results indicate that animals with larger body weight are related to better fertility performance. An unfavourable genetic correlation was found between residual feed intake and days-to-calving.
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Table of Contents

CHAPTER 1: LITERATURE REVIEW ................................................................. 1

1.1 INTRODUCTION ......................................................................................... 1

1.2 CANADIAN BEEF INDUSTRY ............................................................... 1

1.3 ONTARIO BEEF INDUSTRY ................................................................. 2

1.4 REPRODUCTION ....................................................................................... 3

  1.4.1 Natural Estrus and Estrus Synchronization ........................................ 3

  1.4.2 Natural Service and Artificial Insemination ........................................ 3

  1.4.3 Female Fertility .................................................................................. 4

  1.4.4 Fertility Measurements ...................................................................... 4

  1.4.5 Reported Genetic Parameters for Fertility Traits .............................. 6

1.5 FEED EFFICIENCY .................................................................................... 7

  1.5.1 Feedlots ............................................................................................ 7

  1.5.2 Measures of Feed Efficiency ............................................................. 7

  1.5.3 Reported Genetic Parameters for Feed Efficiency Measurements .......... 9

1.6 CONCLUSION .......................................................................................... 10

1.7 TABLES .................................................................................................... 11

CHAPTER 2: GENETIC PARAMETERS OF FEMALE FERTILITY TRAITS IN
A MULTI-BREED BEEF CATTLE POPULATION ............................................. 14

2.1 ABSTRACT .............................................................................................. 14

2.2 INTRODUCTION ..................................................................................... 15

2.3 MATERIALS AND METHODS ............................................................... 16
CHAPTER 3: GENETIC PARAMETERS OF POST WEANING GROWTH AND EFFICIENCY TRAITS IN MULTI-BREED BEEF CATTLE

3.1 ABSTRACT ................................................................................................................. 34

3.2 INTRODUCTION ........................................................................................................... 35

3.3 MATERIALS AND METHODS ..................................................................................... 36

3.3.1 Data ....................................................................................................................... 36

3.3.2 Data Editing ............................................................................................................. 38

3.3.3 Statistical Analysis ................................................................................................. 39

3.4 RESULTS AND DISCUSSION ...................................................................................... 40

3.4.1 Phenotypic and genetic correlations ....................................................................... 42

3.4.2 Conclusion ............................................................................................................... 44

3.5 TABLES ....................................................................................................................... 45
LIST OF TABLES

Table 1. 1: Summary of published heritability estimates for first-service conception rate and pregnancy rate .............................................................. 11

Table 1. 2: Summary of published heritability estimates for number of services pre conception, gestation length and days-to-calving ........................................ 12

Table 1. 3: Summary of published heritability estimates for feed efficiency traits ....... 13

Table 2. 1: The summary statistics of the final data set .................................................. 29

Table 2. 2: Estimates of regression coefficient for heterozygosity and coefficient difference for breed proportion comparing with Angus ......................... 30

Table 2. 3: Estimates of variance components, heritability (h2) and repeatability (r) with standard errors (SE) .............................................................................. 31

Table 2. 4: Genetic (r_g) and phenotypic (r_p) correlation among reproductive traits; standard errors (SD) in brackets ................................................................. 32

Table 2. 5: Expected progeny difference (EPD) and corresponding reliability of the top and bottom 10% of bulls for fertility traits ................................................................ 33

Table 3. 1: Average heterozygosity (%) and breed proportions (%) of the total study group and of each herd ........................................................................ 45

Table 3. 2: Summary of post weaning growth and efficiency measurements ............. 46
Table 3. 3: Heritability, P-value of fixed effects, estimated regression coefficient of AET and heterozygosity, and the coefficient differences for breed proportion when comparing with Angus. ................................................................. 47

Table 3. 4: Genetic (above diagonal, ± SE) and phenotypic correlations (below diagonal, ± SE) among growth and efficiency traits ................................................................. 48

Table 4. 1: Summary information about animals from the EBRC1 and NLARS2 herds. 62

Table 4. 2: Descriptive statistics of fertility and post weaning traits............................... 63

Table 4. 3: Variance components and heritability estimates of fertility and post weaning traits......................................................................................................................... 64

Table 4. 4: Genetic and phenotypic correlations (±SE) between fertility and post weaning traits.......................................................................................................................... 65
CHAPTER 1: LITERATURE REVIEW

1.1 INTRODUCTION

The Canadian beef cattle industry engages in an ongoing effort to enhance beef quality through breed selection and genetic improvement programs (Canada Beef Inc., 2012). Productive and fertility traits are both economically important in this industry; and their performance differs depending on species, breed and location. In animal selection and prediction programs, genetic parameters are an essential part of the selection index. Breeders would like to select high total-breeding-value animals and to predict the offspring of these animals. As a result, the accuracy of heritability and genetic correlation between productive and reproductive traits is critical.

Heritability estimates of both types of traits have been reported in earlier research (Morris et al., 2000 and Schenkel et al., 2004). Most reproductive traits estimated in these previous studies showed low heritabilities, and feed efficiency traits were moderate to highly heritable. However, research on genetic correlations among these traits is limited. To understand these traits clearly, this chapter describes the corresponding operations, general definitions, measurements and reported genetic parameters for these traits.

1.2 CANADIAN BEEF INDUSTRY

The Canadian beef industry is large and successful. Beef production takes place in every province, with a total of approximately 13.5 million head (statistics Canada, 2013). There are 37,406 beef cattle ranching and farming farms (including feedlots) in Canada in
2011, which produced 1.5 billion kg of beef (Statistics Canada, 2012). The industry produces well in excess of the 20.9 kg of beef consumed per person in Canada each year, but also sends a large amount of beef overseas, making it the 6th largest beef-exporting country in the world, and in 2011, the industry contributed $25.96 billion to Canada’s economy (Canadian Beef, 2013).

The process of raising cattle for beef production begins with the cow-calf operation. Breeding typically occurs in the summer, followed by calving the following spring. Once they are weaned, the calves are provided with feed, shelter and bedding. When they reach a target weight, they are transferred to the feedlot (intensive feeding) and are fed a carefully formulated diet to gain weight. Well marbled and flavourful meat are promoted (Canada Beef Inc., 2012).

By using Bos taurus type genetics, Angus, Simmental, Charolais, Limousin and other breeds are included in Canada’s beef cattle industry. Crossbreeding is used to combine the best characteristics of several breeds into one animal. As a result, Canada produces more than 30 different breeds of cattle.

1.3 ONTARIO BEEF INDUSTRY

There are 19,000 beef farmers in Ontario with 316,000 beef cows, which represent 7 percent of Canada’s national beef herd. The province has a large number of small farms, and an average of 66 head per farm in 2012. Nonetheless, these cattle and calves represent 9 percent of farm cash receipts in Ontario (Make it Ontario Beef, 2013).
1.4 REPRODUCTION

1.4.1 Natural Estrus and Estrus Synchronization

The use of natural estrus is the traditional reproductive method used in beef herds. Estrus synchronization is a more recent innovation that is not widely practiced in beef farming. It can be an efficient way of increasing the proportion of females that become pregnant early in each breeding season, which can reduce the calving season and produce a more uniform calf crop (Dziuk and Bellows, 1983). Also, the majority of synchronized females will calve during a two-week period, which makes it easier to manage calving. However, it takes more time (management and labour) and money (drugs) (Odde, 1990). As well, it may result in lower pregnancy rates if procedures and requirements are not matched perfectly (Deutscher, 1985).

1.4.2 Natural Service and Artificial Insemination

In beef herds, cows are bred naturally with herd bulls or by artificial insemination. Both breeding programs have their advantages. Generally, natural service is used more widely than AI due to its lower cost and the ease of overcoming problems with estrus detection (Lima et al., 2010). However, AI has many advantages over nature service. Vishwanath (2003) reported that AI could help to eliminate venereal diseases, provide more accurate dry-off dates, reduce the incidence of dystocia and increase safety for farm employees. It also provides more breeding records for scientific study because each service time can be recorded and there is little doubt as to the sire.
1.4.3 Female Fertility

Female fertility is a complex trait in beef production systems and genetic evaluation procedures, partly due to the numerous measurements needed to assess reproduction (Cammack et al., 2009). Fertility is considered an economically important performance criterion in the beef industry. Melton (1995) reported that improving reproductive performance has a four-times-greater economic implication for the industry compared to improving end-product traits. Besides, the biological and economical efficiencies of cow-calf production depend largely on successful reproduction (Dickerson, 1970). Therefore, fertility should be considered in the breeding objective.

Improving fertility is more important now than it used to be because of the double challenge of limited data collection and analysis procedures have been solved (Evans et al., 1999). Even with more data and better statistical analysis methods today, improving fertility through genetics is still considered slow. This is because of the low heritability estimates for fertility traits. Moderate to high genetic correlations between fertility traits and other production traits have been reported. Consequently, using reproductive traits in selection programs is considered feasible (Meyer et al., 1990).

1.4.4 Fertility Measurements

Fertility is a general term, not a single, easily defined trait (Cammack et al., 2009). Female fertility has two main components: the success at the particular event and the elapsed time to that particular event. The definitions for fertility traits studied in this thesis are as follows:
**First-service conception rate** (FSCR) is a binary trait defined as the probability that a female will conceive from the first AI service in each breeding season. It is a successful trait with a binomial distribution. FSCR is different from the conception rate by natural mating. A female that conceives at the first insemination incurs a lower cost of insemination, lower labour for estrus detection and breeding, and an earlier calving date. Heifers that conceive after their first AI have higher pregnancy rates in subsequent breeding seasons (Minick et al., 2006). Since AI is not a general breeding method, FSCR data is not available on every farm. As a result, this trait would only be used on farms with AI service.

**Pregnancy rate** (PR) is a binary trait defined as the probability of a female being pregnant by the end of the breeding season (Eler et al., 2004). It is an important indicator of fertility. Pregnancy rate is affected by breeding management (estrus synchronization or natural heat cycles), mating methods (natural mating or AI) and the length of the breeding season (the number of AIs or matings). Since PR differs between heifers and mature cows, it is usually studied separately as heifer PR and cow PR. Genetic correlation estimate between PR in heifers and cows has been shown to be at 0.92 (Morris and Cullen, 1994; Mwansa et al., 2000). If a heifer is pregnant at the end of the breeding season, it is more likely to become pregnant in subsequent breeding seasons.

**Number of services per conception** (NS) is defined as the number of AI services until a female conceives. It is one of the major time-related traits in female fertility. As for FSCR, NS data are rarely available on farms that use natural service because each service should be recorded but rarely is (Rust et al., 2001). Since NS is related to
prolonged calving intervals, insemination costs and the number of calves produced, it is considered an economic important trait and a potential selection criterion in fertility.

**Gestation length** (GL) is a traditional time-related trait in fertility. It is defined as the interval between the conception date and the calving date. Hence, the date of each service needs to be recorded, which is only available under AI. The variance in GL within species is small, although it does vary between individual animals. Selecting for GL does not have direct economic value; however, reducing GL may reduce calving problems (Wray et al., 1987).

**Days-to-calving** (DC) is the number of days from first insemination until calving. It was first computed by Meyer et al. (1990) and further described by Johnston and Bunter (1996). This is a continuous variable, and similar to measuring calving date especially when the females’ mating services start on the same day in each breeding season. Because only females that calve successfully will have these records, Johnston and Bunter (1996) suggest that a penalty of 21 days should be applied to females that do not have a subsequent calving record.

### 1.4.5 Reported Genetic Parameters for Fertility Traits

Heritability estimates for fertility are summarized in Table 1.1 and 1.2. Overall, fertility traits are low to moderately heritable. Generally, the estimates of heritability for FSCR and PR were similar and low, with a range of 0.03 to 0.14 (Martínez-Velázquez et al., 2003; Minick et al., 2006; Morris et al., 2000). GL was reported as moderately heritable, with estimates ranging from 0.30 to 0.37 (MacNeil et al., 1984; Wray et al., 1987). NS and DC were lowly heritable (Meyer et al., 1990; Donoghue et al., 2004).
1.5 FEED EFFICIENCY

Genetic programs to improve feed efficiency are now feasible as feed intake recording technology has advanced (Arthur et al., 2001b). In addition, feed costs (Herring and Bertrand 2002) and environmental issues (Herd et al, 2002) are making more efficient cattle more desirable. Herd et al. (2002) reported that selecting for more efficient beef cattle (on the basis of feed intake adjusted for production) should also be accompanied by a significant reduction in greenhouse gas emissions per unit of live weight production. Thus, selection programs improving feed efficiency are expected to benefit the beef industry in more ways than one (Hoque et al., 2005).

1.5.1 Feedlots

In the beef industry, market cattle spend most of their lives grazing on pasture and range. Typically, young cattle are taken off pasture and transferred to intensive livestock operations (ILOs or feedlots) for a short period, where they are fed nutritionally balanced rations that ensure a high quality product for the consumer.

1.5.2 Measures of Feed Efficiency

Feed is a major cost in beef production. However, since feed intake has been difficult and expensive to measure, little attention has been paid to improving the efficiency of feed use in beef cattle through genetics. The current availability of feed intake data is a result of new automated feed intake recording facilities. Recording for dry matter intake (DMI) throughout a standard 112-day test period may cost as much as $50
to $200 per animal (Crews et al., 2005). In earlier studies, the test period ranged from 70 to 200 days (Herd and Bishop, 2000; Archer et al., 2002; Nkrumah et al., 2007). During the test period, clean and unlimited water is offered. Diet may be restricted (Arthur et al., 2001; Hoque et al., 2005) or not, according to the specific study. Based on recorded feed intake, body weight (BW) and growth, several traits are of interest to programs that breed for feed efficiency.

**Dry Matter Intake**

Dry matter intake (DMI) was reported as an economically important trait in beef cattle industry (Lazenby et al., 1998). Usually, a mature cow consumes 1-3% of her body weight per day (Wieland, 2002). DMI is mainly used to maintain BW and to project output (growth). Hence, a prediction equation that uses BW and ADG to estimate the DMI of beef cattle was developed by Minson and McDonald (1987).

**Average Daily Gain and Metabolic Mid-test Body Weight (MMBW)**

Average daily gain (ADG) is an important trait in beef production with higher gains more favourable in the post-weaning feeding period. At the test station, BW is measured during a predetermined period, and ADG and MMBW is estimated by the linear regression of that period BW measurements against test time (Nkrumah et al., 2007). Earlier research shows that growth rate and BW were significantly related with feed intake (Archer et al., 2002; Rolfe et al., 2011).
**Feed conversion ratio**

Feed conversion ratio (FCR) is defined as the ratio between daily feed intake and ADG. It is recommended to use dry feed rather than wet to measure intake. Feed conversion ratio was estimated with moderate heritability, so there is potential to improve FCR. Arthur et al. (2001a) indicated that using ratio traits for genetic selection presents problems, which are associated to predicting changes in the component traits in future generations.

**Residual feed intake**

Residual feed intake (RFI) is defined as observed DMI minus a prediction of DMI based on metabolic body size and rate of growth (Koch et al., 1963). RFI is calculated by a multivariable linear regression with feed intake, ADG and MMBW. Negative RFI is considered efficient because the animal eats less than average. Carstens and Tedeschi (2006) suggest that RFI is a more suitable trait to use in comparing animals during post-weaning tests that differ in production.

**1.5.3 Reported Genetic Parameters for Feed Efficiency Measurements**

As shown in Table 1.3, heritability estimates for feed efficiency traits were reported as moderate. The heritability estimates for DMI ranged from 0.28 to 0.49, suggesting that DMI is moderately heritable, and can be improved by selection. The heritability estimates of ADG were moderate, and ranged from 0.21 to 0.38 (Schenkel et al., 2004; Herd and Bishop, 2000; Rolfe et al., 2011). The heritability estimates for MMBW were moderate to high, with the highest estimate at 0.71 (Archer et al., 2002).
Earlier research showed that feed efficiency traits were low to moderately heritable. In summary, the magnitude of the heritability estimates indicate that selecting for feed efficiency is feasible.

1.6 CONCLUSION

Fertility and feed efficiency have high economic value in the beef industry. According to previous research, fertility is considered as a complicated trait with low heritability. However, the interest in fertility is increasing due to the estimates of genetic parameters and new breeding technologies. For example, the involvement of AI service provides more recordable fertility data for the beef herd. Overall, fertility is worthy to be included in beef breeding programs. Feed efficiency traits have been well studied. Feed efficiency is measured during the feedlot period and highly related to net profit. Feed conversion ratio and residual feed intake are two typical measurements and both of them are moderately heritable. Therefore, feed efficiency can be improved by animal evaluation and selection.
## 1.7 TABLES

**Table 1.1: Summary of published heritability (h\(^2\)) estimates for first-service conception rate and pregnancy rate**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Breed</th>
<th>h(^2)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>First-service conception rate</td>
<td>AN</td>
<td>0.03</td>
<td>Minick et al., 2006</td>
</tr>
<tr>
<td></td>
<td>CR</td>
<td>0.22</td>
<td>Dearborn et al., 1973</td>
</tr>
<tr>
<td>Pregnancy rate</td>
<td>CR</td>
<td>0.04</td>
<td>Morris and Cullen, 1994</td>
</tr>
<tr>
<td></td>
<td>HF</td>
<td>0.06</td>
<td>Toelle and Robison, 1985</td>
</tr>
<tr>
<td></td>
<td>AN</td>
<td>≈0.10</td>
<td>Morris et al., 2000</td>
</tr>
<tr>
<td></td>
<td>AN</td>
<td>0.13</td>
<td>Minick et al., 2006</td>
</tr>
<tr>
<td></td>
<td>BT</td>
<td>0.14</td>
<td>Martínez-Velázquez et al., 2003</td>
</tr>
</tbody>
</table>

\(^1\) AN = Angus; BT = Bos Taurus; CR = Crossbred; HF = Hereford
Table 1.2: Summary of published heritability ($h^2$) estimates for number of services pre conception (NS), gestation length (GL) and days-to-calving (DC)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Breed</th>
<th>$h^2$</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>DC</td>
<td>HF</td>
<td>0.05</td>
<td>Meyer et al., 1990</td>
</tr>
<tr>
<td></td>
<td>AN</td>
<td>0.06</td>
<td>Donoghue et al., 2004</td>
</tr>
<tr>
<td></td>
<td>AN</td>
<td>0.08</td>
<td>Meyer et al., 1990</td>
</tr>
<tr>
<td></td>
<td>ZC</td>
<td>0.09</td>
<td>Meyer et al., 1990</td>
</tr>
<tr>
<td></td>
<td>AN</td>
<td>0.11</td>
<td>Johnston &amp; Bunter, 1996</td>
</tr>
<tr>
<td>GL</td>
<td>SM</td>
<td>0.09</td>
<td>Wray et al., 1987</td>
</tr>
<tr>
<td></td>
<td>CR</td>
<td>0.30</td>
<td>MacNeil et al., 1984;</td>
</tr>
<tr>
<td></td>
<td>SM</td>
<td>0.37</td>
<td>Wray et al., 1987</td>
</tr>
<tr>
<td></td>
<td>SM</td>
<td>0.48</td>
<td>Burfening et al., 1978</td>
</tr>
<tr>
<td>DC</td>
<td></td>
<td>0.03-0.07</td>
<td>Johnson &amp; Notter, 1987</td>
</tr>
<tr>
<td></td>
<td>CR</td>
<td>0.04</td>
<td>Morris and Cullen, 1994</td>
</tr>
<tr>
<td></td>
<td>HF</td>
<td>0.06</td>
<td>MacNeil and Newman, 1984</td>
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<tr>
<td></td>
<td>SM</td>
<td>0.07</td>
<td>Meacham &amp; Notter, 1987</td>
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<td>AN</td>
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<td>Morris et al., 2000</td>
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<td>SM</td>
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<td>Meacham &amp; Notter, 1987</td>
</tr>
<tr>
<td></td>
<td>AV</td>
<td>0.21</td>
<td>Gutiérrez et al., 2002</td>
</tr>
</tbody>
</table>

$^1$ AN = Angus; AV = Asturiana de los Valles; CR = Crossbred; HF = Hereford; SM = Simmental; ZC = Zebu cross.
Table 1.3: Summary of published heritability ($h^2$) estimates for feed efficiency traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>Breed</th>
<th>$h^2$</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>DMI</td>
<td>British Hereford</td>
<td>0.31</td>
<td>Herd and Bishop, 2000</td>
</tr>
<tr>
<td></td>
<td>Angus</td>
<td>0.39</td>
<td>Arthur et al., 2001</td>
</tr>
<tr>
<td></td>
<td>Multi-breed</td>
<td>0.28</td>
<td>Archer et al., 2002</td>
</tr>
<tr>
<td></td>
<td>Multi-breed</td>
<td>0.44</td>
<td>Schenkel et al., 2004</td>
</tr>
<tr>
<td></td>
<td>Brangus</td>
<td>0.48</td>
<td>Lancaster et al., 2009</td>
</tr>
<tr>
<td></td>
<td>Multi-breed</td>
<td>0.49</td>
<td>Crowley et al., 2010</td>
</tr>
<tr>
<td></td>
<td>Crossbreed</td>
<td>0.40</td>
<td>Rolfe et al., 2011</td>
</tr>
<tr>
<td>ADG</td>
<td>British Hereford</td>
<td>0.38</td>
<td>Herd and Bishop, 2000</td>
</tr>
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<td>0.33</td>
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<td>0.30</td>
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<tr>
<td></td>
<td>Crossbreed</td>
<td>0.26</td>
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<tr>
<td>MMBW</td>
<td>Angus</td>
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<td>Japanese Black</td>
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<td>Multi-breed</td>
<td>0.38</td>
<td>Schenkel et al., 2004</td>
</tr>
<tr>
<td></td>
<td>Japanese Black</td>
<td>0.24</td>
<td>Hoque et al., 2005</td>
</tr>
<tr>
<td></td>
<td>Brangus</td>
<td>0.47</td>
<td>Lancaster et al., 2009</td>
</tr>
<tr>
<td></td>
<td>Multi-breed</td>
<td>0.45</td>
<td>Crowley et al., 2010</td>
</tr>
<tr>
<td></td>
<td>Crossbreed</td>
<td>0.52</td>
<td>Rolfe et al., 2011</td>
</tr>
</tbody>
</table>

$^1$DMI = average daily dry matter intake; ADG = average daily gain; MMBW = metabolic mid-test body weight; FCR = feed conversion ratio; RFI = residual feed intake.
CHAPTER 2: Genetic parameters of female fertility traits in a multi-breed beef cattle population

2.1 ABSTRACT

Accurate genetic and phenotypic (co)variance component estimates are necessary to optimize selection response in reproductive traits of economic importance for commercial beef cow/calf operations. The objective of this research was to determine the heritability and relationships among five reproductive traits in a multi-breed beef cattle population. Records on 1,369 cows from two herds, 505 sire and 1,360 dams were collected between 2002 and 2011. Binary traits of first-service conception rate (FSCR) and pregnancy rate (PR) and a categorical trait of number of services per conception (NS) were analyzed by threshold models, while interval traits of gestation length (GL) and days-to-calving (DC) were analyzed using linear models. Models included fixed effects of contemporary groups (herd, year, breeding season and breeding method), age of animal, age of dam and linear regressions on heterozygosity and breed proportions of Angus, Simmental, Charolais and Piedmontese. Additive genetic and permanent environment effects were modelled as random effects. Univariate and bivariate animal models were fitted using ASReml (Gilmour et al., 2009). Estimates of heritability (repeatability) for FSCR, PR, NS, GL and DC were 0.04 (0.05), 0.05 (0.05), 0.04 (0.07), 0.21 (0.21) and 0.07(0.10), respectively. Genetic correlations between FSCR and PR, NS and DC, GL and DC were positive and moderate to high ($r_g = 0.99 \pm 0.14$, $0.60 \pm 0.27$ and $0.75 \pm 0.15$, respectively). Strong and negative genetic correlations were founded for NS with FSCR (-0.95) and PR (-0.98). The remaining pairs of traits appeared to be
genetically independent. Phenotypically, reproductive traits were correlated, with estimated correlation coefficients from -0.77 (FSCR and NS) to 0.77 (NS and DC). To further prove the feasible of fertility selection, the multi-breed expected progeny differences (EPD) was calculated for bulls. The differences between top and bottom ranking bulls were significantly different from zero for FSCR (24%), PR (26%), NS (0.24), GL (2.27 days) and DC (3.42 days). In conclusion, the multi-breed EPDs can be used to selecting female fertility. Based on the estimates of genetic parameters, either FSCR or PR should be included in beef breeding programs, and days-to-calving is the other valuable fertility trait that worth to be included.

Keywords: beef cattle, genetic correlation, heritability, reproduction

2.2 INTRODUCTION

Fertility is determined by several factors, and it is not a single, easily defined trait (Cammack et al., 2009). Genetic evaluation of fertility traits for animals in beef production in Canada is important because of their economic impact. As Melton (1995) has shown, reproductive performance improvement has a four-time-greater economic implication for the beef industry when compared to improvements in end-product traits.

Female fertility has two main components, which are the success at a particular event and the elapsed time for that particular event to occur. In each breeding season, pregnancy rate, first-service conception rate, number of services per conception would not only indicate the number of calves produced, but it is also related to the length of the breeding season along with the cost. The interval trait of days-to-calving (the number of days from the beginning of the joining period to calving) was firstly investigated by
Meyer et al., (1990) and became the standard trait for genetic evaluation now (Robinson, 2007). An early calving date means a shorter open time in the previous breeding season, which is related to a better reproductive performance in the next breeding season. The traditional interval trait of gestation length was also included in the current study. Some previous studies have reported low heritabilities in reproductive traits (Meyer et al., 1990; Rust et al., 2001; Jamrozik et al., 2012). In order to facilitate management of the fixed breeding season with limited time, induced estrus synchronization and artificial insemination were utilized in farms that were studied in current research. Estimations of genetic parameters for fertility traits measured with artificial insemination are limited. Furthermore, to increase the accuracy of the selection index, the genetic and phenotypic correlations needed to be quantified.

The objectives of this study were to estimate heritabilities and repeatabilities for fertility traits, and identify genetic and phenotypic correlations among these traits.

2.3 MATERIALS AND METHODS

2.3.1 Data

The fertility data were collected in the two University of Guelph beef research herds in Ontario from 2003 to 2012 with exclusive use of artificial. The herds were located in Elora with 140 calving cows and New Liskeard with 160 calving cows. Both herds were multi-breed composed of four main breeds of Angus, Simmental, Piedmontese and Charolais, which contributed on average 46.0%, 25.4%, 8.6% and 4.9% of their genes to the total population on average, respectively. In Elora, the breeding
season in each year was from June to September and females were largely under natural
estrus. NewLiskeard had two breeding seasons within each year using entirely fixed-time
AI breeding: spring season from May to June and fall season from September to October,
each of 45 days, which included up to 2 matings per cow. There were two treatments (T1
and T2) of estrus synchronization before 2006 for the first insemination and two
treatments (T3 and T4) for the second insemination. After 2007, only one treatment (T5)
used in for the first insemination and one treatment (T6) utilized for the second
insemination. In each breeding season, females received CIDR insert first (day 0) and
removed CIDR after 7 days (day 7). Artificial insemination was applied after two days
(day 9) of CIDR removal. In T1, Estradiol Benzoate (EB) was injected to females at day
0, Prostaglandin F2alpha (PGF2α, Lutalyse®) was injected at day 7, and Estradiol
Benzoate was injected again at day 8. In treatment 2, Gonadotropin-releasing hormone
(GnRH, Cystorelin®) was used instead of EB at day 0, and PGF2α was used at day 7. In
treatment 5, GnRH was injected at day 0 and day 9 and PGF2α injection was placed at
day 7. Females that were not successfully bred with the first insemination were rebred
within the same season. The second insemination started at day 36 and end up at day 45
with artificial insemination and GnRH injection. In T3, GnRH was injected in day 36,
which was followed by pregnancy check at day 43 and PGF2α injection for all open
females. Treatment 4 and T6 were same, and they add CIDR insert at day 36 and removal
at day 45 compared with T3. Due to breeding management of the two herds,
contemporary group (CG) was defined as the combination of herd, year, breeding season
and the estrus treatment
First-service conception rate (FSCR) was defined as the probability of a female becoming pregnant after the first service, and the pregnancy rate (PR) was the probability of a female becoming pregnant during the breeding season. Both traits are success traits, and females were assigned a “1” for a successful pregnancy and “0” for a failure to become pregnant. Number of services per conception (NS) was classified into 3 classes: ‘1’ indicated a female pregnant after the first insemination; ‘2’ indicated a female pregnant after the second insemination and ‘3’ indicated a failure to be pregnant after two insemination attempts. Although some Elora animals (on an average of 12.2%) may have become pregnant at the 3rd and 4th insemination, but they were still recorded as ‘3’ to be able to combine data for both herds. Gestation length (GL) was measured as the difference between recorded calving date and the final insemination date in previous breeding season. The days-to-calving (DC) was the interval between the first insemination in a herd in the breeding season and the calving date of each female in the following calving season. Observations from cows more than 9 year old were removed from the data set due to small number of records (n<20). Phenotypes for GL and DC were calculated only if they were within three overall SD from their respective contemporary group means.

The summary statistics of the final data set used in the analyses is presented in Table 2.1. A total of 1,369 cows were included. The number of observations for FSCR, PR and NS was 3,863, and the numbers of observations for GL and DC were 2,628 and 2,619, respectively. The mean FSCR and PR were 72% and 76%, respectively. Gestation length was 282.2 days on average, which were similar to previous estimates (Bourdon
and Brinks, 1982). In addition, three generations of pedigree with 504 sires and 1360 dams were used.

### 2.3.2 Statistical Analysis

Fixed effects of the models included contemporary group, age of dam and age of animal. Covariates (from 0% to 100%) included breed proportions of Angus, Simmental, Piedmontese and Charolaise, as well as heterozygosity. Additive genetic (A) and permanent environment (PE) effects due to repeated records on females were included as random effects. An additional random effect of first-service sire (S) was fitted for FSCR, PR and NS. Variance components of each trait were estimated by the software package ASReml 3.0 (Gilmour et al., 2009). Binary models with the ‘logit’ link function were utilized for FSCR and PR. A multinomial threshold model with the ‘logit’ link function was fitted for NS. Linear models were used for DC and GL. Breed difference tests were obtained using “Syslin” procedure in SAS 9.2. All breeds were compared with AN (the major breed in these herds).

The univariate models were as follows:

\[
y = Xb + Z_1a + Z_2p + (Z_3s) + e,
\]

where, \(y\) is a vector of observations for linear traits or liabilities (on the underlying scale) for categorical traits; \(b\) is a vector of fixed effects; \(a\) and \(p\) are vectors of animal additive genetic and permanent environmental effects for all traits, respectively; \(s\) is a random effect of first-service sire for FSCR, PR and NS; \(e\) is a vector of residuals; \(X\) and \(Z_i\) are design matrices relating observations to corresponding effect. Assumptions included:
\( \mathbf{a} \mid \mathbf{A}, \sigma_a^2 \sim N(0, \mathbf{A} \sigma_a^2), \) \( \mathbf{A} \) is an additive relationship matrix, \( \sigma_a^2 \) is an additive genetic variance;

\( \mathbf{p} \mid \mathbf{I}, \sigma_p^2 \sim N(0, \mathbf{I} \sigma_p^2), \) \( \mathbf{I} \) is an identity matrix, \( \sigma_p^2 \) is a permanent environment variance;

\( \mathbf{s} \mid \mathbf{I}, \sigma_s^2 \sim N(0, \mathbf{I} \sigma_s^2), \) \( \sigma_s^2 \) is variance of first service sire random effect;

\( \mathbf{e} \sim N(0, \mathbf{I} \sigma_e^2), \) \( \sigma_e^2 \) is residual variance.

To test the breed proportion effect, all the fixed effects were removed using ASREML.

Heritability \( (h^2) \) and repeatability \( (r) \) were calculated as:

\[
h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_p^2 + (\sigma_s^2 + \sigma_e^2)},
\]

and

\[
r = \frac{\sigma_a^2 + \sigma_p^2}{\sigma_a^2 + \sigma_p^2 + (\sigma_s^2 + \sigma_e^2)}.
\]

Genetic and phenotypic correlations between each pair of traits were estimated using bivariate models. The bivariate models included specific single trait models for each trait as shown above. Distributions of the random effects in bivariate models were assumed as follows:

\[
\begin{bmatrix}
\mathbf{a} \\
\mathbf{p} \\
\mathbf{s} \\
\mathbf{e}
\end{bmatrix} \sim N\left\{\begin{bmatrix}
0 \\
0 \\
0 \\
0
\end{bmatrix}, \begin{bmatrix}
\mathbf{A} \times \mathbf{G}_0 & 0 & 0 & 0 \\
0 & \mathbf{I} \times \mathbf{P} & 0 & 0 \\
0 & 0 & \mathbf{I} \times \mathbf{S} & 0 \\
0 & 0 & 0 & \mathbf{I} \times \mathbf{E}
\end{bmatrix}\right\},
\]

where, \( \mathbf{A} \) is a numerator additive genetic relationship matrix for all animals; \( \mathbf{G}_0 \) is a \( 2 \times 2 \) dimensional additive genetic variance-covariance matrix; \( \mathbf{P}, \mathbf{S} \) and \( \mathbf{E} \) are (co)variance \( (2 \times 2) \) matrices for PE, SS and residual effects, respectively.
Bivariate models were fit in “ASREML” package, which could only treat one trait as a binary trait in each bivariate analysis (Gilmour et al., 2009). Consequently, NS was fitted as a linear trait in bivariate analyses and two bivariate models were used to estimate the correlation between FSCR and PR: FSCR linear and PR binary and FSCR binary and PR linear. In addition, random effect of first-service sire was included for FSCR, PR and NS.

To further describe the possibility of using fertility traits in selection, the Expected Progeny Difference (EPD) of bulls with daughters that had data on fertility traits were estimated. The EPD was calculated as follow:

$$\text{EPD} = \frac{1}{2} \text{EBV} + \beta_{AN}AN + \beta_{SM}SM + \beta_{PI}PI + \beta_{CH}CH,$$

where EBV is solution of estimated Expected Breeding Value for each animal from “ASREML”; AN, SM, PI and CH are breed proportions of Angus, Simmental, Piedmontese and Charolais, respectively; and $\beta_{AN}$, $\beta_{SM}$, $\beta_{PI}$ and $\beta_{CH}$ are regression coefficients for corresponding breed proportions estimated from above models. Top and bottom 10% of bulls for each trait were identified and compared. Bulls with reliability smaller than 0.1 were removed from the comparisons.

By assuming normal distributions of the estimates, Akesson et al. (2008) suggested an approximate rule for significance testing of the estimates of genetic parameters. This rule indicated that a genetic parameter is significantly different from 0 (P < 0.05) when it is at least twice of the value of the standard error of the parameter. When the estimated parameter is at least 3 times of the value of the standard error of the parameter, then the P is smaller than 0.01.
2.4 RESULTS AND DISCUSSION

2.4.1 Breed Proportion and Heterozygosity

Estimates of regression coefficients for heterozygosity and breed proportions are presented in Table 2.2. It can be observed that the breed proportions did not have a significant influence on fertility. None of the four breeds showed significant difference from Angus for all traits, indicating that differences in breed composition did not lead to different reproductive performance of crossbreds. This result was in an agreement with previous researches. Peacock and Koger (1980) reported a small and non-significant difference between Angus and Charolais for genetic effects on fertility (calving rate) but these two breeds were different from Brahman. The research of Gregory et al. (1992) indicated that parental breeds of Angus, Simmental and Charolais did not differ from each other in pregnancy rate. Baker and Lunt (1990) found significantly longer average gestation lengths of Charolais and Peidmontese when compared with Angus. Similar trends were found in this research but the distance was not significantly different from zero.

Heterozygosity had significant regression coefficient on GL at 1.29 days, which indicated that a purebred female probability has a 1.29 days shorter gestation than a crossbreed female. This difference is significant in theory but does not have big economic difference in the running on for beef farms. The estimates of regression coefficient of heterozygosity for PR in the current research (-13%) were smaller than regression
coefficient of 19% in a crossbred beef herd with breeds of Tarentaise, Red Angus and Charolais (Newman et al., 1993). The smaller effect of heterozygosity might be because most animals were crossbred and there was not a good full range of possible breed heterozygosity to adequately test the effect. In conclusion, breed proportions of AN, SM, PI and CH and heterozygosity based on the breeds did not significantly impact the reproductive performance in these data.

2.4.2 Heritability and Repeatability

The variance components, heritabilities, and repeatabilities for fertility traits are shown in Table 2.3. The variance component of the first-service sire for FSCR (0.03) indicated that the service sire would have an impact on FSCR. This was in agreement with the significant effect of service sire on Holstein heifers (Donovan et al., 2003), the variance contributions of service bulls to the conception rate of French Holstein (Boichard and Manfredi, 1994), and to the non-return rate of Canadian Holstein (Jamrozik et al., 2005). The residual variance of FSCR, PR and NS were all 3.29 due to the assumption of normal distribution for residuals on the underlying scale ($\pi^2/3$).

Estimates of heritability were low to moderate, but they were significantly different from zero ($P < 0.05$). The heritability estimates for FSCR, PR, NS and DC were low at 0.04, 0.05, 0.04 and 0.07, respectively, while the heritability of GL was of a moderate magnitude ($0.21 \pm 0.02$). The low heritabilities were mainly due to a large, unexplainable portion of residual variation (Veerkamp and Beerda, 2007), which occupied a great amount of phenotypic variance. Two recent reviews (Rust et al., 2001; Cammack et al., 2009) reported that most fertility traits had low heritability, with the
exception of gestation length, which was moderately heritable. The low estimates of heritability for FSCR (0.04) and PR (0.05) were similar to the estimates by Bormann et al. (2006), Toelle and Robison (1985), and Morris et al. (1994, 2000). Heritability of 0.04 for NS was similar to the estimate that was reported by (Yagüe et al., 2009). The heritability of 0.21 for GL in the current study was moderate but a little lower than most previous literature estimates (Burfening et al., 1978; Bourdon et al., 1982; Wray et al., 1987; Cervantes et al., 2010). Previous estimates of heritability for DC were low and ranged from 0.05-0.11 (Meyer et al., 1990; Johnston et al., 1996; Donoghue et al., 2004). The selection for females themselves may not be efficient due to these small heritabilities for fertility traits. But as these heritabilities were significantly different from zero, selection could be placed on bulls when there are adequate fertility records on their daughters. In summary, female fertility could be improved by selection on these fertility traits.

Fertility is a complex trait and the estimates of genetic parameters vary depending on the trait definition and the estimation method. Since the reproductive performance may differ according to the age and parity of the dam, some research has indicated that reproductive performance in heifers and mature cows may be different traits (Eler et al., 2004; Nishida et al., 2006; Jamrozik et al., 2012). However, the heifer fertility and cow fertility was grouped as female fertility in the current study. This was because fertility records in current study were limited. When there are enough fertility records in the future, the heifer fertility and cow fertility may be considered separate traits. The permanent environmental (PE) effect was included to account for repeated records. The estimates of permanent environmental variances for fertility traits were small. The small
PE variances for fertility traits were also reported in Holstein Friesian dairy cattle (Pryce et al., 1997) and Italian Brown Swiss (Tiezzi et al., 2011). As a result, the estimates of repeatability were of similar magnitude when compared with corresponding heritabilities. The repeatabilities of PR and GL were the same as their heritabilities and the repeatabilities of FSCR, NS and DC were slightly higher than corresponding heritabilities, which were 0.05, 0.07 and 0.10, respectively. The repeatability of DC (0.10) was slightly higher than its corresponding heritability, and it was the same as the estimates for Angus (Meyer et al., 1990). A similar trait of calving date was also indicated as low repeatability for heifers (Morris et al., 1980) and cows (Bailey et al., 1985).

2.4.3 Genetic and Phenotypic Correlations

Genetic and phenotypic correlations among reproductive traits are presented in Table 2.4. Genetic correlations among fertility traits varied greatly. Because of the limitation of “ASREML”, there were two bivariate models fitted to estimate the correlations between FSCR and PR. When comparing the results from the two models, estimates with smaller standard error was considered more accurate than the other. As a result, the genetic correlation between FSCR and PR were extremely high (0.99). This correlation was followed by another high correlation between GL and DC (0.75 ± 0.15). The genetic correlation between NS and DC was also high at 0.6 ± 0.27. Furthermore, there was high negative relationship between FSCR and NS (-0.95 ± 0.11), and between PR and NS (-0.98 ± 0.18), which were followed by the genetic correlation (-0.38 ± 0.22) between FSCR and GL. There was no evidence that the genetic correlations among other traits were significantly different from zero.
Due to the high genetic correlation between FSCR and PR, as well as the similar heritability estimates of these two traits, FSCR and PR can be treated as genetically the same trait. As a result, only one of these traits needs to be considered when performing animal evaluation or animal selection. As pregnancy rate is normally more recordable than first-service conception rate due to the unavailable records of FSCR in natural mating scenarios, PR was recommended as a selection criteria than FSCR to increase the accuracy of bull selection. The genetic correlation between NS and DC indicated that a cow that needs more inseminations is likely to calve later, as would be expected. The genetic correlation was 0.75 (0.15) between GL and DC. This was because days-to-calving was the number of days from first insemination to conception, plus gestation length, so the genetic variance of days-to-calving contains the genetic variance of GL and genetic correlation between DC and GL is expected. Genetic correlations between the two success traits and interval traits of GL and DC (Table 2.4) indicated that success traits and interval traits of fertility are genetically independent, and selection in one group will not improve the performance in the other group. For example, selection to improve FSCR will not improve days-to-calving as the correlation -0.58 ± 0.32 was not significantly different from zero, and the genetic correlations estimated for PR with GL (0.04 ± 0.19) and DC (-0.22 ± 0.45) were not significantly different from zero.

As shown in Table 2.4, most fertility traits were phenotypically correlated with each other. The highest correlations were found between NS and DC (0.77 ± 0.01) and between FSCR and NS (-0.77 ± 0.01). First-service conception rate and pregnancy rate were favourable correlated with NS and DC. However, the genetic correlation (-0.71 ± 0.01) found between FSCR and DC was stronger than the correlation estimate (-0.17 ±
0.03) between PR and DC. This was because a female that got pregnant after first insemination was going to have less (only one here) number of services, and an early calving date as would be expected. However, a dam that becomes pregnant at the end of the breeding season might have required more artificial inseminations, coinciding with a later calving date. Considering of these correlations, first-service conception rate and pregnancy rate are both potential criteria in selection index, but FCSR is stronger related with shorter days-to-calving. The two interval traits, GL and DC, were phenotypically correlated with a coefficient of 0.32 ± 0.02.

Relatively fewer estimates of genetic correlations were available in the literature for fertility traits in beef cattle, but those available were in general agreement with the findings of this study. Jamrozik et al. (2012) found a negative genetic correlation (-0.90 ± 0.02) between calving to first insemination (defined as the probability that a cow will produce a calf from her first service, and similar with FSCR in this study) and DC in Simmental beef cattle, which is agree with the correlation estimated in this study. The small genetic correlation between NS and GL was in agreement with the estimate in dairy (VanRaden et al., 2004). The negative correlation between FSCR and NS agreed with the estimate (-0.92 ± 0.05) reported by Kadarmideen et al. (2003).

2.4.4 Expected Progeny Differences

A total of 258 sires had estimated EPD. As can be seen from Table 2.5, the average EPD of the top and bottom 10 percent of sires for the respective traits differed significantly. There were 0.24% and 0.26% differences between top and bottom bulls for first-service conception rate and pregnancy rate, respectively. The top performance bulls
needed 0.24 less insemination than the worse performance bulls on average and they had 2.27 and 3.42 days less in GL and DC, respectively. The reliabilities of EPDs in fertility traits were low to moderate, which was mainly due to low heritabilities of the traits. However, the significant differences between top and bottom bulls suggested that significant genetic differences between sires is possible to detect overtime and that selection on fertility traits would be feasible.

2.4.5 Conclusions

Most reproductive performance (except GL) of multi-breed beef cattle were not affected by heterozygosity and breed composition. Because of the low heritabilities and repeatabilities of fertility traits, the improvement in reproduction of fertility traits based on selection may be slow, but it is essential because of economic value of these traits. Selection for better reproductive performance in crossbred beef cattle would be possible as indicated by significant differences in EPD among bulls. When performing genetic evaluation and selection, FSCR and PR can be treated as the same trait. When AI is not utilized in breeding system and breeding records for female fertility are limited, PR and DC should be the primary selection criteria. But when artificial insemination is utilized in herds, FSCR should be used as the primary criteria instead of PR.
2.5 TABLES

Table 2.1: The summary statistics of the final data set

<table>
<thead>
<tr>
<th>Trait</th>
<th>Number of animals</th>
<th>Number of records</th>
<th>Scale</th>
<th>Mean</th>
<th>SD</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>FSCR</td>
<td>1,369</td>
<td>3,863</td>
<td>0,1</td>
<td>0.72</td>
<td>0.45</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>PR</td>
<td>1,369</td>
<td>3,863</td>
<td>0,1</td>
<td>0.76</td>
<td>0.43</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>NS</td>
<td>1,369</td>
<td>3,863</td>
<td>1,2,3</td>
<td>1.35</td>
<td>0.58</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>GL</td>
<td>1,369</td>
<td>2,628</td>
<td>Day</td>
<td>282.20</td>
<td>5.29</td>
<td>262</td>
<td>302</td>
</tr>
<tr>
<td>DC</td>
<td>1,369</td>
<td>2,619</td>
<td>Day</td>
<td>299.40</td>
<td>23.05</td>
<td>256</td>
<td>388</td>
</tr>
</tbody>
</table>

\(^1\) FSCR = first-service conception rate; PR = pregnancy rate; NS = number of services per conception; GL = gestation length; DC = days-to-calving.
Table 2.2: Estimates of regression coefficient for heterozygosity and coefficient difference for breed proportion comparing with Angus

<table>
<thead>
<tr>
<th>Trait(^1)</th>
<th>Heterozygosity</th>
<th>Breed(^2)</th>
<th>AN</th>
<th>CH</th>
<th>SM</th>
<th>PI</th>
</tr>
</thead>
<tbody>
<tr>
<td>FSCR, %</td>
<td>-0.30</td>
<td>0</td>
<td>6.42</td>
<td>3.19</td>
<td>1.85</td>
<td></td>
</tr>
<tr>
<td>Prate, %</td>
<td>-0.13</td>
<td>0</td>
<td>-10.4</td>
<td>16.47</td>
<td>9.44</td>
<td></td>
</tr>
<tr>
<td>NS,</td>
<td>-0.30</td>
<td>0</td>
<td>6.83E-02</td>
<td>-2.75E-02</td>
<td>1.02E-02</td>
<td></td>
</tr>
<tr>
<td>GL, day</td>
<td>1.29(^*)</td>
<td>0</td>
<td>0.89</td>
<td>-0.21</td>
<td>0.47</td>
<td></td>
</tr>
<tr>
<td>DC, day</td>
<td>2.09</td>
<td>0</td>
<td>2.78</td>
<td>-0.57</td>
<td>2.69</td>
<td></td>
</tr>
</tbody>
</table>

\(^1\) FSCR = first-service conception rate; PR = pregnancy rate; NS = number of services per conception; GL = gestation length; DC = days-to-calving.

\(^2\) AN = Angus; CH = Charolaise; SM = Simmental; PI = Piedmontese.

\(^*\) Estimates are significantly different from 0 at P value < 0.05.
Table 2.3: Estimates of variance components, heritability ($h^2 \pm SE$) and repeatability ($r \pm SE$)

<table>
<thead>
<tr>
<th>Trait$^2$</th>
<th>Variance component$^1$</th>
<th>$h^2 \pm SE$</th>
<th>$r \pm SE$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\sigma_a^2$</td>
<td>$\sigma_{pe}^2$</td>
<td>$\sigma_s^2$</td>
</tr>
<tr>
<td>FSCR</td>
<td>1.37E-01</td>
<td>4.75E-02</td>
<td>3.13E-02</td>
</tr>
<tr>
<td>PR</td>
<td>1.61E-01</td>
<td>5.07E-08</td>
<td>2.17E-07</td>
</tr>
<tr>
<td>NS</td>
<td>1.73E-07</td>
<td>1.26E-01</td>
<td>-</td>
</tr>
<tr>
<td>GL</td>
<td>4.86E+00</td>
<td>8.44E-07</td>
<td>-</td>
</tr>
<tr>
<td>DC</td>
<td>2.08E+01</td>
<td>9.10E+00</td>
<td>-</td>
</tr>
</tbody>
</table>

$^1 \sigma_a^2 =$ direct additive genetic variance; $\sigma_{pe}^2 =$ permanent environmental variance; $\sigma_s^2 =$ first-service sire variance; $\sigma_e^2 =$ residual variance.

$^2$ FSCR = first-service conception rate; PR = pregnancy rate; NS = number of services per conception; GL = gestation length; DC = days-to-calving.
Table 2.4: Genetic ($r_g \pm SE$) and phenotypic ($r_p \pm SE$) correlation between reproductive traits$^1$;

<table>
<thead>
<tr>
<th>Trait 1</th>
<th>Trait 2</th>
<th>$r_g \pm SE$</th>
<th>$r_p \pm SE$</th>
<th>Scale$^2$ of trait 1</th>
<th>Scale of trait 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>FSCR</td>
<td>PR</td>
<td>0.99 $\pm$ 0.14**</td>
<td>0.54 $\pm$ 0.01**</td>
<td>B</td>
<td>L</td>
</tr>
<tr>
<td></td>
<td>NS</td>
<td>-0.95 $\pm$ 0.11**</td>
<td>-0.77 $\pm$ 0.02**</td>
<td>B</td>
<td>L</td>
</tr>
<tr>
<td></td>
<td>GL</td>
<td>-0.38 $\pm$ 0.22</td>
<td>-0.04 $\pm$ 0.02*</td>
<td>B</td>
<td>L</td>
</tr>
<tr>
<td></td>
<td>DC</td>
<td>-0.58 $\pm$ 0.32</td>
<td>-0.71 $\pm$ 0.01**</td>
<td>B</td>
<td>L</td>
</tr>
<tr>
<td>PR</td>
<td>FSCR</td>
<td>0.70 $\pm$ 1.08</td>
<td>0.41 $\pm$ 0.01**</td>
<td>B</td>
<td>L</td>
</tr>
<tr>
<td></td>
<td>NS</td>
<td>-0.98 $\pm$ 0.18**</td>
<td>-0.63 $\pm$ 0.01**</td>
<td>B</td>
<td>L</td>
</tr>
<tr>
<td></td>
<td>GL</td>
<td>-0.11 $\pm$ 0.29</td>
<td>0.09 $\pm$ 0.03**</td>
<td>B</td>
<td>L</td>
</tr>
<tr>
<td></td>
<td>DC</td>
<td>-0.22 $\pm$ 0.45</td>
<td>-0.17 $\pm$ 0.03**</td>
<td>B</td>
<td>L</td>
</tr>
<tr>
<td>NS</td>
<td>GL</td>
<td>0.28 $\pm$ 0.27</td>
<td>0.04 $\pm$ 0.02*</td>
<td>L</td>
<td>L</td>
</tr>
<tr>
<td></td>
<td>DC</td>
<td>0.60 $\pm$ 0.27*</td>
<td>0.77 $\pm$ 0.01**</td>
<td>L</td>
<td>L</td>
</tr>
<tr>
<td>DC</td>
<td>GL</td>
<td>0.75 $\pm$ 0.15**</td>
<td>0.32 $\pm$ 0.02**</td>
<td>L</td>
<td>L</td>
</tr>
</tbody>
</table>

$^1$ FSCR = first-service conception rate; PR = pregnancy rate; NS = number of services per conception; GL = Gestation length; DC = days-to-calving.

$^2$ Scale: B = binary scale; L = linear scale.

* Estimates are significantly different from 0 at P value < 0.05.

** Estimates are significantly different from 0 at P value < 0.01.
Table 2.5: Expected progeny difference (EPD) and corresponding reliability of the top and bottom 10% of bulls for fertility traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>Bulls</th>
<th>Number of bulls</th>
<th>Mean</th>
<th>Difference</th>
<th>Mean</th>
<th>SD</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>FSCR, %</td>
<td>Top</td>
<td>16</td>
<td>12.8</td>
<td>24.2*</td>
<td>0.20</td>
<td>0.07</td>
<td>0.10</td>
<td>0.37</td>
</tr>
<tr>
<td></td>
<td>Bottom</td>
<td>16</td>
<td>-11.4</td>
<td></td>
<td>0.19</td>
<td>0.06</td>
<td>0.11</td>
<td>0.31</td>
</tr>
<tr>
<td>PR, %</td>
<td>Top</td>
<td>19</td>
<td>13.4</td>
<td>25.6*</td>
<td>0.20</td>
<td>0.08</td>
<td>0.12</td>
<td>0.41</td>
</tr>
<tr>
<td></td>
<td>Bottom</td>
<td>19</td>
<td>-12.2</td>
<td></td>
<td>0.17</td>
<td>0.05</td>
<td>0.11</td>
<td>0.28</td>
</tr>
<tr>
<td>NS</td>
<td>Top</td>
<td>15</td>
<td>-0.12</td>
<td>-0.24*</td>
<td>0.18</td>
<td>0.08</td>
<td>0.10</td>
<td>0.40</td>
</tr>
<tr>
<td></td>
<td>Bottom</td>
<td>15</td>
<td>0.12</td>
<td></td>
<td>0.17</td>
<td>0.06</td>
<td>0.10</td>
<td>0.26</td>
</tr>
<tr>
<td>GL, day</td>
<td>Top</td>
<td>21</td>
<td>-1.14</td>
<td>-2.27*</td>
<td>0.41</td>
<td>0.13</td>
<td>0.22</td>
<td>0.72</td>
</tr>
<tr>
<td></td>
<td>Bottom</td>
<td>21</td>
<td>1.13</td>
<td></td>
<td>0.40</td>
<td>0.13</td>
<td>0.22</td>
<td>0.69</td>
</tr>
<tr>
<td>DC, day</td>
<td>Top</td>
<td>19</td>
<td>-1.82</td>
<td>-3.42*</td>
<td>0.25</td>
<td>0.10</td>
<td>0.11</td>
<td>0.50</td>
</tr>
<tr>
<td></td>
<td>Bottom</td>
<td>19</td>
<td>1.60</td>
<td></td>
<td>0.22</td>
<td>0.08</td>
<td>0.10</td>
<td>0.44</td>
</tr>
</tbody>
</table>

* Estimates are significantly different from 0 at P value < 0.01.

1 FSCR = first-service conception rate; PR = pregnancy rate; NS = number of services per conception; GL = gestation length; DC = days-to-calving.
Chapter 3: Genetic parameters of post weaning growth and efficiency traits in multi-breed beef cattle

3.1 ABSTRACT

Accurate genetic and phenotypic (co)variance component estimates are necessary to optimize selection response in post weaning growth and efficiency traits for growing multi-breed beef cattle in Canada. The main objective of this research was to determine the genetic parameters for average daily dry matter feed intake (DMI), average daily body weight gain (ADG), metabolic mid-test body weight (MMBW), feed conversion ratio (FCR) and Residual Feed Intake (RFI). Tested animals were originally from five herds and tested in one station. Each animal’s DMI was recorded daily, and individual body weight was measured every 28 days. The number of records per trait ranged from 1,514 (FCR) to 1,660 (ADG and DMI), with measures between 1996 and 2009. Main breed compositions were Angus, Simmental, Piedmontese and Charolais with average heterozygosity of 74 percent. Fixed effects of gender, birth contemporary group (herd × birth-year) and feed contemporary group (trial × treatment × year), covariance of age at the end of the test, heterozygosity and breed proportions, and the random effects of genetic and residual errors were modelled using ASREML. Heritability was estimated using univariate models, and genetic correlations were estimated using bivariate trait models. Heritability estimates for all traits were moderate to high from $0.21 \pm 0.05$ (FCR) to $0.88 \pm 0.08$ (MMBW). Strong genetic correlations were found between ADG and DMI ($0.92 \pm 0.03$), DMI and MMBW ($0.9 \pm 0.03$), DMI and RFI ($0.86 \pm 0.03$), and RFI and FCR ($0.88 \pm 0.05$). Genetic and phenotypic correlations for RFI with ADG and MMBW
were not significantly different from zero. This indicates that selection for RFI could be implemented to reduce feed intake without affecting animal growth.

**Key words:** beef cattle, feed intake, genetic parameter, residual feed intake

### 3.2 INTRODUCTION

In the beef industry, profitability of production is a function of revenues and costs. Feed is the largest variable cost in most livestock production enterprises (Arthur et al., 2004). Traditionally, the industry has focused on increased body weight and the associated final market weight to increase income, without taking higher feed requirements and costs into account. This led to lower net profits and, in turn, a proposal to improve feed efficiency. Feed conversion ratio (FCR), which is the ratio of feed intake and body weight gain, was commonly used to identify feed efficiency in beef cattle (Berry et al., 2009). Also, a net feed efficiency measurement (residual feed intake, RFI) was suggested for use in cattle (Koch et al. 1963), since approximately 65-75 percent of total dietary energy intake in beef cows is used only for body maintenance (Ferrell and Jenkins, 1985 and Montano- Bermudez et al., 1990). RFI is the difference between actual and predicted feed intake, and calculated by a multivariate linear regression with feed intake, average daily gain (ADG) and metabolic mid-test body weight (MMBW). The primary reason for developing RFI as a measure of feed efficiency was because it is phenotypically independent of body size and production (Koch et al., 1963), which is body weight gain. As a result, RFI has gained popularity as a measure of feed efficiency in beef cattle (Berry et al, 2009).
Measuring individual animal feed intake has been difficult and expensive (Arthur et al., 2001). Statistical analysis used for estimating genetic variance of feed intake was limited. Now that newer automatic feed intake measurement tools have been implemented and large datasets are becoming available it has provided the opportunity to calculate the (co)variance components accurately for feed intake and related feed efficiency traits. Generally, growth and feed efficiency traits have been reported as moderately heritable. However, most studies focused on beef bulls (Fan et al., 1995; Schenkel et al., 2004; Hoque et al., 2006; Crowley et al., 2010). In contrast, only a few have focused on either multi-breed young feedlot steers or heifers (steers, Nkrumah et al., 2007 and heifers, Lancaster et al., 2009). The objectives of this study were to determine the heritability of post weaning growth and efficiency traits in Canadian multi-breed beef herds, and estimate the phenotypic and genetic correlations among feed intake, growth and feed efficiency measurements.

### 3.3 MATERIALS AND METHODS

Data used in this study came from animals cared for under protocols approved by the University of Guelph Animal Care Committee, which follows the guidelines of the Canadian Council on Animal Care (Olfert et al., 1993)

#### 3.3.1 Data

Data were collected from animals born between 1996 and 2009. Animals were originated from five herds: the University of Guelph Elora Beef Research Centre
(EBRC), the University of Guelph New Liskeard Agriculture Research Station (NLARS), the Agriculture and Agri-Food Canada Kapuskasing Research Centre (KAP) and two cow-calf producers in Ontario, Canada. These herds were multi-breed, and the average breed proportions of these animals and heterozygosity of the total study group and of each herd are presented in Table 3.1. The average heterozygosity was 74 percent, and the major breeds were Angus (AN), Simmental (SM), Piedmontses (PI) and Charolais (CH). Animals were weaned at approximately 200 days of age. With both heifers and steers were brought to the EBRC for post-weaning nutrition trials.

Phenotypes were obtained from detailed studies of growth and feed intake during the post-weaning period. Animals were given a profile on either of two automated feeding system: Calan-gate (American Calan, Northwood, NH; Ferris et al., 2006) and Insentec (Insentec, Marknesse, the Netherlands; Chapinal et al., 2007) systems, which recorded individual feed intake every day. Feed was offered ad libitum throughout the test period, and feeders were filled daily in the morning. Animals were allowed to acclimatise to the facilities, feed and feeding system for 15 days before the start of the trial. Individual body weights were measured on average every 28 days during the test period. Evaluations were conducted for 112 days on average. There were 1to 2 test periods per year for feedlot animals, and there were different feed treatment within tests. Management and facilities remained constant within the year. In the case of replacement heifers and bulls, sex was confounded in trial-treatment. For feedlot steers and heifers some trial-treatment subclasses included both sexes.
3.3.2 Data Editing

ADG for each animal was calculated as the regression coefficient of a linear regression equation of body weight (BW) measurements on the test days using the “nlme” (Linear and Nonlinear Mixed Effects Models) package from R software. Mid-test BW (MBW) was the midpoint of the test in days and computed using the intercept and slope of the body weight linear regression equation.

Metabolic MBW was calculated as MBW to the 0.75 power. Average daily dry matter intake (DMI) was computed as the average of recorded daily dry matter intake during the test period. FCR was defined as average daily DMI divided by ADG. RFI was defined as the difference between actual DMI and the expected feed requirements based on maintenance and growth (Koch et al. 1963). The residual term of a multiple regression model with a random feeding contemporary group (CG) was calculated as follows:

\[ DMI = \beta_1 \times ADG + \beta_2 \times MMBW + CG + \text{residual} (RFI), \]

where \( \beta_1 \) is the partial regression associated with ADG; \( \beta_2 \) is the regression associated with MMBW, and residual is the estimates of RFI. The regression coefficient for ADG and MMBW in the study was 1.73 and 0.09, respectively. Animals with records that exceeded the overall mean \( \pm 3 \times \text{SD} \) of each trait were removed from the dataset. A total of 1600 animals with more than 1514 records of each trait were included. The number of animals in each herd is presented in Table 3.1. Animals were mainly from the NLARS and the EBRC.
3.3.3 Statistical Analysis

Estimates of heritability were obtained using univariate linear models; estimates of genetic and phenotypic correlations were obtained using bivariate models. All genetic models were fitted in ASReml (Gilmour et al., 2009). In the matrix notation, the basic model was

\[ \mathbf{y}_{ij} = \mu + \mathbf{x}_i \mathbf{b}_i + \mathbf{z}_j \mathbf{a}_j + \mathbf{e}_{ij}, \]

where \( \mathbf{Y} \) is a vector of the observations of the \( i^{th} \) trait of the \( j^{th} \) animal, \( \mu \) is the overall mean of the \( i^{th} \) trait, \( \mathbf{b} \) is a vector of all the fixed effects of trait \( i \), \( \mathbf{a} \) is the additive genetic effects of the \( j^{th} \) animal, \( \mathbf{e} \) is a vector of the random residual errors of the \( i^{th} \) trait of the \( j^{th} \) animal, \( \mathbf{X} \) and \( \mathbf{Z} \) are design matrices relating observations to corresponding effects.

Assumptions included:

\[ \text{E} (\mathbf{Y}) = \mu + \text{E} (\mathbf{b}); \]

\[ \mathbf{a} | \mathbf{A}, \sigma_a^2 \sim N (0, \mathbf{A} \sigma_a^2), \quad \mathbf{A} \] is an additive relationship matrix, \( \sigma_a^2 \) is an additive genetic variance;

\[ \mathbf{e} \sim N (0, \mathbf{I} \sigma_e^2), \text{ and } \sigma_e^2 \text{ are residual variances.} \]

A three-generation pedigree was used to create the additive relationship matrix. The complete pedigree included 2882 animals, including 287 sires and 997 dams. Fixed effects for each trait included factors of gender (steer, young bull, heifer and replacement heifer), birth contemporary group (birth-year \( \times \) birth-season \( \times \) birth-herd, \( n=70 \)), feeding contemporary group (trial \( \times \) treatment \( \times \) year, \( n = 84 \)), and covariates of heterozygosity (0 to 100, %), breed proportions (0 to 100, %) of AN, SM, PI, CH, and age of the animal at the end of test (412 ± 53 days). The additive genetic effect was included as a random
variable. Genetic models in bivariate models remained the same as in the univariate model. Breed difference tests were obtained using “Syslin” procedure in SAS 9.2. All breeds were compared with Angus (the major breed in these herds).

3.4 RESULTS AND DISCUSSION

Descriptive statistics for all traits are presented in Table 3.2, which includes 1600 animals with more than 1514 records of each trait. Phenotypic measurements for DMI were similar to previous studies on growing cattle (Nkrumah et al., 2007 and Lancaster et al., 2009). Compared to the reported ADG of purebred bulls by Crowley et al. (2010), the ADG of this population (1.72 kg/d) was similar to CH and SM, but higher than AN. The average FCR of the study population was lower than that of earlier studies (Schenkel et al., 2004; Nkrumah et al., 2007), which indicates a high efficiency performance. The SD of 0.88 for RFI in this population was similar to previous researches (Nkrumah et al., 2007; Lancaster et al., 2009).

Estimates of heritability, the significance (p value) of fixed effects, and the regression coefficient of covariates are presented in Table 3.3. In this study, growth and feed efficiency traits had a significant effect on the two CGs. Gender affected the feed and growth measurements but its effect on the efficiency measurements was not significantly different from zero. As shown in Table 3.3, significant (p < 0.05) differences were found between AN and PI for ADG and DMI at p < 0.05. Angus performed better on ADG, but PI had lower DMI measurements. There were no other significant breed differences. The estimate of regression coefficient for heterozygosity
was positive and significantly different from zero for RFI, which indicates that crossbreed animals are less feed efficient than purebred animals.

Heritability estimates for growth and feed efficiency traits from this study were moderate to high. Heritability estimates for ADG (0.36) were higher than those (0.21) of Brangus heifers reported by Lancaster et al. (2009) and those (0.26) of growing beef reported by Rolfe et al. (2011). However, they were consistent with those reported by Archer et al. (0.33; 2002), Schenkel et al. (0.35; 2004) and Crowley et al. (0.30; 2010).

Heritability estimates (0.54) for DMI from this study were a little higher than those (0.40) of bulls (Schenkel et al. 2004), but similar to recent estimates ranged from 0.40 to 0.49 (Schenkel et al., 2004; Lancaster et al., 2009; Crowley et al., 2010; Rolfe et al., 2011).

Heritability estimates for MMBW were greater than reported in other studies (0.71 and 0.69, Archer et al., 2002 and Crowley et al., 2010, respectively). Since animals brought to the feedlot started at similar body weights, this may be due to small residual errors.

Heritability estimates for FCR were lower than those in some earlier studies. Schenkel et al. (2004) reported 0.37 in purebred beef bulls, and Crowley et al. (2010) reported 0.30 in Irish beef bulls. However, it is consistent with the heritability estimated reported by Herd and Bishop (0.17, 2000), Hoque et al. (0.24, 2005), Hoque et al. (0.15, 2006), and Archer et al., (0.26, 2002).

Heritability estimates (0.40) for RFI is moderate. It is higher than the estimate of heritability reported by Archer et al. (0.23; 2002) and Hoque et al., (0.24; 2005).
However, it is consistent with the most of earlier heritabilities range from 0.38 to 0.47 (Arthur et al., 2001; Schenkel et al., 2004; Lancaster et al., 2009; Crowley et al., 2010).

3.4.1 Phenotypic and genetic correlations

Phenotypic and genetic correlations among feed intake, growth and feed efficiency measurements are presented in Table 3.4. Generally, DMI was highly correlated with growth measurements, indicating that the three traits can be evaluated simultaneously and that selection for any of them would lead to a correlated response in the other traits. The genetic correlation of 0.92 between ADG and DMI was similar with estimates reported by Nkrumah et al. (2007) and Rolfe et al. (2011). The strong genetic correlation of DMI and MMBW (0.90 ± 0.03) was greater than the estimates (0.41) measured in mature cows from the study by Archer et al. (2002). But it was similar with the correlation estimate measured in beef steers (Nkrumah et al., 2007). Phenotypically, the correlations among the three traits were moderate (r > 0.5) and quite similar to those reported by Archer et al. (2002) and Nkrumah et al. (2007). Although the genetic correlations between feed and growth measurements were quite high, they were still different traits, and sufficient independence of traits exists for selection for animals that consume less feed to attain the same growth targets.

The genetic and phenotypic correlation estimates between FCR and ADG were negatively strong and quite similar (r_g = -0.62; r_p = -0.66) to earlier studies (Arthur et al., 2001; Schenkel et al., 2004). Further, the phenotypic correlation estimated for FCR and DMI was positive (0.22 ± 0.03), which is consistent with expectations because of the definition of FCR (FCR = DMI/ADG). However, the genetic correlation between the two
was estimated as negative (-0.27 ± 0.12), which differs from the study by Nkrumah et al. (2007) but is consistent with the correlations estimated by Archer et al. (2002). This finding might due to the strong and positive genetic correlations between ADG and DMI. This result indicates that selection for FCR would increase both ADG and DMI, but ADG relatively more so.

RFI was highly genetically correlated with DMI (r_g = 0.86), which is consistent with earlier studies by Schenkel et al. (2004) and Nkrumah et al. (2007). As expected, the phenotypic correlation of RFI between ADG and MMBW was not significantly different from zero. This finding is consistent with earlier studies (Lancaster et al., 2009; Herd and Bishop, 2000 and Rolfe et al., 2011). In this study, the genetic correlations between RFI and ADG, RFI and MMBW were not significantly different from zero. There were some genetic correlations reported between RFI and ADG (0.15 ± 0.27, Rolfe et al., 2011), and between RFI and MMBW (0.22 ± 0.27, Herd and Bishop, 2000). However, due to the large standard deviation of the estimates, the correlations should not be considered as significantly different from zero. Arthur et al. (2005) found that low RFI (more efficient) cows were heavier than high RFI cows, less efficient counterparts; however, the difference was not significant. Moreover, other correlation estimates were also close to zero (Lancaster et al., 2009). These correlations indicate that selection for RFI would reduce DMI significantly with no negative response on growth.

Strong genetic (r = 0.88) and moderate phenotypic (r = 0.58) correlation estimates were found for FCR and RFI. Nkrumah et al. (2007) reported similar correlations. The positive correlation suggests that selection for either feed efficiency trait might rank of animals quite similarly.
3.4.2 Conclusion

The moderate to high heritability estimates obtained in this study suggest that genetic gain may be obtained by selecting for growth and feed efficiency traits. The genetic correlation estimates for feed intake and growth traits with FCR and RFI indicate that RFI will enable a reduction in feed consumption while maintaining growth rate. Since RFI and FCR were highly correlated, selection in RFI will also result in a strong response in FCR as well.
3.5 TABLES

Table 3.1: Average heterozygosity (%) and breed proportions (%) of the total study group and of each herd

<table>
<thead>
<tr>
<th>Herd</th>
<th>Number of animals</th>
<th>Heterozygosity</th>
<th>Breed</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>AN</td>
</tr>
<tr>
<td>KAP</td>
<td>117</td>
<td>59.97</td>
<td>28.50</td>
</tr>
<tr>
<td>NLARS</td>
<td>627</td>
<td>70.04</td>
<td>52.31</td>
</tr>
<tr>
<td>EBRC</td>
<td>714</td>
<td>79.85</td>
<td>40.94</td>
</tr>
<tr>
<td>Comm1</td>
<td>154</td>
<td>75.13</td>
<td>50.95</td>
</tr>
<tr>
<td>Comm2</td>
<td>48</td>
<td>83.20</td>
<td>54.82</td>
</tr>
<tr>
<td>Total</td>
<td>1,660</td>
<td>74.40</td>
<td>45.69</td>
</tr>
</tbody>
</table>

1 KAP = Agriculture and Agri-Food Canada Kapuskasing Research Centre; NLARS = University of Guelph New Liskeard Agriculture Research Station; EBRC = the University of Guelph Elora Beef Research Centre; Comm1 and Comm2 = two commercial herds from Ontario.

2 AN = Angus; SM = Simmental; PI = Piedmontese; CH = Charolais.
Table 3. 2: Summary of post weaning growth and efficiency measurements

<table>
<thead>
<tr>
<th>Trait</th>
<th>Number of animals</th>
<th>Mean</th>
<th>SD</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADG, kg/d</td>
<td>1,660</td>
<td>1.73</td>
<td>0.42</td>
<td>0.48</td>
<td>2.91</td>
</tr>
<tr>
<td>DMI, kg/d</td>
<td>1,660</td>
<td>9.90</td>
<td>1.70</td>
<td>4.89</td>
<td>14.96</td>
</tr>
<tr>
<td>MMBW, kg²</td>
<td>1,646</td>
<td>96.64</td>
<td>13.34</td>
<td>57.08</td>
<td>136.27</td>
</tr>
<tr>
<td>FCR</td>
<td>1,514</td>
<td>5.56</td>
<td>1.17</td>
<td>2.63</td>
<td>9.08</td>
</tr>
<tr>
<td>RFI, kg/d</td>
<td>1,620</td>
<td>-0.01</td>
<td>0.88</td>
<td>-2.64</td>
<td>2.66</td>
</tr>
</tbody>
</table>

¹ ADG = average daily gain; DMI = average daily dry matter intake; MMBW = metabolic mid-test BW; FCR = feed conversion ratio; RFI = residual feed intake.
Table 3. 3: Heritability, P-value of fixed effects, estimated regression coefficient of AET and heterozygosity, and the coefficient differences for breed proportion when comparing with Angus

<table>
<thead>
<tr>
<th>Item</th>
<th>ADG, kg/d</th>
<th>DMI, kg/d</th>
<th>FCR</th>
<th>MMBW, kg</th>
<th>RFI, kg/d</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heritability</td>
<td>0.36 ± 0.05</td>
<td>0.54 ± 0.05</td>
<td>0.21 ± 0.05</td>
<td>0.89 ± 0.01</td>
<td>0.40 ± 0.06</td>
</tr>
<tr>
<td>Gender</td>
<td>0.03</td>
<td>0.05</td>
<td>0.61</td>
<td>0.05</td>
<td>0.37</td>
</tr>
<tr>
<td>Birth CG</td>
<td>0.01</td>
<td>&lt;.001</td>
<td>0.02</td>
<td>&lt;.001</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>Feeding CG</td>
<td>&lt;.001</td>
<td>&lt;.001</td>
<td>&lt;.001</td>
<td>&lt;.001</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>AET, d</td>
<td>8.38E-03**</td>
<td>8.79E-04**</td>
<td>5.36E-03**</td>
<td>1.63E-03**</td>
<td>1.45E-01**</td>
</tr>
<tr>
<td>H</td>
<td>1.56E-03</td>
<td>5.72E-04</td>
<td>-1.43E-03</td>
<td>1.37E-03</td>
<td>-2.61E-02</td>
</tr>
<tr>
<td>AN</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>SM</td>
<td>-9.30E-05</td>
<td>3.31E-04</td>
<td>1.45E-03</td>
<td>1.53E-04</td>
<td>-1.40E-04</td>
</tr>
<tr>
<td>PI</td>
<td>-7.73E-04**</td>
<td>-1.64E-03**</td>
<td>1.38E-03</td>
<td>-2.87E-03</td>
<td>-3.20E-04</td>
</tr>
<tr>
<td>CH</td>
<td>1.90E-05</td>
<td>1.27E-03</td>
<td>8.70E-04</td>
<td>3.50E-03</td>
<td>-5.50E-04</td>
</tr>
</tbody>
</table>

1 DMI = average daily dry matter intake; ADG = average daily gain; MMBW = metabolic mid-test BW; FCR = feed conversion ratio; RFI = residual feed intake.

2 Birth CG = Birth contemporary group of herd and birth year; Feeding CG = feeding contemporary group of trial × treatment × year; AET = age at the end of the test; H = heterozygosity.

* Estimates are significantly different from 0 at P value < 0.05.
** Estimates are significantly different from 0 at P value < 0.01.
Table 3.4: Genetic (above diagonal, $r_g \pm SE$) and phenotypic correlations (below diagonal, $r_p \pm SE$) among growth and efficiency traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>ADG</th>
<th>DMI</th>
<th>MMBW</th>
<th>FCR</th>
<th>RFI</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADG</td>
<td>0.92 ± 0.03</td>
<td>0.5 ± 0.04</td>
<td>-0.62 ± 0.1</td>
<td>-0.02 ± 0.11</td>
<td></td>
</tr>
<tr>
<td>DMI</td>
<td>0.52 ± 0.02</td>
<td>0.9 ± 0.03</td>
<td>-0.27 ± 0.12</td>
<td>0.86 ± 0.03</td>
<td></td>
</tr>
<tr>
<td>MMBW</td>
<td>0.49 ± 0.02</td>
<td>0.63 ± 0.02</td>
<td>0.37 ± 0.09</td>
<td>0.03 ± 0.06</td>
<td></td>
</tr>
<tr>
<td>FCR</td>
<td>-0.66 ± 0.02</td>
<td>0.22 ± 0.03</td>
<td>-0.01 ± 0.03</td>
<td>0.88 ± 0.05</td>
<td></td>
</tr>
<tr>
<td>RFI</td>
<td>-0.04 ± 0.03</td>
<td>0.71 ± 0.01</td>
<td>0.01 ± 0.03</td>
<td>0.58 ± 0.02</td>
<td></td>
</tr>
</tbody>
</table>

$^1$ADG = average daily gain; DMI = average daily dry matter intake; MMBW = metabolic mid-test BW; FCR = feed conversion ratio; RFI = residual feed intake.
Chapter 4: Genetic correlations between female fertility and post weaning growth and efficient traits of growing animals in multi-breed beef herds

4.1 ABSTRACT

Few studies have been done on the genetic relationship between fertility and post weaning traits, consequently, the purpose of this study was to estimate genetic correlations between female fertility and post weaning growth and efficiency measurements for multi-breed beef cattle in Canada. Animals in this study were kept on two Ontario beef research farms. Fertility data was collected between 2002 and 2011. The study was interested in the following traits: first-service conception rate (FSCR), pregnancy rate (PR), number of services per conception (NS), gestation length (GL) and days-to-calving (DC). Feed efficiency and growth measurements—average daily dry matter intake (DMI), average daily weight gain (ADG), metabolic mid-test body weight (MMBW), feed conversion ratio (FCR) and residual feed intake (RFI) measurements were collected between 1996 and 2009. A three-generation pedigree was included to estimate genetic relationships. Fixed effects of breeding contemporary group (herd × year × breeding season), age of animals and estrus treatment were fitted for fertility traits. Fixed effects of birth contemporary group (herd × birth year), feeding contemporary group (trial × treatment × year), gender and age at the end of the test were included in post weaning trait models. Covariates of heterozygosity and breed proportions were included for all traits. Additive genetic effect and residual error were included as random effects. Heritability was estimated by using univariate models. Phenotypic and genetic
correlations between each pair of traits were estimated using bivariate models. All models were fit in ASReml. Estimates of heritability for fertility traits were low to moderate from 0.03 ± 0.01 (PR) to 0.21 ± 0.02 (GL). However, growth and efficient traits were moderate to high heritable in this study. DMI and MMBW were correlated with most fertility traits from -0.52 to 0.34. ADG was only related with DC (-0.33 ± 0.16). RFI was negatively correlated with DC (-0.34 ± 0.17). In conclusion, bigger cows with more feed intake and faster growth rate are more fertile, and RFI has a significantly unfavourable correlation with DC.

**Key words:** beef, feed efficiency, fertility, genetic correlation

### 4.2 INTRODUCTION

A large number of studies have been done to evaluate possible improvements to the commercial performance of beef cattle—a sector that would benefit from greater productivity and profitability, especially since feed is the largest cost for growing animals (Arthur et al., 2005) and market weight determines the final price of each animal. Genetic evaluation and selection are one of the potential methods used to improve animal performance (Arthur et al., 1999; Weigel, 2006).

Feed conversion ratio (FCR) and residual feed intake (RFI) are commonly used to study feed efficiency in beef cattle (Koch et al. 1963; Berry et al., 2008). Although the concept of measuring feed efficiency has been around for some time, it is only in the past decade or so that genetic evaluations have been available to make significant progress for this trait (Archer et al., 1999). Also electronic equipment has been advancing making it
more feasible to measure intake on farm and on breeding candidates, such as GrowSafe System (Basarab et al., 2002). Genomic predictions will further expand the scope of genetic information for efficiency traits making selection pressure for this trait more possible than ever before (Pryce et al., 2012) With this increased selection pressure on efficiency it is very important that resulting changes expected in correlated traits are well understood.

Female fertility is another trait of economic importance and its relationship with feed efficiency needs to be better understood. Generally, fertility is reported as having low heritability (Rust et al., 2001 and Jamrozik et al., 2012), but improving this trait may provide four times more economic return than improving end-product traits (Melton, 1995). As a result, fertility is an important component of animal evaluation and selection.

Genetic parameters for feed efficiency and female fertility have been studied before, however, few studies have attempted to quantify the genetic relationship between the two (Arthur et al., 2005; Basarab et al., 2007). In order to understand feed efficiency performance, the efficiency traits of FCR and RFI, growth traits of average daily body weight gain (ADG) and metabolic mid-test body weight (MMBW), as well as average daily dry matter intake (DMI) were included in this study. First-service conception rate (FSCR), pregnancy rate (PR), number of services per conception (NS), gestation length (GL) and days-to-calving (DC) were measured to study female fertility. The main objective of this study was to determine the genetic and phenotypic correlations between female fertility and the feed efficiency of growing animals in multi-breed beef herds in order to quantify how improvements may affect one or the other in terms of genetic evaluation and selection.
4.3 MATERIALS AND METHODS

Data used in this study came from animals cared for under protocols approved by the University of Guelph Animal Care Committee, which follows the guidelines of the Canadian Council on Animal Care (Olfert et al., 1993)

4.3.1 Animals and Management

Animals originated from two University of Guelph research farms: the Elora Beef Research Centre (EBRC) and the New Liskeard Agriculture Research Station (NLARS). The two herds were multi-breed with main breed compositions of Angus, Simmental, Piedmontese and Charolais. The breed proportions for these herds are presented in Table 4.1.

In the two herds, females were mated through artificial insemination. In each breeding season, 10-55% of frozen semen was collected from bulls that were raised by the two herds and others were purchased from breeding companies. Approximately 180 and 225 females were bred at the EBRC and NLARS respectively, each year. The EBRC runs one breeding season/year, when artificial insemination follows the natural estrus of each female. Teaser bulls were used for heat detection to determine the best time for breeding. However, the inseminations in NLARS followed estrus synchronization (ES) within two breeding seasons/year. From 2003 to 2006, two ES treatment (T1 and T2) were utilized for the first insemination in each breeding season. After 2007, there was only one treatment (T3) was used for ES. In each breeding season, females received
CIDR insert first (day 0) and removed CIDR after 7 days (day 7). Artificial insemination was applied after two days (day 9) of CIDR remove. In T1, Estradiol Benzoate (EB) was injected to females at day 0, Prostaglandin F2alpha (PGF2α, Lutalyse®) was injected at day 7, and Estradiol Benzoate was injected again at day 8. In T2, Gonadotropin-releasing hormone (GnRH, Cystorelin®) was used instead of EB at day 0, and PGF2α was used at day 7. In treatment 3, GnRH was injected at day 0 and day 9 and PGF2α injection was placed at day 7. Every year, approximately 130 calves are born at the EBRC, and 150 at the NLARS. Calves stayed with their dam until weaned at approximately 200 days of age. Calves from the NLARS were brought to the EBRC for various post-weaning nutrition trials.

Animals were given a profile on two automated feeding system: Calan-gate (American Calan, Northwood, NH; Ferris et al., 2006) and Insentec (Insentec, Marknesse, the Netherlands; Chapinal et al., 2007) systems, which recorded individual feed intake every day. Feed was offered ad libitum throughout the test period, and feeders were filled daily in the morning. Animals were transferred to feedlot after weaning, and they were allowed to acclimatise to the facilities, feed and feeding system for 15 days before the start of the trial. Each animal’s intake was measured daily, and body weights were measured every 28 days during the test. The test lasted approximately 112 days.

4.3.2 Data

Data for fertility traits were collected from 2002 to 2011. A total of 1469 females had fertility records on insemination date, pregnancy check results and calving dates. FSCR and PR were determined according to records of pregnancy checks, using 1 and 0
to indicate pregnant or not. NS was classified into three grades: 1 and 2 indicating pregnancy after the first or second insemination, and 3 indicated failure after two inseminations. Some EBRC animals became pregnant at the 3rd or 4th insemination, but these were still recorded as 3 to combine data from both herds as the NLARS data included only 2 inseminations per female per year. GL was computed as the period between the last insemination date and the calving date. Days-to-calving was defined as the interval between the first insemination date of the entire group and the calving date of each female. Records of females older than 12 years were removed. Records of GL (16) and DC (28) were removed if they exceeded 3 standard deviation (SD) from their respective CG means. 2,619 to 3,863 records of each trait were analyzed.

Data for post weaning traits were collected from all growing animals recorded between 1996 and 2011. Average daily DMI was computed as the average of recorded daily dry matter intake during the test period. ADG for each animal was calculated as the linear regression coefficient from a regression of body weight (BW) measurements on day on test. MBW was computed by the intercept and slope of the BW linear regression equation multiplied by ½ the number of days on test for that group. Metabolic mid-test body weight was determined as MBW raised the power if 0.75. FCR was calculated as the ratio of ADG and DMI. RFI was defined as the difference between actual DMI and the expected DMI based on maintenance and growth (Koch et al. 1963). RFI was calculated as the residual term of a multiple regression model as follows:

\[ DMI = \beta_1 \times ADG + \beta_2 \times MMBW + CG + \text{residual (RFI)}, \]

where \( \beta_1 \) is the partial regression coefficient associated with ADG; \( \beta_2 \) is the regression coefficient associated with MMBW, and residual term is the estimate of RFI. CG refers
to feeding contemporary groups (trial × treatment × year). Animals (363) with records that exceeded the overall mean ± 3SD of any trait were removed from the dataset. A total of 1297 animals were included for study post weaning traits. Descriptive statistics for all measurements are presented in Table 4.2.

### 4.3.3 Statistical Analysis

Estimates of heritability were obtained using univariate linear models. Phenotypic and genotypic correlations between fertility and post weaning traits were estimated using bivariate models. All genetic models were fit in ASReml 3.0 (Gilmour et al., 2009). The single mixed model for each trait was:

\[ Y = \mu + Xb + Za + e, \]

where \( Y \) is a vector of the observations of the estimated trait, \( \mu \) is the overall mean of the trait, \( b \) is a vector of fixed effects, \( a \) is a vector of the additive genetic effects, \( e \) is a vector of random residual errors, and \( X \) and \( Z \) are design matrices for fixed and random effects, respectively. Assumptions of the single linear model were: \( E(Y) = \mu + E(b); a \sim N(0, A\sigma^2_a) \), where \( A \) is the genetic relationship matrix and \( \sigma^2_a \) is the additive genetic variance; and \( e \sim N(0, I\sigma^2_e) \) and \( \sigma^2_e \) are residual variances.

A total of 2882 animals with a three-generation pedigree were included and 270 of them had both fertility and post weaning phenotypes. Fitted fixed effects for fertility traits were: breeding CG (combinations of herd, breeding year and breeding season, \( n = 24 \)), age of animal (from 1 to 12) and estrus treatment (natural estrus or different estrus synchronization treatments, \( n = 10 \)). Fixed effects of birth CG (combinations of herd and birth year, \( n = 34 \)), feeding CG (trial × treatment × year, \( n = 138 \)) and gender (male or
female) were included for post weaning traits. Covariates for post weaning traits included: age at the end of the test (days), heterozygosity (%) and breed proportions (%). Additive genetic effect and residual errors were included as random variables in all models. Models used in bivariate analyses remained the same as in the univariate model.

4.4 RESULTS AND DISCUSSION

The genetic parameters of each fertility trait are shown in Table 4.3. Heritability estimates of fertility traits were low to moderate from 0.03 to 0.21 in this study. This is consistent with two recent reviews on fertility performance (Rust et al., 2001 and Cammack et al., 2009). The low estimates of heritability for FSCR (0.04 ± 0.01) and PR (0.03 ± 0.01) were consistent with estimates by Toelle and Robison (0.06; 1985), Morris et al. (0.04; 1994) and Minick et al. (0.03; 2006). Meyer et al. (1990) reported a heritability of 0.05 for NS, which is similar to that in this study. The heritability estimate for GL in this study (0.21 ± 0.02) was slightly lower than those in most other studies (0.30 to 0.48, Burfening et al., 1978; MacNeil et al., 1984, Wray et al., 1987; Cervantes et al., 2010). Heritability for DC was in the range of that reported in the literature (0.04 to 0.11, Meyer et al., 1990; Johnston et al., 1996; Donoghue et al., 2004; Jamrozik et al., 2012). In summary, the magnitude of these heritability estimates indicated that female reproduction could be improved by selection, but progress would be limited because of these low heritabilities.

Generally, heritability estimates for growth and feed efficiency traits were moderate. This finding indicates the existence of important genetic components for growth feed efficiency traits that may have a significant response to selection.
Heritability estimate for ADG in this study (0.46 ± 0.05) was greater than that for Brangus heifers (0.21, Lancaster et al., 2009) and that of growing beef (0.26, Rolfe et al., 2011). However, it was consistent with those reported by Archer et al. (0.33; 2002), Schenkel et al. (0.35; 2004) and Crowley et al. (0.30; 2010).

Heritability estimates for DMI (0.52 ± 0.05) and RFI (0.37 ± 0.06) in this study were similar to those reported in most studies, with estimates ranging from 0.47 to 0.54 (Nkrumah et al., 2007; Crowley et al., 2010; Lancaster et al., 2009; Rolfe et al., 2011) and from 0.33 to 0.44 (Archer et al., 2002; Koots et al., 2004; Schenkel et al., 2004; Crowley et al., 2010), respectively.

Estimate of heritability for FCR was 0.22 ± 0.06 in this study. It is lower than previous heritability estimates reported by Crowley et al. (0.30; 2010) and Rolfe et al. (0.35; 2011). However, it is consistent with Herd and Bishop (0.17; 2000), Archer et al., (0.26; 2002) and Hoque et al. (0.24; 2005). All these heritability estimates indicated that FCR is a moderate heritable trait.

Heritability estimates (0.89 ± 0.01) for MMBW were greater than previously reported (0.69 and 0.71, Archer et al., 2002; Crowley et al., 2010). Since animals brought to the feedlot started at similar body weight, this may due to small residual errors.

4.4.1 Fertility and growth

Genetic correlations for fertility traits with growth and feed efficiency traits are detailed in Table 4.4. ADG was moderately correlated with DC at -0.33 ± 0.16. MMBW was moderately correlated with FSCR at 0.39 ± 0.14. While genetic correlation estimates for MMBW with NS and DC were negative at -0.42 ± 0.14 and -0.51 ± 0.12, respectively,
indicating that higher MMBW was related to better fertility. Phenotypic correlations for fertility traits with ADG and MMBW were consistent with but smaller than their corresponding genetic correlations. This was mainly due to low heritability and associated environmental variance estimates for fertility traits.

The genetic correlations between growth and female fertility traits indicate a favourable relationship between breeding values for growth and fertility. MacNeil et al. (1984) found a favourable genetic correlation of 0.21 between carcass fat and conception rate. Santana et al. (2012) reported a positive genetic correlation (0.20) between post-weaning gain and heifer pregnancy for Nellore cattle. These estimates indicate that bigger cows are more fertile. In the past decades, bigger cows are considering as less efficient because bigger cows will eat more than others. However, if bigger cows are more likely to perform better in fertility, more feed intake may be valuable. Improvement of growth and reproductive traits would not negatively affect the other.

4.4.2 DMI, RFI and fertility

As can be seen in Table 4.4, there are definite genetic correlations between DMI and fertility traits. DMI was moderately correlated with DC (-0.52 ± 0.14), which indicated that a cow with more feed intake would have a shorter DC. Crowley et al. (2011) also reported negative correlation estimates for DMI between age at first calving and calving to first-service (similar with DC in the research) at -0.23 ± 0.14 and -0.18 ± 0.20, respectively. The genetic correlation estimates for DMI with NS and GL in this study were negative but not significantly different from zero. Overall, better fertility performance was correlated with higher feed intake. This may be because well fed:
heavier animals have more energy balance to devote to superior fertility (Crowley et al., 2011). Besides, due to the high and positive genetic correlations between DMI and MMBW reported previously (Archer et al., 2002; Nkrumah et al., 2007) and the significant genetic correlations estimated between MMBW and fertility traits from this and earlier studies, the genetic correlations estimated between DMI and fertility traits in this study can be considered reliable. Therefore, selection of sires for improving female fertility could lead to larger females with a relative increase in feed intake.

As can be seen in Table 4.4, RFI was significantly negative correlated with DC but other fertility traits. The non-significant genetic correlation between RFI and PR is consistent with a study published by Arthur et al. (2005). In that study, selection was based on low and high RFI, with no significant difference in pregnancy (calving/weaning) rate after an average of 1.5 generations of selection detected. Shaffer et al. (2011) classified RFI into two and three groups to study differences in fertility, and found only age at puberty had significantly difference between positive and negative RFI groups with -13 days difference. The difference indicated that selecting on RFI will delay the puberty of heifer. An unfavorable genetic correlation (-0.37 ± 0.17) was found between RFI and DC in this study. Of the fertility traits studied, DC was the most heritable and could be seen as the best predictor of female fertility from these data. This negative relationship between RFI and DC is consistent with earlier research (Arthur et al., 2005; Crowley et al., 2011). Arthur et al. (2005) found that selection for low RFI would lead to a significant delay of five extra days for calving than selection for high RFI. Crowley et al. (2011) reported negative genetic correlations for RFI between age at first calving and calving to first-service (similar with DC in the research) at -0.29 ± 0.14 and -0.03 ± 0.20,
respectively. The unfavorable genetic correlation between DC and RFI may be due to energy being partitioned toward growth and away from body reserves and other pathways that may affect fertility in animals with better RFI. This suggests that selection for RFI or DC alone without considering the genetic correlations between them will, over time, lead to an unfavorable response for the other trait.

4.4.3 FCR and fertility

Genetic and phenotypic correlations between FCR and fertility traits are detailed in Table 4.4. The genetic correlation estimates ranged from -0.24 to -0.01. However, all of them were not significantly different from zero. This indicates that selection for feed efficiency that based on FCR will not influence fertility performance significantly. In this aspect, selection for FCR will have less unfavorable correlated responses in fertility traits than selection for RFI directly. This is due to the fact that fertility was associated favorable with higher growth and size and unfavorable with DMI, which in combination presents a net zero effect between FCR and fertility traits.

4.4.4 Conclusion

According to the heritability estimates obtained in this study, selection for fertility and feed efficiency traits are feasible. Both groups of traits have the potential to be used as selection criteria in breeding programs for beef cattle. The moderate heritability estimate of days-to-calving and moderate correlations for DC between feed efficiency traits found in this study are showing the potential of this trait in a breeding program. In this study, bigger and faster growing cattle are related with better fertility performance
genetically. Unfortunately, improving RFI could be at the detriment of DC due to their negative genetic correlation found in this and previous researches. Therefore, selection for fertility and efficiency should be done together to be sure that the most profitable cattle are selected for overall.
4.5 TABLES

Table 4. 1: Summary information about animals from the EBRC\textsuperscript{1} and NLARS\textsuperscript{2} herds

<table>
<thead>
<tr>
<th>Item</th>
<th>EBRC</th>
<th>NLARS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of animals</td>
<td>1,133</td>
<td>1,260</td>
</tr>
<tr>
<td>Number of animals with Fertility records</td>
<td>614</td>
<td>752</td>
</tr>
<tr>
<td>Number of animals with Post weaning records</td>
<td>519</td>
<td>774</td>
</tr>
<tr>
<td>Number of animals With both records</td>
<td>0</td>
<td>266</td>
</tr>
<tr>
<td>Heterozygosity, %</td>
<td>74.14</td>
<td>70.65</td>
</tr>
<tr>
<td>Angus, %</td>
<td>38.76</td>
<td>53.25</td>
</tr>
<tr>
<td>Simmental, %</td>
<td>26.43</td>
<td>24.29</td>
</tr>
<tr>
<td>Charolais, %</td>
<td>3.96</td>
<td>5.88</td>
</tr>
<tr>
<td>Piedmontese, %</td>
<td>17.12</td>
<td>0.63</td>
</tr>
</tbody>
</table>

\textsuperscript{1} The University of Guelph Elora Beef Research Centre.

\textsuperscript{2} The University of Guelph New Liskeard Agriculture Research Station.
Table 4. 2: Descriptive statistics of fertility and post weaning traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>Number of records</th>
<th>Mean</th>
<th>SD</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>FSCR</td>
<td>3,863</td>
<td>0.58</td>
<td>0.49</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>PR</td>
<td>3,863</td>
<td>0.76</td>
<td>0.43</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>NS</td>
<td>3,863</td>
<td>1.59</td>
<td>0.79</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>GL, day</td>
<td>2,628</td>
<td>282.17</td>
<td>5.30</td>
<td>262</td>
<td>302</td>
</tr>
<tr>
<td>DC, day</td>
<td>2,619</td>
<td>299.29</td>
<td>21.44</td>
<td>247</td>
<td>394</td>
</tr>
<tr>
<td>ADG, kg/d</td>
<td>1,297</td>
<td>1.68</td>
<td>0.43</td>
<td>0.58</td>
<td>2.91</td>
</tr>
<tr>
<td>DMI, kg/d</td>
<td>1,297</td>
<td>9.64</td>
<td>1.75</td>
<td>4.89</td>
<td>14.96</td>
</tr>
<tr>
<td>MMBW, kg</td>
<td>1,297</td>
<td>95.59</td>
<td>13.25</td>
<td>62.94</td>
<td>133.86</td>
</tr>
<tr>
<td>FCR</td>
<td>1,297</td>
<td>5.79</td>
<td>1.25</td>
<td>2.63</td>
<td>9.01</td>
</tr>
<tr>
<td>RFI, kg/d</td>
<td>1,297</td>
<td>-0.04</td>
<td>0.84</td>
<td>-2.64</td>
<td>2.43</td>
</tr>
</tbody>
</table>

1FSCR = first-service conception rate; PR = pregnancy rate; NS = number of services per conception; GL = gestation length; DC = days-to-calving; DMI = average daily dry matter intake; ADG = average daily gain; MMBW = metabolic mid-test BW; FCR = feed conversion ratio; RFI = residual feed intake.
Table 4.3: Variance components$^1$ and heritability estimates ($h^2$) of fertility and postweaning traits

<table>
<thead>
<tr>
<th>Trait$^2$</th>
<th>$\sigma^2_{genetic}$</th>
<th>$\sigma^2_{error}$</th>
<th>$h^2 \pm SE$</th>
</tr>
</thead>
<tbody>
<tr>
<td>FSCR</td>
<td>1.03E-02</td>
<td>2.29E-01</td>
<td>0.04 ± 0.01</td>
</tr>
<tr>
<td>PR</td>
<td>4.69E-03</td>
<td>1.74E-01</td>
<td>0.03 ± 0.01</td>
</tr>
<tr>
<td>NS</td>
<td>2.63E-02</td>
<td>5.67E-01</td>
<td>0.04 ± 0.01</td>
</tr>
<tr>
<td>GL</td>
<td>4.93E+00</td>
<td>1.85E+01</td>
<td>0.21 ± 0.02</td>
</tr>
<tr>
<td>DC</td>
<td>2.74E+01</td>
<td>2.78E+02</td>
<td>0.09 ± 0.02</td>
</tr>
<tr>
<td>DMI</td>
<td>6.81E-01</td>
<td>6.30E-01</td>
<td>0.52 ± 0.05</td>
</tr>
<tr>
<td>ADG</td>
<td>3.51E-02</td>
<td>4.06E-02</td>
<td>0.46 ± 0.05</td>
</tr>
<tr>
<td>MMBW</td>
<td>5.53E+01</td>
<td>6.66E+00</td>
<td>0.89 ± 0.01</td>
</tr>
<tr>
<td>FCR</td>
<td>1.27E-01</td>
<td>4.48E-01</td>
<td>0.22 ± 0.06</td>
</tr>
<tr>
<td>RFI</td>
<td>2.14E-01</td>
<td>3.69E-01</td>
<td>0.37 ± 0.06</td>
</tr>
</tbody>
</table>

$^1\sigma^2_{genetic} = \text{variance of additive genetic effects}; \ \sigma^2_{error} = \text{residual variance.}$

$^2\text{FSCR = first-service conception rate; PR = pregnancy rate; NS = number of services per conception; GL = gestation length; DC = days-to-calving; DMI = average daily dry matter intake; ADG = average daily gain; MMBW = metabolic mid-test BW; FCR = feed conversion ratio; RFI = residual feed intake.}$
Table 4.4: Genetic (r_g ± SE) and phenotypic (r_p ± SE) correlations between fertility and post weaning traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>ADG</th>
<th>DMI</th>
<th>FCR</th>
<th>MMBW</th>
<th>RFI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phenotypic correlations</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FSCR</td>
<td>0.01 ± 0.03</td>
<td>0.03 ± 0.03</td>
<td>0.00 ± 0.02</td>
<td>0.08 ± 0.03</td>
<td>0.00 ± 0.03</td>
</tr>
<tr>
<td>PR</td>
<td>-0.02 ± 0.03</td>
<td>-0.01 ± 0.03</td>
<td>-0.02 ± 0.02</td>
<td>0.03 ± 0.03</td>
<td>-0.01 ± 0.02</td>
</tr>
<tr>
<td>NS</td>
<td>0.00 ± 0.03</td>
<td>-0.03 ± 0.03</td>
<td>0.00 ± 0.02</td>
<td>-0.09 ± 0.03</td>
<td>0.00 ± 0.03</td>
</tr>
<tr>
<td>DC</td>
<td>-0.07 ± 0.03</td>
<td>-0.12 ± 0.03</td>
<td>-0.01 ± 0.03</td>
<td>-0.15 ± 0.04</td>
<td>-0.06 ± 0.03</td>
</tr>
<tr>
<td>GL</td>
<td>-0.01 ± 0.04</td>
<td>-0.07 ± 0.04</td>
<td>-0.05 ± 0.04</td>
<td>-0.01 ± 0.04</td>
<td>-0.01 ± 0.04</td>
</tr>
<tr>
<td>Genetic correlations</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FSCR</td>
<td>0.05 ± 0.19</td>
<td>0.23 ± 0.18</td>
<td>-0.01 ± 0.24</td>
<td>0.39 ± 0.14</td>
<td>-0.01 ± 0.20</td>
</tr>
<tr>
<td>PR</td>
<td>-0.14 ± 0.23</td>
<td>-0.08 ± 0.22</td>
<td>-0.21 ± 0.30</td>
<td>0.19 ± 0.19</td>
<td>-0.10 ± 0.24</td>
</tr>
<tr>
<td>NS</td>
<td>0.02 ± 0.19</td>
<td>-0.21 ± 0.18</td>
<td>-0.03 ± 0.24</td>
<td>-0.42 ± 0.14</td>
<td>-0.02 ± 0.20</td>
</tr>
<tr>
<td>DC</td>
<td>-0.33 ± 0.16</td>
<td>-0.52 ± 0.14</td>
<td>-0.09 ± 0.22</td>
<td>-0.51 ± 0.12</td>
<td>-0.34 ± 0.17</td>
</tr>
<tr>
<td>GL</td>
<td>-0.03 ± 0.13</td>
<td>-0.22 ± 0.12</td>
<td>-0.24 ± 0.17</td>
<td>-0.02 ± 0.10</td>
<td>-0.02 ± 0.10</td>
</tr>
</tbody>
</table>

1 FSCR = first-service conception rate; PR = pregnancy rate; NS = number of services per conception; GL = gestation length; DC = days-to-calving; DMI = average daily dry matter intake; ADG = average daily gain; MMBW = metabolic mid-test BW; FCR = feed conversion ratio; RFI = residual feed intake.
CHAPTER 5: GENERAL DISCUSSION AND CONCLUSIONS

The main objective of this research was to identify the genetic correlations between feed efficiency measurements of growing beef cattle and the fertility performance of females in multi-breed beef herds. To achieve this goal, the genetic correlations within female fertility and feed efficiency traits were studied separately in chapters two and three. Strong genetic correlations were found within feed efficiency traits and female fertility traits. In chapter four, the genetic correlations between the fertility and feed efficiency traits were estimated. The research found an unfavourable genetic correlation between residual feed intake (RFI) and days-to-calving (DC), and also that more fertile cattle were bigger, with higher DMI. Details are as follows.

5.1 FEMALE FERTILITY

In this study, the heritability estimates for fertility traits were low but significantly different from zero. This is shown in Table 2.5, where the average EPDs of the top and bottom 10 percent of tested bulls were significantly different from zero. This indicates that selections based on female fertility could be effective when genetic evaluations are provided for the traits to enable selection.

First-service conception rate (FSCR) and pregnancy rate (PR) were highly genetically correlated. This indicates that improving either one of the two traits will lead to an almost identical change in the other. In order to increase the total pregnancy rate of females in the herd, only one trait needs to be used. When connected with days-to-calving, FSCR was negatively correlated with it but PR was not, which indicates that selecting on
FSCR will shorten DC. Therefore, if time-related traits are included in breeding objectives, this research recommends selecting for FSCR rather than for PR.

This research also recommends selecting for DC in breeding programs based on fertility because it is moderate heritable ($h^2 = 0.10$), economically important, and available on most farms.

Since fertility is economically important in the beef industry, genetic evaluations and selections based on fertility are valuable. However, there are two primary challenges in improving fertility.

The first challenge is data. Since many females on Canadian farms are serviced with herd bulls based on their natural heat cycles, records of mating dates, pregnancy dates and NS are not available or not accurate. In this situation, many fertility traits, such as FSCR and NS are not available. So even if they are heritable and could be improved in theory, it is a different story in practice.

The second challenge is that earlier research reported low heritability estimates for fertility traits, which this study confirms. As can be seen in Table 2.2, with the exception of GL, no heritability estimates for fertility is more than 0.10. Indeed, they are lower than many other performance traits. As a result, genetic improvement for fertility traits based on selection may be slow.

Improving female fertility in beef cattle requires high quantity and high quality fertility data. Farms using artificial insemination should record every important date and the result of the pregnancy check in their breeding data. Farms using herd bulls should record the pregnancy check of each female at the end of the breeding season and DC so that data can be used in genetic evaluation programs.
5.2 FEED EFFICIENCY

This study shows that heritability estimates for feed efficiency traits are moderate to high. The heritability estimates support earlier research, and suggest that genetic gain may be obtained by selecting for feed efficiency traits.

The negative and favourable genetic correlation between FCR and ADG found in this study pointed out that selection for ADG would improve FCR. Because of the definition of FCR (FCR = DMI/ADG), it was phenotypically positively related with DMI and negatively correlated with ADG. However, the genetic correlation estimated for FCR with DMI and ADG were both negative. This may be due to the high genetic correlation found between DMI and ADG, which suggests that less feed intake is not equal to more efficient cattle, and selecting for better FCR may increase both DMI and ADG but with ADG increasing proportionately higher than DMI. FCR was found positively correlated with MMBW, which means that large animals are inefficient based on FCR.

RFI was highly genetically correlated with DMI. However, the genetic correlations between RFI with ADG and metabolic mid-test body weight (MMBW) were not significantly different from zero. These correlations are favourable in the beef cattle industry, and they indicate that selecting for RFI would reduce DMI significantly, with no negative response on growth rate.

The feed efficiency traits (FCR and RFI) are economically important and proved as moderate heritable. In many applications, interest is in simultaneous improvement of feed efficiency and production traits together (Kennedy, 1993). However, when the components traits (weight, ADG, DMI) are already in the index, there is no advantage to
add RFI or FCR to the index (van der Werf, 2004). As a result, FCR and RFI contribute no new genetic information.

5.3 CORRELATIONS BETWEEN FERTILITY AND FEED EFFICIENCY

As shown in Table 4.4, genetic correlations for fertility traits with ADG was favourable, which indicates that selecting for fertility would lead to a correlated response in body gain. However, better fertility traits are also significantly correlated with bigger females that have higher feed intake. The phenotypic correlations were consistent with their corresponding genetic correlations, but with smaller numbers. This was mainly due to low heritability estimates for fertility traits. These estimates indicate that the genetic improvement of growth and reproductive traits would not negatively affect the other.

In this study, DMI and RFI were unfavourably correlated with DC, meaning that animals with earlier calving date normally have higher feed intake and lower RFI. This may be because well fed, heavier animals have more energy to devote to superior fertility (Crowley et al., 2011). Therefore, selecting sires to improve feed efficiency may lead to a relative increase of DC. To avoid this, bull selection should include the two traits in the index.

Based on their correlation estimates, therefore, selecting separately for fertility or feed efficiency will lead to negligible or favourable responses to the other traits. This study only found significant antagonism between RFI and DC, indicating that genetic selection needs to balance the two traits.
5.4 CONCLUSION

Both female fertility traits and feed efficiency traits are economically necessary measurements in the beef cattle industry. All the results indicate that the traits can be improved through selection. When breeding records for female fertility are limited, PR and DC should be the primary selection criteria. Animals with larger body weight are not feed efficient but relates with better fertility performance. Because of the unfavourable correlation found between RFI and DC, they should both be included in selection indices.
CHAPTER 6: LITERATURE CITED


Carstens, G. E., and L. O. Tedeschi. 2006. Defining feed efficiency in beef cattle. Proceedings from the beef improvement federation 38th annual research symposium and annual meeting, Choctaw, MS, United States,


